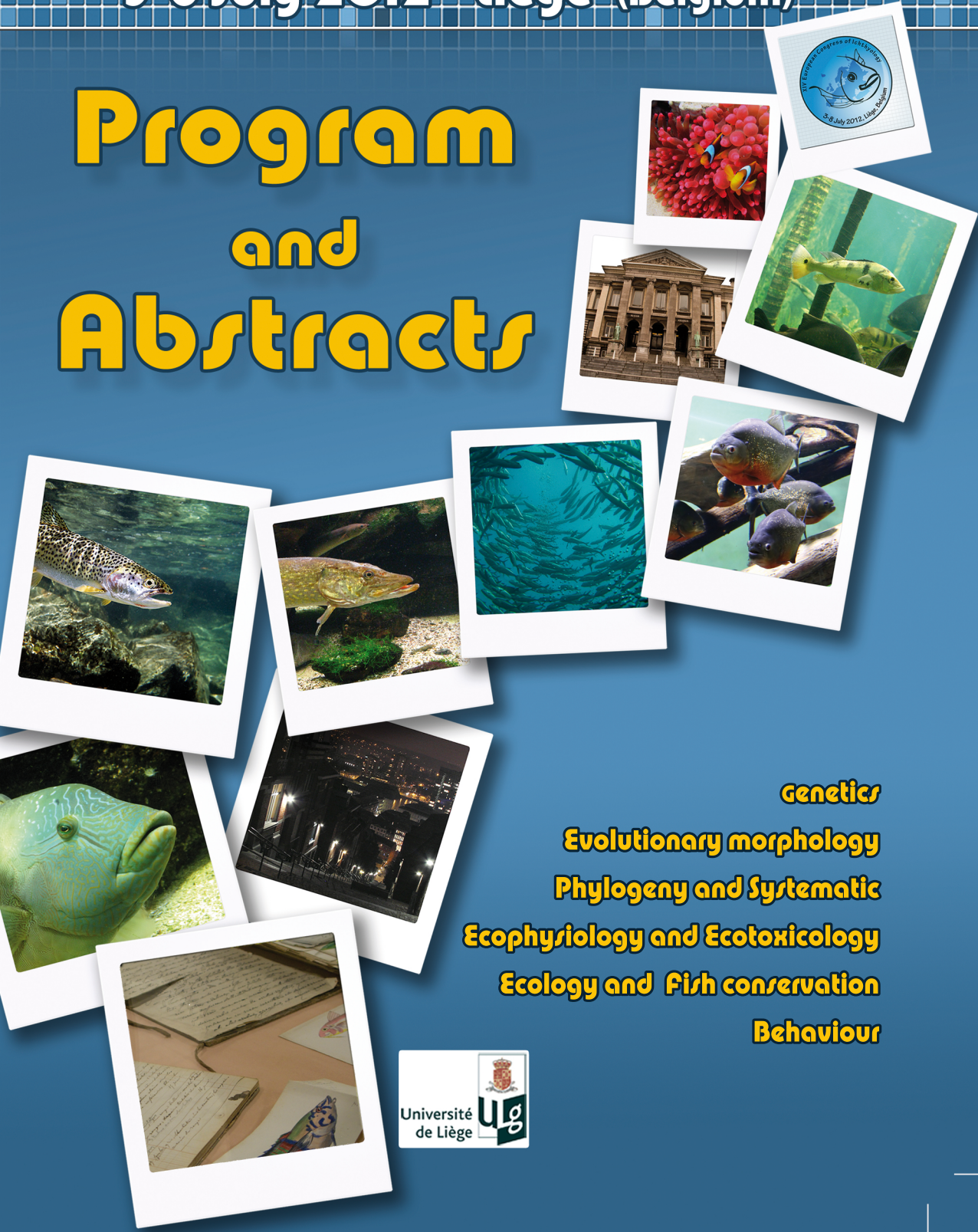


XIV European Congress of Ichthyology

3-8 July 2012 - Liège (Belgium)

Program and Abstracts



Genetics
Evolutionary morphology
Phylogeny and Systematic
Ecophysiology and Ecotoxicology
Ecology and Fish conservation
Behaviour

**XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)**





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Foreword

In November 2012, the **Aquarium-Museum** of Liège will celebrate its 50th anniversary. This event is a great opportunity to bring together ichthyologists from all specialties. Under the auspices of the **European Ichthyological Society**, this international meeting is organized by different laboratories, covering several disciplines of Fish Biology. The congress includes invited plenary lectures, sessions (oral and poster presentations) and two symposia.

Executive Committee

- Behavioural biology, Ethology and Animal Psychology, ULg (Prof. P. Poncin)
- Functional and Evolutionary Morphology, ULg (Prof. E. Parmentier)
- Liège Aquarium-Museum, ULg (F. Paquer, Dr A. Péqueux & S. Wanson)

Congress Secretariat

Mrs. V. Beaupain
University of Liège
Quai Van Beneden, 22
4020 Liège, BELGIUM

Tel: +32 (0) 4 366 50 81
Fax: +32 (0) 4 366 51 13
E-mail: eci-14@ulg.ac.be

Laboratories of the Organising Committee

- Behavioural biology, Ethology and Animal Psychology, ULg (Prof. P. Poncin)
- Functional and Evolutionary Morphology, ULg (Prof. E. Parmentier)
- Evolutionary Morphology of Vertebrates, UG (Prof. D. Adriaens)
- Département de l'Étude du milieu naturel et agricole, Public service of Wallonie (Dr P. Gérard)
- Research in Organism Biology, FUNDP (Prof. P. Kestemont)



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

- CEFRA, The Research and Education Center in Aquaculture, ULg (Dr. C. Mélard)
- Laboratory of Animal Diversity and Systematics, KUL and Laboratory of Ichthyology, RMCA (Prof. J. Snoeks)
- Laboratory of Immunology – Vaccinology, ULg (Prof. A. Vanderplasschen)
- Zebrafish facility and transgenesis, GIGA, ULg (Dr M. Winandy)
- Laboratory of Molecular Biology and Genetic Engineering, ULg (Dr M. Muller)
- Behavioral Ecology and Fish Population Biology, INRA (Dr A. Bardonnet)
- Ecology and Ecosystem Health Research Unit /Conservation and Restauration of Aquatic – Ecosystems Team, INRA (Dr J-M. Roussel)
- Liège Aquarium-Museum, ULg (Dr C. Michel, Curator)

Theme sessions

Organizer

Genetics

Marie Winandy
Charles Mélard
Marc Muller

Evolutionary Morphology

Dominique Adriaens
Eric Parmentier

Phylogeny and Systematic

Jos Snoeks
Emmanuel Vreven

Ecophysiology and Ecotoxicology

Patrick Kestemont
André Péqueux

Behaviour

Agnès Bardonnet
Pascal Poncin

Ecology and Fish conservation

Michaël Ovidio
Jean-Marc Roussel



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Two symposia are organized during the congress :

Adaptive brain morphology and neuroanatomy in fishes

(organizer: Dr. Michael Hofmann, University of Bonn, Germany)

Integration of fish fossil data into phylogenetic and comparative studies

(organizer: Dr. Francesco Santini, University of California, Los Angeles,
Department of Ecology and Evolutionary Biology USA)

Scientific Committee

Dominique Adriaens

Agnès Bardonnnet

Johann Delcourt

Mathieu Denoël

Bruno Frédéricich

Pierre Gérard

Patrick Kestemont

Maurice Kottelat

Charles Mélard

Christian Michel

Marc Muller

Billy Nzau Matondo

Michaël Ovidio

François Petit

Jean-Claude Philippart

Carole Rougeot

Jean-Marc Roussel

Jos Snoeks

Maria Stoumboudi

Alain Vanderplasschen

Pierre Vandewalle

Emmanuel Vreven

Marie Winandy

Marc Ylieff

Technical Staff

Valérie Beaupain

Yves-Eric Corbisier

Arnaud Dierckx

Lucien Hanon

Mariella Lunetta

Frédéric Paquer

André Péqueux

Gilles Rimbaud

Sonia Wanson

With the help of Jean-Philippe Benitez, Valérie Bockiau, Vinciane Bries, Fany Brotcorne, Nicolas Granier, Alain Hambuckers, Patricia Heusdens, Laetitia Hubens, Ludovic Hussin, Marie-Claude Huynen, Anne-Marie Massin, Jacques Ninane, Marie Peeters, Annie Van Leeuw.

Scientific popularization associations

Liège Aquarium-Museum - Dr C. Michel curator.

Embarcadère du savoir association – Prof. J.M. Bouquegneau (delegated administrator) and C. Champenois.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Invited Lecturers

BAROILLER Jean-François – CIRAD - Ifremer (France)

Genetical, physiological and environmental mechanisms of sex determination in fishes

BRITZ Ralph - Natural History Museum, London (England)

Fish systematics today: Can't see the wood for the trees?

FROESE Rainer - Leibniz-Institut für Meereswissenschaften (Germany)

Life-History Traits of Fishes: A Review with Application for Management of Data-Poor Stocks

HARRIS Matthew - Harvard Medical School (USA)

Monsters from the shallows: genetic analysis of postembryonic development revealing developmental capacity, constraint, and architecture of change

HERNANDEZ Patricia - George Washington University (USA)

Using cypriniform fishes to investigate the origin, function, and morphological evolution of trophic novelties

SCHMUTZ Stefan - University of Natural Resources and Applied Life Sciences (Austria)

Fishes, do they ever come back?

SEBERT Philippe – University of Brest (France)

Eel male energetic strategy to cross Atlantic Ocean

SLABBEKOORN Hans - University of Leiden (Holland)

Noise impact on fish : disturbance and avoidance in captivity



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Registration summary

Participants currently registered

116	Participant
45	EIS member
82	Student
15	Student EIS member
258	Total

Abstract submission

Number of abstracts: **247**
Poster presentations : **119**
Oral presentations : **128**

Countries of origin

Algeria (2), Australia (1), Austria (6), Belgium (69), Benin (3), Bosnia And Herzegovina (1), Brazil (11), Croatia (23), Czech Republic (9), Estonia (1), France (18), Germany (22), Greece (7), India (1), Iran, Islamic Republic Of (4), Israel (4), Italy (5), Japan (10), Latvia (1), Malaysia (1), Mexico (2), Netherlands (5), Norway (1), Poland (10), Portugal (1), Russian Federation (14), Slovakia (1), South Africa (1), Spain (1), Sweden (4), Switzerland (4), Tunisia (2), United Kingdom (2), United States (17), Viet Nam (1)

Awards

The EIS Student Awards

The European Ichthyological Society is supporting the best oral and poster presentations given by students at the EIS congresses. Prices for best presentation will be awarded at the end of the congress:

Best oral presentation for PhD students (1st, 2nd and 3rd)

Best poster presentation for PhD students (1st, 2nd and 3rd)

The EIS will reward the 1st, 2nd and 3rd oral and poster presentations with 200 € each. All three winners of both categories will be rewarded with the EIS membership fee for the 3-year period following the congress.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Award Committee

The EIS Board appoints two Award Committees (one for oral and one for poster presentations), formed by prominent Society members, to undertake the task of rating the candidate presentations. The names of the 'judges' will be posted on Congress sites. The results will be announced during the closing ceremony on Saturday.

Evaluation

The presentations are judged by the following criteria: introduction; methods; data analysis and interpretation; conclusions - innovation, originality and scientific significance; presentation; and visual aids or graphic design.

The rating scale is 0-10 points: excellent (9-10), very good (7-8), good (4-6), fair (2-3), poor (0-1).

Only presentations that are rated as excellent or very good are entitled to an award.

The XIV European Congress of Ichthyology is held in the Van Beneden Institute

Edouard Van Beneden, who elucidated, together with Walther Flemming and Eduard Strasburger, the essential facts of mitosis, was zoology professor and the founder of the Van Beneden Institute in 1888.

This site houses the **AQUARIUM-MUSEUM** of Liège, allowing the Aquarium presenting to total up 46 exhibition tanks with some 2,500 inhabitants. It makes it a pillar of tourism in Liège as it is the most visited Museum in Wallonia with more than 80,000 visitors a year. In the Museums halls, 1,000 m² are dedicated to animal diversity: from the smallest of insects to 19 m long whale...over 20,000 preserved specimens from across the globe either stuffed or just the skeletal remains. Please, note aquarium and museum are open and free for all the congress participants. Moreover, visits with guides are kindly organized.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

The Institute houses also a large centre of Scientific, Technique and Industrial: the “knowledge embarcadere”. This centre provides the place for the House of Science, rooms for teachings and meetings, mural painting of Paul Delvaux and exhibition events.

Liège and its University

Established since two centuries ago at the heart of an age-old city, an intellectual centre since the Middle Ages (Liège was ‘the Athens of the North’ in the eleventh century), the University of Liège is an university open to the world, a crossroads of teaching, research and innovation at the junction of international roads and European cultures.

Welcoming over 20,000 students, of whom nearly a quarter are of international origin, plus 2,800 teachers and researchers, and offering one of the most diversified educational offers in francophone Belgium as well as active teaching methods, the University of Liège has links with over 600 institutions world-wide, integrated in vast international academic and scientific networks, which makes it a fully engaged actor in the vast European higher education (Bologna) and research (Lisbon) area.

The University of Liège also qualifies for the ECTS Label granted by the European Commission, which guarantees the quality of the welcome and follow up support given to exchange students.

Attentive to the needs of society, the University of Liège plays an important role as a creator of activities with high value added and in providing dynamism to technological centres uniting business companies and public operators (biotechnologies, the space industry, the environment, etc.). It is the francophone university which creates the largest number of spin-off companies springing from its laboratories.

At the origin of 2,500 publications a year, the University of Liège researchers distinguish themselves in the best scientific and academic journals and are to be found amongst the pioneers of the large international movement in favour of Open Access to knowledge.



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

The abstracts included in this fascicle have been reviewed by the scientific committee of the ECI-14 meeting, in order to evaluate their content as oral or poster communication. The authors remain however responsible of the wording of their abstract.

The abstracts are listed alphabetically by first author.



XIV European Congress of Ichthyology

Liège, 3-8 July 2012 (Belgium)

Program

Monday, July 2nd

14:00 – 18:00	REGISTRATION (<i>main hall of Zoological Institute</i>)
18:00 – 20:00	WELCOME DRINK (<i>Aquarium-Museum</i>)

Tuesday, July 3rd

09:00 – 09:30	WELCOME SPEECH (<i>Zoological Amphitheater</i>) by Prof. Pierre WOLPER, vice-rector of the University
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09:35 – 10:15	Plenary lecture: Fishes, do they ever come back? Stephan SCHMUTZ (<i>Zoological Amphitheater</i>)
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10:15 – 10:45	COFFEE BREAK (<i>Zoological Institute</i>)
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Oral session : Ecology - Fish Conservation (<i>Zoological Amphitheater</i>) Chairman : Maria STOUMBOUDI	
10:45 – 11:00	<u>BERNARD Benoît</u> , LATLI Adrien, KESTEMONT Patrick Population dynamics of the roach, <i>Rutilus rutilus</i> L., in the reach of Tailfer on the river Meuse, Belgium
11:00 – 11:15	<u>BIRZAKS Janis</u> , SPRINGE Gunta, BRIEDE Agrita, JAKOVLEVA Ieva Climate change and long-term salmon smolt migration patterns in wild salmon natural spawning river Salaca
11:15 – 11:30	<u>BLAZEK Radim</u> , DÁVIDOVÁ Martina, JIRSOVÁ Dagmar, MASOVÁ Sárka, OROS Mikuláš, PRIKRYLOVÁ Iva, REHULKOVÁ Eva, JIRKU Miloslav Fish assemblages and their parasites in the Lake Turkana, Kenya
11:30 – 11:45	<u>BODILIS Pascaline</u> , LOUISY Patrick, FRANCOUR Patrice Using citizen science to survey non indigenous invasive species. The case of Kas Peninsula (Turkey)
11:45 – 12:00	<u>COLLETTE Bruce</u> , CARPENTER Kent Red Listing Marine Fishes



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

12:00 – 12:15	<u>KIM Eun-Jin</u> , NAKAJIMA Jun, ONIKURA Norio Habitat preferences of <i>Cobitis kaibarai</i> (Teleostei: Cobitidae) between spawning and non-spawning seasons in paddy fields, Kyushu Island, Japan
12:15 – 12:30	<u>GLOWACKI Lukasz</u> , PENCZAK Tadeusz Geostatistical assessment of impoundment effect on fish metapopulations in a large lowland river

Oral session : Phylogeny - Systematics (*First floor Classroom*)

Chairman : Jos SNOEKS

10:45 – 11:00	<u>RÜBER Lukas</u> , ADAMSON Eleanor, BRITZ Ralf Evolutionary diversification in an endangered biodiversity hotspot: the Southeast Asian peat swamp forest fish fauna
11:00 – 11:15	<u>ADAMSON Eleanor</u> , <u>RÜBER Lukas</u> , BRITZ Ralf Molecular phylogenetics of the liquorice gouramis (<i>Parasphromenus spp</i>): divergence in a fragmented freshwater landscape
11:15 – 11:30	<u>BART Henry</u> , DOOSEY Michael, MIYA Masaki, SAITOH Kenji, TANG Kevin, WOOD Robert, CHEN Wei-Jen, MAYDEN Richard Molecular Phylogenetics of the Cypriniformes: Confronting the Confusion
11:30 – 11:45	BELLI Mathilde, DETTAÏ Agnès, AMIR Aïcha, de PALAMINY Alix, LECOINTRE Guillaume, <u>GALLUT Cyril</u> In search of new markers for the molecular phylogeny of Acanthomorpha
11:45 – 12:00	<u>KOTTELAT Maurice</u> Ontogenetic changes in colour pattern in loaches of the genus <i>Schistura</i> in Southeast Asia (Cypriniformes: Nemacheilidae)
12:00 – 12:15	BRITZ Ralf, <u>JOHNSON David</u> Ontogeny and homology of the skeletal elements that form the sucking disc of remoras (Teleostei, Echeneoidei, Echeneidae)
12:15 – 12:30	<u>BIANCO Pier Giorgio</u> Systematic update of Italian native and exotic freshwater fish

12:30 – 14:00

LUNCH

14:00 – 14:40

Plenary lecturer : Ralf BRITZ (*Zoological Amphitheater*)
Fish systematics today : Can't see the wood for the trees



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Oral session : Ecology - Fish Conservation (<i>Zoological Amphitheater</i>)	
Chairman : Michaël OVIDIO	
14:45 – 15:00	<u>FRANCOUR Patrice</u> Fish Assemblage Survey Technique (FAST): towards a fish index to implement the Marine Strategy Framework Directive?
15:00 – 15:15	<u>MOELANTS Tuur</u> , VREVEN Emmanuel, SNOEKS Jos The enigmatic Congo River fish fauna: the importance of the Wagenia falls on species diversity, ecology and distribution
15:15 – 15:30	<u>GRIMARDIAS David</u> , CARAYON Marie, BARDONNET Agnès, CATTANEO Franck Spatial distribution of European grayling (<i>Thymallus thymallus</i>) post-emergent fry and habitat sub-units preferences: a management-oriented approach
15:30 – 15:45	<u>HABLÜTZEL Pascal</u> Biogeography of the neotropical ichthyofauna at the regional scale: beyond the hydrogeology hypothesis

Oral session : Phylogeny - Systematics (<i>First floor Classroom</i>)	
Chairman : Emmanuel VREVEN	
14:45 – 15:00	<u>BUJ Ivana</u> , CALETA Marko, MIOCIC-STOSIC Jure, MARCIC Zoran, MUSTAFIC Perica, MRAKOVCIC Milorad Past, present and future in extreme habitats: evolutionary history, genetic structure and perspective of <i>Aphanius fasciatus</i> along the Adriatic coast
15:00 – 15:15	<u>CHANET Bruno</u> , GUINTARD Claude, BETTI Eric, GALLUT Cyril, DETTAÏ Agnès and LECOINTRE Guillaume The close relationship of Tetraodontiformes and Lophiiformes enlightened by the study of their soft anatomy
15:15 – 15:30	<u>DE PINNA Mario</u> , BOCKMANN Flavio, APONE Fernando Morphology, molecules & morphology again: the contentious phylogenetic position of planktophagous catfishes, genus <i>Hypophthalmus</i> (Siluriformes)
15:30 – 15:45	<u>DECRU Eva</u> , VREVEN Emmanuel, SNOEKS Jos Unexpected species richness in the African pike <i>Hepsetus odoe</i> (Bloch, 1794) (Characiformes: Hepsetidae)

15:45 – 16:15	<i>COFFEE BREAK (Zoological Institute)</i>
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XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Oral session : Ecology - Fish Conservation (<i>Zoological Amphitheater</i>) Chairman : Michaël OVIDIO	
16:15 – 16:30	<u>KALOGIANNI Eleni</u> , GIAKOUMI Sofia, CHATZINIKOLAOU Yorgos Impacts of the invasive mosquito fish <i>Gambusia holbrooki</i> on the Greek native <i>Valencia letourneuxi</i>
16:30 – 16:45	<u>MADI MOUSSA Rakamaly</u> , GOMEZ GARVIN Jaime, CONDET Manon Impact of coastal development on the recruitment of juvenile commercial coral-reef fish: Mayotte island in the Indian Ocean

Oral session : Phylogeny - Systematics (<i>First floor Classroom</i>) Chairman : Emmanuel VREVEN	
16:15 – 16:30	<u>GOLANI Daniel</u> Revitalizing Research on Lessepsian Fish Migration – from DNA to Taxonomy
16:30 – 16:45	<u>KITAGAWA Tadao</u> , AOKI Nana, FUJII Yota, INUI Takehiro, KANAIWA Minoru, YAMAMOTO Atsuya, KOIZUMI Noriyuki Genetic and morphological divergence between Japanese dojo loach <i>Misgurnus anguillicaudatus</i> populations with three different mitochondrial DNA clades
16:45 – 17:00	<u>LECOINTRE Guillaume</u> , LAUTREDOU Anne-Claire, FISLER Marie, CHANET Bruno, DETTAÏ Agnès, GALLUT Cyril Acanthomorph (Teleostei) large scale interrelationships
17:00 – 17:15	<u>NORÉN Michael</u> , FERNHOLM. B., KULLANDER S. O. Hagfish phylogeny and taxonomy

17:15 – 19:15	POSTER PRESENTATION : Phylogeny & Systematics (1-29)
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XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Wednesday, July 4th

09:00 – 09:40	Plenary lecturer : Jean-François BAROILLER (<i>Zoological Amphitheater</i>) Genetic, physiological and environmental mechanisms of sex determination in fishes
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Oral session : Ecology - Fish Conservation (<i>Zoological Amphitheater</i>) Chairman : Agnès BARDONNET	
09:45 – 10:00	<u>MOSTAFAVI Hossein</u> , COAD B.W., ESMAEILI H.R., MAHINI A.S., MELCHER A.H., PLETTERBAUER F., SCHINEGGER R., TEIMORI A., TRAUTWEIN C., VATANDOUST S., SCHMUTZ S. A probabilistic model characterizing fish assemblages in running waters of Iran: a framework for environmental assessment
10:00 – 10:15	<u>PENCZAK Tadeusz</u> , KRUK Andrzej, GLOWACKI Lukasz, GALICKA Wanda Fish assemblage structures persist in the tributaries of a large lowland river despite continued water pollution
10:15 – 10:30	<u>PERSAT Henri</u> , WINKLER Kathrin, WEISS Steven, GRIMARDIAS David, CATTANÉO Franck Natural and artificial relationships between Rhine and Rhone populations of grayling (<i>T. thymallus</i>): implications for conservation

Oral session : Phylogeny - Systematics (<i>First floor Classroom</i>) Chairman : Maurice KOTTELAT	
09:45 – 10:00	<u>LEDEROUN Djiman</u> , VREVEN Emmanuel, LALÈYÈ Philippe, SNOEKS Jos, PARMENTIER Eric, VANDEWALLE Pierre Actual status of the ichthyofauna of the Mono river basin (Togo and Benin)
10:00 – 10:15	<u>MAAKE Pholosi</u> , SWARTZ Ernst, KRAMER Bernd, GON Ofer Molecular phylogeny and biogeography of the genera <i>Marcusenius</i> and <i>Petrocephalus</i> (Mormyridae) in southern Africa
10:15 – 10:30	<u>MUNROE Thomas</u> Systematic revision of the flatfish Genus <i>Peltorhamphus</i> Günther, 1862 (Pleuronectiformes: Rhombosoleidae), with description of a new species



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Symposium : Integration of fish fossil data into phylogenetic and comparative studies (<i>Classroom Jeuniaux</i>) Organizer : F. SANTINI	
10:00 – 10:15	<u>SANTINI Francesco</u> , CARNEVALE Giorgio, SORENSON Laurie, ALFARO Michael Fossils fishes and phylogenomic analyses
10:15 – 10:30	<u>DORNBURG Alex</u> , MOORE Jon, NEAR Thomas Integrating genes and fossils to measure the West Tethyan influence on a group of nocturnal fishes in contemporary biodiversity hotspots

10:30 – 11:00	<i>COFFEE BREAK (Zoological Institute)</i>
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Oral session : Ecology - Fish Conservation (<i>Zoological Amphitheater</i>) Chairman : Agnès BARDONNET	
11:00 – 11:15	<u>PETER Armin</u> , GERMANN-ARNOLD Brigitte, SCHLAEPPI Thomas New insights into the movement behavior of bullhead (<i>Cottus gobio</i>) by telemetry studies in a small Swiss stream
11:15 – 11:30	PRCHALOVA Marie, KUBECKA Jan, <u>RIHA Milan</u> , CECH Martin, JUZA Tomas, KETELAARS Henk A. M, KRATOCHVIL Michal, PETERKA Jiri, VASEK Mojmir, WAGENVOORT Arco J. Eel attacks – a new tool for assessing European eel (<i>Anguilla anguilla</i>) abundance and distribution patterns with gillnet sampling
11:30 – 11:45	<u>REICHARD Martin</u> , VRTILEK Milan, DOUDA Karel, SMITH Carl An invasive species reverses the roles in a host-parasite relationship between bitterling fish and unionid mussels
11:45 – 12:00	<u>ROLAND Kathleen</u> , KESTEMONT Patrick, PIERRARD Marie-Aline, DIEU Marc, RAES Martine, LOOS Robert, GAWLIK Bernd, SILVESTRE Frédéric Protein expression profiles in European eel (<i>Anguilla anguilla</i>) exposed to perfluorooctane sulfonate; combining in vitro, in vivo and in situ approaches
12:00 – 12:15	<u>SCHULTZ Doron</u> , BENAYAHU Yehuda, FLEISCHER Aliza The ecological and economical effect of recreational fishing in the Eastern basin of the Mediterranean sea
12:15 – 12:30	<u>SENDEK Dmitry</u> Arctic cisco (<i>Coregonus autumnalis</i>) in the eastern part of the Baltic: its evolution, current status and possibilities for preservation



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Oral session : Phylogeny - Systematics (<i>First floor Classroom</i>) Chairman : Maurice KOTTELAT	
11:00 – 11:15	<u>MUSSCHOOT Tobias</u> , <u>BODEN Gert</u> , <u>SNOEKS Jos</u> , <u>VREVEN Emmanuel</u> The distribution of catfishes (Siluriformes) in the Congo Basin
11:15 – 11:30	<u>BANYANKIMBONA Gaspard</u> , <u>NTAKIMAZI Gaspard</u> , <u>VREVEN Emmanuel</u> , <u>SNOEKS Jos</u> The fish diversity of the Upper Malagarazi River basin, East Africa (Burundi)
11:30 – 11:45	<u>SNOEKS Jos</u> , <u>VREVEN Emmanuel</u> African ichthyology : recent results and challenges
11:45 – 12:00	<u>TEIMORI Azad</u> , <u>ESMAEILI H. Reza</u> , <u>REICHENBACHER Bettina</u> Vicariance events and phylogeny of Iranian inland <i>Aphanius</i> species
12:00 – 12:15	<u>STERN Nir</u> , <u>GOREN Menachem</u> , <u>YOKEŞ Baki</u> , <u>GALIL Bella</u> , <u>DIAMANT Ariel</u> What makes a successful invasion? Case study of the Indo-Pacific threadfin bream, <i>Nemipterus randalli</i> , Russel 1987 in the Eastern Mediterranean
12:15 – 12:30	<u>VAN STEENBERGE Maarten</u> , <u>SNOEKS Jos</u> Inter and intraspecific variation in a morphologically static cichlid lineage from Lake Tanganyika

Symposium : Integration of fish fossil data into phylogenetic and comparative studies (<i>Classroom Jeuniaux</i>) Organizer : F. SANTINI	
11:00 – 11:15	<u>BURRIDGE Christopher</u> , <u>MCDOWALL Robert</u> , <u>CRAW Dave</u> , <u>WILSON Mark</u> , <u>WATERS Jonathan</u> The Gondwanan history of galaxiid fishes : inferences from molecular clocks calibrated using fossils and known biogeographic events
11:15 – 11:30	<u>KLOPFSTEIN Seraina</u> , <u>RONQUIST Fredrik</u> A total evidence approach to dating with fossils
11:30 – 11:45	<u>SANTINI Francesco</u> , <u>CARNEVALE Giorgio</u> , <u>SORENSEN Laurie</u> , <u>ALFARO Michael</u> Fossils fishes and phylogenomic analyses
11:45 – 12:15	Discussion
12:30 – 14:00	LUNCH



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

14:00 – 14:40	Plenary lecturer : Rainer FROESE (<i>Zoological Amphitheater</i>) Life-History Traits of Fishes: A Review with Application for Management of Data-Poor Stocks
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Oral session : Ecology - Fish Conservation (<i>Zoological Amphitheater</i>) Chairman : Jean-Claude PHILIPPART	
14:45 – 15:00	<u>STOUMBOUDI Maria</u> , DIMITRIOU Elias, BARBIERI Roberta, KALOGIANNI Eleni, COWX Ian Estimating the minimum ecological flow downstream the Gadouras dam (Rhodes Island, Greece), for conserving the local <i>Ladigesocypris ghigii</i> population
15:00 – 15:15	<u>VRTÍLEK Milan</u> , REICHARD Martin, BLAZEK Radim, POLACIK Matej Reproductive investment of <i>Nothobranchius furzeri</i> females along the rainfall gradient : interpopulation comparison
15:15 – 15:30	<u>TITOV Sergey</u> , SCHERBENOK Yuri Genetic differentiation of European grayling (<i>Thymallus thymallus</i> L.) In the Kama river as reflection of special features of the species expansion

Oral session : Phylogeny - Systematics (<i>First floor Classroom</i>) Chairman : Tom GEERINCKX	
14:45 – 15:00	TEIMORI Azad, JAWAD Laith A., AL-KHARUSI LUBNA H., AL-MAMRY Juma M., <u>REICHENBACHER Bettina</u> "Same same but different": Otoliths of <i>Aphanius dispar</i> (Teleostei, Cyprinodontiformes)
15:00 – 15:15	<u>VANHOVE Maarten P.M.</u> , LARMUSEAU Maarten H.D., ECONOMOU Alcibiades N., ZOGARIS Stamatis, KOVACIC Marcelo, GIAKOUMI Sofia, KOUTSIKOS Nicholas E., VOLCKAERT Filip A.M., HUYSE Tine Tiny worms from tiny fishes: what (functional) genetics and parasitology can teach us about gobies and their radiations
15:15 – 15:30	<u>VASIL'EVA Ekaterina</u> , VASIL'EV Victor Morphogenetic divergence and taxonomic relations between the Mediterranean and Black Sea conspecific / congeneric populations in different fish groups



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Symposium : Integration of fish fossil data into phylogenetic and comparative studies (<i>Classroom Jeuniaux</i>) Organizer : F. SANTINI	
14:45 – 15:00	<u>SANSOM Robert</u> Can fossil fish be used in phylogenies ? Investigating the effects of fossilization on phylogenetic reconstruction
15:00 – 15:15	<u>GIERL Christoph</u> , REICHENBACHER Bettina, GAUDANT Jean, ERPENBECK Dirk, PHARISAT André The value of fossils in phylogenetic analyses of taxonomically difficult lineages : a case study of <i>Lepidocottus aries</i> (Gobioidei)
15:15 – 15:30	<u>STAAB Katie</u> , BETANCUR-R Ricardo, HERNANDEZ L Patricia Investigating the evolution of cypriniform trophic morphology using a time-calibrated phylogeny
15:30 – 15:45	Discussion

15:45 – 16:15	<i>COFFEE BREAK (Zoological Institute)</i>
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Symposium : Integration of fish fossil data into phylogenetic and comparative studies (<i>Classroom Jeuniaux</i>) Organizer : F. SANTINI	
16:15 – 16:30	<u>THIEREN Els</u> Archaeozoology and a DNA analysis document the former occurrence of sturgeon in the North Sea
16:30 – 16:45	<u>ALTNER Melanie</u> , REICHENBACHER Bettina First fossil record of aplocheiloid killifish in Africa
16:45 – 17:15	Discussion

Oral session : Ecology - Fish Conservation (<i>Zoological Amphitheater</i>) Chairman : Jean-Claude PHILIPPART	
16:15 – 16:30	<u>MASSUTÍ Enric</u> , Rueda Lucia, BALBÍN Rosa, RAMON Montserrat, OLIVAR María Pilar, FERNÁNDEZ DE PUELLES M ^a Luz, ORDINES Francesc, TORRES Asvin P., ABELLÓ Pere, QUETGLAS Antoni, BARBERA Carmen, VALLS María, MORANTA Joan The role of environment on body condition of deep-sea fishes in the western Mediterranean



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Oral session : Phylogeny - Systematics (<i>First floor Classroom</i>)	
Chairman : Tom GEERINCKX	
16:15 – 16:30	<u>VREVEN Emmanuel</u> , WAMUINI LUNKAYILAKIO Soleil, SNOEKS Jos, MUSSCHOOT Tobias, SCHLIEWEN Ulrich K. A complex evolutionary history in the large cyprinids from the Inkisi River basin (Lower Congo, DRC)
16:30 – 16:45	<u>POULSEN Jan Y.</u> , Ingvar Byrkjedal, Endre Willassen, Davis Rees, Hirohiko Takeshima, Takashi P. Satoh, Gento Shinohara, Mutsumi Nishida, Masaki Miya Mitogenomic phylogeny of Myctophiformes (Neoteleostei)
16:45 – 17:00	<u>YAZDANI MOGHADDAM Faezeh</u> , DAUD Siti Khalijah, ALIABADIAN Mansour, SIEFALI Mahvash The systematics of Malaysian <i>Puntius</i> and its allies (Pisces: Cyprinidae)
17:00 – 17:15	<u>VISHWANATH Waikhom</u> , ANGANTHOIBI Nongmaithem, LOKESHWOR Yumnam, DISHMA Mayanglambam, RAMESHORI Yumnam Systematics of the Freshwater Fish Diversity of Kaladan River, Mizoram, India
18:00	RECEPTION AT THE TOWN HALL offered by the Mayor of Liège
21:00	STUDENT FISH PARTY (<i>at the Geographic Café</i>)

Thursday, July 5th

09:00 – 09:40	Plenary lecturer : Philippe SEBERT (<i>Zoological Amphitheater</i>) Eel male energetic strategy to cross Atlantic Ocean
Oral session : Ecophysiology & Ecotoxicology (<i>Zoological Amphitheater</i>)	
Chairman : Patrick KESTEMONT	
09:45 – 10:00	<u>BETOULLE Stéphane</u> , FARCY Emilie, MORAT Fabien, VERON Antoine, JAFFAL Ali, GEFFARD Alain, CHILMONCZYK Stefan, BEALL Edward, FOURNIER Michel Immunocompetence of brown and brook trouts living in different subantarctic freshwaters ecosystems
10:00 – 10:15	<u>BUI Thi Bich Hang</u> , MILLA Sylvain, NGUYEN Thanh Phuong, KESTEMONT Patrick Effect of <i>Escherichia coli</i> lipopolysaccharide on immunity of tra catfish (<i>Pangasianodon hypophthalmus</i>)



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

10:15 – 10:30	<u>CORREIA Alberto Teodorico</u> , CAPELA Ricardo Campinho, HAMER Paul, NUNES Bruno Trace elements concentration in otoliths of the European eel (<i>Anguilla anguilla</i>) : a proxy of environmental aquatic exposure to metals
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Oral session : Genetics (*First floor Classroom*)

Chairman : Marc MULLER

09:45 – 10:00	<u>BOROVIKOVA Elena A.</u> , STOLBUNOVA V.V. The problem of the fish species (on example families Coregonidae, Cyprinidae, Gobiidae)
10:00 – 10:15	<u>CIVÁNOVÁ Kristína</u> , ŠIMKOVÁ Andrea, COSTEDOAT Caroline, GILLES André, MARTIN Jean-François Variability, structure and selection of MHCIIb genes in <i>Chondrostoma toxostoma</i> and <i>Chondrostoma nasus</i> in hybrid zones
10:15 – 10:30	<u>GEFFROY Benjamin</u> , GUIGUEN Yann, FOSTIER Alexis, BARDONNET Agnès Aromatase gene expression during the process of sex differentiation of the European eel <i>Anguilla anguilla</i>

10:30 – 11:00

COFFEE BREAK (Zoological Institute)

Oral session : Ecophysiology & Ecotoxicology (*Zoological Amphitheater*)

Chairman : Patrick KESTEMONT

11:00 – 11:15	<u>MATHIEU Cédric</u> , MILLA Sylvain, MANDIKI Robert, DOUXFILS Jessica, KESTEMONT Patrick Do gluco- or mineralocorticoids modulate Eurasian perch (<i>Perca fluviatilis</i> , L.) immune activity?
11:15 – 11:30	<u>PRUVOT Benoist</u> , QUIROZ Y., JEANRAY N., VONCKEN A., CURE Y., WINANDY M., MULLER M. Zebrafish (<i>Danio rerio</i>) behavioral analysis : a new tool in toxicological assays
11:30 – 11:45	<u>RUEDA-JASSO Rebeca A.</u> , DE LOS SANTOS-BAILON Alejandra, GUTIERREZ-OSPINA Gabriel Lethal and sublethal toxicity of nitrites and phosphates : Effects on gills and behavior of <i>Skiffia multipunctata</i> (Goodeidae) fry
11:45 – 12:00	<u>BAGCI Enise</u> , MAEX Margo, HAGENAAERS An, VERGAUWEN Lucia, BLUST Ronny, KNAPEN Dries Development of a refined morphological scoring system using the zebrafish embryo for classification of teratogenic compounds



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

12:00 – 12:15	TRABELSI Awatef, KAMLER Ewa, <u>TELETCHÉA Fabrice</u> , GARDEUR Jean-Noël, JAWORSKI Andrzej, FONTAINE Pascal Hatching time effect on the biochemical composition and energetic content of pike <i>Esox lucius</i> larvae
12:15 – 12:30	<u>VETTER Aurélie</u> , FELIX Christophe, LAZARTIGUES Angélique, BETOULLE Stéphane, DELAHAUT Laurence, SANCHEZ Wilfried, THOMAS Marielle Glycolytic fluxes, a new approach to evaluate the impact of pollutants on energy metabolism in fishes

Oral session : Genetics (<i>First floor Classroom</i>) Chairman : Marc MULLER	
11:00 – 11:15	<u>GEIGER Matthias</u> , FREYHOF Jörg, HERDER Fabian Introducing the FREDIE project with notes on the freshwater fish diversity of the Mediterranean hot-spot
11:15 – 11:30	<u>KACZMARCZYK Dariusz</u> , WOLNICKI Jacek Genetic diversity within 6 Polish <i>Eupallasella percnurus</i> populations and distance between them revealed by polymorphism of the microsatellite DNA
11:30 – 11:45	<u>LARBUISSON Arnaud</u> , DALCQ Julia, MARTIAL Joseph, MULLER Marc Role of Fgf receptors in cranial cartilage development of the zebrafish
11:45 – 12:00	MANKIEWICZ-BOCZEK Joanna, <u>IMSIRIDOU Anastasia</u> , KACZKOWSKI Zbigniew, TSIORA Anna, KARAIKOU Nikoleta, LAPINSKA Malgorzata, MINOS George, ZALEWSKI Maciej Genetic diversity as an important element of sustainable management of perch <i>Perca fluviatilis</i> L. populations in lowland reservoirs in Central Poland
12:00 – 12:15	<u>OTTEN Auke BC</u> , BOSCH van den BIANCA JC, THEUNISSEN Tom EJ, WINANDY Marie, MULLER Marc, SMEETS Hubert JM. Zebrafish models to study mitochondrial function and disease : current status and future perspectives



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Symposium : Adaptive brain morphology and neuroanatomy in fishes (<i>Classroom Jeuniaux</i>)	
Organizer : M. HOFMANN	
10:40 – 11:00	<u>HOFMANN Hans</u> Variations on a Theme: Evolution of a Vertebrate Social Decision-Making Network
11:00 – 11:20	<u>MOGDANS Joachim</u> , SCHMITZ Anke, FRANKEN Johanna Morphology of the lateral line receptor array in Cyprinids with different habitat preference
11:20 – 11:40	<u>WULLIMANN Mario F.</u> Lateral line centers along the brain neuraxis : homologous or convergent ascending pathways in vertebrates?
11:40 – 12:00	CARLSON Bruce, HASAN Saad, HOLLMANN Michael, MILLER Derek, HARMON Luke, ARNEGARD Matthew Neural Innovations Trigger Explosive Diversification of Electric Fishes
12:00 - 12:20	<u>BASS Andrew</u> Developmental and Evolutionary Origins of the Neural Basis for Acoustic Signaling in Vertebrates
12:30 – 14:00	LUNCH
14:00 – 14:40	Plenary lecturer : Mattew HARRIS (<i>Zoological Amphitheater</i>) Monsters from the shallows: genetic analysis of postembryonic development revealing developmental capacity, constraint, and architecture of change
Oral session : Ecophysiology & Ecotoxicology (<i>Zoological Amphitheater</i>) Chairman : André PEQUEUX	
14:45 – 15:00	<u>MASSART Sophie</u> , MILLA S., KESTEMONT P. Sex-steroid receptors localization in immune tissues of the rainbow trout (<i>Oncorhynchus mykiss</i>)
15:00 – 15:15	<u>DEGANI Gad</u> , LEVY Gal High salinity affects brain and pituitary gene expression in blue Gourami males



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Oral session : Genetics (<i>First floor Classroom</i>)	
Chairman : Marie WINANDY	
14:45 – 15:00	<u>PONOMAREVA Ekaterina</u> , PONOMAREVA Maria, SHUBINA Elena Brown trout (<i>Salmo trutta</i> L.) population structure in small streams of White Sea basin, Russian European North
15:00 – 15:15	<u>TARIFEÑO Estefania</u> , MAINFROID Isabelle, VOZ Marianne, PEERS Bernard High-throughput sequencing to study cell differentiation in Zebrafish
Symposium : Adaptive brain morphology and neuroanatomy in fishes (<i>Classroom Jeuniaux</i>)	
Organizer : M. HOFMANN	
14:45 – 15:05	<u>WAGNER Hans-Joachim</u> Mesopelagic barreleye-fishes (Opisthoproctids) : Evolutionary “experiments” in eye designs
15:05 – 15:25	<u>SCHLUESSEL Vera</u> , HOFMANN Michael H. Phylogenetic trends in the evolution of the telencephalon in lower vertebrates
15:25 – 15:45	<u>HOFMANN Michael</u> Brain variations and phylogenetic trends in ray finned fishes
15:45 – 16:15	<i>COFFEE BREAK (Zoological Institute)</i>
16:15 – 17:00	IUCN presentation (International Union for Conservation of Nature) Speaker : Ana NIETO (<i>Zoological Amphitheater</i>)
17:00 – 19:00	POSTER PRESENTATION : Ecophysiology & Ecotoxicology (30-37), Genetic (38-56), Ethology (57-59), Evolutionary morphology (60-67), Adaptive brain morphology and neuroanatomy in fishes (68-72)
17:00 – 19:00	Meet the experts
18:00 – 19:30	General Assembly Of European Ichthyology Society (<i>Classroom Jeuniaux</i>)



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Friday, July 6th

09:00 – 09:40	Plenary lecturer : Patricia HERNANDEZ (<i>Zoological Amphitheater</i>) Using cypriniform fishes to investigate the origin, function, and morphological evolution of trophic novelties
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Oral session : Evolutionary morphology (<i>Zoological Amphitheater</i>) Chairman : Dominique ADRIAENS	
09:45 – 10:00	<u>BOUILLIART Mathias</u> , TOMKIEWICZ Jonna, LAUESEN Peter, ADRIAENS Dominique Functional morphology of the feeding apparatus in preleptocephalus larvae in European eel (<i>Anguilla anguilla</i>): getting ready towards feeding
10:00 – 10:15	<u>BOYLE Kelly S.</u> , PARMENTIER Eric Electric organ discharge and sound production patterns in catfishes of the genus <i>Synodontis</i> (family Mochokidae)
10:15 – 10:30	<u>CORNELISSEN Ilse</u> , DEMMER J., NAGELKERKE L.A.J. Diet of haplochromine cichlids is affected by environment and morphology in Mwanza Gulf, Lake Victoria

10:30 – 11:00	<i>COFFEE BREAK (Zoological Institute)</i>
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Oral session : Evolutionary morphology (<i>Zoological Amphitheater</i>) Chairman : Dominique ADRIAENS	
11:00 – 11:15	<u>DE CROP Wannes</u> , GEERINCKX Tom Anatomy and kinematics of the respiratory apparatus in South American climbing catfishes (Astroblepidae)
11:15 – 11:30	<u>DOOSEY Michael</u> , WILEY Edward Development and Homology of Epurals in the Caudal Fin Skeleton of Euteleost Fishes
11:30 – 11:45	<u>FREDERICH Bruno</u> , SORENSON Laurie, SANTINI Francesco, SLATER Graham J., ALFARO Michael E. Tempo and mode of eco-morphological evolution in damselfishes (Pomacentridae)
11:45 – 12:00	<u>HERDER Fabian</u> , PFAENDER Jobst Do individual fitness or display size differ among colour morphs in "roundfin" sailfin silversides?



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

12:00 – 12:15	<u>KEVER Loïc</u> , DRAGICEVIC Branko, DULCIC Jakov, PARMENTIER Eric Important variations in sonic apparatus morphology and sound characteristics of <i>Ophidion rochei</i> (Ophidiidae)
12:15 – 12:30	<u>MAIA Anabela</u> , ADRIAENS Dominique Tail grasping kinematics in <i>Hippocampus reidi</i>

12:30 – 14:00	LUNCH
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Oral session : Evolutionary morphology (<i>Zoological Amphitheater</i>) Chairman : Bruno FREDERICH	
14:00 – 14:15	<u>MILLOT Sandie</u> , PARMENTIER Eric Ontogeny of sound production and sonic muscle morphology in <i>Pygocentrus nattereri</i>
14:15 – 14:30	<u>MORIMUNE Toshihiko</u> , HOSOYA Kazumi Comparative anatomy on the feeding apparatus in <i>Opsariichthys</i> and related taxa (Teleostei; Cyprinidae)
14:30 – 14:45	<u>MUNYANDAMUTSA Philippe</u> , TKINT Tim, SNOEKS Jos, ADRIAENS Dominique Habitat-related phenotypic plasticity in two <i>Haplochromis</i> species from Lake Kivu (Rwanda)
14:45 – 15:00	<u>NEUTENS Céline</u> , ADRIAENS Dominique, CHRISTIAENS Joachim, VAN LOO Denis, DE KEGEL Barbara, BOISTEL Renaud, VAN HOOREBEKE Luc Evolutionary morphology of the caudal musculoskeletal system in syngnathid fishes: from swimming to prehension...in different ways
15:00 – 15:15	<u>OLIVIER Damien</u> , FREDERICH Bruno, PARMENTIER Eric Feeding mechanism in damselfishes: a comparison between two morphological different species
15:15 – 15:30	<u>PFAENDER Jobst</u> , HERDER Fabian Testing predictions of the syngameon hypothesis in Lake Matano's "sharpfin" sailfin silversides radiation
15:30 – 15:45	<u>SCHULZ-MIRBACH Tanja</u> , METSCHER Brian D., LADICH Friedrich How does swim bladder morphology affect hearing abilities? A case study on Asian and African cichlids

15:45 – 16:15	COFFEE BREAK
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XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

16:15 – 16:30	SHKIL Fedor N., BORISOV V.B., KAPITANOVA D.V., BELAY Abdissa, SMIRNOV S.V. Thyroid hormone induced heterochronies in the early skeletogenesis of Cyprinidae (Teleostei)
16:30 – 16:45	TKINT Tim, DE MEYER Jens, HELSEN Philippe, BOONE Matthieu, VERHEYEN Erik, ADRIAENS Dominique Phenotypic plasticity of jaw morphology as a response to diet in cichlids: suction versus biting
16:45 – 17:00	VAN RIJSEL Jacco C., VAN DER MEER Henny, WITTE Frans Morphological constraints in resurgent haplochromine cichlids: the battle between escape performance, vision and oxygen uptake
17:00 – 17:15	VOSKOBOINIKOVA Olga, NAZARKIN M.V. Comparative Osteology of Cyclopsis tentacularis (Cyclopteridae, Scorpaeniformes)

17:15 – 18:45	POSTER PRESENTATION : Ecology - Fish conservation (73-119)
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19:00 (precisely)	CONGRESS BANQUET at the Castle of Harzé (<i>bus departure in front of the Zoological Institute</i>)
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Saturday, July 7th

09:00 – 09:40	Plenary lecturer : Hans SLABBEKKOORN (<i>Zoological Amphitheater</i>) Noise impact on fish : disturbance and avoidance in captivity
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Oral session : Ethology (<i>Zoological Amphitheater</i>) Chairman : Agnès BARDONNET	
09:45 – 10:00	COLLEYE Orphal, PARMENTIER Eric Implication of aggressive, submissive and reproductive sounds in the way of life of clownfishes
10:00 – 10:15	DELCOURT Johann, YLIEFF Marc, BOLLIET Valérie, BARDONNET Agnès, PONCIN Pascal Video multitracking to study the fish behaviour
10:15 – 10:30	DIRNWÖBER Markus, HERLER Jürgen Toxic coral gobies influence selective corallivory of the obligate corallivorous butterflyfish <i>Chaetodon austriacus</i> in the northern Red Sea

10:30 – 11:00	COFFEE BREAK (<i>Zoological Institute</i>)
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XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Oral session : Ethology (<i>Zoological Amphitheater</i>)	
Chairman :Agnès BARDONNET	
11:00 – 11:15	<u>DONALDSON Terry J.</u> Triggerfish (Balistidae) spawning aggregations and sites : Spatial distribution and characterization
11:15 – 11:30	<u>REZUCHA Radomil</u> , <u>REICHARD Martin</u> The effect of social environment on mating tactic of male Endler's guppy (<i>Poecilia wingei</i>)
11:30 – 11:45	<u>NZAU MATONDO Billy</u> , <u>OVIDIO Michaël</u> , <u>PHILIPPART Jean-Claude</u> , <u>PONCIN Pascal</u> Reproductive performance in F1 hybrids of two phytophilous cyprinid fish, the silver bream (<i>Blicca bjoerkna</i>) × the rudd (<i>Scardinius erythrophthalmus</i>)
11:45 – 12:45	AWARDS & CLOSING CEREMONY : Maurice KOTTELAT & Maria STOUIMBOUDI ACKNOWLEDGMENTS : Pascal PONCIN & Eric PARMENTIER
12:45 – 14:00	LUNCH

Sunday, July 8th

09:30 (precisely)	Whole day CONGRESS TOUR (<i>bus departure in front of the Zoological Institute</i>)
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XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Posters presentations

Phylogeny, Systematics

- 1 **Japanese 'medaka' should be classified into two species !**
ASAI Toshinobu, SENOU Hiroshi, HOSOYA Kazumi
- 2 **FishBase activities at the Royal Museum for Central Africa**
BODEN Gert, MUSSCHOOT Tobias, SNOEKS Jos
- 3 **Ploidy level of progeny from the crosses between allotriploid *Cobitis* females and males of the spined loach *Cobitis taenia* (Teleostei, Cobitidae)**
BORON A., GRABOWSKA A., JABLONSKA O., JUCHNO D., KIRTIKLIS L., KUJAWA R., LESKA A., SPOZ A., ZABINSKA M.
- 4 **Some features of the mtDNA cytochrome b gene's polymorphism of the tubenose goby (*Proterorhinus* sp., Pisces: Gobiidae) of Ponto-Caspian basin**
BOROVIKOVA Elena, GUROVSKI Aleksey, SLYN'KO Yuriy
- 5 **Phylogeography and phylogeny of the Altai osmans (*Oreolueciscus* sp., Pisces: Cyprinidae) of the water bodies of Mongolia**
BOROVIKOVA Elena, SLYN'KO Yuriy
- 6 **Ancient connection among rivers and watersheds revealed from the evolutionary history of the genus *Telestes* (Actinopterygii; Cypriniformes)**
BUJ Ivana, MARČIĆ Zoran, ČALETA Marko, ŠANDA Radek, MUSTAFIĆ Perica, MRAKOVIĆ Milorad
- 7 **The poorly known fish fauna of the Ituri/Epulu basin (Democratic Republic of Congo), Africa**
DECRU Eva, VREVEN Emmanuel, SNOEKS Jos
- 8 **Effect of chronic confinement stress on sperm quality in Eurasian perch**
ESNAULT Stephen, TOMSON Thomas, PRIGNON Christian, PONTIER Jérôme, DELEUZE Stéphane, MÉLARD Charles, ROUGEOT Carole
- 9 **Origin, phylogeny and adaptive radiation of sculpin species flock in Lake Baikal**
GOTO Akira, YOKOYAMA Ryota, SIDELEVA Valentina G.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

- 10 Riddles in the Siebold collection : Heterogeneous type series of Japanese freshwater fishes**
HOSOYA Kazumi, FUJITA Tomohiko, KAWASE Seigo, van OIJEN Martien J.P.
- 11 Where was it caught ? Mapping Swedish type localities of fishes from Linnaeus until exhaustion**
KAJRUP Bodil
- 12 Type series of *Pseudogobio esocinus* (Teleostei; Cypriniformes) in the Siebold collection : its taxonomic problem**
KAWASE Seigo, FUJITA Tomohiko, HOSOYA Kazumi
- 13 Rapid identification of four species of *invasive gobies* using PCR-RFLP**
KOHOUT Jan, PEKÁRIK Ladislav, ŠEDIVÁ Alena
- 14 The arrangement and fixation mechanisms of body plates in straight-nosed pipefish *Nerophis ophidion* (L.)**
LEES Janek
- 15 The Gene divergence of Kamchatka mykiss (*Parasalmo* (*Oncorhynchus*) *mykiss*), by the variability two types of specific genetic markers**
MELNIKOVA M.N., PAVLOV S.D., SENCHUKOVA A.L., SEMENOVA A.V., PIVOVAROV E.A.
- 16 Molecular phylogeny of the South American freshwater fish *Semaprochilodus* (Characiformes: Prochilodontidae) based on nuclear and mitochondrial genes**
MELO Bruno, ABE Kelly, VARI Richard, OLIVEIRA Claudio
- 17 Undetected evolutionary radiation in the pelagic realm : A novel clade in the percomorph fishes as revealed by mitogenomic analysis**
MIYA Masaki, SATOH Takashi, NISHIDA Mutsumi
- 18 Morphological differences between four populations of the soft-mouth trout *Salmo obtusirostris***
DUPLIC A., MRAKOVČIĆ M., CALETA M., MARCIC Z., ZANELLA D., MRDAK D., MUSTAFIC P., BUJ, I.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

- 19 Genetic diversity of common carp (*Cyprinus carpio*) strains revealed by AFLP analysis : Live gene bank in Poland - Preliminary results**
NAPORA – RUTKOWSKI Łukasz, IRNAZAROW Ilgiz, OSTASZEWSKA Teresa, PILARCZYK Andrzej

- 20 Morphological and molecular investigation on the *Romanogobio belingi-vladykovi* complex in the Vistula drainage**
NOWAK Michał, MENDEL Jan, NEUMANN Dirk, SZCZERBIK Paweł, KLACZAK Artur, KOŠČO Ján, POPEK Włodzimierz

- 21 DNA barcoding for identifying neotropical fishes : high molecular diversity in the genus *Astyanax* (Characiformes, Characidae)**
ROSSINI Bruno C., FORESTI Fausto, OLIVEIRA Claudio

- 22 Identification and study of fish species in Zayandehrood River, Iran (Chaharmahal va bakhtiary basin)**
PIRALI KHEIRABADI Esmail, SHAFIE Shafigh, MANSOURI Parviz, TAHERI MIRGHAED Ali, MOHAMADIAN Samira, ROUHOLAHI Shaghayegh, MOKHTARI Abbas

- 23 Evolutionary and biogeographic history of the subfamily Neoplecostominae (Siluriformes : Loricariidae)**
ROXO Fábio Fernandes, ZAWADZKI Claudio Henrique, CHIACHIO Marcio Cesar, FORESTI Fausto, OLIVEIRA Claudio

- 24 Phylogenetic analysis of Otothyrinae (Siluriformes: Loricariidae) with emphasis in *Hisonotus* based in molecular evidences**
ROXO Fábio Fernandes, ZAWADZKI Cláudio H., CHIACHIO Marcio Cesar, FORESTI Fausto, OLIVEIRA Claudio

- 25 The inland ichthyofauna of the Phu Quoc Island : taxonomic and evolutionary aspects**
VASIL'EVA Ekaterina, VASIL'EV Victor

- 26 Comparative analysis of biometric characters of Atlantic Cod *Gadus Morhua* L. from different areas of its distribution**
WIĘCASZEK Beata, DAJBROWSKI Jarosław, ANTOSZEK Artur



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

- 27 Analysis of taxonomic position of Cod *Gadus Morhua* L. from the Baltic sea based on the comparison of meristic characters**
WIĘCASZEK Beata, SOBECKA Ewa, ANTOSZEK Artur
- 28 Biomorphometric characteristics of *Rhinochimaera Atlantica* Holt & Byrne, 1909 (Holocephali: Chimaeriformes) from the Greenland sea**
WIĘCASZEK Beata, SOBECKA Ewa, KESZKA Sławomir, WIELOPOLSKA Magdalena
- 29 Mitochondrial Genetic and Truss Network Differentiation of Spirlin (Actinopterygii : Cyprinidae) In South Caspian Sea Basin of Iran**
SEIFALI Mahvash, YAZDANI MOGHADDAM Faezeh, ALIABADIAN Mansour, ESMAEILI Hamid Reza

Ecophysiology and Ecotoxicology

- 30 Deleterious effects in *Oncorhynchus mykiss* gills after acetaminophen acute exposure : histology, detoxification mechanisms and oxidative damage**
RAMOS Ana Sofia, RODRIGUES Sara, ANTUNES Sara Cristina, NUNES Bruno, GONÇALVES Fernando, CORREIA Alberto
- 31 The sheepshead minnow *Cyprinodon variegatus* as a marine vertebrate model for investigating endocrine disrupting effects of triclosan**
SCHNITZLER Joseph, GAUTHRAY Ghislain, SILVESTRE Frédéric, DAS Krishna
- 32 Effect of ethynylestradiol (EE2) on rainbow trout fry gonads on gene expression, morphology and endocrinology by *in silico* and *in vivo* approaches**
DEPIEREUX Sophie, DEMEULDER Bertrand, DANIS Lorraine, PIERRE Michaël, BAREKE Eric, LEGAC Florence, FOSTIER Alexis, GUIGUEN Yann, DEPIEREUX Eric, KESTEMONT Patrick
- 33 Inflammatory response and heavy metal interactions in roach (*Rutilus rutilus*)**
JOLLY Sabrina, JAFFAL Ali, CARLIER Annie, BLAISE Sébastien, GEFFARD Alain, SANCHEZ Wilfried, BETOULLE Stéphane



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

- 34 Do endocrine stimulating factors mitigate *in vitro* steroidogenesis response of Eurasian perch follicles to stress hormones?**
MANDIKI Robert, MILLa Sylvain, NKOOGO ROBLES Silvia, Kestemont Patrick
- 35 Blood biochemistry profile of softmouth trout *Salmo obtusirostris* from Jadro and Vrljika rivers in Croatia**
CIGROVSKI MUSTAFIC Martina, COZ-RAKOVAC Rozelinda, BEER-LJUBIC Blanka, MRAKOVIC Milorad, SMUC Tomislav, STRUNJAK-PEROVIC Ivancica, TOPIC POPOVIC Natalija, ZANELLA Davor, CALETA Marko, BARISIC Josip, MUSTAFIC Perica
- 36 Effect of cortisol on growth and first sexual maturity in Nile tilapia juveniles, *Oreochromis niloticus***
TOMSON Thomas, JACINTE Mickelson, MANDIKI Robert, MELARD Charles, ROUGEOT Carole
- 37 Effects of dry diet supplementation with natural food on body deformities and growth in juvenile *Carassius carassius* under controlled conditions**
SIKORSKA Justyna, WOLNICKI Jacek, KAMIŃSKI Rafał

Genetics

- 38 Genetics as a tool in a restocking program of *Brycon orbignyanus* (Characiformes, Bryconidae)**
ASHIKAGA Fernando, ORSI Mario L, SENHORINI José A, OLIVEIRA Claudio, FORESTI Fausto
- 39 Population genetic structure of annual *Nothobranchius* fishes in southern Mozambique**
BARTÁKOVÁ Veronika, BRYJA Josef, POLAČIK Matej, BLAŽEK Radim, REICHARD Martin
- 40 Vendace of Solovetskii Islands (the White Sea) as a key for a problem of taxonomical position of northeast Europe ciscoes**
BOROVIKOVA Elena, ALEKSEEVA Yaroslava, SHREIDER Maria, ARTAMONOVA Valentina, MAKHROV Alexandr



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

- 41 Population genetics of the smooth hammerhead shark, *Sphyrna zygaena*, in the equatorial and tropical regions of the eastern Atlantic Ocean.**
DE FRANCO Bruno A., SANTOS Miguel N., COELHO Rui, OLIVEIRA Claudio, MENDONÇA Fernando F., FORESTI Fausto
- 42 Role of *pax4* gene during the pancreatic endocrine cell development in Zebrafish**
DJIOTSA Joachim, VERBRUGGEN V., MARTIAL J., VOZ M., PEERS B.
- 43 Role of the transcription factor Nkx6.1 in the differentiation of the multipotent pancreatic progenitors**
GHAYE Aurélie, PEERS Bernard, VOZ Marianne
- 44 Functional study of the Ser/Arg-rich splicing factor SRp30 during Zebrafish embryonic development**
JORIS Marine, LARBUISSON Arnaud, MULLER Marc, MOTTE Patrick
- 45 Population genetics of the bigeye thresher shark in the Atlantic ocean : low genetic diversity and their implications for conservation**
MENDONÇA Fernando, MORALES Millke, OLIVEIRA Claudio, COELHO Rui, SANTOS Miguel, FORESTI Fausto
- 46 Microsatellite-based genetic diversity and differentiation of Caspian Vimba**
MOHAMADIAN Samira, REZAVANI GILKOLAEI Sohrab, SOLTANI Mehdi, ROUHOLAHI Shaghayegh, GHODRATNAMA Maryam, TAHERI MIRGHAED Ali
- 47 The constitutive heterochromatin distribution on sex chromosomes in *Characidium* (Characiformes, Crenuchidae)**
PAZIAN Marlon, PANSONATO-ALVES José Carlos, OLIVEIRA Claudio, FORESTI Fausto
- 48 Role of the transcription factor Isl1 during the development of the pancreas in zebrafish**
PIRSON Justine, FLASSE Lydie, STERN David, PEERS Bernard, VOZ Marianne
- 49 Transcription factor Egr1 during pituitary development in Danio Rerio.**
QUIROZ Yobhana, WINDHAUSEN T., MARTIAL J.A., MULLER M.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

- 50 Genetic identification and distance between *Chalcalburnus chalcoides* and *Vimba vimba persa* in Southern part of Caspian sea**
ROUHOLAHI Shaghayegh, REZVANI GILKOLAE Sohrab , SOLTANI Mehdi,
MOHAMADIAN Samira, GHODRATNAMA Maryam, TAHERI MIRGHAED Ali
- 51 Population genetic differentiation of Russian , Persian and Siberian Sturgeon species by using mitochondrial and nuclear genetic markers**
SERGEEV Alexey
- 52 Endocrine cells ontogenesis in zebrafish**
STERN David, FLASSE L., PIRSON J., PEERS B., VOZ M.L.
- 53 Phenotypic effects resulting of the reorganizations in rDNA of the hybridsroach (*Rutilus rutilus* L.) and bream (*Abramis brama* L.)**
STOLBUNOVA Veronika, KODUKHOVA Yulia
- 54 Microsatellite-based genetic variability of common carp (*Cyprinus carpio* L.) populations in Croatia**
TOMLIANOVIĆ Tea, TREER Tomislav, ŠPREM Nikica, PIRIA Marina, SAFNER Roman, ANIČIĆ Ivica , MATULIĆ Daniel, JADAN Margita
- 55 The diversification of Ponto-Caspian shads**
SOTELO Graciela, VASIL'ÉVA Ekaterina, FEDORENKO Leonid, MEZH ZHERIN Sergey, NĀVODARU Ion, TURAN Cemal, ALEXANDRINO Paulo, FARIA Rui
- 56 Involvement of the *dhx34* gene in the development of the adenohipophysis in *Danio rerio***
WINDHAUSEN Thomas, MULLER Marc

Ethology

- 57 Radial arm maze as a new paradigm to study collective behaviours in fish**
DELCOURT Johann, GARNIER Simon, MILLER Noam, COUZIN Iain
- 58 Migratory behaviour of European grayling in a one-year radiotelemetry monitoring in Arve river and its tributaries**
VIGIER Laure, BINI Guillaume, CATINAUD Ludovic, CAUDRON Arnaud,
GRIMARDIAS David, RIVES Jacques, PERNETTE Florence, FAUCON-MOUTON Philippe, BARDONNET Agnès, CATTANEO Franck



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

59 Migration of perch *Perca fluviatilis* L. and bream *Abramis brama* (L.) in the Rimov Reservoir

RIHA Milan, KOCVARA Lubos, MRKVICKA Tomas, PRHALOVA Marie, CECH Martin, DRASTIK Vladislav, JUZA Tomas, KRATOCHVIL Michal, MUSKA Milan, PETERKA Jiri, TUSER Michal, VASEK Mojmir, KUBECKA Jan

Evolutionary morphology

60 Heterochronies in skull development of Lake Tana large African barbs (*Labeobarbus*; Cyprinidae; Teleostei)

BORISOV Vasily, SHKIL Fedor, ABDISSA Belay, SMIRNOV Sergey

61 The effect of structure and morphology on the light transmissivity of the mineralized spines of lanternsharks

CLAES Julien, DEAN Mason, NILSSON Dan-Eric, DUNLOP John, SHAHAR Ron, MALLEFET Jérôme

62 Do scale size indices and scale surface morphology allow identification of endemic *Aphanius* species from southern Iran?

GHOLAMI Zeinab, TEIMORI Azad, ESMAEILI H. Reza, SCHULZ-MIRBACH Tanja, REICHENBACHER Bettina

63 Copulatory organ Anatomy in a new viviparous *nomorhamphus* halfbeak (*Atherinomorpha* : *Beloniformes* : *Zenarchopteridae*) from Sulawesi Selatan, Indonesia

HUYLEBROUCK Jan, HADIATY Renny K., HERDER Fabian

64 Effects of hyperthyroidism on the development of *Danio rerio* vertebral column and caudal fin

KAPITANOVA Daria, SHKIL Fedor

65 Morphological characters of *Cobitis elongatoides* (Cypriniformes; Actinopterygii) in Croatia

MIHINJAČ Tanja, BUJ Ivana, MUSTAFIĆ Perica, ZANELLA Davor, ČALETA Marko, MARČIĆ Zoran, MRAKOVIĆ Milorad

66 Microanatomy of the inner ear and hearing abilities in a cyprinodontiform fish

SCHULZ-MIRBACH Tanja, LADICH Friedrich, HESS Martin, PLATH Martin



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

- 67 Structural organization of the nucleolus in different fish species**
THIRY Marc, CLOES Marie, JOHNEN Nicolas, JUCHNO Dorota, LESKA Anna,
THELEN Nicolas

Adaptive brain morphology and neuroanatomy in fishes

- 68 Organization of the telencephalon in cichlids and gouramis based on NADPH-diaphorase activity**
ALJAMAL Mohammed, HOFMANN Michael, KRÜTZFELDT Nils
- 69 Variations in brain morphology within and between populations of silversides**
CLEMENS Michelle, HERDER Fabian, HOFMANN Michael
- 70 The hypothalamus of teleost fishes**
KRÜTZFELDT Nils, HOFMANN Michael
- 71 Morphological investigation of the brain of different populations of threespined sticklebacks**
PRINZ Janine, HOFMANN Michael
- 72 Evidence for an auditory space map in the midbrain torus semicircularis in teleost fishes**
ULAMA Tim, KRÜTZFELDT Nils, HOFMANN Michael

Ecology - Fish conservation

- 73 Use of growth and nutritional indices as indicators of temporal suitability of nursery habitat for newly settled plaice**
AMARA Rachid, SELLESLAGH Jonathan
- 74 Recruitment patterns and spawning periodicity in four cyprinid fish species of Louros River (Greece)**
BARBIERI Roberta, STOUMBOUDI Maria, KALOGIANNI Eleni, LEONARDOS Ioannis



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

- 75 Do reef fish larvae use lagoon sounds to find appropriate settlement environment?**
BERTEN Laetitia, PARMENTIER Eric, LECCHINI David
- 76 Morphological characteristics of bandtooth conger *Ariosoma balearicum* leptocephali in the Adriatic Sea**
BOJANIĆ VAREZIĆ Dubravka, TUTMAN Pero, MATIĆ-SKOKO Sanja, TIČINA Vjekoslav, DULČIĆ Jakov
- 77 Estimation of the exploitable biomass and $F_{0.1}$ of sardine (*Sardina Pilchardus*, Walbaum, 1792) along the central Algerian coast**
BOUAZIZ Ahmed, KERZABI Fedja, BRAHMI Boualem
- 78 Phenotypic plasticity of the South European Toothcarp *Aphanius fasciatus* in the Venice lagoon**
CAVRARO Francesco, CECCONI Ambra, TORRICELLI Patrizia, MALAVASI Stefano
- 79 Diet composition and feeding intensity of brown meagre *Sciaena umbra* linnaeus, 1758 (teleostei, sciaenidae) in the gulf of Tunis**
CHATER Inès, ROMDHANI Ahlem, KTARI Mohamed Hédi, MAHE Kélig
- 80 Mechanism of adaptation of *Protopterus annectens* (Owens, 1839) (Protopteroidea) to the aridity of puddles in the Biosphere Reserve of Pendjari in Benin**
CHIKOU Antoine, LALÈYÈ Philippe, AHOUANSON MONTCHO Simon, TÈHOU Aristide, KOGBÉTO Marie-Josée, WÉNON Dossa, VANDEWALLE Pierre
- 81 Condition and lipid content of chub mackerel, *Scomber colias* in Adriatic Sea**
ČIKEŠ KEČ Vanja, ZORICA Barbara
- 82 Occurrence of encapsulated embryos of *Sympterygia acuta* (Garman, 1877) (Chondrichthyes, Elasmobranchii) in Southern Brazil (SW Atlantic)**
DA FONTOURA MARTINS Mariana, ODDONE Maria Cristina, BIANCHINI Adalto



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

- 83 The effect of interspecific hybridization on the structure of metazoan parasite communities in cyprinid fish**
DAVIDOVA Martina, VETESNIK Lukas, PAPOUSEK Ivo and VETESNIKOVA SIMKOVA Andrea
- 84 Metazoan parasites of Ponto-Caspian gobies introduced into the Rhine River**
ONDRACKOVA Marketa, DAVIDOVA Martina , BORCHERDING Jost, MICHALKOVA Veronika, SLOVACKOVA Iveta, VALOVA Zdenka, JURAJDA Pavel
- 85 The vulnerability assessment of fisheries sector to climate change : the case of the wider area of the mouth of the river Neretva**
ĐOĐO Željana, GLAMUZINA Branko, DULČIĆ Jakov
- 86 Distant travellers : Paranthias furcifer and Holacanthus ciliaris in the Adriatic sea**
DRAGIČEVIĆ Branko, DULČIĆ Jakov
- 87 The Adriatic ichthyofauna : updates and extensions (2009-2012)**
DULČIĆ Jakov, DRAGIČEVIĆ Branko
- 88 Reproductive biology of the black scorpionfish, *Scorpaena porcus* (Pisces, Scorpaenidae) population in the eastern Adriatic Sea**
FERRI Josipa, MATIĆ-SKOKO Sanja, BOČINA Ivana
- 89 Histological analysis of the silver smelt, *Argentina sphyraena* (Pisces, Argentinidae) gonads during the spawning period**
PETRIĆ Mirela, FERRI Josipa, ŠKELJO Frane, BRČIĆ Jure, KRSTULOVIĆ ŠIFNER Svjetlana
- 90 Discarding practices in the commercial trawl fisheries in the eastern Adriatic Sea**
KRSTULOVIĆ ŠIFNER Svjetlana, FERRI Josipa, ŠKELJO Frane, BRČIĆ Jure, PETRIĆ Mirela
- 91 Seasonal fish growth in temperate climates : the effects of temperature and rainfall on the seasonal growth of the stone-loach *Barbatula barbatula***
FONTOURA Nelson



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

- 92 Effects of a generated magnetic field on viability of sea trout (*Salmo trutta m. trutta* L.) spermatozoa and the process of egg fertilization**
SZULC Joanna, TAŃSKI Adam, BIERNACZYK Marcin, KRASZEWSKI Tomasz,
FORMICKI Krzysztof
- 93 Effect of alternating magnetic fields on selected parameters of perch (*Perca fluviatilis* L.) sperm motility**
SZULC Joanna, TAŃSKI Adam, BIERNACZYK Marcin, FORMICKI Krzysztof
- 94 Spreading of new fish species into the western Mediterranean basin : what are the main pathways and what are the triggers?**
FRANCOUR Patrice, BODILIS Pascaline
- 95 Ecological traits of the brook chub *Squalius lucumonis* (Bianco, 1983) in the Tiber River Basin (Italy)**
GIANNETTO Daniela, CAROSI A., GHETTI L., POMPEI L., LORENZONI M.
- 96 Reproductive period of *Spondylus gaederopus* (Bivalvia) and its genetic approach**
GALINO-MITSOUDI Sofia, IMSIRIDOU Anastasia, KOUTRA Athanasia,
SAMARAS Dimitrios
- 97 Seasonal dynamics of the ichthyofauna of a lowland tributary of the Vistula River**
KLACZAK Artur, NOWAK Michał, SZCZERBIK Paweł, EPLER Piotr, POPEK
Włodzimierz
- 98 Study of the carrying capacity of two Belgian rivers, for Atlantic salmon *Salmo salar* L. according to habitat and trophic resource availabilities**
LATLI Adrien
- 99 Diet of the endemic *Telestes karsticus* (Cyprinidae) from Sušik Creek, Croatia**
MARČIĆ Zoran, SUČIĆ Ivana, MUSTAFIĆ Perica, ČALETA Marko, ZANELLA
Davor, BUJ, Ivana, MIHINJAČ Tanja, MRAKOVČIĆ Milorad
- 100 Retention and dispersion of Mediterranean moray eel, *Muraena helena* leptocephali from deep open waters to coastal area**
MATIĆ-SKOKO Sanja, VILIBIĆ Ivica, TUTMAN Pero, PALLAORO Armin



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

101 Feeding habits of blackmouth catshark, *Galeus melastomus*, in the eastern Mediterranean

CHRISTODOULOU Maria, MEGALOFONOU Persefoni

102 The estimation of exploitation status of *Trachurus mediterraneus* (steindachner, 1868), in the central region of the Algerian coasts

MENDIL Hamza, DAMIR Naoual, FILALI Tahar, KHELOUI Hana, KHERCHOUCHE Aldjia, MEGHOUCHE Amine, BOUAZIZ Ahmed

103 Comparative study of the fisheries exploitation using biological indicators in the small lakes in Benin

MONTCHOWUI Elie, AGADJIHOUEDE Hyppolite, PONCIN Pascal, LALLEYE Philippe

104 The diet of *Helicolenus dactylopterus* (Delaroche 1758) in the deep waters of Eastern Ionian Sea

ANASTASOPOULOU Aikaternini, MYTILINEOU Chyssi, DOKOS Jhon, LEFKADITOU Eugenia, BEKAS Petros, SMITH J.Christopher, PAPADOPOULOU Konstantina

105 Spatial and environmental factors of fish biodiversity in the Ionian Sea (Mediterranean Sea)

TSAGARAKIS Konstantinos, MYTILINEOU Chryssi, LORANCE Pascal, HARALABOUS John, POLITOU Chrisi-Yianna, DOKOS John

106 Diel changeover of fish assemblages on sandybanks of a medium-size lowland river

NOWAK Michał, KLACZAK Artur, SZCZERBIK Paweł, KOŠČO Ján, POPEK Włodzimierz

107 Freshwater fishes of the Balkan Peninsula : Delineating biogeographical regions

OIKONOMOU Anthi, LEPRIEUR Fabien, LEONARDOS D. Ioannis

108 BOSS, Biological Object Search Service : An Overview of the Architecture and Features of the FishNet2 Search Engine

RIOS Nelson, BART Henry, BENTLEY Andy, WILEY Edward



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

- 109 Fish isotopic niche concept : a case study with the Atlantic sabretooth anchovy**
RODRIGUES Lucia Ribeiro, FONTOURA Nelson Ferreira, MOTTA MARQUES David
- 110 Age and growth Of *Phycis phycis* (Linne, 1766) in the gulf of Tunis**
ROMDHANI Ahlem, CHATER Ines, KTARI Mohamed Hedi, DUFOUR Jean Louis, MAHE Kelig
- 111 Biological parameters of megrim, *Lepidorhombus whiffiagonis* (Walbaum, 1792) (Osteichthyes : Scophthalmidae) from the eastern Adriatic Sea**
ŠANTIĆ Mate, STAGLIČIĆ Nika, PALLAORO Armin, MARKOV Martina
- 112 Notes on reproductive behaviour of blotched picarel *Spicara maena* L. (Pisces : Centranchidae)**
STAGLICIC Nika, ZULJEVIC Ante, MATIC-SKOKO Sanja
- 113 Role of large river tributaries in conservation of species diversity of fishes at the regulation of their runoff and damming**
STRELNIKOVA Aleksandra, STRELNIKOV Aleksandr
- 114 Estimation of morphometric characteristics of the only confirmed record of *Pristis pectinata* Latham, 1794 in the Adriatic Sea**
SULIĆ ŠPREM Jadranka, DOBROSLAVIĆ Tatjana, KOŽUL Valter, ČIZMIĆ Frane
- 115 Assessment of the fish communities in large Croatian rivers based on the artisan fishermen and anglers' data**
TREER Tomislav, SUIĆ Josip, PIRIA Marina, ŠPREM Nikica, ANIČIĆ Ivica, SAFNER Roman, TOMLIANOVIĆ Tea, MATULIĆ Daniel
- 116 Seasonal changes of species occurrence, abundance and diversity in Neretva river delta (Croatia) fish populations**
TUTMAN Pero, MATIĆ SKOKO Sanja, DULČIĆ Jakov, KRALJEVIĆ Miro, PALLAORO Armin, GLAMUZINA Branko
- 117 Studies of the size and structure of *Eupallasella percunurus* (Pisces, Cyprinidae) populations as a part of programme of its conservation in Poland**
WOLNICKI Jacek, KAMIŃSKI Rafał, RADTKE Grzegorz, SIKORSKA Justyna



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

118 Early development of the freshwater goby *Knipowitschia croatica*

Mrakovčić et al. 1994 (Actinopterygii, Gobiidae)

ZANELLA Davor, MUSTAFIĆ Perica, ČALETA Marko, MARČIĆ Zoran, BUJ
Ivana, MRAKOVČIĆ Milorad

119 Insight in garfish *Belone belone* (L., 1761) diet in the Adriatic Sea

ZORICA Barbara, ČIKEŠ KEČ Vanja



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

**Molecular phylogenetics of the liquorice gouramis
(*Parasphromenus* spp): divergence in a fragmented
freshwater landscape**

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The Southeast Asian liquorice gouramis (genus *Parasphromenus*) are a group of small, brightly coloured labyrinth fishes endemic to the peat swamp forests (PSF) of SE Asia. Approximately 20 species have been described from the Malay Peninsula, Sumatra, Borneo and other small Sunda islands. The group is restricted to acidic black water environments, with most individual species possessing limited, non-overlapping geographical distributions, suggesting that historical landscape fragmentation may have isolated ancestral populations and led to the formation of new species in discrete PSF environments.

Objective: To provide insight into Sundaland freshwater biogeography by reconstructing evolutionary relationships among the PSF genus *Parasphromenus* using a molecular phylogenetic approach.

Materials and Methods: Specimens of each recognised *Parasphromenus* species were collected from PSF across SE Asia. A multi-locus molecular phylogeny was constructed to estimate the evolutionary relationships among species and reveal the level of divergence present among different species. This information was interpreted in conjunction with the historical distributions of PSF habitats and palaeo-drainage basins to elucidate the influence of landscape evolution on promoting diversification within this group.

Main results: Much of the divergence present among *Parasphromenus* species appears to pre-date the Pleistocene, indicating that recent freshwater connections across the Sunda shelf during Pleistocene sea shore regressions have been less significant in promoting diversification within this group. Pliocene paleo-drainages, however, undoubtedly played a major role in the evolution of *Parasphromenus* sister groups.

Conclusion: The dynamic changes in freshwater landscape on the Sunda shelf have promoted diversification and speciation in this group of specialist PSF taxa, highlighting the complex and unique evolutionary history of these endangered and little known freshwater communities.

Keywords : Freshwater biogeography, Molecular phylogeny, Sundaland



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Poster

Organization of the telencephalon in cichlids and gouramis based on NADPH-diaphorase activity

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Fish are the most numerous classes of extant vertebrates, and show great variety in morphology and behaviour, which, in turn, is represented as variation of form and function of the brain. Like in other vertebrates, fish brains are made up of five principal segments, the rostral-most of which is the telencephalon. It contains so-called subpallium and pallium, the latter forming the famous, and generally large, multi-layered cortex of mammals, like ourself. The neocortex of man is thought to be the seat of our consciousness and our cognitive abilities. If such a claim can be made for fish remains to be seen; however, there is evidence that through feed-forward and feed-back loops with pertinent sensory-information processing centres lower in brain, the telencephalon of fish is massively involved in the computation and execution of more cognitive behaviours, e.g. within the frameworks of inter-species and intra-species interaction, homing, and spatial orientation in general. Both total and relative volume of the telencephalon and the segregation of its constituent subdivisions can be regarded as indicators for the species ability to perform cognitive behaviours, and how well 'functional channels' are segregated and/or developed, respectively. While telencephalon size is evident for a large number of species, the structural segregation within the telencephalon has been studied in only a small number of actinopterygians. A contributing complication in surveying not the total telencephalic size, but its subdivisions, is that these are often difficult to delineate based on cytoarchitecture alone. Therefore, we employed a histochemical technique that visualizes NADPH-diaphorase -an anabolic enzyme in the synthesis of nitric oxide (NO) in cells, which use it as a neurotransmitter. We found that by labeling neuronal processes NADPH-diaphorase serves as excellent marker for subdivisions within the pallium and subpallium of the telencephalon.

All major subdivisions of the pallium can be clearly discriminated with sharp boundaries between them. In this study, we used this marker to compare the organization of the telencephalon in cichlids and gouramis, and describe marked differences in pallial areas. One conspicuous finding in gouramis is the fusion of the medial part of the area dorsalis (Dm) in the midline; Dm is an important component of the telencephalon-dependent taste aversion memory system, and its fusion is apparently unique to this group of teleosts. There are also differences in the distribution of NADPH-diaphorase in the area dorsalis that suggest functional differences between cichlids and gouramis that cannot be recognized in Nissl stained histological material.

Keywords : Morphology, Neuroanatomy, Telencephalon



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Integration of fish fossil data into phylogenetic
and comparative studies

Oral

First fossil record of aplocheiloid killifish in Africa

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Introduction: The fossil record represents a very important source of direct information for the understanding of the diversity, biology, and evolutionary history of organisms. The modern African freshwater fish fauna consists of about 3000 species, among which the *Cyprinidae*, catfishes (*Clariidae*, *Mochokidae*), *Cichlidae*, and the *Nothobranchiidae* are dominant. However, their fossil record is scarce and mainly based on isolated fish remains (teeth, vertebrae, bones). Moreover, no fossil record has been reported for the *Nothobranchiidae* and other members of the *Aplocheiloidei* until today.

Objective: Analysis of exceptionally well-preserved fish fossils from palaeolake sediments from East Africa, in order to enhance our knowledge of the palaeodiversity and evolutionary history of Africa's freshwater fish fauna.

Material and Methods: A total of 47 specimens were excavated from the Upper Miocene Lukeino Formation in the Tugen Hills in Central Kenya (East African Rift System), and morphometric, meristic and osteological studies were conducted.

Results: The general shape and proportion of the fossil specimens clearly demonstrate that they represent a member of the Cyprinodontiformes. In particular, they reveal three characters (short dorsal maxillary process; reduced coronoid process of the anguloarticular; one long dorsal fin ray attached to two proximal radials, preceded by one or two short fin rays) that are known as synapomorphies for the *Aplocheiloidei* from literature data. Furthermore, they share some characters with the *Aplocheilidae* (distributed today in South Asia and Madagascar) and *Nothobranchiidae* (distributed today in Africa), but they do not possess the complete suite of derived characters that define these families. Therefore, we consider the fossils as representing a new species, new genus and new family. Additionally, we suggest a picking feeding mode for the fossil species based on the proportion of the jaw elements, which fits well with the feeding mode of many extant cyprinodontiform species.

Conclusion: Articulated fossil fish skeletons are well suitable for comparative anatomical studies and cladistic analyses. The specimens examined represent the first fossil record of an aplocheiloid killifish.

Keywords : Teleostei, Old World, Neogene



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Use of growth and nutritional indices as indicators of temporal suitability of nursery habitat for newly settled plaice

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Evaluation of the specific factors regulating life history dynamics of marine fish population is essential to understand recruitment. Recruitment variability in flatfish is believed to be mainly determined during the pelagic phase with some further adjustment of year-class strength after settlement (Van der Veer et al., 1990).

Temperate nearshore areas serve as nurseries for a number of marine species such as juvenile 0-group plaice. Within these systems, physical and biological factors that regulate the growth and survival of fishes (e.g. temperature, salinity, dissolved oxygen, prey availability, predator abundance) vary substantially in space and time. Rapid growth is particularly important for newly settled fish which can suffer high mortality rates that typically vary inversely with body size.

Larval plaice (*Pleuronectes platessa*) settle in intertidal zone and remain there as juveniles until environmental conditions become unsuitable (late summer) (Amara and Paul, 2003). Because environmental factors likely to regulate growth and survival are highly variable during the plaice settlement period, patterns of habitat suitability for newly settled juveniles may also be dynamic (Selleslagh and Amara, 2007; 2008). Previous research on plaice have shown that settlement occurs over 2 or 3 months and that settling sub-cohorts can have different mortalities on the nursery ground (Alhossaini et al., 1989; Amara and Paul, 2003).

Our objective in this study was to compare growth and nutritional condition of newly settled plaice sub-cohorts collected during the settlement period in different years. Weekly samples were investigated using a 1.5 m beam trawl in the intertidal zone of a sandy beach close to a small estuary of the Eastern Channel (the Canche) during 2000 to 2012.

This will allow us to characterise the temporal suitability of nursery habitat for newly settled plaice, and gain a better understanding of the influence that environmental variability may have on controlling population density of juvenile plaice and hence recruitment.

Keywords : Juvenile plaice, Nursery, Environment



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

The diet of *Helicolenus dactylopterus* (Delaroche 1758) in the deep waters of Eastern Ionian Sea

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The diet of bluemouth, *Helicolenus dactylopterus* (Delaroche 1809) was investigated in the Eastern Mediterranean from specimens collected during experimental bottom long line fishing conducted by HCMR in the Eastern Ionian Sea (Greek waters). Sampling was carried out off Cephalonia Island in deep waters ranging from 300 to 855 m depth in summer and autumn 2010. The stomach and intestine of 380 specimens were examined. The frequency of occurrence (F%), relative abundance (N%), weight percentage (W%), alimentary coefficient (Q%) and the index of relative importance (IRI%) were estimated. Bluemouth diet was dominated by *Pyrosoma sp.* and Osteichthyes. Brachyura, Natantia and Cephalopoda were identified as secondary preys while Ascidiacea, Sponges, Thecosomata, Bivalvia, Gastropoda, Stomatopoda, Thecostraca, Corals, Mysida and Siphonophora represented accidental preys. Most stomachs analysed were in advanced digestion. A high degree of dietary overlap in the intestines was detected between seasons.

Keywords : *Helicolenus dactylopterus*, Feeding, Eastern Ionian Sea



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Japanese 'medaka' should be classified into two species !

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Japanese medaka which is a member of *Oryzias latipes* complex distributed in East Asia and Laos has been believed to be a single species for more than 160 years, since 1846 when "Fauna Japonica" had published by Temminck & Schlegel. In the 1980s, allozyme studies have shown that Japanese wild population of medaka, could be divided into two genetic groups, the Northern and Southern populations. Great genetic differentiation between both populations was also supported by mtDNA analysis. However, these populations has not been fully investigated morphology and taxonomically. Recently, we described the Northern population as a new species, *O. sakaizumii*. This is a historic event in the taxonomy of Japanese medaka. We here review why both populations are treated as a distinct species in each. We have used 119 individuals of both populations to compare osteological system and 22 characters of related morphology. Counts were made mainly from radiograph by soft X-rays, and comparative osteology from cleared and counterstained specimens. As a result, head size to body length ratio in the Southern population was smaller than that of the Northern population. Also, it seems that behavioral difference could be showed between both populations, due to long pectoral fin, anal fin base, anteriorly placed pelvic fin of the Southern population to the Northern populations. Furthermore, the Northern population has slightly notched membrane between dorsal fin-rays 5 and 6 in males; dense network of melanophores and irregular black spots on posterior portion of body lateral. As for the osteology characters, there exists preethmoid cartilage, wing-like apophysis of posterior epiotic, short preopercular sensory canal, enlarged teeth posteriorly on premaxilla of both sexes, ossified epibranchial 2, many abdominal vertebrate, parhypural parapophysis in the Northern population. The Northern and Southern populations coexist parapatrically within the same river drainage, which is the distributional boundary zone of these populations. Both have also been reported to exhibit different schooling behaviors. This implies the ecological diversification between both populations. Furthermore, frequencies of mitochondrial cytochrome b gene mitotype in there have been showed an establishment of reproductive isolation. Therefore, it is recognized that the Northern and the Southern populations differentiate in a specific level.

Keywords : Medaka, *Oryzias latipes*, *Oryzias sakaizumii*



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Genetics as a tool in a restocking program of *Brycon orbignyanus* (Characiformes, Bryconidae)

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The ecological success in the management of impacted ecosystems involves the knowledge of multiple factors. Although the practice of restocking with native species of fish can be considered a frequent procedure, many times the criterions in the choice of breeders are not used. This occurs with the Neotropical fish species *Brycon orbignyanus*, which has suffered the human impact during the past decades and experienced profound changes in natural populations. Thus, efforts have been made to replace individuals in the wild population with individuals produced in captivity. In this context, it's interesting to analyze some aspects as genetic structure and diversity of natural and captive populations of *B. orbignyanus*, to provide information for management programs. Six groups were analyzed by sequencing the mtDNA control region: samples of two groups of wild individuals collected in Ivinhema River and in the Ilha Grande National Park (Parana River), and four captivity groups coming from Jupiá, CEPTA, Itutinga 1 and Itutinga 2. The analysis revealed that the wild groups Ivinhema and Ilha Grande presented a high genetic structure ($F_{ST}=0.16$) with 18 haplotypes in each groups, showing high levels of genetic (0.96 and 0.94) and nucleotide (0.25 and 0.22) diversity. The captivity groups presented high degree of inbreeding, probably by use few individuals as breeders leads to homogeneity of the stocks. The CEPTA group originated from breeders belonging to the Jupiá group was highly homogeneous and only a single haplotype was observed for both groups, expressing an effective loss of the genetic variability. The groups Itutinga 1 and 2 presented better genetic conditions, since the captive breedings are often supplied with new wild breeders from the environment, resulting in four haplotypes for Itutinga 1 and two for Itutinga 2, with genetic diversity of 0.52 and 0.43 and nucleotide diversity of 0.06 and 0.13, respectively. The results identify an expressive decrease in genetic variability from wild to captive population and an increase of genetic structure, probably indicating that an inappropriate process of reproduction is being used for restocking wild populations.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

The loss of genetic variability can reduce fish fecundity and viability, and also affects the opportunities for adaptation in face of evolutionary changes; the probability of the species extinction cannot be discarded in these environments. This study shows the applicability of the molecular markers to better understanding the genetic population structure in fish and its role in the identification of evolutionary significant units for conservation.

Keywords : Genetic diversity, Restocking, *Brycon orbignyanus*



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Oral

Development of a refined morphological scoring system using the zebrafish embryo for classification of teratogenic compounds

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Due to industrial activities a variety of harmful chemicals and wastes are released into the aquatic environment. The European REACH legislation is aimed at collecting chemical toxicity data to protect humans and the environment from their adverse effects. Teratogenic chemicals are prioritized under the EU REACH legislation. The classical developmental toxicity tests predominantly use rats and rabbits and are therefore time-consuming, costly and require a large number of animals. Within this framework there is a need for an efficient, low cost, and high throughput routine alternative testing tool. One of the promising alternative assays is the zebrafish early life stage (ELS) test. At the embryonic stage zebrafish are not considered experimental animals under European legislation and therefore offer substantial potential when considering the 3R principles. The zebrafish embryo has been suggested as a model system that can bridge the gap between cell assays and rodent assays. However, the current ELS tests are mainly based on lethal endpoints and binomial scoring of a restricted set of developmental phenotypes to determine the LC₅₀, EC₅₀, and the teratogenic index (TI). The TI is mostly calculated as the ratio LC₅₀/EC₅₀ to estimate the teratogenicity of compounds. Especially with respect to the EC₅₀ calculations, some questions arise. Since different substances cause different developmental defects, selecting only one developmental defect to compute the EC₅₀ is probably not the way forward. Ideally all developmental defects would be combined into one morphological profile. A number of challenges are encountered when developing such a scoring system. For example, should each developmental defect have the same weight in the final score? In this study we developed a challenging morphological assessment and evaluation method for screening and classification of chemicals. We exposed zebrafish embryos to eight model substances selected from different classes of teratogenic and non teratogenic compounds. A total of 18 developmental parameters was scored using a stereomicroscope and evaluated by using a trinomial morphological scoring (TMS) system.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

First, concentration-response curves for each morphological effect were created. Subsequently, these morphological effects were combined and subjected to a learning algorithm to classify compounds based on their integrated morphological profile. Using this refined analysis strategy we were able to distinguish teratogenic and non teratogenic compounds. This study confirms that the zebrafish embryo is an ideal model system for the development of a routine testing tool for identification of compounds with teratogenic action within the REACH context.

Keywords : Zebrafish embryo, Teratogenicity, Classification



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

The fish diversity of the Upper Malagarazi River basin, East Africa (Burundi)

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The Malagarazi basin constitutes about one third of the catchment area of Lake Tanganyika. Currently, 108 species are known from the entire Malagarazi basin, including 25 endemics. Nearly 60 % of all species have confirmed records from the Burundese part of the basin. This is noteworthy as the Malagarazi in Burundi covers only four percent of the total drainage area. The inventory is by no means complete and certain groups such as the genera '*Barbus*', *Labeo* and *Labeobarbus* (Cyprinidae), *Synodontis* (Mochokidae), and the haplochromine cichlids (Cichlidae), require further taxonomic attention.

During the last three years, new sampling expeditions have been undertaken in the Upper Malagarazi in Burundi. Species identification was often problematic as, to date, no identification key is available for this fish fauna. Specimens belonging to at least two new '*Barbus*' species, one new *Labeobarbus* (Cyprinidae) and one new *Chiloglanis* (Mochokidae), have been collected. One of the new species, '*Barbus*' sp. '*devosi*', belongs to the group of small African '*Barbus*' with a strongly ossified and serrated last unbranched dorsal-fin ray and a blackish midlateral band. In '*B.*' sp. '*devosi*', this band extends from the tip of the snout to the caudal-fin base, or onto the mid-central part of the caudal fin. Specimens of this species had been identified as '*B.*' *eutaenia* and '*B.*' *miolepis miolepis*. However, it can be clearly distinguished from both species in having: a higher number of ceratobranchial gill rakers on the first gill arch (6-9 vs. 2-5); shorter anterior (10.6-19.1 vs. 20.0-34.7 % HL for '*B.*' *eutaenia* and 20.3-36.5 % HL for '*B.*' *miolepis*) and posterior (14.5-26.6 vs. 22.4-43.7 % HL for '*B.*' *eutaenia* and 26.5-45.7 % HL for '*B.*' *miolepis*) barbels; and by the absence of a sheath of enlarged, prominent, scales at the base of the dorsal fin.

The high species diversity within this small portion of the Malagarazi basin in a country with increasing pressures on its natural resources underscores the importance of the national reserve in that area, that is currently being set up.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Recruitment patterns and spawning periodicity in four cyprinid fish species of Louros River (Greece)

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Louros River hosts four cyprinids, endemic to Northwestern Greece. *Telestes pleurobipunctatus*, *Squalius pamvoticus* and *Pelasgus thesproticus* inhabit almost the entire river catchment, but *Luciobarbus albanicus* is found only at the lowland section of the river. The aim of the present work was to investigate the spawning periodicity and the growth pattern of these species at two different sampling sites. Fish were collected monthly or bimonthly (March-September 2006) from Terovo springs (upland) and Xiropotamos stream (lowland). *L. albanicus* was present only at Xiropotamos, while the other three species occurred at both sites. Mean water temperature was 14.3 °C and 18.8 °C at Terovo and Xiropotamos respectively. 0-group fish (larvae and early juveniles) were collected with a micromesh seine net from shallow habitats with low water flow, where they tend to aggregate hidden in vegetation. Samples were preserved in 4% formalin and, in the laboratory, they were photographed and measured with a Digital Image System Analysis. Growth and recruitment were studied using progressive length-frequency histograms. Spawning periodicity and possible presence of multiple spawning events were identified by the presence of discrete additional cohorts. Separation of specimens to seven successive developmental stages aided to the discrimination of the different cohorts. *T. pleurobipunctatus* spawned first at Terovo with two 0-group cohorts at late March and early April, while at Xiropotamos there was a single 0-cohort at the beginning of April. The growth and recruitment patterns of *S. pamvoticus* at Terovo were impossible to discern due to infrequent catches, while the observation of at least two 0-group cohorts at Xiropotamos indicates multiple spawning events. The reproductive period of *P. thesproticus*, which commenced in April, it extended at Terovo to late summer, while at Xiropotamos only to the end of spring. The first and massive spawning of *L. albanicus* occurred in mid- April, followed by two smaller events at the end of the month and at the beginning of May. In conclusion, multiple spawning events were identified in all species investigated, with differences however in the number of 0-cohorts and the periodicity of reproduction between the two sites. In *T. pleurobipunctatus* and *L. albanicus*, the presence of oocytes of a single developmental stage indicates multiple spawning at the population level. In *S. pamvoticus* and *P. thesproticus*, it was not possible to discern whether multiple spawning occurs at the population or at the individual level.

Keywords : Spawning periodicity, Growth, Cyprinids



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology – Fish conservation

Invited speaker

Genetic, physiological and environmental mechanisms of sex determination in fishes

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Unlike mammals and birds which have ancient and well conserved Sex Determining (SD) Systems, teleost fish have unstable, flexible SD with a large array of distinct systems. Fish can have all possible forms of Genetic SD (GSD) from male to female heterogamety sometimes coexisting in sister species, with possible influence of autosomal loci, as well as polyfactorial SD. Fish have also Environmental SD and especially Temperature SD or temperature influences on sex differentiation. Environmental and genetic factors can also interact to bring about sex phenotypes. Frequent switching between SD Systems has been observed in fish with possible emergence of new sex chromosomes. Studies suggest that in tilapia we may be in the transition from a ZZ/ZW system (bleu tilapia) in which the female sex determinant is on the large Chr3-LG3 chromosome towards a XX/XY system (Nile tilapia) with a major male determinant located in a new small Chr1-LG1 chromosome. This transition may be facilitated by temperature induced masculinisation. In the majority of fish, sex chromosomes are not morphologically distinguishable between males and females. For instance, the medaka with an XX/XY GSD has homomorphic chromosomes and only a 258kbp Y-specific region leading to a recombinational isolation of the male sex-determining gene *dmy/dmrt1bY*. This gene originated from a duplicated copy of the autosomal *dmrt1* gene which is a highly conserved gene involved in testis development. Nevertheless, this master sex determining gene evolved rapidly and is not present in closely related species. In contrast, several salmonid species (all with a XX/XY system) may have a conserved male determinant which has recently been identified. A duplicated copy of another downstream testis gene *amh*, has recently been identified in the pejerrey which could be the master SD gene in this species since a knockdown of the *amhy* gene caused male to female inversion. Whereas sex differentiation in fish appears relatively conserved with similar genes to those of other vertebrates, sex determination systems and determinants might frequently undergo changes.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Molecular phylogenetics of the Cypriniformes: confronting the confusion

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Objective: An unreviewed editorial in *Zootaxa* in 2011, without invitation for responses from criticized authors, decried the conflicting molecular phylogenetic hypotheses of cypriniform fishes published by collaborators of the Cypriniformes Tree of Life Project and other investigators, including authors of the editorial, referring to the work collectively as a “tree of confusion”. In this study, we present new molecular phylogenetic hypotheses of order Cypriniformes based on even larger numbers of taxa and genes than previously published analyses (five nDNA genes and wMtDNA for about 150 cypriniform species). However, rather than adding to the confusion, the current analysis addresses the conflicts head on.

Methods and Materials: We assess the effects of including different numbers of Danionines in analysis by comparing our trees to those based on Tang et al.’s (2010) analysis, inclusive of greater sampling of Danioninae (152 species). We analyze character-state transformations across both phylogenies and character support for conflicting branches/nodes. Consensus trees from separate analyses for the 150 cypriniforms dataset investigate 1) five nuclear genes, 2) mitogenomes only, and 3) five nuclear genes plus R-Y coded ND4 data.

Results: All analyses resolve basal relationships of major clades as trichotomies consisting of catostomids plus loaches (inclusive of *Gyrinocheilus*), *Paedocypris*, and all other Cyprinoidea. Reanalysis of Tang et al. (2010) data recovers a different trichotomy: catostomids, loaches (inclusive of *Gyrinocheilus*), and a monophyletic Cyprinidae, but fails to resolve Danioninae *sensu stricto* as monophyletic. We show with character evidence that most of the instability in these analyses result from conflicting character support included in “Danionini.” New hypothesis are provided for cypriniform relationships without these conflicting characters.

Keywords : /



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Genetics

Poster

Population genetic structure of annual *Nothobranchius* fishes in southern Mozambique

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The genus *Nothobranchius* is a group of small fishes that inhabit temporary savannah pools in Eastern Africa. All species are annual; the adults die when the habitat desiccates and new generation survives in the form of eggs encased in the dry mud. We analyzed population genetic structure of two species from the southern periphery of *Nothobranchius* range, using samples covering entire of species' ranges. The first species, *N. furzeri* occurs in the Incomati, Limpopo and Chetu basins in southern Mozambique while its sister species *N. kadleci* is allopatric and inhabits the river basins between the Save and the Zambezi in Central Mozambique. This group of species is a target of recent investigations into the physiology and genetics of ageing and life history evolution. Another interesting aspect is that male *N. furzeri* occur in two colour morphs, which are sympatric over large part of its range. We used a set of 13 microsatellite loci and cytochrome B sequences for a sample of 800 fish from 44 populations to describe the population genetic structure and test hypotheses of the *Nothobranchius* dispersal (adult dispersal during large floods versus egg dispersal in mud on bodies of large mammals). We found profound genetic differences among populations, including adjacent populations that are separated by as little as few kilometres. Genetic structuring was strong and, surprisingly, large rivers (Save, Limpopo) formed major barriers to dispersal. This is unique for a fish taxon and comparable to the situation known for terrestrial animals. There is no indication that the eggs are transported by large mammals and dispersal is likely mediated by flooding. These data will be used for a study of life history evolution of *Nothobranchius* across its range.

Keywords : *Nothobranchius*, Genetic structure



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Oral

Developmental and Evolutionary Origins of the Neural Basis for Acoustic Signaling in Vertebrates

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Vocal-acoustic signaling is widespread among basal and derived lineages of the two major clades of bony vertebrates, *Actinopterygii*, the most species-rich vertebrate lineage, and *Sarcopterygii* that include Tetrapods. This presentation will review new evidence from studies of early development of the hindbrain documenting the developmental and evolutionary origins of central pattern generators for acoustic signaling among fishes, and bony vertebrates in general. The developing hindbrain of all vertebrates is divided into eight segments known as rhombomeres with cranial motor nuclei originating from one or more rhombomeres. Studies in fishes and tetrapods indicate that the premotor-motor circuitry giving rise to the central pattern generating (CPG) networks solely dedicated to sound production, that is vocalization, originate from a compartment formed by the most caudal hindbrain rhombomere (8) and the rostral spinal cord. Vocal muscles also share developmental origins in fishes and tetrapods (laryngeal, syringeal) from occipital somites. Together, the available evidence suggests that vocalization and its morpho-physiological basis are ancestral characters for the major lineages of vocal vertebrates in both clades of bony vertebrates. The rhombomere 8-spinal compartment is also the developmental origins of the premotor-motor circuitry controlling the pectoral appendages in fishes that function in both locomotion and non-vocal, acoustic signaling. Hence, vocal and pectoral phenotypes in fishes share developmental origins and roles in acoustic communication. As will be discussed, these new findings have important implications for the evolution of acoustic communication among tetrapods. This includes the neural basis for the coupling of vocal mechanisms with pectoral functions adapted for non-vocal acoustic and gestural signalling and, even more broadly, the vocal versus gestural origins of speech and language.

Keywords : Vocalization, Brain, Speech



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

In search of new markers for the molecular phylogeny of Acanthomorpha

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Acanthomorph fishes represent almost 17,000 extant species. Although our understanding of their relationships has improved in the last two decades, many parts of their phylogeny are yet to be clarified. To date, advances in Acanthomorphs molecular phylogeny are based on a relatively small set of markers. It has been shown (Dettaï & Lecointre, 2005; Dettaï & Lecointre, 2008; C. Li et al., 2007; B. Li et al., 2009) that adding new markers improves the phylogenetic resolution for the group, emphasizing the need of new markers. Many existing markers were designed empirically, often by adapting markers used for other taxonomic groups. However, the design of new markers became considerably easier since five teleost complete genomes (*Danio rerio*, *Takifugu rubripes*, *Tetraodon nigroviridis*, *Oryzias latipes*, *Gasterosteus aculeatus*) have been made available in the ENSEMBL database. In 2007, C. Li et al. published a computer program to search for new candidate markers by the comparison of two complete genomes. Their technique efficiently yielded new markers, but many are too conserved for Acanthomorph phylogeny. We therefore propose a new method to compare ENSEMBL teleost genomes to find more variable markers. Our method selects candidate genes for new markers among all the genes from the five teleost complete genomes available. In order to make sure that these markers will be suitable for phylogenetic inference, we used several criteria considered as good predictors. We only retained orthologous coding genes, in single copy in the five species, and that have at least one exon of more than 700 bp. The approach takes advantage of the analyse of the orthologies between genomes done in ENSEMBL with the bioinformatic pipeline developed by Vilella et al. in 2009. We have obtained 591 candidate markers. Some of these candidates were tested in the lab and appeared useful within the Acanthomorpha. Most of the markers currently in use are recovered by our method, further validating our approach. The computer program we developed is freely available.

Keywords : New molecular markers, Complete genomes, Phylogeny



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Population dynamics of the roach, *Rutilus rutilus* L., in the reach of Tailfer on the river Meuse, Belgium

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The roach (*Rutilus rutilus* L.) used to be an abundant species in the river Meuse. It benefitted from numerous restockings during the 80's. Once their necessity was proven to be none, such restocking operations were suspended for a trial run of 3 years. In 2003, a second study concluded that the roach population in the Meuse was still doing fine. However, according to indirect indicators such as headcounts in fish ladders and the disastrous results of traditional fishing contests, it appeared that the roach population recently fell dramatically. The reach of Tailfer on the river Meuse and its backwaters were investigated. In March and October 2010, we marked each of 10,100 roaches by respectively cutting off the left and right pelvic fins and scattered them over the study area. Two sampling sessions per month were carried out using complementary catching methods (gill nets, fykes and electrofishing) to collect data. Growth rate was determined by scalimetry and growth parameters were assessed using various mathematical models such as von Bertalanffy, Ford-Walford, Gulland & Holt. The Bertalanffy equation did not show any radical change of pace in growth ($L_{\infty} = 302$ mm, $K=0.2$ and $t_0 = -1$ in 2010) compared to reference value (352 mm, $K = 0.20$ and $t_0 = -0.3$ in 1993). Using Petersen's assessment method, we estimated the density (398 ind/ha in 2010 and 435 ind/ha in 2011 compared to 11817 ind/ha in 1993 and 7219 ind/ha in 2001) and the biomass (8.8 kg/ha in 2010 and 27 kg/ha in 2011 compared to 635 in 1993 and 435 kg/ha in 2001) and noticed a sheer drop (>90%). Capture by unit of effort decreased drastically as well (>97% with 0.86 ind/ m²/ 30' in 2011) and total mortality rate was high ($Z = 0.98$ in 2010 based on Chapman & Robson method) with an impressive fishing mortality ($F = 0.76$). As a consequence, exploitation rate rose over the critical 0.7 threshold for over-exploitation. Though, due to lack of relevant data, our results in 2010 appeared to suffer from poor accuracy, but 2011's results support our preliminary conclusion. Thus, the apparent decline in the roach population is a fact and we stress the necessity to find out the causes and to verify possible implication of actual ecological issues like the spreading of invasive species (*Corbicula spp.*) or the increase of piscivorous predators (catfish, cormorant).

Keywords : Population dynamics, Roach



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Do reef fish larvae use lagoon sounds to find appropriate settlement environment?

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Reef fish larvae are able to travel long distance to reach an island and colonize it. It seems they can find their habitat by using the reef crest sound. As soon as the larvae cross the coral crest, they swim toward their settlement biotope. However, it is not known how they find it. We investigated the effect of different natural lagoon noises on directional swimming behavior of settlement-stage reef fish. Post-larvae were tested in multiple choice chambers, using fringing reef noise, barrier reef noise and mangrove noise. These sounds were recorded at dusk in North and West coast of Moorea (French Polynesia) from February to April 2010. Opunohu's Bay noise was used as a control treatment. Thirty-three species from different families were tested (7 Acanthuridae, 5 Apogonidae, 1 Balistidae, 5 Chaetodontidae, 1 Gobiidae, 4 Holocentridae, 1 Microdesmidae, 1 Mullidae, 5 Pomacentridae, 1 Scorpaenidae and 1 Tetraodontidae). Five to eighteen individuals per species and per treatments were tested from February to May, years 2011 and 2012. We observed that environmental noise affect swimming behavior of some species at settlement-stage, although not all of them. It suggests that typical environmental noise of some lagoon biotope might affect the settlement of a range of the coral fish community.

Keywords : Fish larvae, Acoustic cue, Settlement



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Oral

Immunocompetence of brown and brook trouts living in different subantarctic freshwaters ecosystems

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Between 1955 and 1991, salmonids such as brown trout (*Salmo trutta* Linnaeus, 1758) and brook trout (*Salvelinus fontinalis* Mitchell, 1814) were introduced in the Kerguelen Islands (49°S, 70°E) whose freshwaters had originally no endemic freshwater fish species. The high geographical isolation of Kerguelen Islands may contribute to establish these salmonid populations in the aquatic system of the archipelago, these populations being potentially protected against most parasitic influences. Thus, salmonids in Kerguelen may be interesting biological models to study the natural immuno-physiological variations in fish populations in their natural medium in relation to extrinsic and intrinsic ecological parameters. The present study was realised in Kerguelen between January and March 2007. Two geographical watersheds 10-20 km away from the scientific station of Port-aux-Français were investigated, in order to analyse potential direct anthropogenic pressures. In the two sites (Château and Ferme Rivers) water was sampled to determine its seasonal physico-chemical characteristics. At the same time, fish of the two salmonid species were caught to evaluate some components of their innate immune response. In each individual, number of peripheral blood leucocytes, spleno-somatic index and oxygen-dependent lytic activities of blood and head kidney phagocytes were determined. Some differences in immunologic response of fish were noticed between both sites more or less remote from the sea, in relation to their physico-chemical characteristics and fish physiological status. Results may constitute a major database of these immuno-biological tests in wild fish populations and give major referential information to ecotoxicologists and eco-immunologists in their studies of validation of immunological biomarkers.

Keywords : Immunity, Ecology, Salmonid



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Systematic update of Italian native and exotic freshwater fish

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We provide an updated checklist of freshwater fishes of Italy (including both native and established alien species) based on available molecular, morphological and biogeographical data. About 15 native species, reported as conspecific with transalpine species in the official Italian ichthyological literature, are in fact endemics. Because of the previous taxonomic confusion, several alien species have been brought into Italy, either introduced in official stockings or mixed in as impurities. Rehabilitated species include the cyprinids *Scardinius hesperidicus* and *S. scardafa*, *Telestes savigny* from northern Italy and *T. comes* from southern Italy, and *Squalius ruffoi* from southern Italy. *Squalius albus* is a junior synonym of *S. squalus*. The endemic gudgeon, previously assigned to the genus *Romanogobio*, is returned to the genus *Gobio* (*G. benacensis*). *Phoxinus lumaireul* is a junior synonym of *P. phoxinus*. Among Salmonidae, *Salmo cenerinus* is a junior synonym of *S. marmoratus*, while *Salmo farioides* represents the trout species of the Adriatic lineage and a neotype is designated. The esocid *Esox cisalpinus* is an endemic species of pike in Italy and *Esox flaviae* a junior synonym. Among sculpins, *Cottus scaturigo* and *C. ferrugineus* are regarded as potential junior synonyms of *C. gobio*. At present, there are 49 native living freshwater fish species, and 2 extinct (*Acipenser sturio* and *Huso huso*). Among the 51 introduced species, 4 are recent established (*Oreochromis niloticus*, *Poecilia reticulata*, *Amatitlania nigrofasciatus*, *Hemichromis* sp.), 39 are known to be established, 6 are probably established and 2 non-established Chinese carp, maintained in the wild by intensive stockings.

Keywords : Taxonomy, Freshwater, Italy



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Climate change and long-term salmon smolt migration patterns in wild salmon natural spawning river Salaca

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The largest wild salmon natural spawning river in the East Baltic's is the River Salaca. The river is situated in the North Vidzeme Biosphere Reserve, northern part of Latvia at latitude 57°N where wild salmon smolt migration typically occurs from April to June. It is generally known that the most significant environmental factors regulating smolt migration are photoperiod and water temperature affecting physiological processes of smoltification. At the same time the dynamics of the very migration process is principally affected by water discharge and increased in water temperature. Our study is aimed to clarify i) what changes is going on concerning these two parameters since 1964; ii) are there any significant changes in the salmon smolt migration patterns. Salmon smolt emigration data were collected annually since 1964 as number of caught smolts per day using smolt trap situated at the lower part of the river 0.3 km from the Gulf of Riga. Data on water temperature and discharge (standard daily measurements) were obtained from bulletins of Latvian Environment, Geology and Meteorology Centre. Results show that since 1964 to 2011 a significant increase in water temperature is found for February, March and April. Annual water discharge in the river Salaca tend to increase, especially in winter (December- February) and summer (June- August). Mann-Kendal test statistics indicate significant increase of minimal, average and maximal water temperatures in April and decrease of the number of days, when water temperature is below 6 °C. The mean annual discharge of the river Salaca in studied period is significantly increased. Long-term data show that salmon smolt migration run starts when spring floods decreases (on average at 56 m³/s), but water temperature increases (on average at 8.1 °C). The most intensive smolt migration is observed at water discharge 40 m³/s and temperature 13 °C. Migration commonly ends when water temperature reaches 18°C. The data confirms that in Salaca smolt migration in the last twenty years starts 5 days earlier than until late 1980s. Thus, these differences are not statistically significant. Same changes are observed after the mild winters and on the contrary - after the cold winters when salmon smolt migration begun only in May. In general, in Salaca is observed the increase in water temperature since 1964 that is the most likely effect of climate change. River discharge has changed, too. At the same time concerning smolt migration it is not possible to confirm direct relationship with these climate change indicators. We suggest that changes in smolt migration terms probably could be connected with local adaptation that is observed in the cases of climate extremes. Further analyses are necessary to ascertain this hypothesis.

Keywords : Salmon smolts migrations, Water temperature, Discharge



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Fish assemblages and their parasites in the Lake Turkana, Kenya

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Objectives: Lake Turkana is located in the Great Rift Valley in arid northwestern part of Kenya. Covering an area of 6,750 square km it is the world's largest permanent alkaline desert lake, forming with its only permanent inlet, the Omo River, a closed-basin. Around 300,000 people of five tribes inhabit vicinity of the lake and large proportion of population relies on the wild fishery. According to various sources it can be estimated that the Turkana basin is inhabited by 64-76 fish species. Significant proportion of Turkana basin fish species belongs to widespread Nilo-Sudaninan fish assemblage and only 13 species are endemic.

Materials and methods: Live fish were obtained from local fisherman or by own sampling in three localities characterized by different levels of salinity. Locality Todonyang on the west bank near Omo delta has the lowest salinity. The latter localities, Kalokol on the west bank in middle part and Loiyangalani on the southeast part of the lake are moderately saline. Complete sample examined for presence of metazoan and selected protist parasites consisted of more than 400 fish individuals from 30 species; ten of which are the most common species fished by local fisherman.

Main results: A total of 36 fish species of 16 families were observed. The most common parasites were Crustaceans found on the gills and body surface of 22 fish spp. Likewise, heavy loads of Monogeneans were recorded on the body surface, fins, and gills and rarely in the stomach of 18 fish spp. Other groups of parasites were represented by both larval (*Contracaecum sp.* in 6 fish spp.) and adult stages of nematodes in most fish spp., Digeneans in 8 fish spp., larval gryphorhynchid cestode larvae and numerous adult cestodes in 12 fish spp., acanthocephalans in 3 fish spp., hirudineans in 3 fish spp. and myxosporidians in 6 fish spp.

Conclusion: Two of thirty six fish species determined were considered as new records for Turkana-Omo basin. Significant proportion of parasite species, especially Monogeneans, were found as new for science.

Present study was supported by Ichthyoparasitology Research Centre of the Ministry of Education No. LC 522.

Keywords : Turkana-omo, Fish, Parasite



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

FishBase activities at the Royal Museum for Central Africa

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FishBase was developed at the WorldFish Center (former ICLARM) by Rainer Froese and Daniel Pauly from 1987 onwards. Between 1990 and 2000 it was financed by various grants of the European Commission. Since 2001, FishBase is supported by a consortium that currently incorporates nine institutions: the WorldFish Center (Malaysia), FAO (Rome, Italy), the universities of Kiel (Germany), British Columbia (Canada) and Thessaloniki (Greece), the Chinese Academy of Fisheries Sciences (China), the Natural History Museum of Paris (France) and Stockholm (Sweden), and the Royal Museum for Central Africa (Belgium). Started as an information system on the economically most important fish species, it has now grown to the largest on-line encyclopaedia with information on more than 32.000 fish species. The RMCA has a long history in FishBase with the digitization of its fish collection in the nineties. At present, the main activity consists of providing data on African fresh- and brackish water fishes. Priority is given to new species accounts and taxonomic revisions, but information on distribution, ecology, life history, etc. is also checked and updated. A second important activity of the RMCA is the organization of a yearly 'FishBase and Fish Taxonomy' training for five selected African scientists, alternately in English and French. Two main components, fish taxonomy and FishBase, are treated during this three months training, complemented by a case study that puts theory into practice. Since 2009, an annual follow-up training session for two candidates is organized, which allows them to continue the work on the case study or extend their skills. AquaMaps has become an important tool in FishBase for the prediction of the natural occurrence of marine species based on different parameters.

The RMCA and FishBase are currently developing AquaMaps for African freshwater fishes. This phase mainly involves the delineation of basins and subbasins in Africa, an update of species distributions, and an evaluation of the preliminary results.

Keywords : Fishbase



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Using citizen science to survey non indigenous invasive species : The case of Kas Peninsula (Turkey).

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Engaging non-scientists to survey ecosystems, called participative science, has been adopted worldwide. For the first time, this was applied to monitor fish assemblages in the Kas Peninsula, Turkey, an area known for its important Lessepsian fish populations. For three years (2004, 2007 and 2010), fish assemblages were surveyed using underwater visual census by transect method. A total of 28 species was observed, six of which are Lessepsian species. Results show a significant increase in the abundance of Lessepsian species over the study period. In 2004, they represented 34% of the total abundance, increasing to >61% in 2010. Differences were observed in the progression of populations between two invasive herbivores, *Siganus rivulatus* and *S. luridus* (Siganidae), and two native herbivores, *Sparisoma cretense* (Scaridae) and *Sarpa salpa* (Sparidae). The siganids were recorded each year in all sites whereas *S. cretense* was regularly observed in fewer numbers while *S. salpa* was rarely censused. *Siganus* spp. abundance increased three-fold in 6 years while *S. cretense* and *S. salpa* remained stable. *S. rivulatus* was the most abundant among the four species. Its competitive superiority may be due to its greater adaptability to fluctuating environmental conditions and biological traits, e.g. rapid growth, earlier sexual maturity, high fecundity. Because siganids are herbivores, their presence can strongly impact algal ecosystems. It is then important to follow their spreading, but this can be challenging due to the limited number of scientists. Adopting participative science is thus a useful strategy to monitor the spread of invasive species in the Mediterranean.

Keywords : Non indigenous species, Citizen science, Monitoring



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

**Morphological characteristics of bandtooth conger
Ariosoma balearicum leptocephali in the Adriatic Sea**

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Eight leptocephali of the bandtooth conger *Ariosoma balearicum* (Delaroche, 1809) were collected with small mid-water trawl net in September 2011 during the monitoring project PELMON in the open waters of the middle Adriatic. Detailed description, including morphometric measurements and meristic counts are presented. This represents the first record of *A. balearicum* leptocephali in the Adriatic Sea.

Keywords : Congrid leptocephali, Biometry, Adriatic sea



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Poster

Heterochronies in skull development of Lake Tana large African barbs (*Labeobarbus*; *Cyprinidae*; *Teleostei*)

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Large African barbs (genus *Labeobarbus*) of Lake Tana (Ethiopia) form a species flock, i.e. a diverse group of closely related sympatric forms/species in an isolated area, which includes 15 species differing in biology, ecology, and morphology, including skull proportions. It's suggested that the Tana species flock has a monophyletic origin from *L. intermedius* and originated recently about 15 thousand years ago. The most probable mechanism of such explosive evolutionary transformation are considered heterochronies, i.e. changes in developmental rate and timing leading to changes in definitive morphology. Both major global heterochronies, pedomorphosis and peramorphosis, are proposed to contribute to morphological diversification of Tana barbs. The early development of chondro- and osteocranium was studied in four species of Lake Tana barbs: i) *L. intermedius*, a proposed ancestor of Tana species flock, ii) *L. brevicephalus* is likely a pedomorphic species, and iii) *L. megastoma* and *L. macrophthalmus* are regarded as the peramorphic species. The general sequence of cranial cartilages and bones appearance is the same for investigated barb species. However, they differ greatly in the temporal pattern of skull bones appearance. The osteogenesis of *L. brevicephalus* progresses gradually: cranial bones appear in a gradual manner. The osteogenesis of *L. intermedius*, *L. megastoma* and *L. macrophthalmus* is represented by two peaks of bones appearance separated by a period of stasis – a stage when skull continues to grow whereas new skull bones do not arise. The stasis period in two peramorphic species is longer than in ancestral. The chondrocranium develops in investigated species without any temporal differences. Thereby, as compared to *L. intermedius*, the bony skull development in *L. brevicephalus* is accelerated, whereas, bony skull development in *L. megastoma* and *L. macrophthalmus* is retarded relative to chondrocranial development. These differences in the temporal pattern of craniogenesis are proposed to account for different cranial proportions displayed by these barbs. Consequently, obtained results favor the assumption that heterochronies are the most probable mechanism of the explosive divergence of Tana barbs.

Keywords : Heterochrony, Skull development, Large african barbs



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

**Ploidy level of progeny from the crosses between
allotriploid *Cobitis* females and males of the spined loach
Cobitis taenia (Teleostei, Cobitidae)**

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Some species of the genus *Cobitis* through hybridization processes followed by genome duplication during meiosis, produce polyploidy occurring naturally mainly as gynogenetic triploid females. Most of the Polish populations of *Cobitis* are mixed, diploid-polyploid and composed of the spined loach *C. taenia* and/or the danubian loach *C. elongatoides* and their allopolyploid taxa; triploid females and tetraploid males and females. Numerous occurrence of triploid females with very low number of *Cobitis* males in the mixed populations seems surprising.

Under this study we have made several experiments of crossing between triploid females dominated in the diploid-polyploid population in the Bug River with co-existing *C. taenia* males and with males from an exclusively diploid population. All the parental females and males were injected with human chorionic gonadotropin hormone (hCG). Hatching success and early survival of progeny up to yolk sac absorption was observed; the mortality was relatively low, about 20 %. The ploidy levels of all the loaches were determined according to karyotypes. The progenies before karyotyping have been reared to attain at least 30 - 40 mm of the body length. The chromosomes of at least 20 individuals resulted from each crossing were analyzed. Chromosome counting revealed that most of them were triploids ($3n = 74$) with the karyotypes similar as parental $3n$ *Cobitis* females. The results seem to support gynogenesis as a mode of reproduction of triploid *Cobitis* females. However, some of the individuals resulted from crosses were tetraploids with the modal number of $4n = 98$ chromosomes. Additionally the ploidy level of some samples of progeny was determined according to DNA content using flow cytometry. In conclusion, we proved that some of oocytes produced by $3n$ *Cobitis* females (from the population in the Bug River) may be fertilized by the sperm of *C. taenia* and develop into tetraploid individuals.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Oral

The problem of the fish species (on example families Coregonidae, Cyprinidae, Gobiidae)

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The problem of the species is one of the most important problems of biology. The search for practical criteria for delimiting species was always topical. In now time many concepts exist in biology for explaining species meaning. However no one of the many species concepts is universal and we can see examples both confirming, and disproving them. The reason of it is attempt to prove specific independence of the group of organisms on one feature. Moreover, the use of molecular-genetic methods allowed to obtain the expanded field of the new data for describe species. All these facts involve the peak of splitting wave in description of species diversity. In this report we analyzed some examples of the discrepancies for the base species concepts that we revealed in our experimental works and by analyzing the literature. For example hybridization process detection between roach (*Rutilus rutilus*) and bream (*Abramis brama*) and also between many species of family Coregonidae disturbs the conditions of the biological species concept (BSC). By genotypic cluster species concept (GCSC, Mallet, 1995) the species are group of organisms that recognized by existence of hiatus of the morphological or genetic characters from other similar groups of organisms. Indeed for coregonine fishes many discrete groups can be described with using various morphological, physiological and ecological traits. However molecular-genetic analyses did not reveal any genetic differentiation between many groups of coregonine fishes that exactly differed by morpho-ecological features. Phylogenetic species concept (PSC, Cracraft, 1989) does not offer an accurate way of measurement of scale of differences between two monophyletic clusters of the organisms. In this case even one nucleotide substitution discriminating two groups of specimens from one population give us an opportunity to consider each of them as the monophyletic cluster on a dendrogram. Thus meaning species more exist in the mind of investigators than in nature. We supposed that useful species concept must take into account the complex of features of organisms (morphological, physiological, ecological and genetic) and dynamic character of groups of organisms which we call species.

This work is financially supported by the RFBR Grant N° 11-04-00697-a.

Keywords : Species concepts



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Vendace of Solovetskii Islands (the White Sea) as a key for a problem of taxonomical position of northeast Europe ciscoes

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The northeast of Europe is traditionally considered to have extensive area where transition between two forms (species) of the ciscoes, *Coregonus albula* (vendace) and *C. sardinella*, have been observed. One of the first mentions of presence in the northeast of Europe the Siberian ciscoes reported by L.S. Berg (1916). New form of ciscoes finding in White Sea near Solovetskii Archipelago was named as *C. sardinella marisalbi* Berg. But subsequent investigations cast doubt on Berg's point of view because the ciscoes with vendace's morphological features were finding in the island's lakes. Moreover, it became known that many vendace's invasions were carried out by monks of Solovetskii monastery in 19 century. Notice, that before the middle 19 century any references about ciscoes in lakes of island were not made. For the purpose of correct understanding of the nature of a transitive zone between European and Siberian ciscoes we have carried out research of ciscoes' populations from Great Solovetskii Island as typical habitat of subspecies *C. s. marisalbi*. During 1995-2009 we have collected 344 ciscoes from five lakes of island and studied diagnostic morphological traits for the two species. In addition, for 135 specimens the polymorphism of the creatine kinase isoloci and ND-1 fragment of mitochondrial DNA was analysed. Accordingly one of the main taxonomical characteristics, number of the vertebrae, ciscoes of Solovetskii Island have intermediate position between *C. albula* and *C. sardinella*: mean number of vertebrae are 57-58. Type specimen of ciscoes that was used for describing subspecies *C. s. marisalbi* has 59 vertebrae. However molecular-genetic markers did not reveal any differences ciscoes of Solovetskii Island from typical vendace: all specimens had characteristic for *C. albula* allele of creatine kinase (CK-A*100) and widespread in populations of vendace haplotypes mtDNA (E).



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

We consider that morphological characters are strongly depending on environmental conditions. Indeed, water temperature at which embryos develop has an effect on the number of vertebrae: decreasing of water temperature lead to increasing of the number of vertebrae. Thus these facts allow concluding, that morphological criteria do not make it possible to differentiate between two ciscoes because they substantially depend on environmental conditions. On the other hands, a presence the populations with intermediate features is a strong argument for combining *C. albula* and *C. sardinella* into a single species. In this case European and Siberian ciscoes can be considered as ecological forms (lake and river) of one Eurasian species.

Keywords : Vendace, Least cisco



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Some features of the mtDNA cytochrome b gene's polymorphism of the tubenose goby (*Proterorhinus sp.*, Pisces: Gobiidae) of Ponto-Caspian basin

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Our investigation embraced 21 populations of tubenose goby from Ponto-Caspian basin including one of the most northern invasive populations of the Rybinsk reservoir (Volga Uppers). Polymorphism was screened at sequence 365-bp fragment of the mitochondrial DNA cytochrome b gene (Cyt-b mtDNA) that is polymorphic in Gobiidae. Moreover, we quantified the morphological variability of tubenose gobies using meristic and morphometric characteristics. A total 10 Cyt-b gene haplotypes were revealed by sequencing; 50 nucleotide positions (13.7 %) were polymorphic. All haplotypes were clustered by maximum likelihood analyses in two main clades. The first clade combined haplotypes detected in tubenose goby populations from Odessa Bay (Black Sea). The second clade included haplotypes from very large geographical region: from Caspian Sea to Volga Uppers and Danube River. This clade had not discrete structure, but interesting feature was observed into it: basal haplotypes were revealed in populations from Caspian Sea, water bodies of the Don and Volga basins while distal position occupied haplotypes from rivers Dniester, Dnieper, Danube, Mzymta (all this water bodies belong to Black Sea basin). Haplotype network supported result of the maximum likelihood cauterization: haplotypes from Odessa Bay population were separated. Moreover, distances between this group and other groups of the tubenose goby haplotypes were comparable with interspecific distances. Populations of the tubenose goby from Volga and Don basins were characterized more high frequency of the haplotype H1. This haplotype was revealed also for one of three specimens from Caspian Sea. Haplotype H2 was characteristic for Dnieper populations of the tubenose goby only. Haplotype H4 was found in populations of Dniester, Danube and as well as was characteristic for one of the twelve tubenose gobies from Dnieper. Thus, the data under consideration allow reconstructing some features of phylogeography of the tubenose goby of the Ponto-Caspian basin. So, population of Caspian Sea is more ancient and is characterized by higher level of variation. Radiation of the tubenose goby from Caspian Sea basin has been occurring in two directions: 1. more ancient expansion to Dnieper-Dniester-Danube basins; 2. colonization of the Don-Volga basins that took place in recent historical time. At the same time, morphological data did not reveal any accurate differentiations between tubenose gobies from different basins and water bodies. Notice also that hypothesis by Nielson&Stepien (2009) about existence "freshwater" and "marine" species is not supported by our data.

Keywords : Tubenose goby, Phylogeography



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Phylogeography and phylogeny of the Altai osmans (*Oreoleuciscus* sp., Pisces: Cyprinidae) of the water bodies of Mongolia

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The genus *Oreoleuciscus* (Pisces: Cyprinidae) is endemic to western Mongolia and Tuva. Taxonomy of the genus *Oreoleuciscus* is controversial: during last decades different researchers referred this genus to the distinguish lineages of family Cyprinidae — aspinine, leuciscine and phoxinine. However in recent years close relation of Altai osmans to Amur minnow (*Phoxinus lagowskii*) was shown by molecular-genetic methods. At the same time phylogeography of populations *Oreoleuciscus* sp. from Western Mongolia are unknown. Thus, the main aim of this study was to clarify of features of the population structure and radiation for this group. For 25 specimens of Altai osman from 16 inland water bodies of Mongolia the nucleotide sequences of cytochrome b gene (Cyt-b) mitochondrial DNA (mtDNA) were determined; 17 haplotypes mtDNA were revealed. These haplotypes were discriminated to two major clusters, designated as A and B. Cluster A comprised specimens of *Oreoleuciscus* from the Valley of Lakes (the Goby Lakes Valley). The cluster B consisted of two subclusters; one of them (B1) included populations *Oreoleuciscus* of the Hollow of the Big Lakes (the Great Lakes Basin) and lakes of the Big Altai Range. The second subcluster (B2) combined specimens of *Oreoleuciscus* from Hollow of the Lake Uvs, some isolated lakes of the Northwestern Khangay and water bodies of the Arctic Ocean Basin (Selenga and Orchon basins). Genetic differentiation (p-distance) between clusters ranged from 0.018 to 0.048; populations of Valley of Lakes were more differentiated from other. According to Kartavtsev&Li (2006) these estimates correspond to the sibling species level. On the basis of evolutionary rate in Cyt-b gene for Cyprinidae the time of divergence of the population's groups of Altai osman was estimated. We revealed that the populations of the Valley of Lakes had diverged from the populations of the Hollow of the Big Lakes, lakes Big Altai Range and Arctic Ocean Basin approximately 5.5 million years ago (MYA). Time of divergence of the populations of the subclusters B1 and B2 equals 3 MYA. Our estimated divergence dates are in full agreement with the fossil record of Khyar-gas Lake (Khirgis-Nur) strata series (Sychevskaya, 1983). So, the basic events of expansion of the genus *Oreoleuciscus* were connected with geological history of territory of Mongolia, in particular, orographical factors and volcanic activity. At this moment three groups of Altai osman populations are distinguished in inland water bodies of Mongolia.

Keywords : Altai osman, Phylogeography, Phylogeny



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Estimation of the exploitable biomass and F0.1 of sardine (*Sardina Pilchardus*, Walbaum, 1792) along the central Algerian coast

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During the past 20 years, sardine (*Sardina pilchardus*, Walbaum, 1792) production continues to decline to reach 5600 tons in 2011, in the central part of Algeria between Cherchell and Bejaia. We found it useful to study the state of the exploitation of the sardine, and to adjust its production to $F_{0.1}$. The biological study of *S. pilchardus* was conducted between 2010 and 2011 on 4776 individuals, all sexes combined, with sizes ranging from 7 to 21.5 cm. Following FAO recommendations, the VIT software (LLEONART and SALAT, 1997) was used to determine biomass, virtual population analysis (VPA), and yield or productivity per recruit. The mean catch size, estimated at 12.8 cm, is higher than the stock size estimated at 10.4 cm. Furthermore, the exploitation of sardine mainly targets individuals that are 14.5 cm in size, and have reached their size of first sexual maturity ($L_{50} = 12.3$ cm, both sexes). The analysis suggests that young immature individuals are spared from overexploitation by recruitment overfishing. The exploitable mean biomass of the sardine was estimated at 3339,6 tons by the V.P.A. The yield (production) per actual recruit ($Y/R = 7.317$ g, Factor of Terminal Fishing Mortality = 1) is very close to the MSY or (7.334 g, Factor of Terminal Fishing Mortality = 0.88). This result indicates that the sardine stock is in a state of overexploitation. The biomass per actual recruit ($B/R = 4.363$ g), which refers to the mean annual biomass of survivors as a function of fishing mortality, is lower than the maximum sustainable biomass ($B_{max}/R = 4.721$ g). Given the state of over fishing of the sardine stock in the central part of the Algerian coast, an adjustment of the ratio Y_{actual}/R is recommended. To do this, fishing effort is set at $F_{0.1}$, and the values obtained for $Y_{0.1}/R$ and $B_{0.1}/R$ then correspond to 6.764 g and 7.326 g, respectively. Fishermen are more interested in the total production of the exploitable stock than the imaginary yield per recruit. To compute this value, we simply multiply the number of recruits ($R = 765,356,177.82$) by $Y_{0.1}/R$. In conclusion, by adopting a precautionary approach, we recommend the adjustment of the annual production to 5,176.9 tons, a decrease of 7.6 % from the actual production (5,600 tons). Applying this recommendation would allow the preservation of the *S. pilchardus* in the central part of the Algerian coast and ensure its sustainable production.

Keywords : Sardine, Algeria, $F_{0.1}$



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Functional morphology of the feeding apparatus in preleptocephalus larvae in European eel (*Anguilla anguilla*): getting ready towards feeding

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The European eel (*Anguilla anguilla*, Linnaeus 1758) is faced with a severe decline in its natural populations over the last 30 years. In order to decrease the pressure on these populations, a lot of effort is recently put in obtaining a complete artificial breeding program for this endangered species. Unfortunately, the artificial reared eel larvae are, at present, unable to stay alive for more than three weeks after hatching. To gain some information on the feeding capacities of these larvae at the onset of active food uptake, a functional morphological analysis of the feeding apparatus of these extremely small larvae (< 1cm) is performed using a graphical 3D-reconstruction of the musculoskeletal system. Based on 3D data of joints, levers and muscles insertions, as well as muscle data, biting performance is modeled to predict theoretical bite force. Preliminary data on kinematics (from video recordings) of jaw and hyoid movements in pre-feeding larvae demonstrates a rather limited ability of jaw movement. Therefore, small and soft food items are suggested to be preferable in both natural and artificial environments, where biting through piercing of prey items seems unlikely.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Electric organ discharge and sound production patterns in catfishes of the genus *Synodontis* (family Mochokidae)

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Mochokid catfishes are one of eight catfish families (order Siluriformes) with a modified transverse process of vertebra four (*Müllerian ramus*) and an associated protractor muscle, collectively termed the elastic spring apparatus (ESA). The Müllerian ramus of the ESA is attached to the anterior swim bladder and is known to be involved in sound production in several catfish families. Most sound production descriptions from the speciose mochokid catfish genus *Synodontis*, however, detail stridulatory sounds produced by the pectoral spine, while fewer accounts of low frequency swimbladder sounds exist. Several previous studies documented electrical discharges (EODs) from several *Synodontis* species and found evidence for an electric organ function of the protractor muscle. We examined further the role of EOD formation and sound production in additional *Synodontis* species by conducting experiments with simultaneous acoustic and electrical recordings from *Synodontis euptera*, *S. nigriventris*, and *S. robbianus*. EODs were produced by all three species. *Synodontis euptera* produced spike EODs while hand-held, *S. nigriventris* produced burst EODs only during social interactions with conspecifics, and *S. robbianus* produced spike and bursts EODs during social behavior, and less frequently spontaneous spikes. Spikes were characterized by a single prominent, phase dependent head-positive pulse and low fundamental frequency f_0 , *S. robbianus* (mean \pm s.e.) 51 ± 6.5 ms, f_0 105 ± 20 Hz, and *S. euptera* 95 ± 16 ms, f_0 33 ± 4.1 Hz. Bursts comprised a series of head-positive bipolar pulses of varying duration and low f_0 , and varying amplitude: *S. nigriventris* 26-299 ms, 56-105 Hz, and 154-128 μ V, *S. robbianus* 38-278 ms, 82-148 Hz, and 3-17 mV. The number of cycles per burst duration was correlated with fundamental frequency (*S. nigriventris* $r=0.88$, *S. robbianus* $r=0.61$). Bursts were characterized by strong harmonics ($\geq 99^{\text{th}}$ percentile of spectral energy) and first harmonics were present in 93% of *S. nigriventris* and 53% of *S. robbianus* burst EODs. Weak, low frequency, non-stridulatory sounds were recorded when fish were hand-held and usually when pectoral spines were held to prevent stridulations. Sounds from all species were of relatively low peak frequency (300-400 Hz) and were emitted as a series of short pulses (3-20 ms) or sometimes, in *S. euptera* and *S. robbianus*, as continuous growls (100-500 ms). Further physiological investigations will be conducted to verify the production of low frequency sounds and to examine the putative role of the protractor muscle in EOD and sound generation in *Synodontis* spp.

Keywords : Electric communication, Acoustic communication, Swimbladder muscle



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Invited speaker

Fish systematics today: Can't see the wood for the trees ?

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The ordering of fish taxa into a system is a scientific task with a long tradition that started centuries ago. Various systems were created by different authors usually based on a selection of criteria considered the most important. Since 1966, the publication of Hennig's *Phylogenetic Systematics*, the system considered ideal by the vast majority of systematic ichthyologists is a phylogenetic one, in which taxa are grouped according to their genealogical relationships. While the goal seems to be universally accepted, the path to reach it is controversially debated. Up to the 1980's systematic ichthyology was based almost exclusively on morphological characters. With the ability to sequence chunks of DNA cost effectively and with little effort molecular systematics has rapidly gained popularity. Molecular systematic hypotheses are being generated for an ever growing number of fish taxa at all systematic ranks. This 'revolution' has shifted the emphasis from the detailed study of characters towards the production of the phylogenetic tree. For some fish taxa a multitude of different phylogenetic trees are now available and a decision which one brings us closer to the truth is impossible. A good example of this dilemma are the anatomically very interesting, highly-derived, miniature Asian cyprinids discovered during the last few decades. I will use them to illustrate the issue of losing sight of the wood because of too many trees.

Keywords : Phylogenetic systematics, DNA sequences, Morphology



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Ontogeny and homology of the skeletal elements that form the sucking disc of remoras (*Teleostei*, *Echeneoidei*, *Echeneidae*)

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Fishes of the echeneoid family Echeneidae are characterized by a complex, adhesive, ovoid suction disc on top of the head with which they attach themselves to various marine hosts, including other fishes, sea turtles, and cetaceans. The moveable parts of the disc are serially arranged, bilaterally paired, rectangular, spinulose laminae that can be raised and lowered like the shutters of Venetian blinds; these laminae are collectively encircled by a thick, marginal “lip” of flexible connective tissue. Since its earliest descriptions, there has been general agreement that the bony components of the echeneid disc are those of a highly modified, spinous dorsal fin that has migrated from the usual postcranial location to a supracranial one and would thus comprise the proximal, middle and distal radials of spinous dorsal pterygiophores and dorsal spines. Most early authors (e.g., Gunther, 1860; Beck, 1869; Storms, 1888; Regan, 1912), who studied the anatomy of the disc proposed that the bilaterally paired laminae represent two halves of a transformed spinous ray, although there was considerable disagreement about exactly how this transformation occurs. Surprisingly, however, three recent papers (O’Toole, 2002; Fulcher and Motta, 2006; Richards, 2006) rejected the earlier hypotheses that the paired disc laminae are dorsal spines and proposed instead that they represent “a laterally expanded distal pterygiophore, while the medial spine is a reduced dorsal-fin spine.” An ontogenetic perspective is clearly critical to ultimate resolution of this long-standing homology question, but echeneid larvae of sizes at which the bony components develop and elucidate the precise ontogenetic trajectory through which this extraordinary transformation occurs are rare in larval fish collections. We managed to cobble together a series of larval and juvenile echeneids ranging from 9 to 28 mm SL from historical collections from the Far Seas Research Laboratory in Tokyo and the NMFS Southeast Fisheries Center in Miami. With this series, we revisited the question of the homology of the different skeletal parts that form the disc using an ontogenetic approach, comparing the initial stages of development of the disc with early developmental stages of the spinous dorsal fin in a representative of the morphologically basal percomorph *Morone*. Our results confirm that the paired disc laminae do indeed represent two halves of a transformed spinous ray, and more importantly, elucidate the precise ontogenetic trajectory through which this extraordinary transformation occurs, which demonstrates that the most recent hypotheses, published in 2002 and 2006, are erroneous.

Keywords : Echeneidae, Ontogeny, Homology



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Oral

Effect of *Escherichia coli* lipopolysaccharide on immunity of tra catfish (*Pangasianodon hypophthalmus*)

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Lipopolysaccharide (LPS), one component of outer membrane protein of gram negative bacteria, were reported to induce a number of biological effects in fish including stimulation of the immune system. In the present study, tra catfish (*Pangasianodon hypophthalmus*) were injected with different concentrations of *Escherichia coli* LPS (3 mg, 15 mg and 45 mgLPS/kg fish) and then challenged with the bacteria *Edwardsiella ictaluri* to find out how the LPS affects the tra catfish immunity for protecting it against the bacteria. Plasma cortisol and glucose, measured as stress biomarkers, were rather low and did not differ significantly among treatments ($p>0.05$). On the other hand all LPS treatments induced significant differences in blood cell count and immune variables such as plasma and spleen lysozyme, complement as well as antibody titre, except total red blood cell ($p<0.05$). After challenged by *Edwardsiella ictaluri*, accumulated mortality of LPS injected fish (3, 15, 45 mg LPS/kg fish) and control were 23.4, 32.8, 37.7 and 52.5%, respectively. The result of immune assay also showed higher values of LPS treated animals than the control and the best results were obtained in fish treated with 3mg LPS/kg. An increase of 1.5-2 folds were seen in the lysozyme activity of LPS treated fish compared with controls. Complement activity in fish from LPS treatments was also higher (1.6-2.5 folds) than in control fish. The total of antibody was enhanced in LPS injected fish (96.5-123.02 mg/ml) compared with control fish (75.4 mg/ml). It could be concluded that injection of *E. coli* LPS in tra catfish could enhance some innate immune responses and increased protection the fish from bacterial damages.

Keywords : Lipopolysaccharide, Immunity, *Pangasianodon hypophthalmus*



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Past, present and future in extreme habitats: evolutionary history, genetic structure and perspective of *Aphanius fasciatus* along the Adriatic coast

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Differences in the levels of genetic substructuring in marine, anadromous and freshwater fishes have already been documented. However, data on the genetic structure and evolutionary history of fish species inhabiting specific habitats, such as hypersaline water bodies are still scarce. Suitable model species for investigating evolution in such waters is the South European Toothcarp, *Aphanius fasciatus* (Valenciennes, 1821), a cyprinodont that is distributed over the central and eastern coastal zone of the Mediterranean. In order to enable better understanding of the evolutionary course in such extreme habitats, the phylogenetic relationships and genetic structure of several *A. fasciatus* populations inhabiting hypersaline waters along the eastern Adriatic coast have been analyzed. Phylogenetic trees constructed using maximum parsimony and Bayesian methods, as well as median-joining and statistical parsimony networks based on two genetic markers with different mutation rates revealed more complicated intraspecific structure than expected, whereas measures of genetic polymorphism detected different levels of genetic diversity in various populations. Insight into the past history, together with better understanding of the present status of *A. fasciatus* enabled more precise prediction of its future alterations, which was conducted by population viability analyses.

Keywords : South european toothcarp, Genetic polymorphism, Evolution



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

**Ancient connection among rivers and watersheds revealed
from the evolutionary history of the genus *Telestes*
(*Actinopterygii*; *Cypriniformes*)**

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The genus *Telestes* Bonaparte, 1837 comprises primary freshwater, obligate riverine fishes that are adapted to moderately cold waters. Its distribution has not been influenced by human alteration, so it represents suitable model for investigating evolution of European freshwater fish taxa. The phylogenetic relationships of *Telestes* with other genera inside the Leuciscinae subfamily have already been investigated and several geological events have been proposed to shaped its evolutionary history (in particular the Alpine orogenesis, the uplifting of the Dinarides, the Messinian salinity crisis and the Pleistocene glaciations). However, due to the lack of the comprehensive and detailed investigation of the *Telestes* phylogeography and evolution throughout its distribution range, there are still some controversies regarding its evolutionary course. In order to reveal differences in genetic structure of each *Telestes* species and to discover details of their evolutionary paths, we have analyzed samples of all *Telestes* species throughout their distribution ranges. Phylogenetic reconstruction based on several molecular markers was conducted using maximum parsimony, maximum likelihood and Bayesian inference, whereas Nested clade analysis was carried out in order to make inferences about the processes underlying phylogeographic structure. The obtained results revealed interesting evolutionary history of the genus that affirms complex geological history of the Dinaride region. On the other hand, differences in intraspecific genetic structure enabled detection of local events that shaped the unique evolutionary course of each species and created differences between them.

Keywords : *Telestes*, Phylogeography, Dinaride region



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Integration of fish fossil data into phylogenetic
and comparative studies

Oral

The Gondwanan history of galaxiid fishes : inferences from molecular clocks calibrated using fossils and known biogeographic events

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The aim of this study was to determine the contributions of Gondwanan vicariance and marine dispersal to the contemporary distribution of galaxiid fishes. This group has been central in arguments concerning the roles of dispersal and vicariance in the Southern Hemisphere, as some taxa have marine life history stages through which trans-oceanic dispersal may have been facilitated, yet other galaxiids are entirely restricted to freshwaters. Biogeographic hypotheses of Gondwanan vicariance and marine dispersal were tested for the first time using estimates of lineage divergence times derived from molecular clocks calibrated using fossils and dated biogeographic divergence events. Phylogenetic relationships were reconstructed from 4,531 mitochondrial and nuclear nucleotide characters, and 181 morphological characters, across 53 of the 56 presently recognised species. Trans-oceanic disjunctions were exhibited at 16 nodes, but only three predated relevant continental fragmentation events; furthermore, ancestral distribution inheritance scenarios for two of these nodes reflected cladogenesis within rather than between Gondwanan landmasses, and ancestral marine dispersal capability could not be rejected for all three. Instead, the evidence surveyed suggest that Gondwanan vicariance occurred twice, but in both instances was preceded by marine dispersal between landmasses, and in at least one instance was initiated by the cessation of marine dispersal subsequent to continental fragmentation. All other trans-oceanic disjunctions reflect marine dispersal, and Gondwanan vicariance appears to have been preceded by marine dispersal in the few instances where it may explain contemporary galaxiid distribution, such that these biogeographic mechanisms may sometimes have a synergistic relationship.

Keywords : Molecular clocks, Fossils, Biogeography



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Oral

Neural Innovations Trigger Explosive Diversification of Electric Fishes

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Animal communication signals are critical for species recognition and mate choice. As a result, evolutionary divergence between communication signals can promote speciation and reinforce reproductive isolation between existing species. However, the potential for signal divergence is limited by the abilities of senders to generate different signals, as well as the perceptual abilities of receivers to detect different signals and differentiate among them. Here we describe dramatic increases in the rates of signal evolution and species diversification that are related to evolutionary change in the electrosensory and electromotor systems of African mormyrid fishes. These fishes communicate by generating a pulse-type electric signal that is species-specific and often sexually dimorphic, and playback experiments in a few species have demonstrated that electric signals are used for species recognition and mate choice. These signals are detected by epidermal electroreceptors followed by signal processing within the exterolateral nucleus (EL) of the midbrain. We analyzed the gross anatomy of the midbrain in 26 species of mormyrids and discovered two distinct patterns of EL organization: a relatively small and homogenous EL vs. a relatively large EL that is differentiated into separate anterior and posterior subdivisions (ELa/ELp). This neuroanatomical difference is related to the spatial distribution of electroreceptors on the body surface: all species with an enlarged ELa/ELp have electroreceptors distributed all over the head and body, whereas the majority of species with a small EL have electroreceptors limited to three distinct clusters on the head. Behavioral playback experiments revealed that species with an enlarged ELa/ELp can detect electric signal variation, whereas species with a small EL cannot. Phylogenetic reconstruction suggests that EL is the ancestral character state for mormyrids and that ELa/ELp has evolved twice independently. In one of these two lineages, called 'clade A', evolutionary change in the electromotor system that controls electric signal production led to an increased capacity to generate signal variation. We hypothesized that the combined ability to both generate and detect a wider range of signal variation would lead to increased rates of signal evolution and species divergence.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Indeed, we found that the rate of signal evolution in 'clade A' is over ten-times faster than that of other mormyrids, and that the rate of species diversification in 'clade A' is three- to five-times faster than in closely related outgroup lineages. These results support the general hypothesis that neural innovations leading to novel sensory or motor abilities can lead to increased diversification. Current studies are focused on the cellular and network mechanisms that establish these perceptual differences, as well as the selective pressures responsible for the origin of these neural innovations.

Keywords : Animal communication, Sensory coding, Speciation



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Phenotypic plasticity of the South European Toothcarp *Aphanius fasciatus* in the Venice lagoon

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The South European Toothcarp *Aphanius fasciatus* (Valenciennes, 1821) is a small euryhaline killifish, inhabiting shallow brackish waters in the central and eastern coastal zones of the Mediterranean sea. It is an estuarine resident, present commonly in lagoons and other brackish water ecosystems. In the Venice lagoon it is mainly found in salt marsh systems, but it also inhabits small artificial ditches within lagoon islands. Preliminary analysis of population genetic structure conducted within the Venice lagoon suggested that genetic polymorphism is very low, ascribing all the fish to one population. Therefore the aim of this study is to investigate the phenotypic plasticity expressed by *A. fasciatus* populations in response to the typical instability and the high spatio-temporal variability characterizing transitional water systems. Four sampling sites were chosen, including both natural and artificial habitats, differing in their structural characteristics, such as tidal regime and trophic richness. Fish were collected by one-year monthly samplings using a beach seine. All fish were photographed and then released, only a subsample was preserved for laboratory analyses. Phenotypic plasticity was studied both in terms of life history traits and body morphology. Life history traits varied between the two main habitat types. In particular, fish from salt marshes produced a higher number of smaller eggs, whereas bigger and fewer eggs were found in the two artificial habitats. Morphometric analyses showed a relative homogeneity within the two natural salt marshes, while major differences were found in fish from the artificial ditches. Basically, fish from salt marshes showed a more elongated body compared to those from not tidally influenced artificial habitats, where body depth was higher. Results were discussed in the light of the effects of structural habitat properties on phenotypic diversification.

Keywords : Killifish, Lagoon, Phenotypic plasticity



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

The close relationship of Tetraodontiformes and Lophiiformes enlightened by the study of their soft anatomy

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Recent phylogenetic studies based on the comparisons of DNA sequences have shown that Lophiiformes (anglerfishes) and Tetraodontiformes (puffers, triggerfishes and sunfishes) were closely related while no morpho-anatomical work assessed this point. Dissections of fresh animals coupled with analyses of literature lead to show the existence of possible soft anatomy synapomorphies for Lophiiformes and Tetraodontiformes. Even if only few species were studied, anglerfishes, puffers, and triggerfishes share: i) rounded and anteriorly disposed kidneys, ii) a compact thyroid nested in a thyroidian sinus, iii) an abbreviated spinal cord, iv) clusters of supramedullary neurons in the rostral part of the spinal cord. These features are not present in taxa shown by molecular studies to be among the closest relatives to tetraodontiforms and lophiiforms (like sparids and caproids). The sharing of these unusual characters by these two groups might be synapomorphies supporting a close relationship between Lophiiformes and Tetraodontiformes. The present study shows both the importance of comparative anatomy and the necessity of correlations between morpho-anatomical and molecular works.

Keywords : Lophiiformes, Phylogeny, Tetraodontiformes



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Diet composition and feeding intensity of brown meagre *Sciaena umbra* Linnaeus, 1758 (teleostei, sciaenidae) in the gulf of Tunis

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Analysis of diet composition and feeding intensity of the brown meager (*Sciaena umbra* Linnaeus, 1758) was realised seasonally and according to the fish size in the Central Mediterranean sea (Gulf of Tunis).

Specimens were collected, monthly from October 2008 to September 2011 from the landings of the small-scale fisheries. In all, 272 stomachs of brown meagre measuring between 15.3 and 49.2 cm total length (TL) were examined.

The prey items identified in stomachs belong to six groups: Crustacea (Decapoda, Amphipoda, Isopoda, Mysidacea, Stomatopoda...), Annelida, Mollusca, Teleostei, Angiosperma and Algae.

118 stomachs were empty (43.4 %). This percentage varied throughout the year. The lowest feeding intensity was recorded in summer during spawning period (June – August), feeding activity increased in October and November. Coefficient of vacuity is lower for individuals smaller than 25 cm.

The Index of Relative Importance (IRI) was calculated to measure the trophic preference. According to this index, crustaceans were the main preys (%IRI = 99 %), in both the small and large size classes, whereas other prey groups had minor importance. Among the crustaceans, the most important taxon identified was decapods, which was present in 96 % of stomachs and represented 92 % of total prey weight. The others most categories of crustaceans were amphipods and isopods which occurred in 25 % and in 23 % respectively. Diet composition showed little seasonal variation, decapods were the most important prey in all season. Cannibalism has not been observed for this species. The brown meagre is an opportunistic predator, stomach contents were dominated by the benthic organisms.

Keywords : *Sciaena umbra*, Diet composition, Gulf of Tunis



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Mechanism of adaptation of *Protopterus annectens* (Owens, 1839) (Protopteridae) to the aridity of puddles in the Biosphere Reserve of Pendjari in Benin

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Searches in the dried sandbank at Sangoun village, not far from the puddle Bori of the National Park of Pendjari, allowed to find many nests of the fossorial fish *Protopterus annectens* (Lungfish of the family Protopteridae) and to describe its mechanism of adaptation to the aridity. The fish is endowed with a branchial and pulmonary organ of breath which allows him to live in the water or outside the water in difficult conditions. When waters become very low, the fish enters into the mud and locks itself into a cocoon which it hides the inside of mucous secretions. The cocoon remains opened towards the outside by a communication near which the fish sticks its mouth to breathe of the air. When the plain is flooded of water, the fish goes out the mud to live normally in the water. A few studies exist today on the hibernation of this primitive fish actively research by the populations who consume them. It would be interesting to conduct detailed studies on this mechanism in the park. Such studies should identify suitable sites to develop ecotourism on the phenomenon while ensuring the conservation of the species.

Keywords : Lungfish, Hibernation, Pendjari



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Feeding habits of blackmouth catshark, *Galeus melastomus*, in the eastern Mediterranean

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The purpose of this study was to investigate the feeding habits of *Galeus melastomus* and estimate its TROPH index in the eastern Mediterranean Sea. A total of 250 specimens were collected from three different fishing areas in the Greek waters and their stomach content was recorded considering the major prey groups. Diets were studied taking into account sex, body size, fishing area and season. The gender of each specimen was recorded (140 females, 110 males) with total lengths ranging from 155 to 570 mm and the length – weight relation was calculated. Osteichthyes were found as the most important prey (42.3% in terms of IRI, Q = 971) with crustacean - natantia and cephalopods following as secondary prey. There were significant differences of prey selection and prey size among the studied groups although no differences were found between the diets of males and females. The body size was found to be the most important factor concerning prey selection. The small specimens consumed mainly osteichthyes while the larger ones preferred cephalopods and crustaceans. Moreover, it was estimated that this species can consume prey lengthen 46 % of its own length and weighted 39 % of its own weight. TROPH index was 3.39 ± 0.57 while breadth (B) and omnitority (OI) indexes were also considered.

Keywords : Blackmouth catshark, Feeding, Trophic level



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Poster

Blood biochemistry profile of softmouth trout *Salmo obtusirostris* from Jadro and Vrljika rivers in Croatia

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The objective of this study was determination and discrimination of biochemical data among two populations of softmouth trout (*Salmo obtusirostris*) from rivers Jadro and Vrljika, and brown trout (*S. trutta*) from river Gacka based on machine-learning methods. Fish were sampled by electrofishing. Blood samples for biochemical analyses were collected from all sampled fish by caudal vein puncture after anesthesia with MS-222. After blood sampling, all sampled fish were released back in the wild. Blood samples were collected in tubes coated with anticoagulant, centrifuged at 12,000 g for 60 seconds and the resultant plasma was frozen at -20°C for storage until the analysis a week later. The biochemical analyses of parameters, such as aspartate aminotransferase (AST), albumin (ALB), creatine kinase (CK), lactate dehydrogenase (LDH), alkaline phosphatase (ALKP), glucose (GLU), urea (URE), creatinine (CRE), total proteins (TP), triglyceride (TRIG) and plasma cholesterol (CHOL), were carried out using a SABA-18 auto-biochemistry analyser (AMS Analyzer Medical System, Rome, Italy). Analysis of blood biochemistry parameters in the present study used a number of machine-learning methods, including Naïve Bayes (NB), Decision Trees (C4.5), Random Forests (RF), Logistic Regression (LR), Support Vector Machine using Radial Basis Function kernel (SVM-RBF), and K-Nearest Neighbour (KNN). Results of the machine-learning models indicated that using three of the blood biochemistry variables simultaneously - urea, glucose, and albumin - is enough to discriminate accurately between different populations of trouts.

Keywords : *Salmo obtusirostris*, Blood chemistry, Croatia



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Condition and lipid content of chub mackerel, *Scomber colias* in Adriatic Sea

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The chub mackerel, *Scomber colias* Gmelin, 1789, is a pelagic, schooling fish species widely distributed in temperate and warm waters of the Atlantic, Pacific and Indian Ocean, as well as in the Mediterranean and the Adriatic Sea. Besides its importance in the food web, chub mackerel is also commercially important fish that is traditionally exploited in the Adriatic Sea by purse seiners. The main goal of this investigation was to provide information on condition and lipid content of this species as it was not previously investigated in the Adriatic Sea. A total of 4,189 chub mackerels were sampled randomly from commercial landings between January 1998 and December 2007. Samples were collected during the night, with artificial light; using a purse seine net with a stretched mesh size of 10 mm. Sex was determined macroscopically by shape, appearance and gonad structure. 1,085 of the analysed specimens were male, 1,611 were female and for 1,493 specimens, sex could not be identified. Amount of mesenteric fat in the visceral cavity was also determined macroscopically. Condition of *S. colias* was described with 3 condition coefficients (Fulton's, allometric and relative coefficient). To diminish length influence on fish condition, only specimens in length range between 20 and 30 cm were analyzed and presented as variations of condition during the time.

Fork length and weight of analysed specimens ranged from 10.1-39.1 cm (mean \pm SD: 23.8 \pm 4.68 cm) and 8.90-804.50 g (mean \pm SD: 164.49 \pm 102.70 g), respectively. Seasonality of the fat reserves as well as condition had been noticed in this investigation. Namely, during the warmer part of the year, precisely in spawning period, fishes were without fat reserves and condition coefficients (Fulton's, allometric and relative) were low - possibly due to fish usage of all available energy for maturing and releasing of its sexual products. The fattest fishes were found scarcely during the entire year although large quantities of chub mackerels were expressed during the colder months of the year. This could be due to swimming speed consuming the fat reserves or with conditions of poor nutrition during the winter when chub mackerel should be summing up the reserves. Females had shown lower values in all condition coefficients than males. After the spawning season, chub mackerel males accumulated fat more efficiently and faster than females.

Keywords : *Scomber colias*, Mesenteric fat, Condition



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Oral

Variability, structure and selection of MHCII B genes in *Chondrostoma toxostoma* and *Chondrostoma nasus* in hybrid zones

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To characterise the overall genetic diversity, population structure and selection processes in cyprinid fish, MHC genes of IIB class have been analyzed. As the model organism in this study, two congeneric cyprinids, the introduced *Chondrostoma nasus* and native, protected and endemic *C. toxostoma* that live in sympatry and form a hybrid zone in the Durance River (South France, Mediterranean Sea drainage) were studied. For the individual determination (pure species versus hybrid) all fish were genotyped for mtDNA (cyt b) and 41 microsatellite loci. The allelic variability in exon 2 of two MHCII B genes (*DAB1*-like and *DAB3*-like) representing the most variable region with the nonsynonymous sites specifying the peptide binding region was analysed in total of 229 individuals from eight different localities collected in the summer period of 2008, 2010 and 2011. Two approaches were applied to analyse MHC polymorphism: classical (combining cloning of PCR amplicon, CE-SSCP and Sanger sequencing) and modern ("cloning sequencing" by NGS - Roche 454 GS-FLX pyrosequencing technology, serviced by Beckman Coulter Genomics, USA). Pros and cons of both used methods were evaluated. The obtained sequence data were used for allele determination. The sequence analyses and the analyses of selection pressure were performed. The results reveal the non uniform allele expression within individuals, duplication of both studied loci (previously showed in several cyprinid species) and that the exon 2 of *DAB* genes is subjected to positive selection. The difference in the MHCII B profiles was found between allopatric and sympatric populations. Based on the hypothesis of parasite-mediated selection maintaining MHC polymorphism it could suggest the difference in parasite load between chondrostomes living in allopatric area and those living in hybrid zone. This study was funded by the Czech Science Foundation, project no. P505/10/1138.

Keywords : *Chondrostoma*, MHC, Parasite-mediated selection



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Poster

The effect of structure and morphology on the light transmissivity of the mineralized spines of lanternsharks

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In the darkness of the deep ocean a surprising diversity of organisms generate light to find food, communicate or avoid predation. The lanternshark, *Etmopterus spinax*, from one of the few families of luminous sharks, emits a blue glow from thousands of photophores embedded in its skin. *Etmopterus*, like most luminous and non-luminous dogfish sharks, possesses defensive, mineralized spines on the leading edges of its two dorsal fins; in this species, however, the spine tips appear to glow from photophores localized behind them. In order to characterize the interaction of *Etmopterus* spines with their light production we correlated light transmission properties with aspects of gross- and ultrastructural morphology from spines of closely-related luminous and non-luminous dogfish. Luminometry experiments —in which a laser of luminescence-wavelength was shone through spines— illustrate that *Etmopterus* spines transmit 60% of incident light, in contrast to only 10% through spines from a non-luminescent species (*Squalus*). In both species, the single light source was split into two components when passing through the spine, with those of *Etmopterus* oriented more anteriorly than those of *Squalus*. Quantitative modeling based on luminometry results, *in vivo* measures of light from spine-associated photophores, and *in situ* measures of ambient light indicate that spine-associated light would be visible from several meters away in the shark's natural environment. Species' difference in transmissivity is reflected in both the cross-sectional shape and mineral content of spines, quantified through microCT scans and backscatter electron imaging (SEM-BEI) of spines from several *Squalus*, *Etmopterus*, and outgroup species. Whereas the tips of all spines were comparatively highly mineralized, spines of *Squalus* exhibited an absolute higher level and more uniform distribution of mineral content. Also, in comparison with inverted heart-shaped cross-sections of non-luminescent species, cross-sections of *Etmopterus* spines are half-ovals, with flattened incident faces and convex refractive faces.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

A raised ridge on the spine forms an additional smaller ovular cross-section anterior to the spine's large primary chamber; we discuss and model the possibility of this ancillary chamber acting as a secondary lens and whether pressures of mechanical integrity for defensive purposes are competing factors with those for light transmission. These results, in demonstrating correlations between differences in gross-geometry, mineral content, and light transmissivity amount and orientation, support our hypothesis that spine-associated luminescence acts as a signal, warning predators away. The presence of distinct structural features associated only with luminescence, suggests that these features co-evolved, rather than spine morphology being pre-adapted for light transmission.

Keywords : Elasmobranch, Luminescence, Biomaterial



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Poster

Variations in brain morphology within and between populations of silversides

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Adaptive radiations of freshwater fishes are among the most important model systems in speciation research. Several ancient lakes harbour such radiations, offering ideal conditions for studying the role of different modes and mechanisms contributing to the rapid emergence of species diversity. The comparatively few studies available relating brain morphology to ecology in adaptive fish radiations strongly suggest that ecological selection pressure has influenced brain structure evolution, and own pilot data show that differences occur even among evolving, very closely related habitat specialists in Indonesian sailfin silverside fishes. The problem addressed here is that differences in brain morphology can be also due to plasticity during individual life histories. It is very important to determine whether differences in brain morphology are the result of behavioural phenotypes or whether different life styles of populations or species are the result of genetically determined differences in brain morphology. We investigated the brain of several silverside species with normal histological methods as well as with marker for specific neuropeptides to reveal differences in brain organization within a population and compared the pattern of variation to the one found in closely related species. There seems to be considerable variation especially in the size of the hypothalamus that may be related to differences in the individual life histories within a population. Consistent species differences in brain morphology are only apparent in more distantly related species. Species differences can also be obscured by the fact that there may be differences between sexes. The cerebellum, for example, is larger in females of *Telmatherina antoniae* than in males. Our results show that the brain is highly plastic even at the population level and that brain factors causing speciation can only be determined if they can be discriminated from neuronal plasticity due to different phenotypes.

Keywords : *Telmatherina*, Adaptive radiation, Brain morphology



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Red Listing Marine Fishes

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The IUCN (International Union for the Conservation of Nature) Red List Categories and Criteria are intended to be an easily and widely understood system for classifying species at high risk of global extinction. The aim of the system is to provide an explicit, objective framework for classification of a broad range of species according to their extinction risk. There are 9 Red List Categories including three threatened categories: Vulnerable (VU) when a taxon faces a high risk of global extinction; Endangered (EN) a very high risk of extinction; and Critically Endangered (CR) an extremely high risk of extinction. Since their adoption 1994, the Red List Categories have become widely recognized internationally and they are now used in a range of publications and listings by IUCN as well as by various governmental and non-governmental organizations. Until recently, Red Listings have been mostly of terrestrial and freshwater taxa but there are efforts underway to expand the Red Listing procedures to add 20,000 marine taxa to the Red List by the Global Marine Species Assessment (GMSA). Red Listing workshops have been held both regionally (Mediterranean, Eastern Tropical Pacific), by taxon, or regionally by taxon. About 10,000 marine species have been assessed since 2006. Habitat building primary producers such as mangroves, seagrasses, and corals have high levels of species in threat categories relative to other marine species, largely because of human impacts in the coastal zone. All species of sea turtles and a large proportion of marine mammals, sharks and rays, and groupers fall into one of the three threatened categories. Global assessments have been completed for groupers, butterfly fishes, angelfishes, Sciaenidae, hagfishes, surgeonfishes, triple fins, and damselfishes. Reef fishes such as butterflyfishes, angelfishes, wrasses and parrotfishes all have 5% or less of species in threatened categories despite the fact that they typically inhabit coastal areas partly because most of these colorful reef species are not heavily exploited for food. Groupers rely on degraded coastal habitats but a major threat is also heavy fishing pressure. Consequently, at 12% in threatened categories, groupers have much higher levels of threatened species compared to other reef-related fishes. Two thirds of the highly valuable and heavily fished species of tunas and billfishes are Least Concern and only 17% are in one of the three threatened categories. Heavy exploitation of tunas and billfishes is the primary threat to these species.

Keywords : Red list, Marine fishes, Conservation



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ethology

Oral

Implication of aggressive, submissive and reproductive sounds in the way of life of clownfishes

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Clownfishes are brightly coloured coral reef fishes well known for their mutualistic symbiosis with tropical sea anemones. These fishes live in social groups in which there is a size-based dominance hierarchy. In this structure where sex is socially controlled, agonistic interactions are numerous and serve to maintain size differences between individuals adjacent in rank. Clownfishes are also prolific callers whose sounds seem to play an important role in the social hierarchy. Agonistic interactions being involved in daily behaviour suggest how important acoustic communication might be in their way of life.

Recording the different acoustic behaviours indicated that sounds are divided into two main categories: aggressive sounds produced in conjunction with threat postures (charge and chase), and submissive sounds always emitted when fish exhibited an appeasement display (namely the head shaking movements). Both types of sounds showed size-related intraspecific variation in dominant frequency and pulse duration: smaller individuals produce higher frequency and shorter duration pulses than larger ones. Consequently, these sonic features might be useful cues for individual recognition within the group. On the other hand, no acoustic call was associated with courtship and reproductive behaviours.

Unlike other pomacentrids, sounds are not produced for mate attraction in clownfishes but to reach and to defend their breeding status, which explains why constraints are not important enough for promoting call diversification in this genus. However, acoustic signals seem to be an integral part of the peculiar way of life of clownfishes, although they are restricted to agonistic interactions only.

Keywords : Clownfishes, Sounds, Agonistic behaviours



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Diet of haplochromine cichlids is affected by environment and morphology in Mwanza Gulf, Lake Victoria

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We studied the diets and morphology of zooplanktivorous and detritivorous haplochromines at three locations, covering a distance of 60 km in Lake Victoria's Mwanza Gulf, (Tanzania). We found that location had a significant effect on diet, most probably related to the abundance of food items. In addition, the morphology had a significant effect on diet composition, suggesting that the species' attributes influence feeding of haplochromines to some degree, irrespective of the composition of food items in the environment. Moreover, the influence of morphological attributes is predictable and follows known relationships between morphology and feeding performance. We studied these relationships by collecting haplochromine cichlids by surface trawling in 2010-2011. More than 95% of these belonged to the zooplanktivorous and detritivorous groups, which, after the decline of haplochromines in the 1980s, have started to recover since the 1990s. Before the decline, both trophic groups had distinct diets with detritivores mainly feeding on detritus and phytoplankton and zooplanktivores feeding on micro-crustacean zooplankton. After the recovery, they are reported to have switched to a diet with bigger-sized and increasingly abundant prey such as shrimps and insects. Despite changes in morphology within both groups, they are still different, but it is unknown what the differential effect on diet of environment and morphology is. We studied 97 haplochromines (48 zooplanktivores and 49 detritivores), recorded their diet by estimating stomach fullness and volume percentage of food items and measured 21 morphological variables with a known relationship to feeding. Both groups fed on zooplankton and insects, but diets were still separable with detritivores feeding more on detritus. There was a significant environmental influence (3 locations) on diet: haplochromines fed more on insects and detritus in inshore areas than offshore areas of Mwanza Gulf. Binomial regression was used to analyse the different aspects of morphology on diet. We found that there was a significant influence of overall morphology (first and second principal components), as well as of specific morphological variables. Gill raker, mouth gape and protrusion characteristics were mainly related to a zooplankton based diet. Head, jaw and mouth gape characteristics were more related to a detritus based diet. Our findings suggest that, besides a strong environmental influence, morphology still affects feeding of zooplanktivorous and detritivorous haplochromines, despite the reported changed diets and changed morphology.

Keywords : Haplochromines, Morphology, Diet



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Oral

Trace elements concentration in otoliths of the European eel (*Anguilla anguilla*) : a proxy of environmental aquatic exposure to metals

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Aquatic organisms, namely fishes, accumulate trace metals from the environment into hard and soft tissues. The European eel (*Anguilla Anguilla*), for instance, as a catadromic species, presents a complex life cycle, in which individuals cross several habitats, from salt to freshwater grounds, including also estuarine brackish areas, potentially affected by anthropogenic activities. Some studies have reported high elemental concentrations in otoliths for aquatic contaminated areas, suggesting the use of the chronological properties of the otoliths for monitoring the quality of waters suspected of metallic contamination. However these studies are scarce, limited to a few fish species and generally inconclusive. One hundred and sixty wild individuals of *A. anguilla*, collected in Ria de Aveiro (North Portugal), were used to test the incorporation of some important metals (zinc, cadmium, copper and lead) into the otoliths, through absorption from the water, during a chronic exposure of 28 days. Prior to the experiments, yellow eels were subjected to an acclimation/quarantine period of 2 weeks. Individual experiments were carried out in aquaria of 50 liters under laboratory-controlled conditions (photoperiod, temperature and salinity). Exposure involved one control (without contamination) group, and 3 different ecologically relevant metallic concentrations (low, medium and high). A total of 10 individuals were used in each group (i.e. 5 fish in 2 replicates per concentration). Fish were daily fed (basal rate of 0.8% body weight) with mussels for human consumption. A static system with a water renewal rate of 80% every two days was used. An independent experiment, to estimate the otolith growth rate during the exposure period, was performed using a dye marker (tetracycline). This information was used to define the beam electron diameter (ICPMS-LA, 30 µm) used for otolith metal concentrations assessment.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Although our results suggest that the trace metal concentrations in the otoliths appear to increase from the lower to the higher tested concentrations, the obtained differences are not statistically significant. Furthermore there were no significant relationships between the otolith elemental and water concentrations. Our data indicates that water trace metal concentration has no significant effect on incorporation of Cu, Cd, Zn and Pb in otoliths of *A. anguilla*. However, these results should be interpreted with caution, since the obtained data were highly variable, and probably much of this variation is related to poor analytical precision, at such low concentrations, as a consequence of a small ablation spot size.

Keywords : Sagitta, Metals, Contamination



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Occurrence of encapsulated embryos of *Sympterygia acuta* (Garman, 1877) (*Chondrichthyes, Elasmobranchii*) in Southern Brazil (SW Atlantic)

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An important part of the evolutionary success of the elasmobranch fishes is associated with the complexity of their reproduction. The suborder Rajoidei is composed by oviparous skate species, such as *Sympterygia acuta*. This species is endemic from the Southwestern Atlantic coast and occurs from Brazil to Argentina. It is a single oviparous species laying encapsulated eggs on marine debris, where the complete embryonic development takes place. The morphology of the *Sympterygia* egg capsule is unique because of the presence of extremely long (up to 50 cm) tendril-like posterior horns. Egg capsules are fixed through these structures, forming nests with more than hundred units. Such complex structures are not seen in any other skate or shark genus. Differently from other areas of occurrence, nests of *Sympterygia* spp. are commonly found over Cassino Beach (Rio Grande, Rio Grande do Sul State, Southern Brazil) after storms or windy days. Under these conditions, capsules bear live embryos that can survive for hours on the sand, exposed to the air. Unfortunately, the *Sympterygia* spp. embryology is poorly studied. Therefore, a program for collection of skate egg capsules was implanted since September 2009 at Cassino Beach. In September 4th 2011, eight encapsulated embryos were collected near the tide line, transferred to aquatic animal care room at the Physiological Sciences building (FURG), and kept in seawater (30-35 ppt) under fixed temperature (~22°C) and photoperiod (12h L: 12h D) conditions. Medium was 100% renewed every two days using natural seawater. Three out of the eight encapsulated embryos were successfully hatched (all females). The first neonate, hatched in November 1st 2011, had 8.8 cm total length (TL) and 4.5 cm disc width (DW). Total weight (TW) was not available, since this neonate was released alive. The second neonate, hatched in November 3rd 2011, had 8.4 cm TL, 3.8 cm DW and 3.5 g TW. The third neonate, hatched in November 5th 2011, had 8.6 cm TL, 3.6 cm DW and 2.4 g TW. TL values observed in these specimens are in agreement with those reported in the literature (7.7-8.4 cm for males and females). However, the TL of 8.8 cm observed in the present study represents the maximum TL recorded to date. The occurrence of encapsulated embryos in the studied area is crucial for the understanding of both biology and physiology of the embryonic development in *S. acuta* which so far is poorly understood due to the difficulty of obtaining biological material for study. Therefore, a systematic sampling program directed to the collection of *S. acuta* embryos is being performed at Cassino Beach.

Keywords : Elasmobranch, Oviparity, Skate



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

The effect of interspecific hybridization on the structure of metazoan parasite communities in cyprinid fish

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Interspecific hybridisation occurs widely across a taxonomically diverse fish species. In the present study, two cyprinids, *Cyprinus carpio* and *Carassius gibelio*, and their respective hybrids were investigated for the presence of metazoan parasites. We focused on specific metazoan parasites to analyse how interspecific hybridization affects host specificity. 39 fish specimens (12 *C. carpio*, 14 *C. gibelio* and 13 hybrids) were collected from the Hlohovecký fish pond (Danube River Basin, Czech Republic) in November 2009 and 2010. The hybrids were confirmed using both meristic traits and molecular identification. A total of 23 metazoan parasite species were recorded. The majority of parasite species found belongs to Monogenea (15 species). In *C. gibelio*, the highest values of total parasite abundance were observed, mainly due to the presence of *Gyrodactylus* species. The hybrids harboured more parasite species than each of the pure species, including parasites strictly specific to *C. carpio* or *C. gibelio*. In contrast, the total parasite abundance in hybrids was lower than in both parental species.

This work was supported by the Grant Agency of the Czech Republic, Project No. P505/12/0375.

Keywords : Cyprinid fish, Hybridization, Parasites



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Anatomy and kinematics of the respiratory apparatus in South American climbing catfishes (Astroblepidae)

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'Climbing catfishes' are a small group of neotropical catfishes which are characterized by an extremely specialized head morphology. They are among the few fishes living in the highest altitude rivers in the Andes of South America. By alternating use of their suckermouth and pelvic fins they are able to climb vertically on waterfalls. Not only expiration, but also inhalation occurs through the gill slits, which enables them to continue breathing while the mouth is used as a sucker for locomotion. This is a remarkable convergence with certain Asian cypriniforms. In this study, morphological data obtained by dissections, clearing and staining, serial sections and CT-scanning were combined to study skeletal and muscular structures in an *Astroblepus* species from central Peru, and their integration in a functional and atypical feeding, respiration and climbing apparatus. A kinematic analysis, using high-speed recordings made in an experimental setup in Oxapampa, Peru, yields insights into the functions of the mobile elements of the head: the concerted movements of the sucker-like lip, the jaws and the opercular apparatus to enable this exquisite combination of respiratory and locomotory functions.

Keywords : Climbing catfishes, Morphology, Kinematics



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Population genetics of the smooth hammerhead shark, *Sphyrna zygaena*, in the equatorial and tropical regions of the eastern Atlantic Ocean

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Elasmobranch fishes are particularly susceptible to overfishing, mainly because of their life history traits typical of top predators. Because of increasing concerns on this group, as well as other by-catch species, the International Commission for the Conservation of Atlantic Tunas (ICCAT, the management body for the Atlantic Ocean) has been recommending more biological studies on pelagic sharks, aiming a better management and conservation of these fishing resources. Considering the current lack of information on Atlantic populations of the smooth hammerhead shark, *Sphyrna zygaena*, this study aimed to characterize the genetic structure of this shark species along the Eastern Atlantic Ocean, using molecular markers. Fragments of muscle tissue were obtained from samples collected along the Eastern Equatorial region (Gulf of Guinea: n=31) and from the Eastern Tropical area (Cape Verde Archipelago: n=10). The genomic DNA was extracted and used for a polymerase chain reaction (PCR) amplification of the mitochondrial DNA control region (D-loop) and for sequencing. The sequences were aligned and an Analysis of Molecular Variance (AMOVA) was carried out. Within the studied sample, four polymorphic sites were found corresponding to two haplotypes. The nucleotide diversity (π) in the samples presented a low value of 0.00182, and the haplotype diversity (H_d) was 0.3512. The AMOVA analyses resulted in a negative F_{ST} value, indicating an absence of genetic structure, which seems to indicate a high gene flow of this species in the studied area. Those preliminary results seem to indicate that only one population occurs in the two studied regions, which has implications for management in terms of fisheries stocks. However, further analyses are required before consistent conclusions regarding the populations and stock structure along the entire Atlantic Ocean can be drawn. For that, additional samples from other regions of the Atlantic Ocean are currently being collected and analyzed. Financial Support: FAPESP, I.P./IPIMAR, CCMAR

Keywords : Overfishing, Population genetics, Conservation



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Morphology, molecules & morphology again: the contentious phylogenetic position of planktophagous catfishes, genus *Hypophthalmus* (Siluriformes)

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In the course of its taxonomic history, the genus *Hypophthalmus* has been allotted in its own family and even suborder. This is a reflexion of its extraordinary set of morphological modifications, which place it among the most aberrant of all catfishes. In modern times, most of those dramatically distinctive characteristics have been correctly identified as autapomorphic, and the genus has been proposed as a member of the large neotropical family Pimelodidae. Beyond that, its position within the group remain controversial. Apparently contradictory evidence place it at widely divergent positions in the pimelodid phylogeny. More recently, data from both nuclear and mitochondrial sequences further added to the uncertainty. Here we review the evidence relevant to the problem, including new data. Our conclusion is that complete data strongly support the placement of *Hypophthalmus* as the sister group to the genus *Parapimelodus*. Apparently contradictory previous morphological evidence is actually a result of character states modified beyond meaningful comparison in adult specimens of *Hypophthalmus*. Such limitations are overcome by examination of conditions in juvenile specimens, which allow surprisingly clear views of phylogenetically informative characters. The fact that species of both *Hypophthalmus* and *Parapimelodus* are planktophagous offer interesting opportunities for understanding the evolution of that mode of feeding, highly unusual in catfishes.

Keywords : Phylogeny, Systematics, Evolution



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

The poorly known fish fauna of the Ituri/Epulu basin (Democratic Republic of Congo), Africa

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The Ituri constitutes the upper part of the Aruwimi, a north-eastern right bank tributary of the Central Congo basin. A first rough estimate lists 118 species with a high amount of Cyprinid species (23.7 %), Alestiidae (13.6 %) and Mormyridae (12.7 %). During a recent expedition in the area, *Oreochromis leucostictus* was found for the first time in the Ituri. This species is known to naturally occur in lakes Albert, George and Edward and therefore its presence may be the result of an introduction in the Ituri region. Interestingly, also a *Haplochromis* species was discovered for the first time from the Ituri. The species is clearly distinct from the other 12 *Haplochromis* species known from the Congo basin but appears to be very similar, if not identical, to *H. aeneocolor* from Lake George and the Kazinga Channel. While this *Haplochromis* could have been accidentally introduced together with tilapia, the occurrence of some other species like *Platypanchax modestus* and *Barbus pellegrini* in both regions may result from past faunal exchanges between the regions of the East-African lakes and the Congo basin. The most important right bank affluent of the Ituri is the Epulu River, which is largely situated within the Okapi Wildlife Reserve, the fish fauna of which has hardly been studied. At present only 31 fish species have been found in the Epulu River. This low number can be explained by the presence of the Ngoy falls (± 15 m high) that appear to form an important physical barrier to fish migration from the Ituri to the Epulu. As such, the Epulu has an impoverished ichthyofauna that is mainly composed of Cyprinidae with 12 species (38.7 %) and Clariidae with 5 species (16.1 %). In contrast with the Ituri River, the families of the Alestiidae and Mormyridae are poorly represented in the Epulu by only two species each. On the other hand, the families Amphiliidae, Kneriidae and Notobranchiidae, and some species like certain cyprinids are present in the Epulu, but not in the remaining part of the Ituri. Currently only a single endemic, *i.e.* *Labeobarbus macroceps*, is known from the Epulu River.

Keywords : Ituri, Epulu, Ichthyofauna



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Unexpected species richness in the African pike *Hepsetus odoe* (Bloch, 1794) (Characiformes: Hepsetidae)

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The widespread African pike, *Hepsetus odoe* (Bloch, 1794), is a member of the monogeneric and, until recently, also monospecific family Hepsetidae. Although in the past one additional nominal species and two subspecies have been described, these were all formally synonymized with *H. odoe* by Roberts (1984). This act apparently has found general acceptance without any further reservation. Based on a detailed morphometric study including 36 measurements and 18 counts on about 450 preserved specimens, a complete revision of the genus *Hepsetus* was undertaken. This study revealed that *Hepsetus* contains six well delineated, valid species instead of one. Recently, the southern African *H. cuvieri* (Castelnau, 1861), was rehabilitated (Zengeya et al., 2011). The junior synonyms *H. odoe lineata* and *H. odoe microlepis* were found to represent valid species with *H. lineata* occurring in Lower Guinea and some adjacent parts of the Congo basin, while *H. microlepis* is endemic to the Lower and Middle Congo basin. Furthermore, two new species were discovered: one recently described as *Hepsetus akawo* (Decru et al., 2012) from the eastern part of West Africa and the northern part of Lower Guinea; and the other *Hepsetus* sp. 'kingsleyae', a species endemic to the Ogoowe basin in Gabon which is currently under description. *Hepsetus odoe* is now restricted to the westernmost part of West Africa. Interestingly, while *Hepsetus* species mostly have allopatric distributions, in the Ogoowe basin both *H. lineata* and *H. sp. 'kingsleyae'* were found sympatrically and even syntopically, the former mainly occurring in the main stream, while the latter seems to prefer the associated lakes. Preliminary genetic results (COI-bar coding) appear to confirm the morphological results.

Keywords : Revision, *Hepsetus*, Diversity



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Oral

High salinity affects brain and pituitary gene expression in blue Gourami males

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This study examined the effect of underground water conditions (0 %, 50 % and 100 %) with various NaCl concentrations (0.2±0.02 ppm, 0.56±0.05 ppm, 1.11±0.06ppm) on reproduction- and growth-related hormones in blue gourami males under non-reproductive and reproductive conditions. An increase in the percentage of males building nests under the highest water condition (100 %) were compared to fish that maintained a lower percentage of NaCl in the first two days. The % GSI of males building nests was higher than non-reproductively active males in water containing the lowest concentration of NaCl. In non-reproductively active males, GnRH1, βLH, βFSH and PRL mRNA levels were significantly higher in males maintained in underground water having a high NaCl concentration. In reproductively active males, mRNA levels of brain GnRH1, PRL and GnRH3 mRNA levels were significantly higher than males maintained in underground water having a high NaCl concentration. Thus, it is suggested that a high NaCl concentration affects the gene expression of reproduction-related hormones; in reproductively active males, it shortened the duration of nest-building by blue gourami males.

Keywords : Reproduction, Salinity, Teleosts



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ethology

Poster

Radial arm maze as a new paradigm to study collective behaviours in fish

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Collective decision-making is based on both environmental information perceived by individuals and social interactions with other group members. Determining and analyzing separately both interactions is a real challenge. If the environmental influences on group behaviours can be determined, new possibilities to collect information about processes inside the group become possible.

To improve our knowledge of these processes, an experiment where collective decision-making can be measured easily and without any ambiguity is needed. For this perspective, a new paradigm in the study of collective behaviour is introduced here. The radial arm maze is a classical method used to study individual cognitive abilities. Its advantages are firstly to allow control of environmental information; secondly, to realize multi-way tests, and thirdly, to give the opportunity to collect categorical responses like presence/absence. We apply this paradigm for the first time to a whole animal group.

We have also developed an image analysis system able to automatically count the number of individuals in every defined zone. Due to this counting, the degree of cohesion, the group stability, the activity and zone preferences can be described as function of factors such as the group size, the defined zones, or the experimental time. The degree of cohesion can be measured by a new index taking into account the number of sub-groups and the size of each ones. Group activity can be measured by the movement of the majority group between arms. This activity allows determining exploratory processes but also whether zone preferences or homing phenomena appear in the absence of any stimulus. To illustrate, our first results from the exploratory behaviour study of shoals of golden shiners (*Notemigonus crysoleucas*) are introduced. Using this new paradigm, it is now possible to quantify rapidly in a standardised way the collective responses of fish shoals according to the absence or presence of environmental stimuli, and to create experiments where environmental information is controlled.

Keywords : Shoals, Video analysis, Collective decision-making



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ethology

Oral

Video multitracking to study the fish behaviour

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With the development of digital imaging techniques over the last decade, there are now new opportunities to study complex behavioural patterns and rhythms in fish (from individual to collective group) and to track a very large number of individuals. These new technologies and methods provide valuable information to fundamental and applied science disciplines such as ethology, animal sociology, animal psychology, veterinary sciences, animal welfare sciences, statistical physics, pharmacology, as well as neuro- and ecotoxicology. Specifically in situations where a large number of individuals are involved, the use of video tracking data is essential, as manual analyses would be complicated, time-consuming and sometimes even impossible. Today, multitracking allows us to observe directly the behaviours of groups, and to determine the real interaction rules by sampling data collected in nature or in the laboratory, without any a posteriori rules as it was and is frequently the case in computer simulation of collective behaviours. With these technologies, the quantitative measures of collective behaviours is now easily accessible, and allow to define social behaviours with more accuracy than just qualitative criteria as is always the case for instance with the definition of shoaling and schooling behaviours.

Firstly will be introduced a review of fish video multitracking techniques. This review describes the possibilities of tracking individuals and groups at different scales, but also outlines the advantages and limitations of the different detection methods. The problem of occlusions, during which errors of individual identifications are very frequent, will be discuss. Secondly, our recent contribution in colour-based multitracking will be introduced, notably the new application of fluorescent VIE (Visible Implant Elastomer) tags in automatic tracking technology to study the behaviour of transparent animals like glass eels (*Anguilla anguilla*) in dim light or in darkness. The method makes it possible to measure the activity (notably distance and speed) of four individuals as a function of tidal and nycthemeral rhythms in the same flume (circular aquarium simulating the river or estuarine conditions) across a wide time scale (from seconds to weeks) in the context of migration in estuary.

Keywords : Video multitracking, Shoal and school, Collective behavior



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Poster

Effect of ethynylestradiol (EE2) on rainbow trout fry gonads on gene expression, morphology and endocrinology by *in silico* and *in vivo* approaches

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Teleosts fish show flexibility in the process of sex determination; their germ cells can develop into oogonia or spermatogonia. This makes them sensitive to xenoestrogens, endocrine disruptors which interfere with the natural female hormone estradiol. Xenoestrogens are present in the environment at sufficient concentration to disrupt reproduction in fish, causing mainly feminisation of male fish and/or infertility. Our objective is to address the question: "how a germ cell with XY genotype can develop into oocyte within a testis under chronic exposure to a potent xenoestrogen (EE2) ?". To address our issue, we combine approaches *in silico* and *in vivo* by using the microarray technique on rainbow trout (*Oncorhynchus mykiss*) fry. First, we re-analysed available microarray data using most recent bioinformatics methods, with the R software. However, microarray data on fishes are scarce and the platforms used are heterogeneous. Several datasets obtained from 'home-made' array technology in INRA-SCRIBE and characterised by complex experimental protocols were used. We performed a new way of analysis of these data, based on the use of the R package Limma, the only able to perform ANOVA on more than two experimental conditions, followed by contrasts analysis. We choose physiologically relevant contrasts to screen differentially expressed genes (DEG) of interest. The top list of statistically differentially expressed probesets has been screened to highlight genes potentially involved in the studied process by pathways analysis using the DAVID software. In parallel, an *in vivo* study was conducted on trout male fry exposed to a range of EE2 concentrations (0.01; 0.1; 1 and 10 µg/L) from the first feeding to 136 days post fertilisation (dpf). Histopathological analysis reveals female structures in the testis from the first concentration, with intersexes at the lower concentration (0.01 µg/L) and sex reversal in the upper ones (0.1; 1 and 10 µg/L). Microarray analysis on the Agilent array 60K was done with 6 replicates per condition. First results show up to 12 000 DEG between the conditions tested, with a good separation in the gene expression profiles between each concentration used. QPCR analysis of selected genes demonstrates the method effectiveness. We are currently working on the analysis of genes expression profiles, in correlation with the gonad histology and endocrinology in order to highlight signatures of EE2 contamination.

Keywords : Microarray, Bioinformatic, Endocrine disruption



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ethology

Oral

Toxic coral gobies influence selective corallivory of the obligate corallivorous butterflyfish *Chaetodon austriacus* in the northern Red Sea

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The obligate coral-dwelling gobiid genus *Gobiodon* inhabits *Acropora* corals and has developed various physiological, morphological and ethological adaptations towards this life habit. Its scale-less skin is covered by mucus that is toxic and multi-functional by reducing predation as well as affecting parasite attachment sites. While the advantages of this coral-fish association are well documented for *Gobiodon*, possible fitness-increasing factors for the coral partner are unknown. This study examines the influence of coral-dwelling gobies on the selective corallivory of obligate corallivorous butterflyfishes. In an aquarium experiment using video observation, the corallivorous butterflyfish *Chaetodon austriacus* fed significantly less on corals inhabited by two *Gobiodon* species compared to equally sized but uninhabited colonies. In the more agonistic species *G. histrio*, which mostly displayed directed movements towards butterflyfishes, the bite rate was 3.8 to 5.5 times lower on inhabited colonies. For *G. species 3*, which mostly displayed undirected body movement as a response to visits by *C. austriacus*, the bite rate was 2.7 to 3.1 times lower. A choice flume experiment suggests that the highly diluted skin mucus of *Gobiodon* spp. also functions as a coral predator repellent. This study demonstrates that *Gobiodon* spp. exhibit resource defence against coral-feeding butterflyfishes and that uninhabited coral colonies suffer higher predation rates. Although the genus *Gobiodon* is probably a facultative corallivore, this study shows that by reducing the predation on inhabited colonies by other fishes, the association between *Gobiodon* spp. and their host corals should be regarded as mutualistic.

Keywords : *Gobiodon*, *Chaetodon*, Coral-fish association



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Role of *pax4* gene during the pancreatic endocrine cell development in Zebrafish

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Pax genes encode a family of transcription factors crucial for embryogenesis. Pax4 is known to be required for the differentiation of endocrine pancreatic β and δ cells in mouse, however its mechanism of action is still unclear. Only one target gene (*arx*) has been identified to date. In this study, we have analysed the expression and function of *Pax4* in zebrafish. The *pax4* ortholog was identified in zebrafish and we amplified the corresponding cDNA. We found that its expression is restricted to the pancreatic region. Surprisingly, we observed by double fluorescent *in situ* hybridization that *pax4* is not expressed in the insulin β cells like in mouse but in endocrine precursors and in somatostatin δ cells. Knockdown of *pax4* using splicing-blocking morpholinos did not affect β and δ cell differentiation but led to a clear upregulation of the target gene *arx*, and consequently to an increase of glucagon α cells. Interestingly, as the altered spliced *pax4* transcript was trapped in nuclei of morphants, this allowed us to follow the fate of *pax4* expressing cells. We found that their fate is switched to α cells. Indeed, while the *pax4* expressing cells rarely express glucagon and *arx* in wild-type embryos, the altered *pax4* transcripts were mainly located in glucagon (*arx*+) α cells in morphants. In conclusion, our data indicate that *pax4* is not required for β and δ cell differentiation in Zebrafish but rather controls the amount of α cells by repressing the transcription factor *arx*.

Keywords : Pax4, Pancreas, Arx



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

The vulnerability assessment of fisheries sector to climate change : the case of the wider area of the mouth of the river Neretva

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In this review article is an overview of previous findings of invasive species in the wider area of the mouth of the Neretva River, and recent data on the propagation of sea bream *Sparus aurata* in the wider area of the delta of the river Neretva and Mali Ston Bay, as well as bluefish *Pomatomus saltator* and *Trachinotus ovatus* in the delta of the Neretva. Amounts to some socio-economic aspects of the emergence of new species of fish in the Adriatic are also presented. Result of climate change is also the introduction of new species. The impact of previously introduced new species in the area has been economically both positive and negative. Groupers and bluefish provide two examples where the effects on fish populations and the industry were mixed. Two potentially poisonous species of pufferfish have also been found. Although still rare public awareness should be raised about the potential threat of these fish to the public-especially amongst subsistence fishermen. Overall, changes in the distribution of species will result in revenue changes in the distribution for the fishing sector and benefits and losses may not be distributed equally. Climate change is also likely to have some impacts on species currently under mariculture in the area.

Keywords : Vulnerability assessment, Fisheries sector, Invasive species



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ethology

Oral

Triggerfish (Balistidae) spawning aggregations and sites : Spatial distribution and characterization

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Some species of triggerfishes (Balistidae) form spawning aggregations that are predictable both spatially and temporally. Large-bodied species such as *Balistoides viridescens* and *Pseudobalistes flavimarginatus* have transient spawning aggregations that include benthic spawning in nests prepared or selected by, and defended by males prior to spawning with females. In contrast, smaller species, such as *Melichthys niger*, have resident spawning aggregations. Spawning aggregation sites may be shared by these species but are utilized differently. Alternatively, these species may be utilized only by a single species and seem dependent upon both reef geomorphology and habitat. Spawning aggregations of transient spawning aggregation species follow semilunar cycles and have lek-like characteristics. Those of resident *M. niger* show tendencies suggestive of group socialization in the water column that may lead to paired courtship and spawning on the bottom. Patterns of distribution within a spawning aggregation site vary with individual male *P. flavimarginatus* restricted to specific nest sites, while *B. viridescens* and *M. niger* tend to move about the spawning aggregation site throughout much of the day. There is some plasticity in nest site characteristics, as well. *Pseudobalistes flavimarginatus* favor nests in sand and rubble, with nests excavated and tended by males. *Balistoides viridescens* appears to be more flexible in that they may defend holes or fissures in coral pavement as nest sites or they may excavate nests in sand and rubble depending upon where the spawning aggregation site is located. Variation in temporal and sexual patterns of post-spawning nest defense exist for both species, as well.

Keywords : Lek-like mating, Spawning aggregation, Triggerfish



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Development and Homology of Epurals in the Caudal Fin Skeleton of Euteleost Fishes

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Objective: We describe the early ontogeny of the caudal fin with special reference to the epurals for selected species of teleosts. In the past, epural bones of teleost fishes have been labeled sequentially from anterior to posterior (e.g. epural 1, epural 2, etc.) without regard to their position relative to centra and ventral elements of the caudal fin. We aim to demonstrate that euteleost fishes show a variety of patterns of epural formation and development and that some of these may be phylogenetically informative characters.

Materials and Methods: Specimens from growth series of several teleost species were cleared and double stained to display cartilage and bone. Specimens were examined with both a dissecting and compound microscope. The development of epurals is detailed beginning with the earliest detection of chondrocytes in growth series of various teleosts.

Main Results: Teleosts typically have three epurals; however, epurals can vary from zero to five depending on the group and intraspecific variation. Recent research on caudal fin development of basal teleosts (e.g. *Elops saurus* and *Hiodon* species) and salmonids (e.g. *Thymallus thymallus* and *Oncorhynchus* species) indicates that simple numbering of epural bones is not phylogenetically meaningful. Our observations indicate that epurals form after notochord flexion in the examined otomorphs and salmonids, as well as in *Chauliodus macouni* and *Synodus foetens*. Epurals form before flexion in *Mallotus villosus* and in the examined ctenosquamates, which allows for simple association of an epural with a hypural. After notochord flexion, epurals may reposition relative to their corresponding hypurals and this is a factor that can confuse homology assessment in large specimens.

Conclusion: The results of the caudal fin developmental studies indicate that the epurals of euteleost fishes cannot be matched by numbering with those in the basal teleosts. It is recommended that epurals be named using the polyural terminology according to their position relative to ventral caudal elements early in ontogeny (e.g. epural of preural segment 1 or epural of hypural 2). The names of epurals are associated with hypurals because this method best assesses the serial matches of epurals.

Keywords : Hypural, Ontogeny, Vertebral centrum



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Integration of fish fossil data into phylogenetic and comparative studies Oral

Integrating genes and fossils to measure the West Tethyan influence on a group of nocturnal fishes in contemporary biodiversity hotspots

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One of the most striking contemporary biodiversity patterns is the uneven distribution of marine species-richness, with species diversity in the Indo-Australian Archipelago (IAA) vastly exceeding any other marine area for most organisms. However, the IAA formed fairly recently in geologic time, and marine biodiversity hotspots have shifted across nearly half the globe in the last 50 million years. Understanding how the diversification dynamics of marine lineages have been influenced by the rise and fall of biodiversity hotspots represents a necessary historic perspective on the formation and maintenance of global marine diversity. However, evolutionary inferences are often challenged by a lack of fossil evidence that would facilitate insights into historic patterns of abundance and diversity. Squirrelfishes and Soldierfishes (*Holocentridae*) provide an exception to this. Holocentrids are among the most conspicuous fishes in the nocturnal reef fish community and reach their greatest diversity in the IAA. However, holocentrids also represent some of the most numerous fossil taxa in deposits from the Eocene West Tethyan biodiversity hotspot. We sample DNA sequence data from most genera and over fifty percent of extant holocentrid species for multiple single copy nuclear genes and one mitochondrial gene and integrate this data with a morphological character matrix that includes stem holocentrine and myripristine lineages from the West Tethys and stem holocentrid fossils that date back to the Cretaceous. We utilize a Bayesian time-calibrated phylogenetic framework and estimate a similar origin of extant holocentrids to predictions based on the fossil record. Our study further demonstrates how inferences of biogeographic history can potentially be misled in the absence of fossil data.

Keywords : Biogeography, Reef-fish, Nocturnal



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Distant travellers : *Paranthias furcifer* and *Holacanthus ciliaris* in the Adriatic sea

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In January 2011, a semi-submersible oil platform “Zagreb 1” was towed to the Trogir shipyard (Eastern Adriatic Sea, Croatia) for repair. The platform was towed a long way, from the Gulf of Mexico to the Croatian coast and more than 6400 Nm were passed in 60 days. On 17th June 2011 a specimen of *Paranthias furcifer* was caught in the Marina Bay in the Adriatic Sea. The location of the capture was just a few miles away from the anchored platform and it seemed possible that the fish was somehow connected with the presence of the platform. In October of the same year, a specimen of *Holacanthus ciliaris* was caught in the close vicinity of the platform and a couple of sightings of strange fishes were reported from the fishermen from the same area. Due to unusual findings of these fishes, which are abundant in the Gulf of Mexico where the platform originated, we presume that the platform was indeed a vector of introduction of these fishes and possibly other organisms.

Keywords : *Paranthias furcifer*, *Holacanthus ciliaris*, Alien fish



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

The Adriatic ichthyofauna : updates and extensions (2009-2012)

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In the period of 2009-2012, six new fish species have been added to the Check list of Adriatic fishes (*Lobotes surinamensis*, *Siganus luridus*, *Paranthias furcifer*, *Holacanthus ciliaris*, *Elates ransonnetti*, *Enchelycore anatina*). Northward spreading of dusky spinefoot *Schedophilus ovalis* was observed. New additional record or rare species *Tylosurus acus imperialis* was observed in 2011, while new record of the oarfish, *Regalecus glesne*, occurred in 2009; this is only the second record of this species for the Adriatic. Of 13 Lessepsian migrants that were recorded in the Adriatic, it seems that *Fistularia commersonii* and *Siganus luridus* are successful invaders.

Keywords : Adriatic sea, Ichthyofauna, Biodiversity



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Morphological differences between four populations of the soft-mouth trout *Salmo obtusirostris*

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We determined the morphological characteristics of *Salmo obtusirostris* (Heckel, 1851), from the Jadro and Vrljika Rivers (Croatia), the Neretva River (Bosnia and Hercegovina) and the Zeta River (Montenegro). *S. obtusirostris* is an endemic salmonid of the eastern Adriatic Basin. Historically, its populations were divided into four subspecies. Detailed measurements included 42 morphometric measures and 8 meristic measures. Diagnosis was based on 8 specimens from the Zeta River, 20 from the Jadro River, 20 from the Vrljika River and 20 from the Neretva River. The results of analysis were compared with those from literature as well as with recent results of molecular analysis. Marked differences between the obtained results and literature data were found. The results will be used in the planning of conservation measures for recovery of some populations of *S. obtusirostris*.

Keywords : Salmonids, *Salmo obtusirostris*, Endemic



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Effect of chronic confinement stress on sperm quality in Eurasian perch

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Stress plays a key role in the ability of fish to perform reproduction. Given the huge variability in fish reproductive strategies, large variability in the effects of stress on reproductive efficiency could be expected. Eurasian perch (*Perca fluviatilis*) is mainly represented in Europe and reared under intensive rearing conditions (*e.i.* high confinement or stocking density), which are known to impair with many physiological function. In perch, stress induces an increase of cortisol and a decrease of immunity, but little is known regarding the effect of stress on male reproductive capacity. The aim of the present study was to examine the impact of chronic confinement stress on sperm quality of *Perca fluviatilis* during the final maturational period (mid-February to late-March).

Perch breeders (>3 years) were reared in 3 confinement conditions (0,70 m³, 0,5 m³ and 2,0 m³) in duplicate (except for 0.70 L) at the same density (12 ind/m³) from September 2011 at a 50:50 sex ratio. The 5th and 26th March, 3 males from each tank were randomly handled, anesthetized and sperm collected by stripping. 100 µL were dissolved in extender, sperm concentration assessed by counting spermatozoa with a Burkert's cell and sperm motility determine by CASA system. Velocity parameters studied were % progressive (Prog) and motile (MOT) spermatozoa and VAP, VCL and VSL. Sperm concentration decreased with confinement: 70.5±17.2 x10⁹, 65.3±10.7 x10⁹, 61.5±9.9 x x10⁹ for 2,0 m³, 0,5 m³ and isolated (0,70 m³) fish respectively. For the date of analysis VAP (from 32.6 to 40.2 mm/sec and from 36.8 to 37.1mm/sec for 5th and 26th March respectively), VSL (from 23.5 to 30. mm/sec and from 22.0 to 26.5mm/sec for 5th and 26th March respectively), VCL (from 81.6 to 89.0 mm/sec and from 78.8 to 89.5mm/sec for 5th and 26th March respectively), MOT (from 56.0 to 70.4 % and from 73.0 to 85.0 % for 5th and 26th March respectively) and PROG (from 21.5 to 23.3 % and from 21.9 to 28.7 % for 5th and 26th March respectively) were not influenced by the confinement level.

Keywords : Sperm, Stress, Confinement



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Reproductive biology of the black scorpionfish, *Scorpaena porcus* (Pisces, Scorpaenidae) population in the eastern Adriatic Sea

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The reproductive parameters of the black scorpionfish, *Scorpaena porcus*, collected by trammel nets along the eastern Adriatic coast were analysed by studying the seasonal histology of the gonads, fecundity and other various indices related to reproduction. Females of the investigated species are larger than males and become sexually mature at total lengths of 11.0 cm, while males reach maturation at 10.0 cm of the total length (L50 in both cases). All individuals with total lengths of over 15.0 cm were sexually mature. Gonadosomatic index and histological examination of gonads suggest that spawning takes place between May and September and peaks in July. Developmental stages of germ cells of the black scorpionfish are described for both sexes. Furthermore, histological observations of oocyte development show that the oocyte diameter increases about 40-fold during oogenesis. The fecundity of *S. porcus* was determined by the size and weight of the individuals and ranged from 1599.90 to 76934.00, with an average of $15438.69 \pm \text{SD } 1436.00$ eggs per female. Average diameter of mature oocytes was $0.49 \text{ mm} \pm \text{SD } 0.08$.

Keywords : *Scorpaena porcus*, Reproduction, Adriatic



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Seasonal fish growth in temperate climates : the effects of temperature and rainfall on the seasonal growth of the stone-loach *Barbatula barbatula*

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It is well known that temperature is a major factor driving fish growth and modelling temperature effects has been tried both on laboratory and field experiments. Proposed models for seasonal fish growth in which temperature variation was included explained most of the seasonal growth variability. Nevertheless, even after extracting the major effects of seasonal temperature some unexplained residual pattern could still be present. Fish seasonal growth is also related to food availability, which in nature is frequently related to river flood level. This idea derives from the observation of growth cycles in tropical rivers, where growth rates increase when the river level reaches the flood plains during the rainy season. A similar proposal has been made for temperate fish, since ice-melting flood in spring is considered as an important factor driving fish growth. Spring brings both temperature increase and access to new food items carried by snow melting, what leads to increasing fish growth rates. The goal of this study is to test the hypothesis of food-driven increased growth rates for temperate freshwater fish, using the stone-loach *Barbatula barbatula* as a biological model and rainfall as a correlate of access to allochthonous food supply. To test this hypothesis, published data on the stone-loach *Barbatula barbatula* (Linnaeus, 1758) (Cypriniformes, Balitoridae) from southern England were used. Fish length, age and water temperature data were available at Docken's Waters in a sample program carried out from 1964 to 1967. Average precipitation (from 1961 to 1990) was used as a correlate of river level and potential access to drift-food. The total amount of monthly sunshine hours was used as a strong correlate of the total energy input to the systems. Considering that in temperate regions water temperature is the major factor driving fish seasonal growth, a mathematical model for seasonal growth including temperature variation was adjusted. After extracting the temperature effects, residuals were correlated to total radiation and rainfall. It was identified that precipitation (or flood level) is positively related with seasonal partial residues when temperature effects were extracted ($R^2 = 0.3687$). So, although flood contribution is usually hidden by the major effects of temperature, it can be identified by partial residual that, at least for *Barbatula barbatula* at Docken's Waters, increased access to food supply could explain additional 36 % of residual pattern, supporting previous findings for both marine and freshwater temperate fish.

Keywords : Seasonal growth, Temperature, Rainfall



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Fish Assemblage Survey Technique (FAST): towards a fish index to implement the Marine Strategy Framework Directive?

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According to the recent Marine Strategy Framework Directive (MSFD), fish assemblages are one of the key biological components that need to be monitored. The MSFD recommends that populations of all commercially exploited fish are within safe biological limits, exhibiting a population age and size distribution that is indicative of a healthy stock. There is then a need to develop technical specifications and standardised methods for monitoring fish assemblages at the community level. The Fish Assemblage Survey Technique (FAST) was developed to fulfil several objectives: (i) to be able to monitor fish species targeted by fisheries in marine coastal areas, (ii) to be sensitive to human induced impacts, and (iii) to be simple to implement to avoid a long training of observers. In this method, data acquisition for one station consists of six 15-minute visual censuses by SCUBA divers, performed along a random pathway over all kinds of substratum (sand, seagrass, rock) between 0-25 m depths. The presence/absence of 28 pre-defined fish species are recorded during each census. The selected species are all targeted by professional and recreational fisheries (net fishing, spearfishing, angling, etc.). The size of each fish observed is estimated and assigned to two size classes: large fish, if longer than 2/3 of the maximum size; and small/medium fish, if smaller than 2/3 of the maximum size. The two size classes and number of censuses were chosen to make the FAST a rapid and relevant assessment method. Several parameters are then calculated relative to the maximal value that can reach the fish assemblage (all species and both size classes observed): mean index, cumulative index, proportion of species with a full demographic structure, number of species, coefficient of variation. The data collected from 1999 to 2007 (spring, summer and autumn) on more than 35 stations allowed us to validate the FAST as a low cost method for fish bio-indicator and to propose a 5-level interpretation grid that can be used to assess the environmental status of the fish assemblages. The application of FAST as a tool for general fish assemblage bio-indicator is discussed in relation to the implementation of the MSFD, monitoring of marine protected areas, and the siting of sampling networks along the Mediterranean coast.

Keywords : Bio-indicator, Sampling strategy, Marine strategy framework dir.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Spreading of new fish species into the western Mediterranean basin : what are the main pathways and what are the triggers?

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The species composition of the western Mediterranean ichthyofauna changed during the last decade: some lessepsian species well established within the eastern Mediterranean basin started to spread into the western basin; during the same time, some other Atlantic species crossed the Gibraltar Strait to spread in the western basin. A review of the spreading and/or establishment of these species allowed us to highlight three main pathways: (1) a recent spreading through the Siculo-Tunisian Strait, from the eastern to the western basin, (2) a permanent spreading in the western basin through the Gibraltar Strait since the first noticed entrance into the Mediterranean and involving the establishment of Mediterranean populations or assemblages, (3) a sequential spreading in the western basin through the Gibraltar Strait, with alternation of spreading phases spaced of several decades. These pathways are considered as natural, i.e. they are not human induced. This review allows us to discuss the links between some oceanographic events (e.g. current modification) and these spreading through straits. However, the geographical distribution of some species are sometimes more complex to understand because the natural pathways can be disturbed with anthropogenic transportation.

Keywords : New species, Lessepsian species, Spreading



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Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

**Tempo and mode of eco-morphological evolution in
damselishes (Pomacentridae)**

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Coral reef fishes represent one of the most outstandingly diverse assemblages of vertebrates on the planet but our understanding of their mode of diversification remains limited. Here we test whether the damsselfishes (Pomacentridae), one of the most species-rich families of reef-associated fishes, adaptively radiated during their evolutionary history. Tests of the tempo of lineage diversification using a time-calibrated phylogeny including 208 species did not support the expected pattern of rapid initial diversification that slowed through time as predicted by macroevolutionary theory. Evolutionary modeling of trophic traits similarly rejected the hypothesis of early among-lineage partitioning of ecologically relevant phenotypic diversity. Instead, damsselfishes are shown to have experienced iterative convergent radiations wherein subclades converge on similar trophic strategies (i.e. pelagic feeders, benthic feeders, intermediate) and morphologies. We discuss that regionalization of coral reefs, bipartite life cycle of reef fishes, competition and functional constraints are good candidate of causal factors underlying the iterative ecological radiation and convergent evolution of damsselfishes.

Keywords : Coral reef fishes, Morphospace, Rate of diversification



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Invited speaker

Life-History Traits of Fishes: A Review with Application for Management of Data-Poor Stocks

FROESE Rainer

Leibniz Institute IFM-GEOMAR to Helmholtz Centre for Ocean Research - GEOMAR

Well over 4,000 species of fishes are harvested from the wild for human consumption or use as fish meal. However, full stock assessments as a basis for management are available for only a few hundred species. Thus there is a need for reasonable proxies based on life history traits and resilience of species to derive precautionary reference points and indicators for the management of data-poor stocks. Here I present life history relationships between environment, longevity, body size, somatic growth, natural mortality, and population growth. I show the relation to the internationally agreed reference points for exploitation rate and stock size that can produce the maximum sustainable yield. I propose a new size-based indicator for the estimation of the current stock status. Finally, I propose some reference points that would indicate a good environmental status of the marine environment with respect to commercial fish stocks.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Reproductive period of *Spondylus gaederopus* (Bivalvia) and its genetic approach

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The aims of this work were for the first time to find the reproductive period as well as the genetic structure of Greek spiny oyster *Spondylus gaederopus*, contributing to the gap for autoecology and genetics of this famous and unstudied edible bivalve. The samples were collected by scuba diving from rocky substrate of the Kelyfos Island in Toroneos Gulf (Chalkidiki, Greece), in a depth from 8 to 20 m. Specimens were collected from November 2007 until October 2008, in a bi-monthly basis and more frequently approaching the time of the shell reproduction. In the laboratory, the length, the wet and dry weights (body and valves) were measured. Condition Index (CI) of the spiny oysters was calculated by the formula: body weight/total shell weight X 100. The two sexes were recognized by the gonadal colour and stereo and microscopic observation. For the reproductive period determination the gonads are classified according to their maturity, based on a rank of six stages. Total DNA was extracted from the anterior adductor muscle, with the CTAB methodology. A universal primer set was used for the amplification of the 16S rDNA gene of mitochondrial DNA, in all the individuals of the population. A sequencing analysis on a 3730XI DNA Analyzer (Applied Biosystems) is being made, using both forward and reverse primers for crosschecking. DNA sequences will be deposited to GenBank. According to the results, the spiny oyster is a gonochoristic species with a sex ratio of 1:1. The males are generally smaller (younger) while the females are larger in order to safe greater fecundity. The smaller size of spiny oyster with gonads was 3.8 cm in length and the gonadal activity was observed in all larger shells from spring to summer. The spawning took place during the summer. The condition index for wet and dry weights was high in spring, low from summer (during the reproduction) up to winter and not exceeding an average of 15 %, because the ratio of shell/total weight was 0.86.

Keywords : *Spondylus gaederopus*, Reproductive period, 16S rdna gene



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Oral

Aromatase gene expression during the process of sex differentiation of the European eel *Anguilla anguilla*

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Sex determination in European eel appears to be highly influenced by the environment. While heterochromosomes were found on the 19 chromosome pair of females eels, most studies suggested that environmental factors could easily overcome genetic sex. However, the period during which environment may affect sex determination remains unknown. Gonad differentiation in eel is a long and complex process where males could only be microscopically discriminate from females at a size of 30 cm. In this gonochoristic species, the undifferentiated gonad could develop into either an intersexual stage (Syrski organ) or directly into ovaries. The Syrski organ could then develop into either an ovary or a testis. In vertebrates, the development from the undifferentiated stage to one sex or the other is generally triggered and regulated by many sex specific genes. Among these genes, the gene encoding the aromatase enzyme was reported to well discriminate females from males at the earliest stages of sexual differentiation in other fish species. Indeed, the aromatase enzyme plays a key role in hormonal regulation since it converts androgens to oestrogens. In order to obtain a precocious indicator of sex, we investigated aromatase gene expression during the sexual differentiation process of eels. For this purpose, glass eels were raised in an INRA aquaculture facility until they reach a critical size for sex histological assessment. In addition some undifferentiated individuals were sampled in a female-biased population (Oir River). Using real-time PCR we compared aromatase gene expression between undifferentiated eels, males, females and intersexual eels at different stages of gonad development. Results revealed that gonad of males do not necessarily pass through an intermediate intersexual stage and that it is very unlikely that ovaries develop from the Syrski organ. The aromatase gene expression was higher in female when compared to males and intersexual eels. In addition, level of aromatase appeared to be dependent on the development stage with gonad presenting cysts of meiosis exhibiting higher aromatase gene expression level than gonad presenting oocytes at the oil droplet stage. Interestingly, undifferentiated individuals sampled in the female-biased population exhibited level of aromatase almost as high as females at the earliest development stage. Aromatase gene expression may thus be used as an early marker of female sex development, alone or in conjunction with others markers.

Keywords : Physiology, Sex, Eel



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Genetics

Oral

Introducing the FREDIE project with notes on the freshwater fish diversity of the Mediterranean hot-spot

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FREDIE stands for 'Freshwater Diversity Identification for Europe' and is a nationally funded project aimed at bringing together DNA barcoding with taxonomic expertise for European freshwater organisms (www.fredie.eu). Included are freshwater fishes, mayflies and freshwater molluscs, and we aim to develop an online available identification system for species diversity of these groups in Europe. Although DNA barcoding offers the possibility to accelerate detection and monitoring of biodiversity, its quality and significance is strictly bound to availability and quality of underlying reference data, especially reliable species determinations. Within the FREDIE project, resources and expertise of three core institutes and a web of associated partners are combined to create a reliable and sustainable reference system for European freshwater fishes, molluscs and mayflies. Representatives of nearly all species of the three groups occurring between Portugal and the Ural are collected, identified by experts and sequenced to become barcode references. In selected cases where conventional barcode markers do not lead to unambiguous species identifications a refined identification system is planned including morphological characters and other genetic markers with better taxonomical resolution. In addition to the DNA sequence data generated, we will provide the respective voucher specimens and a DNA collection as permanent references available to the scientific community. FREDIE also provides molecular and morphological estimations of species numbers of the three organism groups for Europe, as well as deeper insights into their spatial structure on a large scale. In a first sub-project we focused on the freshwater fish diversity of the Mediterranean hot-spot, which harbors about 557 extant species. We were able to obtain so far more than 90 % of these species, represented by >3,500 individuals by own collecting efforts and support by European colleagues. Through intensive sampling of widely distributed taxa from several major European drainages, some possessing different levels of morphological divergence and specific designation, we evaluated the performance of barcoding in distinguishing sister-species and glacial lineages. Results demonstrate that DNA barcoding can be an extremely efficient tool for species identification across various families of European freshwater fishes. In many cases, the approach identified also biological meaningful intra-specific groups. The analysis of geographic variation revealed both, previously known but also underappreciated phylogeographic breaks among different taxa. This has important conservation implications for those species and populations and further enhances our understanding of the biogeography and evolution of European freshwater fish diversity.

Keywords : European freshwater diversity, DNA barcoding, Mediterranean hot spot



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Role of the transcription factor Nkx6.1 in the differentiation of the multipotent pancreatic progenitors

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Type 1 diabetes is an autoimmune disease in which the immune system attacks and destroys *beta* cells that produce insulin. *Beta* cells regeneration from multipotent progenitors is a promising therapeutic approach for patients suffering from type 1 diabetes. To demonstrate the existence of multipotent progenitors in the pancreas and characterize them, it is essential to identify specific markers of these cells.

The expression pattern of the transcription factor Nkx6.1 suggests that it could be a marker of multipotent progenitors in the pancreas. To determine it, we will mark the Nkx6.1 expression cells and follow their fates. For that purpose, we used 3 BACs (Bacterial Artificial Chromosome) which contain the *nkx6.1* gene and its regulatory elements located downstream. By recombination in *Escherichia coli*, we inserted the GFP in the first exon of *nkx6.1* (in collaboration with the team of Alain Vanderplassen). In this way, GFP should be under the control of all regulatory elements of *nkx6.1*. This strategy will be shown on the poster.

Keywords : Nkx6.1, Bacs, Multipotent progenitor



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Poster

Do scale size indices and scale surface morphology allow identification of endemic *Aphanius* species from southern Iran?

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Introduction: The Iranian inland *Aphanius* species have mainly been described based on the data achieved by fish morphology and morphometry, and recently by adding otoliths characters and molecular data. However, due to the conservatism of the traditional morphological characters in most of these species, the use of other informative characters such as scale morphology is essential. In addition, identification of local populations and their taxonomic and phylogenetic interpretation are a major point for the conservation and management of vulnerable species such as the here studied endemic *Aphanius* species. Structures of fish scales have been used as a taxonomic tool since the beginnings of systematic ichthyology. In addition, it is known that scale sizes can provide important information for the identification of fish species.

Objectives: We test whether scale surface morphology and scale size indices can be used to assess inter- and intraspecific variation of three closely related species of *Aphanius* from Iran.

Material and Methods: We have analysed qualitative data, i.e. scale surface morphology using SEM images, and quantitative data, i.e. four scale size indices, from several populations of *Aphanius sophiae*, *A. farsicus* and *A. pluristriatus*.

Results: Clear differences appear between species and also between some populations with regard to scale microstructures such as focus position, presence of focus granules, distribution of *radial* in the rostral fields, tubercle shape as well as shape, size and distribution of lepidonts. Scale size indices show that males represent a higher scale width and length than females, and that scale width is higher than scale length in both males and females of all studied species. Furthermore, the mean values of the scale sizes are clearly different between the studied species and therefore allow a safe identification of the *Aphanius* species studied. Moreover, some populations of *Aphanius sophiae* and *A. farsicus* can be separated based on their scale sizes.

Conclusions: Investigation of scale surface morphology and scale size increase our knowledge on *Aphanius* with regard to sexual dimorphism, inter- and intraspecific variation, and can significantly improve the identification of species that are difficult to separate based on traditional morphological characters.

Keywords : Cyprinodontidae, Scale characters, Endemic *Aphanius* species



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Ecological traits of the brook chub *Squalius lucumonis* (Bianco, 1983) in the Tiber River Basin (Italy)

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The brook chub *S. lucumonis* (Bianco, 1983) is an Italian endemic species restricted to the Tuscany-Latium district in three river basins located in central Italy: Tiber, Arno, Ombrone-Serchio. Many authors reported about a progressive decline in its original range and its disappearance is mainly due to habitat modification and competition with alien species. Thus, *S. lucumonis* has been considered as a threatened fish, it is assessed as endangered species according to IUCN Red List and is also listed in the Appendix III of the Bern Convention and in the Annex II of the European Union Habitats Directive as a species requiring designation of Special area of conservation

The objective of this research was to investigate some ecological traits of this species by analyzing the relationships with the main environmental variables which influence the distribution and the abundance in the Tiber River Basin fish populations. Moreover the research focused on the dealings between *S. lucumonis* and the other fish species which inhabiting the Tiber River Basin, especially the congeneric *S. squalus* (Bonaparte, 1837).

Data from 333 sampling sites, collected from 1998 to 2009 in 132 different watercourses throughout the Tiber River Basin, were used in the research. For each station a set of environmental parameters was used to characterize the river sectors and a census of the fish fauna was kept by electrofishing using the removal method. Then the data were analyzed by means of the Canonical Correspondence Analysis (CCA).

The results of study allow investigating the role of the environmental variables in the fish communities' assemblages and represent a useful tool for the identification of management strategies aimed at conservation of the species.

Keywords : Ecological traits, *Squalius lucumonis*, Cca



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Integration of fish fossil data into phylogenetic
and comparative studies

Oral

The value of fossils in phylogenetic analyses of taxonomically difficult lineages : a case study of *Lepidocottus aries* (Gobioidei)

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Introduction: The current classification of gobioid fishes is based on osteological characters, the lateral line system and molecular data. However, several lineages, including the Eleotridae and Butidae, remain difficult to resolve because synapomorphies are rare (Eleotridae) or have not yet been determined (Butidae), and because the fossil record of these groups is scarce.

Objective: We provide a critical re-evaluation of the extinct genus *Lepidocottus* savage based on its type species *L. aries* (Agassiz) that is aimed at clarifying the phylogenetic position of this taxon. *L. aries* originally was assigned to the Cottidae, but in subsequent studies referred to the Gobiidae.

Material and Methods: The study is based on newly discovered articulated skeletons, in part with otoliths in situ, from Upper Oligocene sediments in Aix-en-Provence, southern France (near the type locality of †*L. aries*). Methods include morphological analysis of the skeletons and otoliths and a review of literature data.

Results: We show that *Lepidocottus* is a valid genus of the Butidae. Thus, *L. aries* represents the first fossil evidence of articulated skeletons belonging to this family. In addition, two otolith-based species, in previous studies described as "*Gobius*" and/or "*genus Eleotridarum*" (in the old definition, i.e. including the present-day Eleotridae + Butidae) can now be identified as belonging to *Lepidocottus*. In all, five species of *Lepidocottus* were distributed during the Oligocene and Early Miocene of Western Europa in fresh- and brackish water environments.

Conclusions: The pterygiophore arrangement (2211) of the first dorsal fin and a rectangular shaped otolith of the gobioid type (i.e. characterized by a shoe-sole like sulcus) are proposed as new, and at present the only discovered, synapomorphies for the Butidae. Based on additional otolith characters and the occurrence of cycloid (= reduced ctenoid) scales, we suggest that *L. aries* is sister to the extant *Kribia kribensis* (Boulenger), and that these two are sister to *Bostrychus*. Our phylogenetic reconstruction is suggestive of a Late Eocene/Early Oligocene (about 33–34 m.y. ago) dispersal of ancient Butidae from their likely center of origin in the Indo-/Western Pacific via the Mediterranean into the eastern Atlantic.

Keywords : Gobioidae, Osteology, Otoliths



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Geostatistical assessment of impoundment effect on fish metapopulations in a large lowland river

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Fish communities were quantitatively sampled in several dozen sites established along the whole length of the large lowland temperate zone Pilica River, Poland, in the late 1960s. A few years later an impoundment 27 km² in surface area and with no fish pass was constructed in the river's middle course, as the first and only barrier in the river. Fish communities were sampled along the Pilica again in the mid 2000s, when the impoundment had functioned for 30 years. Geostatistical (semi-variogram) methodology was applied to the fish abundance data sets obtained during the two samplings. Differences in species abundance between each two sampling sites a specified distance apart were calculated and distance-related variance assessed, both in the upper (upstream of the reservoir) and lower courses of the river and in the pre-impoundment and post-impoundment periods. The semi-variogram differences between species, in different river courses and periods, were discussed from the viewpoint of the impact of the impoundment on fish colonization and extinction processes, and on community homogenization.

Keywords : Freshwater, Dam reservoir, Metapopulation/metacommunity



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Revitalizing Research on Lessepsian Fish Migration – from DNA to Taxonomy

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The rate of Red Sea (Lessepsian) fish migration population establishment in the Mediterranean and their westward dispersal has dramatically accelerated in the last fifteen years. Molecular studies in the last two decades have added a new dimension of precision, thus increasing the resolution on, inter alia, the origin of Lessepsian migrant fish, their parasitofauna, founder effect and hence rate of invasion. Molecular studies have greatly increased our understanding of fish taxonomy and biodiversity in the target area. These studies have shown that several of these successful invasive species that were previously considered as having a wide Indo-Pacific distribution, actually belong to a different taxon than the Red Sea populations that are most likely confined to the Red Sea. An example of a species change that has already been published is the silverside *Antherinomorous forskalii* which was previously considered to be *A. lacunosus*. Other examples still under study include *Saurida* (Synodontidae), *Sillago* (Sillaginidae), *Pempheris* (Pempheridae), *Etrumeus* (Clupeidae), *Pomadasy* (Haemulidae).

Keywords : Lessepsian fish, Taxonomy, Molecular studies



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Origin, phylogeny and adaptive radiation of sculpin species flock in Lake Baikal

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In the Lake Baikal which is the oldest (about 30 million years) and deepest (1640 m) freshwater lake, 33 species of Cottoid fish generally called as Baikalian sculpins belonging to 12 genera and 3 families, Cottidae, Abyssocottidae and Comephoridae inhabit all depth of the lake, from littoral to abyssal (Sideleva, 2003). Although recent molecular data supported that Baikalian Cottoid fish are monophyletic, it was not made clear what fish species or group is ancestral to Baikalian sculpins (Kontula et al., 2003; Yokoyama and Goto, 2005; Kinziger et al., 2005). To understand the evolutionary history of Baikalian sculpins more deeply, we were carried out (1) to estimate the origin of them by constructing more comprehensive mtDNA phylogeny of freshwater Cottoid fish including Baikalian sculpins, *Cottus* species and their related taxa, and (2) to elucidate the process of adaptive radiation in a part of benthic fishes in Baikalian sculpins, 4 species of *Procottus* which inhabit from littoral to bathyal zone of underwater slope, by using mtDNA and nuclear DNA sequence data. As the results, we found for the first subject that Baikalian sculpins probably derived from an ancestral species belonging to the lineage Ulanidea (*sensu* Kinziger et al., 2005) which are distributed in North America and Far East Russia. As for the second subject, we found specific substitutions in rhodopsin gene causing the blue shift in their optic ability, change of amino acid from tyr to phe at the 261st position and from asp to asn at the 83rd position detected in *P. jettelesii* and *P. major* both of which inhabit deeper zone compared with that of shallow water species, *P. gotoi* and *P. gruwici*, respectively. These changes leading to blue shifts in optic absorbance in photoreceptive protein (rhodopsin) suggest that a case of adaptive radiation and speciation occurred among the benthic Baikalian sculpins, *Procottus* species, in direction from littoral to bathyal habitat.

Keywords : Baikal sculpins, Origin, Adaptive radiation



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Spatial distribution of European grayling (*Thymallus thymallus*) post-emergent fry and habitat sub-units preferences: a management-oriented approach

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The first habitat shift in grayling (*Thymallus thymallus* L.) fry has been widely described, but information about the habitat use by larval grayling only relied on microhabitat scale preferences, mainly considering the “water depth”, “velocity”, and “substrate size” variables. Furthermore, comparison between rivers of fry habitat preference curves showed that they were poorly transferable, suggesting that fish is adapted to local habitat conditions. Thus, the variability of these microhabitat conditions used by fry could support the assumption that a more integrative, larger scale approach (“macrohabitat”) which would combine habitat variables might be more relevant to management issues than usual methods based on univariate preference curves. The aim of our study was to describe the temporal and spatial pattern of downstream movement (banks colonization) and the habitat use by post-emergent grayling fry on the Allondon river, a tributary of the Rhône River in Southwest Switzerland, using a large scale and management-oriented approach. In this purpose, the longitudinal distribution of fry was sequentially determined during all the early-life period of fry using riverbank habitats, by walking along the banks all over the study area and seeking for each individual or school (then numbered) to pick up its precise location. The habitat use was established in the same time, as well as the available habitat on the colonized area later, with a typological approach of the shoreline habitats on the basis of five descriptive variables, decomposed in a small number (i.e. 3 to 4) of categorical and easily discernible modalities. Then, a practical typology of riverbank habitats was developed to easily distinguish different habitat types (HT) available on the studied river, and how grayling fry were distributed across all these types of habitat was finally determined, in order to describe habitat type preferences. Results firstly showed that fry was longitudinally distributed in a reduced portion of the river, and concentrated on areas providing suitable conditions. Secondly the multidimensional macrohabitat approach provided differential modality preferences from the ones obtained when considering independently each variable (univariate analysis) of microhabitat. The present study enlightened how such a larger scale approach of habitat type preferences can bring useful ecological information and improve the identification of suitable habitat. This multidimensional and categorical typology of habitats, easily applicable by managers, can guide them in riverbank conservation and restoration actions for the management of threatened fish populations.

Keywords : *Thymallus thymallus*, Fry habitat preference, Management



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Biogeography of the neotropical ichthyofauna at the regional scale: beyond the hydrogeology hypothesis

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With more than 5,600 species, the Neotropics harbor the highest diversity of freshwater fishes in the world. To explain the geographical distribution of the neotropical ichthyofauna, several hypotheses have been proposed. A hypothesis enjoying increasing acceptance is the hydrogeology hypothesis, which suggests that headwater stream capture events enabled species to disperse into adjacent basins and that local tectonic uplifts lead to vicariance events, followed by allopatric speciation. However, in single basins without hydrogeological barriers, empirical evidence for geographical structure in species distribution patterns remains scarce. In the present study, distribution patterns of cichlid fish species in the upper río Madera drainage (south-western Amazon), a large basin lacking substantial hydrogeological barriers, were evaluated. Cichlids may be especially suited for such regional analysis as their low dispersal ability conserves traces of historical hydrogeographical events and their high speciation rate accelerates diversification processes. Species identity is typically manifested in conspicuous phenotypic traits, enabling reliable species identification. Over 2000 reports of 45 species were obtained from field expeditions, local museum collections and the literature. The analysis revealed a considerable geographic structure in species distributions, which cannot be explained by the current hydrogeological setting and the physicochemical environment alone. Species distributions rather be determined by a complex interplay of dispersal abilities, historical hydrogeological events and spatial differences in environmental parameters. The observed spatial structure does not follow the bifurcating pattern of the riverine drainage system and therefore contrasts earlier biogeographical subdivisions of the upper río Madera basin. Regional studies may significantly improve the delimitation of operational geographical units and therefore increase the explanatory power of supra-regional analyses, leading to a better understanding of Neotropical biodiversity.

Keywords : Biogeography, South america, Cichlidae



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Invited speaker

Monsters from the shallows: genetic analysis of postembryonic development revealing developmental capacity, constraint, and architecture of change

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The diversity among fish is a rich resource to address the process and means of evolutionary change and the hidden potential within developing organisms. The specification of form, physiology, behavior, and life history can be found in the regulation of development and its response to the environment. My lab uses comparative studies of development to help understand the mechanisms underlying the evolution of morphological and physiological diversity. Fish have several established, experimental models for genetic analysis. Additionally, the morphological and genetic diversity among fish provides a wealth of new models in which to look at the genetic and developmental basis of character change. Mutation analysis in experimental model organisms is at the core of our understanding of how development works, and these findings have proven important in the identification and functional support of genetic variations associated with character change in natural populations. However, many genes have early essential roles in development and these genes are often reused multiple times during development. Thus, it has been argued that the essential and pleiotropic effect of many developmentally important genes limits the utility of such mutational study of development toward understanding the process of evolution. By focusing on late developmental events however, one limits the type of genes as well as the types of genetic and developmental changes that may be identified; this selective bias in the types of changes that permit change while retaining viability and reproduction undoubtedly holds true for cases of artificial and natural selection. This analysis of the regulation of late developmental events may then refine the predictive value of such mutational analysis. I will discuss the use of fish as experimental and natural models to address these questions. A broadening of comparative genetic analysis across many genera may resolve the bias against genetic 'monsters' and what they can tell us about potential within developing systems and the capacity for evolutionary change

Keywords : Genetics, Evolution, Development



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Do individual fitness or display size differ among colour morphs in “roundfin” sailfin silversides?

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Lake Matano harbors the small radiation of “roundfin” sailfin silversides (Atheriniformes: Telmatherinidae: *Telmatherina*). Its three morphospecies are characterized by substantial, but incomplete, reproductive isolation, morphological traits such as body size and shapes of head and body, and distinct patterns of habitat use. These findings are consistent with a sympatric mode of divergence of roundfins within this extraordinarily deep, ancient lake. Focus analyses revealed resource partitioning and corresponding adaptations also between male and female roundfins, demonstrating that sexual dimorphism contributes to further ecomorphological and trophic diversity in this emerging fish radiation. In contrast, there are no indications that the conspicuous male colour polymorphisms present in sailfin silversides are related to divergence in terms of morphology, ecology or population structure. Here, we focus on male colour polymorphisms in roundfins and test the hypotheses that male colour ornaments or display size correlate with individual fitness proxies. We find no indication that blue and yellow morphs differ in individual condition or relative mass of the liver, the two proxies for individual fitness applied, or in display sizes of body and unpaired fins. This clearly supports previous findings suggesting that environment contingent selection in terms of heterogeneous visual background likely explains male colour polymorphism in sailfin silverside lake radiations.

Keywords : Lake fish, Adaptive radiation, Speciation



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Invited speaker

Using cypriniform fishes to investigate the origin, function, and morphological evolution of trophic novelties

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Cypriniform fishes, which comprise approximately 25% of all freshwater fishes are characterized by a number of evolutionary innovations associated with feeding that may have played an important role in their adaptive radiation. Cypriniform fishes present an excellent model for investigating such innovations given that they possess a number of poorly investigated novelties associated with feeding: enlarged pharyngeal jaws opposed to an enlarged basioccipital process of the neurocranium (instead of upper pharyngeal jaws); a muscular palatal organ found on the roof of the buccal chamber used in feeding; and the kinethmoid, a rostral ossification associated with premaxillary protrusion. Although cypriniform fishes comprise an enormous proportion of the freshwater biota relatively little is known about these feeding novelties that characterize this diverse group. Here we combine developmental techniques, functional morphological approaches, and comparative methods to investigate the origin, functional consequences, and ultimate evolutionary consequences of cypriniform morphological novelties. The developmental mechanisms involved in the generation of these novelties were investigated using zebrafish. While most often used as a model for biomedical studies the zebrafish actually provides an excellent system with which to investigate the origin and early development of these trophic novelties. A number of experimental approaches (high-speed video, PIV, and XROMM) were used to investigate functional implications of kinethmoid-driven premaxillary protrusion. Finally, histological and developmental tools were used to examine both the origin and subsequent morphological evolution of the palatal organ. Here we present data on the size, structure, and myosin composition of palatal organs within several subfamilies. A complex mesh of predominantly fast muscle fibers characterized all but one species of cypriniform palatal organs examined. This evolutionary developmental project is unique in examining novelty at several levels starting from a developmental genetic level, through performance, and ultimately to evolutionary consequences. Moreover, identifying the developmental mechanisms responsible for the origin of these feeding adaptations will enhance our understanding of how functional novelties arise and evolve.

Keywords : Cypriniformes, Feeding, Evolutionary novelty



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Oral

Variations on a Theme: Evolution of a Vertebrate Social Decision-Making Network

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Animals evaluate and respond to their social environment with adaptive decisions. Revealing the neural mechanisms of such decisions is a major goal in biology. We analyzed expression profiles for 10 neurochemical genes across 12 brain regions important for decision-making in 88 species representing five vertebrate lineages (teleosts, amphibians, reptiles, birds, mammals). We found that behaviorally relevant brain regions are remarkably conserved over 450 million years of evolution. We also find evidence that different brain regions have experienced different selection pressures, because spatial distribution of neuroendocrine ligands are more flexible than their receptors across vertebrates. Our analysis suggests that the diversity of social behavior in vertebrates can be explained, in part, by variations on a theme of conserved neural and gene expression networks.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Oral

Brain variations and phylogenetic trends in ray finned fishes

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Ray finned fishes are the largest vertebrate group and show enormous variations in morphology and behavior. This is also reflected in brain morphology. We have investigated the brains of a large number of actinopterygians to study the evolution of the brain in different radiations. Early actinopterygian brains were probably relative simple as found in polypterus, sturgeons and paddlefish, and garfish. Within teleosts, there is a marked increase in size and complexity of the hypothalamus in acanthopterygii. In addition, there are structures associated and connected to the hypothalamus like the nucleus glomerulosus and the nucleus of the posterior tubercle that are not found as such in the rest of the teleosts. The hypothalamus and associated structures are heavily interconnected with the telencephalon, which suggests a role in certain cognitive functions. Correlations with ecology reveal that most diurnal coral reef species are acanthopterygii (possessing a nucleus glomerulosus), whereas most fresh water fish are not. Notable exceptions are cichlids, which may be so successful because of cognitive abilities associated with the nucleus glomerulosus. The hypothalamus further increased in relative size in tetraodontiforms and syngnathiforms for reasons that we do not yet understand. There are also marked trends in sensory related areas. Particularly taste and smell show enormous variations in size that are not immediately apparent by inspecting the receptors. There are primary, secondary, and tertiary gustatory centers in the brain, each of them can vary in size independent from each other. Primary gustatory centers are especially large in some cyprinids in accordance with their elaborate feeding mechanism. In some species (e.g. *Elops saurus* and *Amia calva*) we found an enlargement of tertiary gustatory centers for reasons that we do not understand yet. The cerebellum also varies in size enormously ranging from gigantic in mormyrids to minute in scorpion fish. It is also very large in tunas and may well be associated with motor skills involved in active hunting. Some coral reef fish have large cerebelli, but, in this case, this is probably due to motor skills associated with maneuvering in a spatially complex habitat. Marked differences in size and complexity are present also in a newly discovered auditory area in the midbrain, which could reflect the varying importance of acoustic orientation in different species. Morphological specialization of brain areas may play an important role during evolution of species and the integration with ecomorphological data could greatly enhance our understanding of the driving forces of the evolution of ray finned fishes.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Riddles in the Siebold collection : Heterogeneous type series of Japanese freshwater fishes

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Philipp Franz von Siebold (1796-1866) was a pioneer for Japanese modern natural history as well as a Military surgeon at Deshima, the Dutch trading post in Nagasaki. Siebold's vigorous collecting activities during his stay in Japan from 1823-1829 laid the basis of the "Fauna Japonica". Taxonomically, the Siebold collection plays a very important role for the nomenclature of fishes in Far Eastern Asia. Many specimens of fishes which had been brought from Japan by Siebold and his assistant and successor Heinrich Burger, were described as new species on the basis of syntypes by Temminck and Schlegel, curators at "Rijks Museum van Natuurlijke Historie" (now Netherlands Centre for Biodiversity Naturalis), Leiden. As syntype series are composed of multiple specimens without a name-bearing type, they often bring about taxonomic confusion. Although Boeseman (1947) in his revision unraveled some type series that were polyspecific and selected many lectotypes in syntype series of Temminck & Schlegel species, many problems were not recognized at the time. We give examples of three cases of heterogeneous type series in which a lectotype has been designated. In all cases the lectotypes and paralectotypes) are contained in a single jar. 1. *Cobitis biwae* Jordan and Snyder, 1900, "shima-dojou" in Japanese. Lectotype of *Cobitis taenia japonica* Temminck and Schlegel, 1846, RMNH 2703a. Contaminated by *Cobitis striata* Ikeda, 1936, RMNH 2703b-e, and *Cobitis matsubarae* Okada and Ikeda, 1939, RMNH 2703f-h. (See also Sawada and Aizawa, 1983; Yamaguchi, 2003). 2. *Pseudogobio esocinus* (Temminck and Schlegel, 1846), "kamatsuka". Lectotype of *Gobio esocinus* Temminck and Schlegel, 1846, RMNH 2478a. Contaminated by *Abbottina rivularis* (Basilewsky, 1855), RMNH 2478h-j. (See Authors, 2012). 3. *Pseudobagrus aurantiacus* (Temminck and Schlegel, 1846), "ariake-gibachi" Lectotype of *Bagrus aurantiacus* Temminck and Schlegel, 1846, RMNH 2952a. Contaminated by *Pseudobagrus nudiceps* Sauvage, 1883, RMNH 2952c. In the Fauna Japonica, the type locality is simply expressed as "near Nagasaki", i.e., Satsuma, Kurume, and Higo. These localities are limited to Kyushu Island, while the "contaminating species" mostly occur outside Kyushu, i.e., in the Lake Biwa basin on Honshu. This discrepancy may have been caused by the way of fish storage in the Siebold collection. Presumably specimens, which were roughly identified as the same species, were kept in a single lot regardless of sampling locality and date.

Keywords : Siebold, Contamination, Paralectotypes



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Poster

**Copulatory organ Anatomy in a new viviparous
nomorhamphus halfbeak (Atherinomorpha : Beloniformes
: Zenarchopteridae) from Sulawesi Selatan, Indonesia**

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Halfbeaks of the family Zenarchopteridae occur in freshwaters and estuaries of the Indo-West Pacific region, with five genera and 54 species recognized so far. The viviparous genus *Nomorhamphus* is endemic to Sulawesi and islands of the Philippines, where these halfbeaks inhabit mostly hillstream habitats. In Sulawesi, the species known so far occur either in the highlands of Maros in the island's south-west, the south-eastern peninsula, or in eastern Central Sulawesi. Morphological species discrimination strongly rests on the structure of the andropodium, the male copulatory organ, composed of the anterior five to seven anal-fin rays modified for sperm transfer. Examination of specimens collected in Central Sulawesi during the last years showed that these are only partially covered by current halfbeak taxonomy, suggesting that species diversity of *Nomorhamphus* in Sulawesi is strongly underestimated. Here, we present results of a closer examination of a so far undescribed species, based mostly on copulatory organ anatomy.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Virology and Immunology

Poster

Inflammatory response and heavy metal interactions in roach (*Rutilus rutilus*)

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Fish's survival and resistance to environmental stress are reduced and controlled by pathogens. A net increase of sensitivity to viral, bacterial and parasitic infections is linked to the presence of contaminants in the environment. Aluminium (Al) is the third most abundant element on Earth's crust; its high bioavailability is associated with toxic effects on freshwater fish at neutral pH. This metal is present in natural surface waters. In Champagne (France), high concentrations of Al are detected in association with viticultural practices. Different studies showed that exposure to high concentration of Al can induce oxidative stress, neurotoxicity, genotoxicity in numerous fish species but nothing is known about the possible immunotoxicological-related effects. The aim of the present study was to analyze interactions between chronic aluminium contamination and some components of the immune inflammatory response in roach. For this purpose, roach stimulated or not with bacterial lipopolysaccharides were exposed to environmental concentrations of aluminium (100 µg/L) under laboratory-controlled conditions for 21 days. Some cellular and humoral components related to the LPS-induced inflammatory response were performed on possible tissular targets: Head kidney and spleen. Phagocytosis, oxidative burst and metallothionein levels were measured on splenic and kidney leucocytes by flow cytometry. Lysozyme and Tumor Necrosis factor-alpha (TNF-α) biosynthesis were revealed in the same both tissues by immunohistochemistry. Results were examined in regards to the metallic bioaccumulation levels in immune tissues.

Keywords : Immunotoxicology, Roach



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Functional study of the Ser/Arg-rich splicing factor SRp30 during Zebrafish embryonic development

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Nuclear pre-mRNA splicing is a key process regulating gene expression in eukaryotes. Splicing consists of the removal of introns and the joining of exons within a dynamic macromolecular complex called the spliceosome, which consists of five small nuclear ribonucleoproteins (snRNPs) and numerous non snRNPs proteins. Amongst these non snRNPs proteins, the SR proteins family constituted an important group of splicing factors that are involved in constitutive and alternative splicing. SR proteins are structurally related as they are characterized by a C-terminal domain enriched in dipeptide Ser/Arg preceded by one or two RNA-recognition motifs (RRMs). Phylogenetic inference using the RRM domain allowed us to identify 16 encoding genes for SR proteins in the vertebrate model organism, *Danio rerio*. Zebrafish is increasingly recognized as powerful models for the study of vertebrate embryonic development in a physiological context. The roles of SR splicing factors during animal cell differentiation and development are largely unknown. The aim of the present research is to investigate SR proteins functions during zebrafish development by using molecular and genetic approaches. In this study, we investigated the role of the SR splicing factor SRp30. The expression profile was determined by *in situ* hybridization at 24, 48 and 72 hours post-fertilization and showed *SRp30* expression mainly in brain, retina and pharyngeal arches at these stages. Furthermore, *SRp30* knock-down by morpholinos microinjection strongly suggests an important role of this specific splicing factor during early cartilage, retinal and brain development. In order to gain insight into the molecular function of *SRp30*, we analysed control and morphant transcriptomes using high throughput RNA sequencing.

Keywords : Alternative splicing, Development, Transcriptome



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Oral

Genetic diversity within 6 Polish *Eupallasella percnurus* populations and distance between them revealed by polymorphism of the microsatellite DNA

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Introduction: The lake minnow, *Eupallasella percnurus* (Pall.), is listed in the Polish 'red book' as critically endangered species and is strictly protected by the Polish law. It is also a priority species within the Natura 2000 Network. The successful conservation and management of *E. percnurus* populations require an assessment of the level of genetic variability specific for both populations existing long and those newly established through translocations. An assessment of the observed genetic differences among the populations is also indispensable.

Material and Methods: Six populations of this fish from Kowalicha (newly established), Bledzewo, Siedliszcze, Sosniak, Mikołajki Pomorskie and Podpakule were investigated. The samples were taken from 298 fish ($n = 49-50$ per population). Polymorphism of 13 microsatellite loci was investigated. Genetic variation and genetic distance among these populations were evaluated. The size of genetic bottleneck/founder effect that has affected genetic variation was also studied.

Results and Discussion: In most of the examined microsatellite loci, only 2-3 alleles/population were detected. Some loci were found to be monomorphic in one or more populations. The overall number of alleles detected in each population across investigated loci varied from 24 in Mikołajki to 48 in Kowalicha. The observed heterozygosity (H_o) and expected heterozygosity (H_e) calculated across the investigated loci were low and ranged from H_o 0.23 and H_e 0.19 for Mikołajki to H_o 0.55 and H_e 0.50 for Podpakule. All populations remained at Hardy-Weinberg equilibrium. The investigated populations differed in M value. The lowest value of this indicator (0.39) was detected for Mikołajki Pomorskie population, the highest (0.53 and 0.52) was specific for Podpakule, Kowalicha and Sosniak populations. The M values detected within populations suggest that all of them have lost some of their genetic variation because of founder/bottleneck effect, but the size of this reduction was different. The level of genetic variation and M value estimated for newly established Kowalicha population were similar to the values specific for the most genetically diverse population from Podpakule, what therefore seem to portend well for future. The largest genetic distance (F_{st} 0.64, $\delta\mu^2$ 15.24) was found between populations from Siedliszcze and Mikołajki, but other populations were also highly genetically differed between each other. High genetic differences existing among all investigated populations indicate that in order to protect their genetic identity, the inter-population transfers of individuals of this species should be preceded by evaluation of genetic differences between the source and destination populations.

Keywords : Genetic variation, Lake minnow, Microsatellite DNA



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Where was it caught ? Mapping Swedish type localities of fishes from *Linnaeus* until exhaustion

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The type locality is the geographic location where the name-bearing type specimen(s) for a certain species was found. A literature survey of Swedish type localities for fishes was performed using original descriptions, supplementary documentation and digital maps. More than 200 species descriptions were scrutinized. Of these, 148 were descriptions of new species. Geographical coordinates were established for 133 species, where the description of the locality was sufficiently detailed. Some species have several syntypes from different localities, giving a total of 166 type localities. For little more than half of these species at least one preserved type specimen still exists. The localities are unevenly spread over Sweden. Southwestern Sweden is favored by higher biological diversity, and ease of travel access since centuries back. Only few type localities are present in northern Sweden, where also the diversity is lower, and travel options were subject to considerable difficulties into the 19th Century. Notable localities include the precise location of the type locality of *Cobitis taenia*, based on a description by Ardeï (1738) of specimens from Vårdsätra near Uppsala.

Keywords : Type locality



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Impacts of the invasive mosquito fish *Gambusia holbrooki* on the Greek native *Valencia letourneuxi*

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The rapid decline of the Greek native *Valencia letourneuxi* has been mostly attributed to habitat degradation, as well as aggression from or resource competition with the mosquitofish *Gambusia holbrooki*, but there is no documentation available on these negative impacts of *G. holbrooki*. For this purpose, specimens of *V. letourneuxi* were obtained from eight sampling sites in Western Greece with various *G. holbrooki* densities during the dry season (June to mid-October 2005, 2006 and 2009). To test for a population response of *V. letourneuxi* to *G. holbrooki*, mean densities of the two species per sampling site were examined for the best curve estimation regression model. Logarithmic regression proved to have the best response of the *V. letourneuxi* density (dependent variable) to the *G. holbrooki* density (independent variable). From the created model, a unique *G. holbrooki* density threshold value was defined, that had a pronounced effect on the corresponding values of *V. letourneuxi*. The mean values of *V. letourneuxi* life history variables (condition and reproductive variables) were compared between “low *G. holbrooki* density (i.e. below *G. holbrooki* threshold) and “high *G. holbrooki* density” (i.e. over *G. holbrooki* threshold) *V. letourneuxi* samples. Results show that in the summer, there were no significant differences in the condition of juvenile and adult *V. letourneuxi*, whereas in autumn (at the end of the reproductive period) the somatic condition of both juveniles and adults was significantly poorer in sites with high *G. holbrooki* densities. Female gonadosomatic index (GSI), in contrast, did not differ significantly either in summer or in autumn.

Keywords : Mosquito fish, Native fish, Somatic condition



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Poster

Effects of hyperthyroidism on the development of *Danio rerio* vertebral column and caudal fin

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Thyroid hormones play a crucial role in the teleost development. The influence of TH on the skeletogeny is still insufficiently explored. We investigated the effects of the hyperthyroid conditions, attained by the administration of the exogenous triiodothyronine T₃ (1 ng/ml), on the development of *Danio rerio* (zebrafish) vertebral column and caudal fin. The skeletal structures differ in the reaction to the hyperthyroidism: from the absence of any visible changes (most of vertebral bodies, ribs, scaphium of the Weberian apparatus, lateral processes of the second vertebra, hemal arches and spine of the preural 2, hypurals 1-4, parhypural) to significant changes in timing of appearance, abnormal development or disappearance. Supraneural 3 of the neural complex and the claustrum arise earlier, whereas the lateral processes of the first vertebra, the basidorsals of the second vertebra, supraneurals 5-9 appear later than in fish reared under normal conditions. Intercalarium, usually consisted of three processes, lose one or two of them in many cases. Absence of the supradorsals associated with the neural arches three and four results in the underdeveloped neural complex. Neural and hemal arches and spines in many cases are absent or develop abnormally and acquire the irregular shape. Such structures as an epural, hypural 5, ural-2 centrum, supraneural 2 of the neural complex and the dorsal process of the supraneural 3 fail to appear during the development of many specimens. As one may conclude, hyperthyroidism seriously affects the development of the zebrafish vertebral column and caudal fin and causes the changes in the fish adult morphology. The elements of the vertebral column and caudal fin differ in the reaction to the hyperthyroidism. Moreover, specimens, even siblings, display the different thyroid hormone responsiveness – from the absence of changes in the development to the numerous developmental abnormalities.

The present study was partially funded by the Russian Foundation for Basic Research (10-04-00787-a). Authors are recipients of the Grant of Russian President (MK-2026.2011.4).

Keywords : Hyperthyroidism, Skeletogeny, Zebrafish



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Type series of *Pseudogobio esocinus* (Teleostei; Cypriniformes) in the Siebold collection : its taxonomic problem

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Von Siebold had been collecting many Japanese animals and plants, thereby accomplished a great achievement for Japanese natural history entitled as "Fauna Japonica". The Siebold collection comprises not only the oldest specimens of Japanese freshwater fishes, but also provides the keys to give us important information about taxonomy and past original fish faunae. However, there are some problems in the Siebold collection; 1) taxonomic study is not adequate because of the way of type designation: 2) each sampling site is very unclear, particularly on type locality.

Pseudogobio esocinus belonging to Cyprinidae, Gobioninae, is a freshwater bottom dweller and distributed in Japan and Korea. This species was described as "*Gobio esocinus*" by Temminck & Schlegel (1846), namely one of the typical Siebold's collection on the basis of syntypes, and then designated as type species of the genus *Pseudogobio* by Bleeker (1860). Boeseman (1947) designated the lectotype for *P. esocinus*, referring to some variation in several characters. Tominaga et al. (2009) found two different forms by mitochondrial cytochrome b gene in western Honshu Island, Japan, and indicated the existence of cryptic species within *P. esocinus*. Additionally, taxonomic relationship between *P. esocinus* and closely related *P. vaillanti* distributed in China is still uncertain. Furthermore, type locality of *P. esocinus* is not obviously known as in other Siebold collection. Hence, we examined syntypes of *P. esocinus* (RMNH 3478) to define its taxonomic position and state. Type observation on 7 specimens of syntypes for *Pseudogobio esocinus* led us to reconfirm proper lectotype designation by Boeseman (1947). At the same time, we happened to find the contamination of 3 specimens of *Abbottina rivularis* in syntypes. Above observation resulted in no effect on nomenclature of *P. esocinus*, because these three heterogenous specimens were regarded as paralectotypes.

Pseudogobio esocinus is widely distributed in the Honshu Island in Japan, but distribution of *A. rivularis* is restricted in the northeastern Kyushu, Sanyo District and Lake Biwa-Yodo river basin. Siebold went through these regions except the Sanyo region when the single court journey to Edo (Tokyo) in 1826. Therefore, type locality of *P. esocinus* would be specified to the north-east Kyushu and Lake Biwa-Yodo River basin.

Keywords : *Pseudogobio esocinus*, *Abbottina rivularis*, Siebold collection



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Important variations in sonic apparatus morphology and sound characteristics of *Ophidion rochei* (Ophidiidae)

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Despite sounds were recorded in few Ophidiiform species (five Carapidae and two Ophidiidae), the importance of acoustic communication in this taxa is well supported by morphological data. In Ophidiidae, there is an important sexual dimorphism in sonic apparatus but sounds were never recorded from females. This study focuses on *Ophidion rochei* that inhabits shallow water of Mediterranean and Black Seas. The aims of this study were 1) to obtain sounds in captivity, 2) to give a description of the different morphotypes, and 3) to investigate how morphological data and abiotic parameters affect sounds characteristics. Fish were recorded in the field and in tanks at different temperatures before being dissected, cleared and stained to describe the morphology of sonic apparatus. Temporal and spectral characteristics of all recorded sounds were investigated with Avisoft software. Sounds were made by males, females, and juveniles. The call signature could be divided in two principal types. The first was emitted by males while the second was attributed to females and juveniles. Males produced 'pulsed sounds' composed of a single or many pulsations (3 to 55). Multiple pulsed sounds lasted from 167 to 6578 ms and the mean pulse period was around one 100 ms. Females and juveniles produced 'classical swimbladder sounds'. The call duration in females was much shorter and ranged from 0.6 to 60 ms. In this case, the period was around 4 milliseconds. Females and juveniles also displayed closely-related morphologies in comparison to males that showed huge differences in the anatomy of first vertebrae, ribs, sonic muscles, and swimbladder ('rocker bone', anterior neck, internal posterior tube). Males sound also present variations in some sounds characteristics such as pulse duration, pulse period, and sound amplitude. These variations seemed correlated with the development of the sonic apparatus, from the juvenile morphotype to the adult morphotype. The temperature also affects some sound characteristics of males and females sound. Pulse period, for example, becomes shorter when the temperature rises. In conclusion, in correlation with completely different morphologies, calls in females and juveniles were clearly distinct from male calls. The high complexity of the male sound producing anatomy suggests the important role of acoustic communication in this species.

Keywords : Morphology, Acoustic, Ophidiidae



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Habitat preferences of *Cobitis kaibarai* (Teleostei: Cobitidae) between spawning and non-spawning seasons in paddy fields, Kyushu Island, Japan

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Habitat preferences between relative abundance of the species and environmental factors would be useful in understanding their population ecology and for evaluating their potential for interaction with surrounding. In addition, their microhabitat requirements would be valuable when planning management to alleviate the effects of habitat alteration occurred by stream modification. *Cobitis kaibarai* is one of the *Cobitis striata* complexes that distribute in the rivers flowing Ariake estuary, northern Kyushu, Japan. This spined loach is endemic species in northwestern part of Kyushu. Even if it is designated as endangered (EN) level would be possibilities of extinction in the future due to its limited distribution on the Japanese Red List, there were few ecological data about this species. It is only known that this species inhabit in the agricultural creeks or mid-lower reach of rivers. In this study, the habitat selection of spined loach, *C. kaibarai* was researched by analysis monthly environmental data between spawning and non spawning seasons in Ushizu river system, Saga prefecture, Kyushu Island, Japan. The study area is located in paddy fields, including deep concrete-sided revetments and traditional-style channels irrigated with river water through shallow ditches. The individuals were captured using a hand net (mesh size, 1 mm) and released after counting the number of specimens and measuring SL with weight from October 2009 to June 2011 monthly and 10 physical environmental parameters (water temperature, water velocity, water depth, water width, MPS, PCS, existence of four hydrophytes type) were measured to assess the microhabitat in 12 sites each month. Akaike's Information Criterion (AICc) and Generalized Linear Model (GLM) were utilized for analysis to detect the effect of the important environmental variables on the habitat of *C. kaibarai*. The capture and recapture method using illustration marking was conducted to confirm the movement of the individuals between spawning and non-spawning seasons on 12 stations. A total of 2018 individuals were captured. The population was expected to be correlated with the water temperature and emergent hydrophytes with silt substrate in non-spawning season. There were no correlative relationships with environmental variables by habitat selection on statistical analysis in spawning season (from April to July). However the adults seem to move from concrete sided channel to traditional-style temporary water channels for spawning normally characterized as very low water depth or no water in winter season from verification of marked individuals migrating and differences of the population density. The floodplain is not useful for agricultural farming without advantages but if the temporary water areas are changes by modification, then this would be risk suspected to affect the reproductive population on conservation perspective of this species.

Keywords : Cobitidae, Floodplain, Habitat selection



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Genetic and morphological divergence between Japanese dojo loach *Misgurnus anguillicaudatus* populations with three different mitochondrial DNA clades

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The dojo loach (or the oriental weather loach) *Misgurnus anguillicaudatus* inhabits the waters of East Asia, including the waters of the Japanese Islands. The Japanese population of *M. anguillicaudatus* includes two major mitochondrial DNA (mtDNA) clades: Type I (with ancestral, non-introgressed mtDNA) and Type II (with introgressed mtDNA from the genus *Cobitis*). The latter clade with introgressed mtDNA includes two sub-clades: Type IIa (Japanese native) and Type IIb (introduced from the Asian continent). The taxonomical relationship between the populations with the three different mtDNA clades has not been established. In this study, we compared *M. anguillicaudatus* populations with the three different mtDNA clades on the basis of their genetic and morphological characteristics. Genetic analysis using nuclear *RAG-1* gene sequences (897 bp) indicated low levels of genetic divergence between the populations with the three different mtDNA clades. Moreover, populations with the Type I and Type IIa clades could not be distinguished from each other, despite a high degree of mitochondrial divergence between them. Morphological characteristics were examined by measuring 19 distances and counting five characters using soft X-ray photography. We observed a difference in morphological characteristics, including the number of vertebrae (range, 48 to 50 vs. 43 to 48) and the proportion of caudal peduncle length to standard length (approx. average, 0.17 vs. 0.14), between the populations with the Type I and Type II clades. In addition, we observed differences in morphological characteristics including the number of dorsal pterygiophores (mode, eight vs. seven) between the population with the Type IIb clade and the populations with the other clades. These findings suggest that populations of *M. anguillicaudatus* with the three different mtDNA clades can be regarded as different taxonomic units. To elucidate their taxonomic relationship, sympatric populations with the different mtDNA clades need to be analyzed further.

Keywords : Dojo loach, Introgression, Rag-1



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Seasonal dynamics of the ichthyofauna of a lowland tributary of the Vistula River

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Seasonal changover of fish assemblages, especially in regard to the species commercially exploited, is widely known and appreciated by professional fishermen for centuries. Irrespective, quantitative data are rather scarce and only several studies focused on marine ecosystems and freshwater lakes are available. Data regarding temperate lowland rivers are minor. For that reason, in 2011 we conducted an introductory research, consisting of triple sampling (in spring, summer and autumn) in the Nida River, the longest left-bank tributary of the Upper Vistula River. The sampling was performed by the means of downstream boat electrofishing. During each season the electrofishing was made on exactly the same 20 sites along the 100-km stretch of the Nida River. On overall, we recorded 33 species belonging to the 11 families. Taking into account abundance, more than 90 % of the total fish catch belonged to the following nine species: *Alburnus alburnus*, *Rutilus rutilus*, *Gobio gobio*, *Squalius cephalus*, *Leuciscus leuciscus*, *Esox lucius*, *Leuciscus idus*, and *Blicca bjoerkna*. The structure of the ichthyofauna significantly differed among the seasons. In spring the most dominant fish was *R. rutilus* (26.5 % of total fish catch), followed by *A. alburnus* (20.5 %), *S. cephalus* (11.6 %), *L. leuciscus* (7.8 %), *E. lucius* and *G. gobio* (each of 6.0 %), *L. idus* and *P. fluviatilis* (each of 5 %), and *B. bjoerkna* (2.4 %). In summer the most dominant was *A. alburnus* (49.0 %), along with *R. rutilus* (23.1 %). Far less frequent were *S. cephalus* (4.9 %), *B. bjoerkna* (4.2 %), *L. leuciscus* (3.3 %), *G. gobio* (3.0 %), *L. idus*, *P. fluviatilis*, and *E. lucius* (altogether 6.9 %). In autumn the dominant was still, however not so significantly, *A. alburnus* (27.7 %), then *G. gobio* (14.5 %), *R. rutilus* (12.9 %), *E. lucius* (8.3 %), *P. fluviatilis* (8.0 %), *L. leuciscus* (7.1 %), and *S. cephalus* (7.0 %). It was striking that in autumn sampling *B. bjoerkna* was only 1.1 %. It should be noted that summer and autumn samplings were undertaken during the extremely low water level, what could significantly affected the results. These data clearly show that in a medium-sized lowland river, as the Nida River, the composition of the ichthyofauna varies noticeably over a year. This is an important information for further monitoring samplings, which are usually performed only one time a year, most often in autumn.

Keywords : Electrofishing, Fish assemblages, Seasonal changeover



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Integration of fish fossil data into phylogenetic
and comparative studies

Oral

A total evidence approach to dating with fossils

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Phylogenies are usually dated by calibrating interior nodes against the fossil record ("node dating"). This relies on indirect ad hoc methods that, in the worst case, misrepresent the fossil information. Here, we compare standard node dating to an approach based on simultaneous analysis of fossil and extant taxa ("total-evidence dating") within a Bayesian context. As a test case, we focus on the early evolution of the Hymenoptera (Insecta). For node dating, we use nine calibration points derived from the fossil record, while total-evidence dating is based on 343 morphological characters scored for 45 fossils (4-20 % complete) and 68 extant taxa. In both cases we used molecular data from five markers (about 5 kb) for the extant taxa. We use relaxed-clock models to accommodate rate variation across the tree but find it necessary to introduce a rooting constraint to avoid errors in tree topology. The order Hymenoptera is estimated by our approach to date back to the Carboniferous with an approximate age of 309 My (291-347 My). Despite considerable uncertainty in the placement of most fossils, we find that they contribute significantly to the estimation of divergence times, as indicated by usually narrower posterior distributions that are less sensitive to prior assumptions when fossils are included as terminals. From a theoretical standpoint, total-evidence dating is preferable simply because it explicitly incorporates the fossil data instead of relying on secondary interpretation. Our results suggest that it can also improve the precision and accuracy of divergence time estimates.

Keywords : Molecular dating, Calibration, Fossil



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Rapid identification of four species of invasive gobies using PCR-RFLP

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Studying various aspects and consequences of biological invasions is of great importance in scientific and economic points of view. However, the identification of invaders, and especially their juveniles, could be substantially difficult if they are represented by several morphologically similar species. The aim of our work was to develop a rapid, cost-effective molecular method for identification of the four species of invasive gobies occurring in the central Danube basin, namely *Neogobius melanostomus*, *Neogobius fluviatilis*, *Ponticola kessleri* and *Babka gymnotrachelus*. First, the fragment of cytochrome oxidase I gene was amplified and sequenced for representative samples of the four species. The appropriate sequences of the four species available in GenBank were also used. Low intraspecific sequence variation was detected, whereas substantial interspecific differences were found. The fragment was digested with the Bfal enzyme, which showed unique restriction patterns for each of the species. The four patterns were clearly distinguishable from each other using the standard agarose gel electrophoresis. This method proved valuable for discriminating the four invasive gobies in the Danube basin as well as in other native and non-native areas of their distribution.

This contribution is the result of the project implementation: Development and application of the innovative diagnostic approach for the molecular identification of animals (ITMS: 26240220049) supported by the Research & Development Operational Programme funded by the ERDF.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Discarding practices in the commercial trawl fisheries in the eastern Adriatic Sea

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Discards of unwanted or undersized fish and other non-target species represent a significant proportion of global marine catches that enhance the negative impact of fishery, especially when using fishing tools with low selectivity as bottom trawl nets. In order to estimate both retained and discarded catch composition of the commercial trawl fisheries in the eastern Adriatic, we used scientific observer records during 2010 and 2011. A total of 49 fish species, 12 cephalopods and 7 crustaceans were recorded in the catches, of which 29 species were always discarded and 39 species were only partially retained (discarding practice was generally market-driven). During the investigation period, it was estimated that 76.5 % of the total catch by number and 39.6 % by weight were discarded. When focused only on the sampled fish species, 18 were always discarded with *Seranus hepatus*, *Boops boops*, *Gadiculus argenteus*, *Lepidopus caudatus*, *Lesueurigobius friesii* and *Callionymus sp.* being the most numerous among them. On the other hand, the most abundant commercial fish species that were only partially discarded were *Merluccius merluccius*, *Trachurus sp.*, *Lophius budegassa*, *Mullus barbatus*, *Lepidorhombus sp.* and *Micromesistius poutassou*. Estimated percentages of discard for these species were as follows: for *M. merluccius* 49.2 % by number and 12.4 % by weight, for *Trachurus sp.* 41.2 % by number and 12.6 % by weight, for *L. budegassa* 56.5 % by number and 5.9 % by weight, for *M. barbatus* 5.7 % by number and 2.8 % by weight, for *Lepidorhombus sp.* 84.4 % by number and 48.4 % by weight, for *M. poutassou* 79.7 % by number and 73.3 % by weight. Catches of *M. barbatus* were almost always retained and small amounts of discard mainly referred to the individuals of TL bellow 11 cm (MLS for this species) and therefore of no commercial interest for the fishermen. On the contrary, *M. poutassou* was usually discarded and was retained only when the overall catch was low. For the remaining four species, although discard percentages by weight may be considered as low, it should be noted that discard percentages by number are quite high and are further emphasizing the significant impact of discards on the state of fish populations.

Keywords : Trawl fishery, Discard, Adriatic



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Poster

The hypothalamus of teleost fishes

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The hypothalamus is the single largest constituent of the diencephalon in most teleosts, and its prominence surpasses that of the species' thalamic nuclei. The latter are commonly regarded sensory relays in higher vertebrates, but play a lesser such role in fish. The hypothalamus varies in relative size across species, which may reflect its integration in sensory and premotor pathways, and its involvement in higher order behaviours, which the hypothalamus is thought to support through feed-forward and feed-back loops with the dorsal pallium. Furthermore, morphometric analyses (volume brain-part / volume brain) of representatives of several fish groups show that each is clustered around a different ratio of telencephalon vs. hypothalamus volumes (with respect to total brain size). A large telencephalon, but small hypothalamus is characteristic for osteoglossomorphs, a moderate hypothalamus is present in the remaining non-acantopterygians. Acanthopterygians, in contrast have a larger hypothalamus and tetraodontiformes have both, a large telencephalon and a very large hypothalamus. We presume correlations can be made between these clusters and behaviours / cognitive abilities of the species they contain. Despite the hypothalamus' assumed importance as both sensory-information relay and feedback station for cognitive behaviours computed in the dorsal pallium, little is currently known about functional subdivisions and their respective differential connectivity. We sought to remedy this situation by investigating the hypothalamus of two species, i.e. the goldfish and the pufferfish (*Carassius auratus* and *Colomesus asellus*) by means of histology, neurochemistry (NADPH and cytochrome oxidase), and calcium-binding-protein immunocytochemistry (Calretinin, Calbindin, and Parvalbumin). The results presented here will lay the basis for forthcoming studies of the differential hodology of the identified subdivisions, in order to elucidate the complexity of the functional anatomy of the teleost hypothalamus and its possible role in the evolution of fishes.

Keywords : Hypothalamus, Evolutionary morphology, Brain morphology



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Oral

Role of Fgf receptors in cranial cartilage development of the zebrafish

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The Fgf pathway is involved in various processes such as cell growth, differentiation, axis patterning or cell migration. In zebrafish, cranial cartilage of the viscerocranium results from migration and differentiation of cranial neural crest cells (cNCC). These processes are governed by reciprocal interactions between cNCC and other tissues such as pharyngeal endoderm, mediated by secreted morphogenic factors such as Fgfs. We study expression of Fgf receptors in the zebrafish pharyngeal region and their function in pharyngeal cartilage formation.

Between 24 and 48 hpf (hours post fertilization), only receptors 1 and 2 are expressed in the pharyngeal region, while mRNA encoding receptors 3 and 4 was not detected. At this stage, fgfr1 and fgfr2 mRNA are mainly localized in the endoderm. Fgfr1 and Fgfr2 Knock down by morpholino injection, analyzed by Alcian Blue staining at 4 dpf, caused modifications in the mandible, the hyoid and the ceratobranchial arches. Similar phenotypes are obtained by using transgenic zebrafish ((Hsp70-dnFgfr1-eGFP)^{pd1}) containing a hsp70-controlled gene for a dominant-negative Fgfr1 mutant after a 30 minutes heat shock at 37°C. Our results confirm that the Fgf signaling pathway is important for cranial cartilage formation in zebrafish.

Investigating expression of genes known to be involved in cartilage formation revealed that Fgfr1 is involved in ventral migration of cNCC at 48 hpf. Endoderm formation and expression of chondrocyte maturation markers are reduced in both Fgfr1 and Fgfr2 morphants. Moreover, endodermal targets of Fgf signaling, crucial for endodermal function, are affected when Fgf receptors expression is reduced. Thus, both Fgfr1 and Fgfr2 are involved in endoderm formation and signaling and are crucial for later stages of chondrocyte maturation.

Keywords : Zebrafish, Development, Cartilage



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Study of the carrying capacity of two Belgian rivers, for Atlantic salmon *Salmo salar* L. according to habitat and trophic resource availabilities

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The Atlantic salmon *Salmo salar* L. used to be a common species in most rivers of Europe and North America. However, it disappeared from most European rivers due to human activities such as overfishing and dams in the middle of the 20th century. During the last decades, several countries have set up reintroduction or protection programs in order to restore the populations involving restocking operations with eyed eggs, fry, parr or smolts. A similar project, called "Meuse Saumon 2000", is led in Wallonia (Belgium) since 1987. During its freshwater life stage, the salmon lives in riffles and rapids, characterized by high flow velocity, shallow water and coarse substrates and chase drifting invertebrates. However, habitat and feeding preferences vary over time with development. The aim of this study was to evaluate the carrying capacity of two rivers (Ourthe and Samson) in Belgium, by evaluating habitat and food availability. First, based on orthophotoplans, we used the Geographic Information System (ArcGIS) to determine the riffles' and rapids' areas auspicious for young of the year. Thus, on the Ourthe, we identified 111ha out of 324 to be potential habitats and 3 ha on the Samson. These estimations were verified *in situ*. Then, the availability of trophic resources was estimated, through 50 sampling sessions of benthic and drifting macroinvertebrates carried out during June and August 2011. Macroinvertebrates were determined, quantified and measured. Up to 17 and 16 families were observed in the rivers Samson and Ourthe respectively with an average of 9411 and 8718 ind./m². Ephemeroptera and diptera were the most common taxa collected. During the same period, parrs were caught in the riffles using electrofishing. Biometry, fish-length and mouth-width were measured and the stomach contents were sampled. Pearre index was calculated in order to characterize the salmon's feeding behaviour. We conclude that, in both rivers, young salmon are opportunistic predators which hunt preferentially abundant and low mobility species likes Chironomidae, Simuliidae and Baetidae. Based on feeding capacity, food availability and feeding preferences, the carrying capacities of Ourthe and Samson Rivers were evaluated at 21 parr /100 m² and 24 parr/100 m² respectively.

Keywords : Salmon, Mapping, Carrying capacity



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Acanthomorph (Teleostei) large scale interrelationships

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Interrelationships among orders or suborders of spiny teleosts (Acanthomorpha) have deeply changed during the last ten years thanks to japanese, american and french large-scale molecular phylogenetic studies. These changes will be reviewed with a focus on clades repeatedly found by independent teams and data, recent results from our team and significance for some morphological characters.

Keywords : Acanthomorpha, Phylogeny



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Actual status of the ichthyofauna of the Mono river basin (Togo and Benin)

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In order to assess the impact of human activities on the fish diversity of the Mono river basin, in general, and the planned construction of a dam at Adjarrala, in particular, an update of the knowledge on its ichthyofauna was initiated. The data were obtained from Museums collections and literature. A list of fish species was compiled and updated following the last systematic revisions. A total of 61 species, distributed over 39 genera and 22 families, was found. With 10 species, Cyprinids are the most numerous. Cichlids and Mormyrids follow with respectively nine and seven species. Further, Alestids and Clariids are represented each with 6 species. The remaining groups are represented by three or less species only. Among the 61 currently inventoried species, three are marine species and one (*Oreochromis niloticus*), a freshwater species has been introduced. Two species, i.e. *Heterotis niloticus* and *Raiamas senegalensis*, were not reported in the literature but were found to be present in the Museum collections. The presence of *Marcusenius brucii*, *M. cyprinoides*, *Petrocephalus simus*, *Phractura ansorgii*, *Synodontis melanopterus* and *Brycinus leuciscus*, in the Mono river could not be confirmed. Specimens identified as such and housed in the collections, turned out to be misidentified.

Keywords : Ichthyofauna, Mono river basin, Togo and Benin



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

**The arrangement and fixation mechanisms of body plates
in straight-nosed pipefish *Nerophis ophidion* (L.)**

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Instead of elasmoid scales, which are widespread among teleost species, the body of straight-nosed pipefish *Nerophis ophidion* (L.) of the order Syngnathiformes is completely enclosed by dermal bony plates. Using the scanning electron microscope (SEM) images, the main objective of present study is to observe locating features of the body plates of *N. ophidion*. In addition, to find out fixation mechanisms between the body plates. The study shows that the shape of these superficial skeletal elements is dependent on the position on the body. The bony plates, forming rows on the body, have processes fixing the adjacent plates with each other, but also the sculpture on the plates plays an important role in fixation.

Keywords : *Nerophis ophidion*, Bony plates, SEM study



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Molecular phylogeny and biogeography of the genera *Marcusenius* and *Petrocephalus* (Mormyridae) in southern Africa

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The family Mormyridae comprises 18 genera and about 200 species of freshwater fishes endemic to tropical Africa. Mormyrids are unusual in having an electric organ that they use for electro-communication and electro-location. The electric organ signal or discharge (EOD) is species specific and has been used as a taxonomic character in systematic studies of this family. Local populations of *Marcusenius* in southern Africa exhibited unusual variability in molecular genetics, morphology and EOD, but little is known about the characteristics of *Petrocephalus* populations. This study incorporates morphology, molecular genetics and EOD data to provide a better understanding of the taxonomy, biogeography and phylogenetic relationships of these mormyrid fishes. Standard DNA isolation methods were used to isolate DNA from muscle tissue preserved in 100% ethanol. The genetic data, morphology and EODs were analysed using various statistical and phylogenetic packages. Analyses of mitochondrial DNA cytochrome *b* phylogenies of *Marcusenius* and *Petrocephalus* revealed species level differentiation between different river systems. The genetic results confirm morphology and EOD results in identifying new species of both genera in southern Africa that can be distinguished from the widespread *M. macrolepidotus* and *P. catostoma*. *M. macrolepidotus* is more closely related to a newly discovered *Marcusenius* form in the South African Limpopo system than it is to *M. pongolensis* and *M. altisambesi*. *P. catostoma* from the type river system is the sister species to the South African population, *P. wesselsi*, and the newly discovered species from the Rovuma system. The results also indicate that populations from the Congo basin are most likely ancestral to the *Marcusenius* and *Petrocephalus* populations of southern Africa. A separation time of at least 1-5 mya is in agreement with geological data, indicating that the evolution of major river systems have been important in facilitating dispersal and isolation.

Keywords : Mormyridae, Molecular Phylogeny, Biogeography



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Impact of coastal development on the recruitment of juvenile commercial coral-reef fish: Mayotte island in the Indian Ocean

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Tropical coasts, and particularly those of Mayotte, are characterized by particularly rich coastal ecosystems: mangroves and coral reefs. There are multiple biological and physical interactions between these two ecosystems which are essential for the balance of the tropical coastal environment. In the recent years there has been a strong demographic increase at Mayotte Island causing increased pressures and human alteration of these ecosystems. This study examined the effects of anthropogenic disturbance of coastal areas on the recruitment of commercial fishes to two habitat types (reef crests with an without mangroves on the shoreline. The relationship among anthropogenic effects, coral reefs, mangroves and fish populations was studied using multiple sampling techniques (study of coastline modification, measures of coral health and fish visual census). This study found a positive relationship between human disturbance, destruction of corals and changing shifts in the trophic structure and abundance of fish populations. Moreover, the presence of mangroves appears to play an important role in the life cycle of Mayotte's reef fishes, in particular for Scaridae. Finally, the negative effects of human activities contribute significantly to the fragility of the reef environment and at the same time decreases their resilience capacity. All these findings highlight the necessity to protect and conserve these valuable habitats. However, only community management integrating terrestrial and marine environments can reduce the negative impacts on these environments.

Keywords : Juvenile coral reef fish, Human disturbance, Mangroves



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Tail grasping kinematics in *Hippocampus reidi*

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Seahorses have a large set of novel characters that set them apart from other Gasterosteiformes. One of the less studied of these characters is the prehensile tail similar an analogous structure to that of some reptiles and mammals. The longsnout seahorse, *Hippocampus reidi*, inhabits gorgonian coral reefs, seagrass beds and Sargassum patches in the western Atlantic and is found frequently attached to these substrates. Based on previous morphological studies that show highly modified ventral hypaxial musculature, we hypothesize that attachment is powered by these muscles, while detachment is passive and powered mostly by the dorsal fin. We recorded four trials for each of five male seahorses while attaching and detaching to a 1 cm diameter dowel in an aquarium setting and recorded 3D high-speed video kinematics. We analyzed the tail kinematics over five equidistant points between the tail base and the tail tip and measured event duration, 3D components, 3D distance travelled and speed of landmarks and internal tail angles. Tail attachment was characterized by ventral bending accompanied by considerable lateral movement, with the tip landmark showing significantly higher displacement than all the other landmarks during attachment. In addition, bending is higher distally as indicated by lower internal tail angles during both attachment and detachment. Contrary to what was expected, landmark velocity during attachment is lower than during detachment. However, velocity is constant during detachment but not during attachment, suggesting that detachment could still be a passive mechanism powered by the dorsal fin. At this point it is not possible to discard the possibility of storage of energy in the tail that is released during detachment. Tail prehension is a more complex behavior than first thought, showing high tridimensionality. This would be advantageous to attach to vertical substrates that are ubiquitous in the habitat of the longsnout seahorse.

Keywords : Functional morphology, Prehension, Seahorse



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Poster

Do endocrine stimulating factors mitigate in vitro steroidogenesis response of Eurasian perch follicles to stress hormones ?

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Background: Stress-induced corticosteroid modulation hampers endocrine regulation controlling the steroidogenesis in fish but a stimulating action sometimes may be observed in some fish species such as tilapia submitted to stress depending to the oocyte maturation stage. In percid fish, the interaction between endocrine stimulating factors and stress hormones are not yet clarified. Therefore, the objective of the study was to determine the effects of some endocrine metabolic factors, namely insulin-like growth factor-1 (IGF-1) and thyroid hormones and their interactions with glucocorticoids (cortisol) or mineralocorticoids (11-deoxycorticosterone, DOC) on the in vitro steroidogenesis capacity of Eurasian perch follicles.

Methods: Ovaries were collected from sexually mature females during (March) and at the end (beginning of April) of the final oocyte maturation. Then, ovarian tissues containing about 12-15 oocytes were incubated during 6 hours in control Cortland medium or in medium containing either endocrine stimulating factors or stress hormones, as follows:

- Control medium without endocrine factors,
- Medium containing endocrine stimulators (IGF-1, T3, T4, HCG),
- Medium containing stress hormones (cortisol, DOC),
- Medium containing endocrine stimulators and stress hormones

The in vitro follicle steroidogenesis was evaluated by aromatase activity and steroid (testosterone-T, estradiol-E2, 11-ketotestosterone-11KT, and 17 α -20 β -dihydroxy-4-pregnen-3-one-17,20 β P) production.

Results: IGF-1 treatment at 100nM induced a significant (P<0.05) enhanced steroidogenesis capacity comparable to HCG at 50 UI/ml and the control follicles in terms of aromatase activity and steroid production as already reported for Eurasian perch and other fish species (Chourasia and Joy, 2007; Milla et al, 2009).



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

The stimulation of steroidogenesis process by HCG and IGF-1 was related to the oocyte developmental stage, especially for aromatase activity and some steroid hormones (17,20 β P). Thyroid hormones did not affect steroidogenesis capacity whatever the doses and the oocyte developmental stage.

Both cortisol and DOC induced a dose-dependent inhibition of the steroidogenesis capacity, with DOC being more inhibitory than cortisol at the same concentration. Except at high doses, gonadotropin supplementation such as HCG contracted the inhibition of aromatase activity, while all the metabolic factors were ineffective in such regulation. Moreover, neither HCG nor any metabolic factor could contract the inhibition of steroid production by stress hormones, except for low doses of cortisol (10 ng/ml) or DOC (1 ng/ml).

Conclusion: The results demonstrated that stress-induced corticosteroid elevation inhibit steroidogenesis capacity in percid fish by decreasing aromatase activity and mainly steroid production. They also indicate a positive interaction In the case of gonadotropin stimulation but not with endocrine metabolic factors such as IGF-1 or thyroid hormones.

Keywords : Stress hormones, Endocrine stimulators, Eurasian perch follicles



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Oral

Genetic diversity as an important element of sustainable management of perch *Perca fluviatilis* L. populations in lowland reservoirs in Central Poland

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European perch *Perca fluviatilis* L. is a species that is common and widespread in Europe and northern part of Asia. Proper multidimensional management of abundant European freshwaters species such as perch, is challenging both from ecological (e.g. food web impact through top-down and bottom-up effects) and commercial perspective (e.g. important game species). However, all activity relating to the knowledge-based management of such natural resources as fish should be based on genetic background in order to provide species conservation and biodiversity. Therefore, in the present study, the mtDNA cytb and D-loop restriction analysis was applied in order to estimate genetic differentiation within and among three perch (*Perca fluviatilis* L.) populations in three reservoirs in Central Poland: Sulejow (Pilica River catchment), Proba and Jeziorsko (Warta River catchment). All individuals were obtained by electrofishing. Live perch were transported to the laboratory, where euthanasia was carried out using an anesthetic overdose. Total DNA was extracted from muscle according to the CTAB method and PCR was applied to amplify a segment of control region (D-loop) and the complete sequence of cytochrome b gene of mitochondrial DNA. Ten and eleven restriction endonucleases were used to digest the amplified cyt b and D-loop fragments, respectively. REAP and ARLEQUIN packages were used for studying the genetic profile of the populations. Anglers' catch return forms for years 2005-2007 were used for fishing pressure evaluation. Nucleotide diversity values of the three investigated perch populations were much lower (0.003 to 0.02) than those reported previously for perch samples in Europe.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

The highest value of haplotype diversity (0.361) was observed for the population of less polluted and less overfished Sulejow Reservoir, while for the polluted and overfished environment of Jeziorsko Reservoir and the youngest and the smallest Proba Reservoir, it reached lower levels (0.133). In each reservoir perch represented one of five most frequently caught species. A minimum average landing per annum for the two biggest reservoirs reached 1.5 tons, while for Proba it reached 0.2 ton across the studied years. Hydrotechnical conditions, pollution and/or recreational fishing are supposed to be the main factors limiting genetic variation in perch populations. Due to the lack of genetic differentiation among populations studied (values of nucleotide divergence ranged from 0.00 to 0.128), various fish management strategies focused on water quality maintenance, such as eggs translocation to enhance fisheries suffering from significant pressure caused by anglers, or perch aquaculture development can be applied.

Keywords : Perch (*Perca fluviatilis* L.), Mitochondrial DNA, Genetic differentiation



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Diet of the endemic *Telestes karsticus* (Cyprinidae) from Sušik Creek, Croatia

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Telestes karsticus Marčić & Mrakovčić 2011 is a newly described, endemic, cyprinid fish species from the Danube Basin. Although understanding of the biology and ecology of an endangered species is crucial for its conservation, the current knowledge of the life history of *T. karsticus* is very limited. The objective of this study was to ascertain the diet of this species. The ratio of gut length vs. standard length was 0.9 ± 0.12 . Gut contents revealed that benthic invertebrates accounted for the majority of food consumed, although terrestrial insects, plant material, algae and fish were also found. Since this is the only fish species in this creek, we can conclude that *T. karsticus* is cannibalistic. *T. karsticus* can be classified as a euryphagus omnivore.

Keywords : Diet, *Telestes karsticus*



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Oral

Sex-steroid receptors localization in immune tissues of the rainbow trout (*Oncorhynchus mykiss*)

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In vertebrates, sex hormones behave on the reproductive system but also affect the functioning of several non-reproductive tissues, notably the immune system. In teleost fish, reported adverse effects of endocrine disrupting chemicals (EDC) include population decline, inhibition of reproductive function, and disruption of the nervous and immune systems. Although much is known about the end effects of EDC exposure, less is known about the mechanisms induced by the endocrine disruptors on the immunity. Our objective is to understand the physiological and molecular immunotoxicity processes induced by some typical EDCs in a teleost model, the rainbow trout *Oncorhynchus mykiss*.

To achieve this goal, the estrogen receptors (ER) and androgen receptors (AR) was, first, quantified and located in various immune organs (gill, pyloric caeca, spleen, anterior and posterior intestine, skin, liver, anterior and median kidney) and in testis, as a positive control. Afterwards, the gene expression of ER α 1, ER β 2 and AR α was quantified by quantitative real-time PCR. Then, we used immunohistochemistry to locate the receptors (ER α and AR α). Currently, the ER α and AR α proteins are quantified by western blot.

We observed that the genes of ER α , ER β and AR α have significantly higher levels of expression in liver and testis than in other immune organs. However, it is worth noting that the expression of all receptors has been detected and quantified in all immune organs. This ubiquitous distribution supports the idea of a potential influence of sex steroids on the fish immune system in rainbow trout. This hypothesis has been confirmed by the immunohistochemistry results. Indeed, a positive staining of specific cells or tissues involved in immunity was observed. For example, ER α was detected in the mucous cells of different tissues, in the hematopoietic tissues in kidney or, again, in the lamina propria in intestine which contains lymphocytes, plasma cells, granulocytes and macrophages. This expression in immune related cells and tissues indicates a possible regulation of the immune activity by the sex steroids.

Keywords : Sex-steroid receptor, Immunity, Endocrine disruptors



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

The role of environment on body condition of deep-sea fishes in the western Mediterranean

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Despite the long Mediterranean tradition in fishery investigations, studies on the influence of the environment on the population dynamics of exploited species are scarce, especially for deep-sea fishes. The aim of this contribution is to assess the link between body condition of nekto-benthic fishes and environmental features in two areas of the western Mediterranean, located in the Balearic (BsB) and the Algerian (AsB) sub-basins, with different geomorphological and hydrodynamic characteristics. Two multidisciplinary surveys were carried out in December 2009 and July 2010. In each survey two vessels were used simultaneously: (i) a commercial fishing boat to sample nekto- and epi-benthic communities; (ii) and a research vessel to collect hydrographic data and to sample zooplankton along the water column, as well as the meso-pelagic species of the main scattering layers, which were detected by acoustic methods. Depths in the survey ranged from 200 to 1000 m. Differences in community structure, fish condition of 15 exploited deep-sea fish species (*Helicolenus dactylopterus*, *Lepidorhombus boscii*, *Lepidorhombus whiffiagonis*, *Lophius budegassa*, *Merluccius merluccius*, *Micromesistius poutassou*, *Raja clavata*, *Scyliorhinus canicula*, *Trigla lyra*, *Etmopterus spinax*, *Galeus melastomus*, *Lepidion lepidion*, *Mora moro*, *Nezumia aequalis* and *Phycis blennoïdes*) and environmental parameters were compared between areas and seasons, by means of uni- and multi-variant analysis and Generalized Linear Models. To estimate fish condition Fulton's and relative condition indices, as well as standardized residuals from the weight-length relationship, were used. Results showed a better fish condition in the BsB during summer, despite differences among the three indices used. The spatial and temporal differences in fish condition are discussed in the context of the main environmental variables characterizing both study areas, which include data on the oceanography (temperature, salinity, potential density, dissolved oxygen and fluorescence) as well as potential preys for the nekto-benthic fish assemblages (meso-zooplankton, meso-pelagic, supra- and epi-benthic communities). Significant variations between areas and seasons were also observed for some of these variables. These results show the importance of the environment on the condition of deep-sea fishes and suggest an important trophic coupling between the benthic and the pelagic domain in the Balearic Islands, one of the most oligotrophic areas of the western Mediterranean.

Keywords : Fish condition, Environment, Trophic coupling



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Oral

Do gluco- or mineralocorticoids modulate Eurasian perch (*Perca fluviatilis*, L.) immune activity?

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Cortisol is well studied as stress indicator as it is released in blood circulation following an acute stress. It is the main corticosteroids in fish and it can bind to gluco (GR) and mineralocorticoid receptors (MR). In a large diversity of fish species, it has already been described that cortisol regulates various physiological systems such as immunity, glucose metabolism and hydromineral balance. The mammal mineral balance regulator aldosterone is also described to regulate some immune parameters such as leucocytes abundance or cytokines expression. Recently 11-deoxycorticosterone (DOC) has been highlighted to bind MR and maybe counteracts the lack of aldosterone in fish. Even if the DOC functions are not well described in fish yet, it was demonstrated that thymus of medaka exposed to DOC acetate lost all their thymocytes, the T-cells precursors. We studied at short-term the modulation of the Eurasian perch immune system following an intraperitoneal injection of these two corticosteroids. During this study, we demonstrated that cortisol but also DOC affect the immune status of fish. Blood lymphocyte proportion was drastically decreased in favour of neutrophil ones in cortisol injected fish. Cortisol also up-regulated blood lysozyme activity 72h after the injection. Moreover, cortisol and DOC regulated the expression of immune related genes in two secondary lymphoid organs, the gills and the spleen. DOC up-regulated the expression of the gene coding for apolipoprotein A1, an antimicrobial factor in fish. Transcript level of C-type lysozyme increased in the gills and in the spleen following DOC injection. Cortisol had the same effects on the expression of this gene but only in the spleen. Moreover, cortisol decreased the expression of TNF- α , a pro inflammatory cytokine, in the spleen. The study of gene expression also demonstrated that the DOC injected stimulated its pathway in the spleen by increasing the expression of its receptor MR and by stimulating the expression of the 11 β -HSD-2, an enzyme described to clear cortisol around the MR. This could indicate an implication of this organ in the action of DOC in fish. All these regulations showed that these two corticosteroids can modulate the immune activity in fish. The results indicated that cortisol seems to favour innate immunity compared with the adaptive ones. This indicated that DOC should be studied as hydromineral balance regulator but also as an immune regulator in fish.

Keywords : Corticosteroids, Receptors, Immunity



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Retention and dispersion of Mediterranean moray eel, *Muraena helena* leptocephali from deep open waters to coastal area

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Unfortunately, biological aspect, particularly knowledge of spawning determinations and larvae dispersion and retention of most economic valuable or ecologically interesting fish species in the Adriatic and Mediterranean Sea is still insufficient. This is particularly true for those fishes undertaking more extensive spawning migrations to open sea deeper waters. In this study, evidences regarding South Adriatic Pit (SAP) as reproductive area for Mediterranean moray eel, *Muraena helena* (family Muraenidae), as well as that at least one spawning area of morays exist in the Mediterranean Sea, will be presented. Leptocephali samples were collected in the south and middle Adriatic Sea by using a small pelagic trawl. The circulation and mean current fields were taken from previous studies. Larvae ranged in length from 7.7 to 13.1 cm, and were most abundant along the off-shore islands. Age studies revealed age of leptocephali to be from 8 to 11 months, indicating a 3-4 months long spawning season from late August to late December. We propose a scenario of the leptocephali dispersion and retention from SAP to coastal area. We believe that future studies should be carried out in the SAP, leading to the support of hypothesis about this place as spawning place for numerous meso-and bathypelagic and bathybenthic Adriatic fish, but also for a number of coastal fishes that undertake open sea spawning migration to circle the life cycle. This knowledge is exceedingly important to override some of the largest gaps related to the recruitment and processes affecting survival of the early life stages. All of that is necessary for better species conservation and stock assessment.

Keywords : *Muraena helena*, Spawning area, South Adriatic Pit



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

The Gene divergence of Kamchatka mykiss (*Parasalmo (Oncorhynchus) mykiss*), by the variability two types of specific genetic markers

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Kamchatka mykiss (*Parasalmo O. mykiss*) is an object of the Red Book of Russia, and its resident form (mikizha) is one of the most valuable objects of world aquaculture and fish farming. At the same time, the status of this species is debatable; there is no consensus of opinion among authors regarding its genus. Different authors assign mikizha to the genera *Salmo*, *Parasalmo*, or *Oncorhynchus*. In our work we tried to explore the different populations and locality of using two types of specially designed species-specific markers: SCAR and ISSR - markers. We created seven SCAR-and seven ISSR-markers which have significant population-variability of DNA-products from Kamchatka mikizha geographical group, which can be used in further studies of the species *Parasalmo (O.) mykiss*. After research of samples from the west (river Sopochnaya, Utkholok, Tigil, Sedanka and Kol') and the east coast (river Zhupanova, Bystraya, Elovka and Dvuhyrtochnaya) of Kamchatka, and out-group samples from Chile and North Americano, we obtained a new data are well supported by previously studies of this species. By SCAR-markers all populations of *Kamchatka mykiss* is strictly divided along geographical lines, with clearly observed the proximity of the North American and Chilean populations. In the other group are the Kamchatka populations, but the West Kamchatka group occupies a separate domain, and the East Kamchatka group tends to Chilean populations. This is especially pronounced in populations from the Zhupanova River. This similarity is very interesting and needs further investigation. Proximity is Chilean and North American groups are well explained by the fact that the mykiss inhabiting in the rivers of Chile has a North American origin. The value of Θ_{ST} (analog FST (Weir, 1995)) on average over all loci takes the values 28 %, it is statistically significant value. By ISSR-markers were obtained similar results with the difference that the population of the East Kamchatka River Zhupanova clustered with North American populations. The value of Θ_{ST} for this type of research was even higher – 34 %. These results were also confirmed in our laboratory studies of these samples at microsatellite loci.

This work was supported by the Russian Foundation for Basic Research (11-04-00778-a), by the grant of the Presidium of Russian Academy of Sciences for the leading scientific schools (NSh-2104.2008.4), Federal Agency of Science and Innovations within the framework of the Federal Target Program "Scientific and Scientific-Pedagogical Personnel of Innovative Russia" (02.740.11.0461, 14.740.11.0633, 14.740.11.0165 15).

Keywords : Mikizha, Issr-marker, Scar-marker



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Molecular phylogeny of the South American freshwater fish *Semaprochilodus* (Characiformes: Prochilodontidae) based on nuclear and mitochondrial genes

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The Neotropical freshwater fish genus *Semaprochilodus* Fowler, 1941, consists of six species restricted to the Amazon and Orinoco basins and the coastal drainages of Suriname and French Guyana in northern South America. The hypothesis of the monophyly of the genus is supported by thirteen morphological synapomorphies involving cranial ossifications and body pigmentation. The interspecific relationships are only partially resolved and supported solely by morphological characters. We present the first phylogeny of *Semaprochilodus* based on partial DNA sequences of two mitochondrial (16S and Cox1) and three nuclear (Myh6, Rag1 and Rag2) genes commonly used in other phylogenetic studies among characiforms. All species were analyzed except for *S. varii* (due to a lack of tissues) with *Prochilodus argenteus* used as outgroup. The analysis yielded clusters supported by high bootstrap values from the parsimony analysis that partially corroborate a previous morphological study. The Amazonian *S. taeniurus* forms the sister group to all remaining congeners. We found a close strongly supported (99%) relationship between *S. brama* from the rio Araguaia and *S. laticeps* of the Río Orinoco. These species along with the not included *S. varii*, have very dark pigmentation along the posterior border of the operculum (an apomorphy for this group of species). *Semaprochilodus insignis* from the Amazon and *S. kneri* from the Orinoco were confirmed as sister species with high bootstrap support (89%) as suggested by their common possession of two morphological synapomorphies. The last two species have, however, very low genetic distances (0.3%), as indicated by DNA barcoding. Morphologically, these two species are distinguished by differences in ranges and modes, principally in the number of horizontal rows of scales above and below the lateral line and their allopatric distribution in the Amazon and Orinoco basins. Our results suggest a reanalysis of the morphological characters is necessary to better evaluate the phylogenetic position of *S. taeniurus* and that a species level taxonomic review of *S. kneri* (Pellegrin, 1909) is necessary to determine whether it is a valid species or a junior synonym of *S. insignis* (Jardine, 1841) as suggested by our molecular data.

Keywords : Systematics, Neotropical fish, DNA sequences



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

The estimation of exploitation status of *Trachurus mediterraneus* (Steindachner, 1868), in the central region of the Algerian coasts

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Mediterranean horse mackerel, *Trachurus mediterraneus* (Steindachner, 1868), is widely distributed along the north eastern and central Atlantic, in the hole Mediterranean and Black sea. It's one of the most pelagic species targeted by fishermen in the central region of Algerian coasts, located between Dellys and Bou-Ismaïl. Therefore we found it useful to study its exploitation status by adjusting its production to F0.1. To determine the main biological parameters, we used the FISAT II 1.2.0 (2005), the FISHPARM (version 3.0S) and VONBIT (2011). Finally, the choice fell on the software VIT (Lleonart and Salat, 1997), which is highly recommended by FAO, the fact that it is designed for the Mediterranean fisheries. To do this, we compiled our data with those of our Fisheries Laboratory, whose total number of horse mackerel - both sexes combined - is 6210. Their total lengths are between 8.5 and 26.5 cm. All these individuals are from the trawl fishery. The growth parameters obtained shows that *Trachurus mediterraneus* has a longevity of 5 years and an asymptotic length $L_{\infty} = 36.33$ cm with a body growth coefficient $K = 0.21 \text{ year}^{-1}$ and a $t_0 = -0.43$ year. Exploitable biomass of *Trachurus mediterraneus* (Steindachner, 1868), was estimated at 535.7 tons. The current yield per recruit ($Y / R = 19.26$ g; for a factor $F = 1$) exceeds the maximum sustainable yield ($MSY = 19.94$ g; with an $F = 0.62$). In the same time, current biomass per recruit ($B / R = 27.49$ g.), is less than the maximum sustainable biomass ($B_{max} / R = 38.49$ g.). From this diagnosis, it appears a state of overexploitation of the stock of *T. mediterraneus* in the central region of the Algerian coast. Therefore, we recommend adjusting the performance threshold $Y_0 .1 / R$ - corresponding to 18.56 g ($F_{0.1} = 0.33$). In reality, managers are not interested in a theoretical yield per recruit but to a total production of the exploitable stock. To do this, we should simply multiply the yield per recruit Y/R by 19487516.6, the number of recruits. In conclusion, it would be judicious to reduce the production to 361.49 tons, which corresponds to a decrease of 3.66% of the current production 375.23 tons. Mean exploitable biomass will be equal to 535.71 tons. The implementation of this recommendation would allow the preservation of *T. mediterraneus* of the central region of the Algerian coast and ensure a sustainable long term production.

Keywords : *Trachurus mediterraneus*, Exploitation, F0.1



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Population genetics of the bigeye thresher shark in the Atlantic ocean : low genetic diversity and their implications for conservation

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Populations of several elasmobranchii species have decreased in the last decades, especially because of the increasing interest for shark products. Since sharks are particularly susceptible to overfishing, mainly due to their biological traits, studies regarding their population dynamics are important to provide advice for their management. Genetic tools addressing species variability are efficient and widely used to the identification and discrimination of the stocks. Among the elasmobranchii exploited by commercial fisheries, the bigeye thresher shark, *Alopias superciliosus*, may be under considerable population pressure, and has been classified as “vulnerable” according to the IUCN Red List. Moreover, ICCAT (the management body for the Atlantic Ocean) has recently prohibited the retention and the commercialization of this by-catch species. Considering the lack of information regarding *A. superciliosus* populations in the Atlantic, this study aimed to determine the levels of genetic variability and the population structure in the Atlantic Ocean. The analyses were carried out using mitochondrial DNA control region (D-loop) sequences from 142 samples collected along a wide Atlantic area. Only seven haplotypes were found. Among these, haplotype H1 was shared by 93.7 % of the sharks. Five other haplotypes (H2 to H6) were considered rare, and were found on only one specimen each. Haplotype H7 was also rare and shared by four specimens. The nucleotide and haplotype diversity indexes found were $\pi=0.00140\pm0.00047$ and $Hd=0.123\pm0.00142$ respectively. This suggests a low genetic variability, no population structure and an intense gene flow across the studied area. Therefore, for fisheries management and species conservation purposes, a single *A. superciliosus* stock should be considered in the sampled area. The low genetic variability found can be a risk factor for the evolutive potential of the species, and reduces the population ability to respond to environmental changes.

Keywords : Marine biodiversity, Pelagic fisheries, Sharks



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Poster

Morphological characters of *Cobitis elongatoides* (Cypriniformes; Actinopterygii) in Croatia

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The species *Cobitis elongatoides* Băcescu & Mair, 1969 is distributed through the rivers of the Danube basin. It has an exceptionally narrow ecological niche and its body is adapted for life in shallow waters with slow to no flow with a fine sediment substrate. The objective of this study was to obtain new information on the morphology of this species, and to determine whether there are morphological differences between populations in Croatia. The study examined populations in four rivers: Kupa, Petrinjčica, Sava and Drava. Morphological analyses included examining the morphometric and meristic traits and the external appearance. Populations from all four rivers were compared in the context of the available literature. The morphometric traits were analysed statistically and the obtained results compared with literature data.

Keywords : *Cobitis elongatoides*, Morphology, Danube basin



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Ontogeny of sound production and sonic muscle morphology in *Pygocentrus nattereri*

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The ability of sound production is well known in the red piranha (*Pygocentrus nattereri*). The dominant frequency of the calls was shown to correspond to the sonic muscle contraction rate. The aim of this study was to compare the sonic characteristics and sound muscle morphology in fish of different size classes: 3-8 cm SL (n = 13 fish), 14-15 cm (n = 6) and 23-26 cm (n = 4). The sound production has been recorded when fish were held by hand. Sounds have been successfully recorded for all fish except for two of the largest piranhas. The smallest fish produced a sound composed of 10 ± 1 pulses, with a dominant frequency of 146 ± 13 Hz and a duration of 69 ± 11 ms. The sound of the medium class size was composed of 14 ± 2 pulses, with a dominant frequency of 102 ± 3 Hz, lasted 149 ± 19 ms. The largest fish produced a sound with 12 ± 2 pulses, with a dominant frequency of 53 ± 4 Hz and which lasted 203 ± 37 ms. The duration of the sound increased significantly with the fish size whereas the sound frequency decreased with fish increasing size. The microscopic analyse of the sonic muscles has revealed a different morphological structure for each size class. First, there was a strong positive relationship between the sonic fibre diameter and the fish size. However, the sonic fibres were always smaller than the epaxial ones. Secondly, in small and medium class sizes, the proportion of sarcoplasmic reticulum in sonic muscle was higher than in larger fish. This morphological feature is well known in fast contracting muscles and could explain why small fish are able to realise higher pitched sounds. Moreover, the largest fish which were not able to produce any sound presented a sonic muscle with very large fibres surrounded with few sarcoplasmic reticulums, as it is the case in white epaxial fibres. They showed also numerous lipidic inclusions between muscular fibres. This observation should explain the incapacity of the sonic muscle to contract rapidly and their inability to produce sounds. In conclusion it seemed possible to draw relationships between the sonic muscle abilities and its morphological features.

Keywords : Piranhas, Sound characteristics, Sonic muscle structure



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Undetected evolutionary radiation in the pelagic realm : A novel clade in the percomorph fishes as revealed by mitogenomic analysis

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Marine pelagic realm is the largest habitat on the Earth, comprising >99.9% of the world's water and harboring diverse fishes from epipelagic to abyssopelagic zones. A recent mitogenomic study found that some marine pelagic perciform taxa formerly placed in 4 different suborders (Percoidei, Stromateoidei, Scombroidei, Trachinoidei) unexpectedly share a common ancestry, suggesting that future addition of pelagic species from the percomorphs with unknown identity would further expand the limits of this previously unrecognized clade. To confirm this prediction, we extensively assembled mitochondrial (mt) and nuclear (nc) gene sequences from all percomorphs deposited in the database and analyzed the unambiguously aligned sequences from 6 mt and 3 nc genes separately using ML method. The resulting mt and nc phylogenies strongly suggest that 15 families across 6 percomorph suborders (the 4 suborders listed above plus Icosteioidei and Scombrobracoidei) share a common ancestry and these fishes are found to be all dwellers in the pelagic realm occurring at various depths. Based on these preliminary results, we further assembled mt genomic data from these selected taxa (29 spp. from the 15 families) plus various percomorphs and outgroups (67 spp.; total = 96 spp.) and subjected the data to partitioned ML analyses. The resulting phylogenies indicated that those selected taxa from the 15 perciform families across the 6 suborders form a monophyletic group with 100% bootstrap probabilities. These results strongly suggest that there has been an evolutionary radiation in the pelagic realm that cannot be predicted from previous taxonomy and classification in the percomorphs.

Keywords : Phylogeny, Evolutionary radiation, Percomorpha



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

The enigmatic Congo River fish fauna: the importance of the Wagenia falls on species diversity, ecology and distribution

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The Congo River is, after the Amazon, the second largest river basin on earth and harbours, with more than 1125 valid species, the largest fish fauna of the African continent. However, despite the fact that the Congo basin is a fish diversity hotspot, its fish fauna is not well known, as illustrated by the lack of an updated species list of the basin. The Wagenia falls in Kisangani have traditionally been identified as the ichthyofaunal barrier between the Central and Upper Congo faunas, although no in depth study was ever undertaken. Therefore, this study wants to explore the taxonomic, trophic and genetic diversity of the fish fauna of comparable locations up- and downstream of the falls. Prerequisite for such analyses are correct species identifications. However, persistent taxonomic problems remain. A case in point can be found within three morphologically similar species of Distichodontidae, i.e. *Distichodus antonii*, *D. atroventralis* and *D. fasciolatus*. In the past, the use of the number of lateral line scales as the major diagnostic character for these three species has been the source of numerous misidentifications, even in the type series. Therefore, a morphometric study on 10 counts and 30 measurements has been undertaken, using a multi- (Principal Component Analysis) and univariate (Mann-Whitney U-tests) statistical approach to both data sets separately. Results show that *D. antonii* is most distinct and can be separated from both *D. atroventralis* and *D. fasciolatus* by: its low number of scales between the lateral line and the dorsal fin, i.e. 10-12 (vs. 13-15 for *D. atroventralis* and *D. fasciolatus*); its large internasal distance, i.e. 9.7-26.5 %HL (vs. 7.6-21.3 % HL), although this character is positive allometric; and its terminal mouth (vs. inferior). *Distichodus atroventralis* and *D. fasciolatus* are very similar and present a considerable overlap in measurements. However a combination of the following meristics proved to be diagnostic: 11 pelvic fin rays (exceptionally one specimen with 10 rays) and 22-24 dorsal fin rays for *D. atroventralis* vs. mainly 10 pelvic fin rays (exceptionally three specimens with 11 rays) and 24-28 dorsal fin rays for *D. fasciolatus*. Moreover, smaller specimens ($\pm \leq 200$ mm SL) show only six to nine vertical bars on the flank in *D. atroventralis* vs. 11-20 in *D. fasciolatus*. For these three species, the Wagenia falls do not seem to have been a barrier as they can be found above and below the Wagenia falls, even syntopically.

Keywords : Congo, Wagenia, Distichodontidae



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Oral

Morphology of the lateral line receptor array in cyprinids with different habitat preference

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The fish lateral line consists of an array of neuromasts that occur freestanding on the surface of the fish and/or within subdermal canals. It has been speculated that differences in lateral line design represent adaptations to the hydrodynamic conditions prevailing in the habitat of different species. To test this hypothesis, we investigated lateral line design in species that are near relatives but show different life styles and/or habitat preferences. We chose representatives of the cyprinid family, i.e. the limnophilic goldfish (*Carassius auratus*) and bitterling (*Rhodeus sericeus*), the indifferent gudgeon (*Gobio gobio*) and golden ide (*Leuciscus idus*), and the rheophilic minnow (*Phoxinus phoxinus*). For comparison, we chose *Gyrinocheilus aymonieri* from the family Gyrinocheilidae (Cypriniformes), a species that lives in flowing water. For these species we described number, position, distribution and orientation of neuromasts to obtain a complete map of the lateral line receptor array using scanning electron microscopy, methylene blue, DASPEI and rhodamin-phalloidin labelling. The results did not reveal a systematic relationship between array morphology and presumed habitat preference. Thus, lateral line array morphology in cyprinids may not only depend on habitat preference, but also on other factors, e.g. micro-habitat or behavioural use of the lateral line.

Keywords : Lateral line, Neuromast, cyprinid



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Microsatellite-based genetic diversity and differentiation of Caspian Vimba

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Genetic diversity of Caspian vimba (*Vimba vimba persa*) was investigated using microsatellite markers from two regions along the Iranian coastline of Southern Caspian Sea (BaborRoud River in Mazandaran province and GorganRoud in Golestan province). Genomic DNA from 60 specimens was extracted from fin tissue by phenol-Chlorophorm method and PCR reaction was accomplished with 17 microsatellite primers, out of 17 microsatellite primers 13 loci were amplified, in which 10 of them were amplified with reasonable polymorphism and 3 were monomorphism. Out of 17 microsatellite primers 13 loci were amplified, in which 10 of them were amplified with reasonable polymorphism and 3 were monomorphism. Totally 143 alleles were identified that the highest mean number of alleles per CA3 loci was observed 14 and the lowest 3 in Z8145 loci. Observed and expected heterozygosity averages were 0.81 and 0.78 respectively. Most cases significantly deviated from Hardy-Weinberg equilibrium ($p \leq 0.01$). The estimation of F_{st} ($p \leq 0.01$) revealed significant population structuring and two population of *Vimba vimba persa* is identified in the Caspian Sea. These studies were to apply and develop population genetic approaches to assist conservation, sustainable harvest and restocking of these populations.

Keywords : Microsatellite, Genetic diversity, Caspian Vimba



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Comparative study of the fisheries exploitation using biological indicators in the small lakes in Benin

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A comparative study, using biological indicators, was conducted in Benin in two lakes (Hlan and Toho) for investigating the impact of fishing effort on the fish assemblage. The comparison is based on a three-month survey of commercial fisheries, focusing on fishing activities and catches on the two lakes. The results show that some indicators are useful for evaluating fishing impacts. Among these indicators are: catches per unit effort (lower at Toho Lake than at Hlan following a ratio ranging from 1.5 to 4 according to the gears used), the average fish total lengths in the catches (9.12 cm at Toho and 28.87 cm at Hlan) and the maximum lengths of the targeted species generally smaller at Toho (4 to 34.5 cm) than at Hlan (8.3 to 106.4 cm). A second class of indicators exhibit values that are in accordance to expectations: the species richness (31 at Hlan compared to 18 at Toho), the species diversity ($H' = 2.45$ at Hlan compared to 0.03 at Toho) and evenness (0.91 at Hlan compared to 0.01 at Toho) were higher at Hlan. 5 species accounted for 90% of the landings at Hlan compared to only 1 species at Toho. The population size structure was markedly different in lake Hlan (bimodal distribution) and the lake Toho (unimodal). Even with many small fish forming the first mode in the size distribution, the average body size was larger in lake Hlan than the lake Toho. Even if a good understanding of the two fisheries can explain the trends obtained, it clearly appears from this study that the first class of indicators is interesting and can be used for comparative studies across ecosystems.

Keywords : Fish populations, Population structure, Fishing activities



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Comparative anatomy on the feeding apparatus in *Opsariichthys* and related taxa (Teleostei; Cyprinidae)

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The closely related genera *Opsariichthys*, *Zacco*, *Candidia* and *Parazacco*, presumably the most primitive cyprinids, differentiate to various feeding habits such as piscivorous, insectivorous, omnivorous and adhesion algal feeders. The adaptive radiation in feeding habits is considered to reflect remarkable variations in morphology of the cephalic musculature, pharyngeal apparatus and intestine. The purpose of the present study, aims to elucidate the relationship between feeding habits and these relevant structures in the opsariichthine fishes. The adductor mandibulae complex of *Opsariichthys* species has a specialized structure: the adductor mandibulae A₁ has a tendinous structure at posterodorsal portion; the adductor mandibulae A₃ is completely covered by the adductor mandibulae A₂; the adductor mandibulae A₃ is divided by the levator arcus palatini (except in *C. barbatus*). *Opsariichthys uncirostris*, in the adductor arcus palatini, the levator arcus palatini, the protractor hyoidei and the sternohyoideus to open the lower jaw has the most voluminous among the examined species. The musculature development is considered to allow stronger exertion and enable more rapid responses than rudimentary musculature. In *O. uncirostris*, the mechanical advantage indicates lower ratio for velocity in comparison with other examined species, and the adductor mandibulae A₂ works efficiently for biting force and velocity. Only the pharyngeal bone musculature in *Opsariichthys* species is rudimentary in comparison with other examined species. The level of musculature, development may be effective when masticating with the pharyngeal teeth and the pharyngeal pad. The intestinal coiling patterns were classified into six distinctive morphotype groups: *O. uncirostris* and *Z. temminckii* were classified into Group A. Group B was observed in *Z. sieboldii*, *Z. koreanus* and *C. barbata*. Group C was seen in *O. pachycephalus* and *Z. platypus*. Group D, E and F are represented by *Z. platypus*. The intestine length showed a general evolutionary trend that well matched each specific feeding habit. Morphological specializations were interpreted in a functional context, and assessed based on feeding habits. In particular, the well developed and characteristics of the adductor mandibular complex in *Opsariichthys* species can be a specialization and evolutionary trend to a piscivorous feeding behavior.

Keywords : Ecomorphology, Myology, Evolution



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

A probabilistic model characterizing fish assemblages in running waters of Iran: a framework for environmental assessment

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Iran is a large country over 1.6 million km² with an enormous diversity. Unfortunately, man's activities have profound and usually negative influences on freshwater ecosystems in Iran. Current assessment methods for the evaluation of the ecological integrity of riverine ecosystems only use chemico-physical water quality parameters and biological quality elements like macroinvertebrates. Among potential indicators, fish assemblages are of particular interest because of their ability to integrate environmental variability at different spatial scales. In this study we developed a fish-based index to assess the ecological integrity of Iranian rivers for the first time through the use of the 'reference condition approach'. We tested fish assemblages exposed to stress, in so called "impacted sites" versus sites which are unexposed to stress, "reference sites". Based on the land use we discriminated reference sites and impacted sites. Our dataset contains records of 202 fish species in 1700 sites covering different habitats all over Iran. Based on this information and abiotic data such as slope, temperature, river width, we predicted the potential distribution for around 60 key species. Accordingly, we predicted a potential assemblage at the sites. The models were validated using an independent set of reference sites. Finally, we used an additional set of disturbed sites to compare observed versus potential assemblages. The deviation between the potential and the observed assemblage within these sites is used as a measure of degradation.

Keywords : Biological assessment, Fish-based index, Iranian rivers



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Systematic revision of the flatfish Genus *Peltorhamphus* Günther, 1862 (Pleuronectiformes: Rhombosoleidae), with description of a new species

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The rhombosoleid genus *Peltorhamphus* Günther was thought to contain only three species, *P. novaezeelandiae* Günther, *P. latus* James, and *P. tenuis* James, that are widespread in shallow, continental shelf waters of New Zealand, and also at nearby Chatham Islands and Norfolk Island. The only systematic revision of *Peltorhamphus* (in 1972) developed a key to assist in identifying specimens. During on-going studies updating taxonomic information for *Peltorhamphus*, problems were encountered when attempting to identify specimens, especially juveniles. Examination of 1106 specimens of *Peltorhamphus*, representing 203 lots, revealed that 81 of 203 lots (40%) contained misidentified specimens (including lots with paratypes). In addition to three previously-described species, a fourth species, with a much more limited geographic range than the others, was also discovered. Discovery of this undescribed species, most often misidentified as juvenile *P. novaezeelandiae* or as adult and juvenile *P. latus*, in addition to the large number of other misidentified specimens in collections required taxonomic re-evaluation and redescription of all species in the genus, and an appraisal of characters used to differentiate them. Some characters traditionally used to differentiate species continue to be useful, whereas, others were found to overlap too much to be useful in separating the species. Novel characters related to scales, gillrakers and pigmentation, were also discovered during this study that further facilitate species identifications of *Peltorhamphus*. Re-assessment of the number of valid species of *Peltorhamphus* provides better understanding of species diversity within this genus as well as that of the flatfish assemblage residing in New Zealand waters.

Keywords : Rhombosoleidae, *Peltorhamphus*, New Zealand



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Habitat-related phenotypic plasticity in two *Haplochromis* species from Lake Kivu (Rwanda)

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The phenomenon of intraspecific variation reflecting environmental conditions in which populations live, and the patterns emergin from it, may reflect local adaptive responses to a given environment. This is particulary relevant in a Lake environment where niche segregation is known to have resulted in sympatric speciation. This study aims to look at the phenotypic differentiation in relation to habitat segregation of two closely related and sympatric species *Haplochromis kamiranzovu* and *H. insidae* from Lake Kivu. Both species could be found both in littoral and pelagic zones, as well had a north-south distribution across the lake. Using landmark-based geometric morphometrics, it could be revealed that *H. kamiranzovu* and *H. insidae* differ in external morphology at all levels: species, sex, region (north-south) and even habitat (littoral-pelagic). Shape variation is found in the head, the upper jaws, orientation of the lower jaw, position of the eye, at the level of the body depth, and in the caudal peduncle. The relevance of the observed shape difference in relation to differences in the habitat is further discussed.

Keywords : Geometric morphometrics, Lake Kivu, Phenotype



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

The distribution of catfishes (Siluriformes) in the Congo Basin

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The Congo River basin is the second largest drainage system in the world, preceded only by the Amazon in South America. At present, just over 1000 valid fish species are known from its drainage (excluding the endemics from Lakes Tanganyika and Kivu). The present study involved two steps in analysing the catfish distribution in the Congo. First, the vast Congo Basin was split up in ichthyogeographically meaningful subbasins, based on environmental and geographic parameters (geographic barriers, habitat type and subbasin size). This exercise resulted in the delineation of 29 subbasins for the Congo River basin *sensu stricto* between its source and estuary, and an additional four for Lakes Tanganyika and Kivu and their drainages. In a second step, the distribution of the catfishes of the Congo Basin *sensu stricto* was mapped and analysed using the new subbasins. Mapping was based on the most important collection records of African fishes, including but not limited to the Royal Museum for Central Africa (Tervuren, Belgium), the Musée National d'Histoire Naturel (Paris, France), the Natural History Museum (London, UK) and the American Museum of Natural History (New York, USA). In addition, localities from reliable literature sources were taken into account, while recent revisions were used to update distributions from collection records. This resulted in a data matrix with presence data for all catfishes in the various subbasins of the Congo basin *sensu stricto*. In total, 201 catfish species were recorded, representing 7 families and 39 genera. Three families (Mochokidae, Amphiliidae and Clariidae) comprised almost 75% of these species. About three quarters of all catfish were found to be endemic to the Congo River system. A third was found to be restricted to a single subbasin. Endemic species richness (number of species only known from a single subbasin) varied between 0 and 12 (average 2.3), or up to a maximum of 18.2 % of the total catfish species in a subbasin. The number of species per subbasin varied from 8 to 81 (average 41), which corresponded to 0.05 to 11.9 species per 1000 km² (average 1.1). Distribution patterns of individual species showed to be very variable, with relatively few species occurring throughout the Congo River Basin. In addition, some subbasins appeared to be characterized by a rather unique combination of species.

Keywords : Congo Basin, Catfish, Distribution



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Genetic diversity of common carp (*Cyprinus carpio*) strains revealed by AFLP analysis : Live gene bank in Poland - Preliminary results

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Introduction: AFLP markers provide an efficient method for DNA fingerprinting and genetic linkage mapping. As many as 22 common carp pure bred lines and distinct varieties are cultured in Poland. Recently, the project aimed at genetic analysis of this carp breeding lines using set of 13 microsatellite loci and AFLP analyzes was launched. In this preliminary results we are presenting preliminary results of AFLP analyses.

Materials and methods: In total 37 animals representing 9 breeding lines of common carp (Polish landecka(R2), Polish Knyszynska(K), Hungarian(W), Ukrainian(U), German(N), Polish Jaktorowska(J), Polish Sobieszynska(S), Israeli DOR-70(D), Lithuanian Bubijska(B)) were analysed. Four fish from each line were analysed except Dor-70 where 5 fish were sampled. AFLP analysis using the enzyme combination EcoRI/TaqI was performed. AFLP protocol with fluorescently labeled primers described in Papa et al. (2004) was used in this study. GenomeLab GeXP (Beckman Coulter) was used. Statistic analyzes were done using FAMD 1.21 beta software.

Results: Seven primer combinations generated very good AFLP profiles. 225 polymorphic peaks were produced. Mean number of peaks per individual was 84. Unique peaks were observed in all analysed strains: R2 and K strain–2 peaks; W–2 peaks; N–3 peaks; S, U, B–5 peaks; D-8 peaks and J–18 peaks.

The AMOVA revealed that the total genetic variation among lines was 30%, whilst variation within lines was estimated to be 70%. Genetic distance was estimated using method of Cavalli-Sforza and Edwards (1967), based on single-locus chord distance. Most of the carp lines formed two clusters: first one consisted of 6 carp lines (N, S, D, R2, W and B) followed by a cluster of two lines - Ukrainian and Polish Knyszyn. The UPGMA dendrogram (not shown) separated Polish Jaktorowska line from all the others.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Discussion: Our results demonstrated the usefulness of the AFLP loci in distinguishing and monitoring the genetic diversity of cultured common carp lines. We show that AFLP generated polymorphism could correctly reflect the history and genetic relationship between common carp breeds. High amount of unique peaks confirm known difference of Polish Jaktorowska carp from other studied lines. This breeding line has long documented history of isolated breeding. Our study, which is still in progress, will provide the set of markers to be used in the national program for the conservation of genetic resources and monitor genetic diversity and purity of different carp lines.

The present work was financed by a grant funded by the Ministry of Science and Higher Education N311629038

Keywords : AFLP, Common carp, Genetic markers



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Evolutionary morphology of the caudal musculoskeletal system in syngnathid fishes: from swimming to prehension...in different ways

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Seahorses and pipehorses possess the unique characteristic of extensive tail bending, allowing them to grasp onto the substrate. Current phylogenetic hypotheses suggest that grasping performance evolved more than once, as it seems to have arisen independently in pipehorses and seahorses. Most pipehorse species, which possess a prehensile tail, are nested within pipefish species (that lack this prehensile tail), and hence are not a sister group to the seahorses. Considering the different evolutionary strategies giving rise to a prehensile tail (starting from a rigid one in pipefishes), it is hypothesised that some crucial (and hence shared) structural modifications to increase prehensibility occurred at the level of (1) body armour organisation, (2) vertebra organisation, (3) interaction between plates and vertebra and (4) muscle organisation. To test these hypotheses, the caudal system in pipefish (representing the ancestral condition), pipehorse and seahorse are compared, using histological and micro-CT data. The results confirm some hypotheses, but not all. As such, body armour organisation in pipehorses proved to be different from that of seahorses, providing both an increased capacity for flexibility between consecutive segmented plates (overall to partial plate reduction). Modifications in the musculature are also extensive, where seahorses represent a unique organisation of the muscle-tendon complexes for syngnathids (plate-like myosepta in seahorses and muscle fibre extension versus ancestral conical myoseptal organisation). This study thus confirms that within a single clade (syngnathids), at least two different evolutionary strategies have independently yielded an adaptive solution for a novel function, *i.e.* tail prehension).

Keywords : Tail prehensibility, Syngnathid fishes, Musculoskeletal morphology



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Hagfish phylogeny and taxonomy

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A 587 bp fragment of the 16S RNA gene was sequenced in 9 putative species of the Myxinidae and analyzed together with sequences from 19 putative species from GenBank. The phylogenetic analysis of the molecular data is compatible with the monophyly of the subfamily Myxiniinae but incompatible with the monophyly of the subfamily Eptatretinae, characterized by having one pair or several pairs of external gill apertures, respectively. The genera *Paramyxine* and *Quadratus* are non-monophyletic and are synonymized with *Eptatretus*. *Eptatretus fernholmi* becomes a junior homonym of *Paramyxine fernholmi*, and needs to be renamed. *Eptatretus wisneri* becomes a junior homonym of *Paramyxine wisneri* and needs to be renamed. *Eptatretus lopheliae* and *Eptatretus rubicundus* form a monophyletic group characterized by the presence of an elongated tubular nostril and reddish coloration. The validity of the Western Atlantic *Myxine limosa* as distinct from the Eastern Atlantic *Myxine glutinosa* is confirmed. There is no type species for *Eptatretus*, with more than 50 species, and the historical search for the candidate type species goes back to the travels of Cook and Banks in the South Seas.

Keywords : Myxinidae, 16S, Bayesian analysis



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Diel changeover of fish assemblages on sandybanks of a medium-size lowland river

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It is generally known that the composition of fish assemblages varies over a cycles, either seasonal or diel. This knowledge is appreciated by commercial fishermen and anglers to catch fish more efficiently. Especially large-scale seasonal dynamics, usually attributed to spawning and wintering migrations, are extensively studied and commercially exploited. On the other hand, there are only a few studies concentrating on more discrete diel changeover of fish groupings in lowland rivers of temperate zone. Thus, the aim of this study was to investigate diel changeover of fish assemblages in the Nida River, the longest left-bank tributary of the Upper Vistula. Fish were sampled by beach seining, using a fry net (7 x 2 m, mesh size of 7 mm). Three sampling sites were chosen in the upper, middle and lower course of the river. Sampling was performed every 2 h over a 24-h cycle, in April, August and October 2010 and 2011. One sampling took place on an additional site in the middle course of the Nida River in August 2009. In result, during the 216 sampling events, a total of 5023 specimens identified to 28 species and one hybrid were collected (out of 45 species ever seen in this river system). From 0 up to 770 specimens were collected on a single site (mean 295.4 ± 223.2 S.D.). The number of individuals per single sampling varied noticeably in the range of 0–342 (25.8 ± 41.7). Number of species per single sampling amounted from 0 to 11 (3.8 ± 2.5). As expected, some species were recorded only or mainly during daytime (*Alburnus alburnus*, *Leuciscus leuciscus*, *Chondrostoma nasus*), whereas several other were found mainly in night (*Romanogobio belingi-vladykovi*, *Gobio gobio*, *Blicca bjoerkna*, *Rutilus rutilus*). On overall, the structure of the ichthyofauna was dominated by cyprinids, mainly *L. leuciscus* and *G. gobio*. Percids were recorded mainly in night. Surprisingly, young specimens of predatory species occurring in this river (*Perca fluviatilis*, *Sander lucioperca*, *Esox lucius*, *Lota lota*) were caught only sporadically. In 2011 one specimen of invasive *Percottus glenii* was collected and that was the first record of this species in the Nida River drainage.

Obtained dataset was analysed by Mixed Effects Models, using a Generalized Least Squares (GLS) technique. As expected, the analyses pointed to the time of the day and season as the most important factors, responsible for the composition of fish assemblages in the Nida River.

This study was supported by the funds BW2201/KIiR/2010 and DS3202/KIiR/2011.

Keywords : Diel cycle, Fish ecology, Lowland river



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Morphological and molecular investigation on the *Romanogobio belingi-vladykovi* complex in the Vistula drainage

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Taxonomic status of the Vistula populations of the "whitefin" gudgeon has been discussed over decades, since the discovery of this fish on that territory. Various authors have assigned them either to *Romanogobio belingi* or *Romanogobio vladykovi*, whereas some others (e.g., P. Bănărescu) have placed them "somewhere in-between". To resolve this issue, we applied combined morphological-molecular approach. 31 specimens identified morphologically as the "whitefin" gudgeon from the Vistula drainage were analysed along with several dozens of *Gobio gobio* and *Romanogobio kesslerii*. A set of 35 morphometric measurements and 13 meristic characters was undertaken on each specimen. Two molecular markers (control region (CR) and first intron of the S7-protein gene) were checked in each specimen, using the primers specified previously (Mendel et al., 2008). The material from the Vistula drainage was compared with samples of a number of species of both genera, *Gobio* and *Romanogobio*, from adjacent drainages (Dniestr, Dniepr, Danube, Elbe, Rhine, and Odra), which are deposited in the Bavarian State Collection of Zoology in Munich (ZSM), Natural History Museum in Kiev (NMU), Institute and Museum of Zoology in Warsaw (MIZ), and Department of Ichthyobiology and Fisheries in Kraków (KIR). Principal component analysis (PCA) performed on set of morphological data revealed that the specimens from the Vistula drainage are much more similar to *R. belingi* than to *R. vladykovi*, however several noticeable differences were found, too. Contrary, it was found that the samples from the Dniestr and Rhine drainages resemble much more Danubian *R. vladykovi* than *R. belingi* from the Dniepr. Sequencing of the mitochondrial marker (CR) pointed to the occurrence of two evolutionary lineages: *R. belingi* and an unique lineage (Lineage_I). Nuclear marker (S7) results shown that the vast majority of the analysed specimens are either clear hybrids between *R. belingi* and *R. vladykovi* (7 individuals), or *R. vladykovi* in cytonuclear disequilibrium (16 individuals). Only five "pure" *R. belingi* specimens were found. Additionally, frequent intergeneric hybridization (*Romanogobio* sp. x *Gobio* sp.) was recorded.

The study was supported by the project no. 206/09/P60 of the Grant Agency of the Czech Republic and Polish funds BW2201/KIIR/2010 and DS3202/KIIR/2011.

Keywords : Biodiversity, Gobioninae, Hybridisation



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ethology

Oral

Reproductive performance in F1 hybrids of two phytophilous cyprinid fish, the silver bream (*Blicca bjoerkna*) × the rudd (*Scardinius erythrophthalmus*)

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Reproductive performance including the spawning behaviour and quality of gametes in cultured F1 hybrids of two phytophilous cyprinid fish species, the silver bream *Blicca bjoerkna* × rudd *Scardinius erythrophthalmus* was investigated in this study at their first sexual maturity. The spawning behaviour was studied in terms of egg release, courting and mating acts under reproductive conditions between hybrids or mixed with the silver bream males. Behavioural experiments were conducted in experimental environments simulating natural reproductive conditions of the species using the spawning ground, high temperature, mixing of sex, natural photoperiod and no hormonal injections. The quality of gametes was evaluated by analysing egg production, sperm density, and F2 and backcross offsprings. For the egg production, the gonadosomatic index, absolute fecundity and egg diameters were analysed at spawning. Sperm density was estimated by counting spermatozoa in a hemocytometer. F2 and backcross offsprings were produced from eggs of the female hybrid fertilised with the sperm of a corresponding hybrid male and a male silver bream. The results revealed that these hybrids exhibited all the reproductive behaviours of the parental species with an intense courting activity. Each egg-release act was accompanied by mating activity, involving simultaneously and successively all the experimental males, hybrids and silver bream, resulting in fertilised eggs. The quality of female sexual products was close to that found in parental species. However, the male sexual products were found more diluted, and F2 generations produced with a significantly lower hatching rate than backcrosses. This study has proven that these F1 hybrids have the capacity to exhibit all the reproductive behaviour as observed in the wild population of parental species. These hybrids are fertile and thus biologically viable. In rivers, their backcrossed offsprings have a greater chance of occurring than F2 progeny.

Keywords : Behaviour, Gametes, Hybrids



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Freshwater fishes of the Balkan Peninsula : Delineating biogeographical regions

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Objective: Understanding the major determinants shaping biodiversity patterns remains a primary challenge in ecology and conservation. Yet, biodiversity patterns vary in space and over time, and this variation is thought to be driven by several biogeographical processes that act upon species. Freshwater fishes are characterized historically by their relative antiquity, are good zoogeographic indicators as they are unable to cross both saltwater and terrestrial barriers and are suitable for investigating the possible existence of shared biogeographic history. Although, regional patterns of biodiversity confirm the notion that the Balkan Peninsula is a hotspot of European biodiversity, still it remains the most understudied region of Europe. Therefore, the need to contribute to the existing knowledge that remains poor, compared to other regions of Europe, is urgent. The first step to untangle the mechanisms establishing diversity of freshwater fishes in the region is the delimitation of discrete biogeographic regions. The aim of the present work is to delineate biogeographical regions in the Balkan Peninsula based on freshwater fish distributions.

Materials and methods: Fish species lists from drainage basins distributed in nine Balkan countries were compiled from bibliographical sources including published papers, books and grey literature databases. Only native species per drainage were considered including migratory species but excluding obligatorily estuarine species with no freshwater life stage. To delineate biogeographical regions, we applied a hierarchical cluster analysis (UPGMA algorithm) that allows a representation of the relative distance between drainage basins based on their fish fauna composition. We quantified compositional dissimilarity between drainage basins using two beta diversity measures accounting for the spatial species turnover and nestedness, respectively. Finally, we compare the relative degree of endemism between the defined biogeographic regions by standardising the number of endemic species, *i.e.* by taking into account the overall number of indigenous species in each biogeographic region (percentage of endemic species per biogeographical region).

Main results and conclusion: The biogeographical regions identified here reflect the major role of historical contingency in shaping the present-day distributions of freshwater fish in the Balkan Peninsula. From a conservation perspective, our biogeographical regionalisation would be useful for prioritizing action plans towards the regions the most unique in regards to their freshwater fish fauna.

Keywords : Balkan peninsula, Freshwater fishes, Biogeographical regions



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Feeding mechanism in damselfishes: a comparison between two morphological different species

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The success of a zoological group can be enhanced by the presence of a “key morphological trait” which allows the group to be competitive in its feeding habits. Good examples can be found in teleosts like the specialized pharyngeal jaws in cichlids or the intramandibular joint in some squamipinnes. Pomacentridae (damselfishes) are one of the most species-rich coral reef fish families and have a relatively great trophic diversity including benthic feeders grazing on filamentous algae, pelagic feeders catching small elusive preys in the water column and a third intermediate group of species feeding on algae, zooplakton and small benthic invertebrates in various proportions. A ligament joining the mandible to the hyoid bar (cerato-mandibular ligament) is a pomacentrid synapomorphic character. This ligament is at least involved in a sound production mechanism of the damselfish *Amphiprion clarkii*: it forces the mouth closing during the lowering of the hyoid bar. In this way, it represents a peculiar mechanism of mouth closing in teleosts because the work of adductor mandible muscles is not required. The hypothesis of this study is that this ligament could also be involved in feeding mechanisms, playing a role in the success of damselfishes. The goal of this preliminary study was to compare the kinematic patterns during feeding behaviors using high-speed video recordings between two species: *Amphiprion clarkii* and a species deprived of the cerato-mandibular ligament: *Chromis chromis*. The way of catching three different kinds of food was tested: artemia, mussel lump attached to pliers and free mussel lump. A mechanical pattern similar to sound production was observed only in *A. clarkii* during the catching of free mussel lump. It results the potential use of the ligament seems correlated to the kind of preys. In this species, the presence of two feeding mechanisms should give some advantages such as an increase of functional plasticity.

Keywords : Damselfish, Feeding mechanism, Evolutive success



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Metazoan parasites of Ponto-Caspian gobies introduced into the Rhine River

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Metazoan parasites of *Neogobius fluviatilis*, *N. kessleri*, *N. melanostomus* and *Proterorhinus semilunaris* were investigated in the lower stretch of the Rhine River from 2009 to 2011. A total of 16 parasite species were found. Larvae of nematodes *Anguillicoloides crassus* and *Raphidascaris acus*, acanthocephalan *Pomphorhynchus laevis* and monogenean *Gyrodactylus proterorhini* occurred in all four goby species. The highest parasite species richness and mean abundance was observed in *P. semilunaris*, compared to *N. kessleri* with the lowest parasite species richness and *N. fluviatilis* with the lowest mean parasite abundance. *Pomphorhynchus laevis* was the dominant species in the parasite community with highest abundances and prevalences in all *Neogobius* species; glochidia of *Anodonta* sp. and *Unio* sp. together with metacercariae of *Apatemon cobitidis proterorhini* and *Diplostomum* spp. were the dominant parasite species in *P. semilunaris*. The temporal dynamics of parasite community structure did not differ in *N. fluviatilis* and *P. semilunaris*, species with limited occurrence in the sampling region. Oppositely, both mean parasite abundance and infracommunity richness increases with time in *N. kessleri* and *N. melanostomus*, the species with regular occurrence and high densities. This work was supported by the grant No. P505/12/2569.

Keywords : Gobiid fish, Invasive species, Parasites



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Oral

Zebrafish models to study mitochondrial function and disease : current status and future perspectives

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Introduction: Mitochondrial disorders are often fatal multisystem disorders, associated with abnormalities of the terminal component of mitochondrial energy metabolism, i.e. oxidative phosphorylation (OXPHOS). Mitochondrial disorders include neurological syndromes, myopathies, heart diseases and developmental disorders. Because of its dual genetic control, defects in OXPPOS can be due to mutations in either the mitochondrial (mtDNA) or nuclear DNA. Mitochondrial disorders are clinically and genetically heterogeneous, but mtDNA replication defects appear as a common cause, mainly due to a defective mtDNA replicating enzyme polymerase gamma (POLG).

Objective and Methods: As existing models have considerable limitations, we developed zebrafish as a new model to study mitochondrial diseases by establishing appropriate phenotypic assays and knocking down the POLG gene by injecting morpholinos in the 1-4 cell stage embryos. Specific optimized assays for mitochondrial replication defects involve measurement of mtDNA copy number and integrity (mtDNA deletions) and staining with BrdU and Mitotracker combined with general sectioning and HE staining or DHE staining for the involvement of ROS (Reactive Oxygen Species).

Main results: First, we studied normal mtDNA replication in wildtype zebrafish. Compared with other species, mtDNA replication initiation occurs quite late during zebrafish embryonic development at the end of the somitogenesis stages, implying that the amount of mtDNA drops to only a few copies per cell. This suggests that apart from the known germ line mtDNA bottleneck, a bottleneck also occurs in somatic cells. The first MO experiments resulted in fish with neurological abnormalities, a bad swimming response (upon touching), low heart beat and some growth retardation. These observations are compatible with human pathologies due to POLG mutations.

Conclusion: Based on these initial data, we consider the zebrafish model highly promising to study POLG-related mtDNA replication defects and the pathogenesis of mitochondrial disorders, also for functional testing of genetic variants and to study the effect of mitochondrial genes with unknown functions.

Keywords : Mitochondrial disease, Zebrafish models, Mitochondrial DNA copy number



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

The constitutive heterochromatin distribution on sex chromosomes in *Characidium* (Characiformes, Crenuchidae)

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Chromosome studies in fish of the genus *Characidium* have shown particular characteristics as in species and/or population level. Despite cytogenetic data indicate conservation in diploid number ($2n = 50$ chromosomes) for most species which have been studied, there are structural karyotype variations among them, especially due to events involving constitutive heterochromatin regions. Some species are characterized by the presence of heteromorphic sex chromosomes of ZZ/ZW type (A group), in which the W is almost or totally heterochromatinized. Currently, the application of chromosome painting and micro-FISH techniques have allowed the chromosomal location of specific sequences, the detection of chromosomal rearrangements and the painting of whole chromosomes, becoming important tools for cytogenetic evolutionary studies. Considering the existence of the heteromorphic sex chromosome Z with heterochromatin located only in the pericentromeric region and the W chromosome completely heterochromatic in *Characidium cf. gomesi*, a W chromosome probe was obtained by microdissection and DOP-PCR amplification methods. Six genomic sequences were obtained of W chromosome (CgW1, CgW2, CgW4, CgW9, CgW10, CgW13) which showed no significant similarity with any sequence deposited in GenBank. FISH experiments using a labeled W chromosome probe marked the pericentromeric region of Z chromosome and painted the whole chromosome W. The probe was applied in chromosome preparations of a different population of *C. cf. gomesi*, and also in *C. cf. fasciatum* and *Characidium sp.*, which showed a similar label pattern that found in *C. cf. gomesi*. However, no sign of hybridization was detected in other *Characidium* species as *C. cf. zebra*, *C. cf. lagsantense* (B group) and *Crenuchus spilurus*. It can be considered that the heterochromatinization process of these chromosomes probably began in homologous and homomorphic chromosomes in the ancestral form of the A group, and probably must have occurred after the ancestral separation of the A and B groups, which can be explained by the fact that no labeling occurred in the chromosomes of *C. cf. zebra*, *C. cf. lagsantense* and *Crenuchus spilurus*. The repetitive DNA sequences have been considered as important tools to elucidate the processes of morphological differentiation presented by sex chromosomes of fishes, and to explain the significant diversity of systems found in morphological diversification of sex chromosomes.

Financial support: FAPESP, CAPES, CNPq

Keywords : *Characidium*, Sex chromosomes, Repetitive DNA



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Fish assemblage structures persist in the tributaries of a large lowland river despite continued water pollution

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The Pilica River tributaries (the Vistula catchment, Poland) were sampled in the mid 1990s and mid 2000s by CPUE electrofishing. A significant reduction in water pollution occurred between the two sampling periods, but in the main channel and not in the tributaries, and particularly in its middle and lower course. This was the probable cause of a significant increase in species number and total fish biomass by the mid 00s. The biomass of fish sampled in both periods was analysed using the SOM (self-organizing map) technique, which produces maps consisting of neurons; a neuron contains groups of samples that are more similar to one another than to samples of other neurons. The neurons were then grouped by the Ward clustering method into clusters and subclusters. The clusters and subclusters seem to have been distinguished mostly by differences in the tributaries' water chemical composition, which was different in given tributaries or their sections, because of different river substrate. An attempt to distinguish indicator fish species of both decades was made using the IndVal technique and fish abundance data, but species that had highest significant IndVal values were usually also tributary-specific.

Keywords : Long-term pollution, Fish fauna stability, Statistics



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Ecology - Fish conservation

Oral

Natural and artificial relationships between Rhine and Rhone populations of grayling (*Thymallus thymallus*): implications for conservation

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The natural distribution of European grayling (*Thymallus thymallus*) in Western Europe is discontinuous; dramatic declines in population sizes as well as local extinctions have occurred in many regions. The species is now recognized to be threatened. Causes of this decline probably are multifaceted. In an attempt to counteract this trend, many fishery managers are attempting to increase stock sizes through the rearing, transport, and stocking programmes. While there are many potential problems with such efforts, there is a lack of basic information concerning the adaptive suitability of stocked material for site-specific conditions. Basic data on the phylogeographic as well as population genetic structure of the species are needed to help guide conservation strategies. We sampled most of the populations still existing in Rhone catchment and compared them to those of the close Swiss upper Rhine catchment in order to 1) gain insights into the lineage diversity that could result from the geological history of connections between these two catchments; 2) assess the population genetic structures with respect to important natural processes and potential anthropogenic disturbances; and 3) prioritise populations for conservation goals. Results revealed that the main genetic pattern biogeographically match with the history of hydrographical networks. Microsatellite analysis showed highly variable mean allele diversity across populations. Both haplotype and microsatellite analyses revealed a strong geographical structure of populations among the main Rhone catchment, a close, more or less natural, affinity between the Upper Rhone (Leman lake) and the Swiss Rhine-Aar catchments, and a determinant contribution of stockings in some populations of the Upper Ain River sub-catchment. The potential persistence of strong genetic structure within some rivers suggests ecological constraints that might prevent the full introgression of contiguous gene pools. These results, complemented with detailed probabilistic analyses, enabled assignment of a conservation status for each population as well as sound recommendations for a national and cross-border management strategy.

Keywords : Phylogeography, Stocking, Conservation



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

New insights into the movement behavior of bullhead (*Cottus gobio*) by telemetry studies in a small Swiss stream

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In literature there is only limited information available on the residency and movement behavior of small-sized fish species. This is also the case for the bullhead, a small bottom-dwelling fish species. New telemetry methods and modern tags allow more detailed studies on the movement behavior of small-sized fish species. In order to detect the home range, movements and reaction after active displacement of bullhead two different telemetry methods were used: radio tracking with nano tags (weight: 0.4 g) and PIT tagging with 12 mm tags (0.1 g). Over a period of two years we radio tagged 39 bullheads in a small stream in a trout zone in Switzerland. Bullheads were caught by electrofishing, tagged with a nano tag, which was placed in the body cavity. The incision was closed with surgical suture. Individuals were regularly tracked with a YAGI antenna for a period of 57 days till the lifetime of the battery expired. The PIT tags were implanted with a syringe into the body cavity of bullhead. PIT tagged individuals were less often tracked but over longer periods (up to 2 years). The detection was carried out with a mobile antenna and a mobile reader. The detection rate of PIT tagged fish was very high, about 4 times higher compared to recapture rates by electrofishing. After tagging, some of the bullheads were actively displaced from the habitat where they were caught (displacement distance 50-150 m). Within the observed time period of 57 days none of the fish showed a complete homing movement to the areas from which they were caught prior to tagging, although most individuals showed a clear upstream migration tendency for the first few days after displacement. Depending on the season most radio tagged fish showed very limited home ranges (a few tens or a few hundred meters). Few radio tagged individuals however carried out longer movements, the maximum movement distance from the area where they were caught is 1.3 km. PIT tagged fish showed a clear downstream movement tendency up to a distance of almost 400 m. However, few bullhead migrated quite long distances in an upstream direction (up to 700 m). Our findings confirm the restricted movements of bullheads, but clearly show a distinct dispersal of a few individuals which was not yet described in prior studies. We discuss the importance of our results for recolonization of new habitat, river restoration practice and the establishment of the longitudinal connectivity in streams.

Keywords : Bullhead, Telemetry, Movement



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Ecology - Fish conservation

Poster

Histological analysis of the silver smelt, *Argentina sphyraena* (Pisces, Argentinidae) gonads during the spawning period

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The silver smelt, *Argentina sphyraena* is a bathydemersal species inhabiting the continental shelf and upper slope waters of the eastern North Atlantic and the Mediterranean. This species is usually found at depths between 100 and 200 m in the Adriatic where its spawning period is extended from winter to spring. Enhanced by the lack of data on the silver smelt reproductive biology, female and male gonads were processed for routine histology in order to describe developmental stages of germ cells during the spawning period of investigated species in the eastern Adriatic. Analysis revealed asynchronous development of the ovaries and testes with germ cells of both sex being in different stages of development. Four stages in oocyte development were observed. Primary growth stage included oocytes in perinucleolus phase, while chromatin nucleolar oocytes were not observed. Average cellular diameter of perinucleolar oocytes was 96.73 μm (\pm 15.07 SD) and oocytes in cortical alveolus stage 215.22 μm (\pm 45.02 SD). Vitellogenic growth stage included early and late vitellogenic oocytes, with their diameters of 365.53 μm (\pm 39.37 SD) and 519.15 μm (\pm 30.04 SD), respectively. Maturation stage was characterized by advanced yolked oocytes with an average diameter of 705.50 μm (\pm 67.43 SD). Testes were staged as mid-spermatogenic, since approximately equal numbers of spermatocytes, spermatids and spermatozoa were observed. The diameter of seminiferous tubules varied from 143.32 to 239.66 μm , with an average value of 188.34 μm (\pm 22.50 SD). Presented data indicate that *A. sphyraena* is an asynchronous spawner that has prolonged spawning season.

Keywords : *Argentina sphyraena*, Reproduction, Adriatic



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Testing predictions of the syngameon hypothesis in Lake Matano's "sharpfin" sailfin silversides radiation

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The mechanisms driving divergent evolution in sympatry remain only partially understood. Evolving radiations restricted to habitat islands are particularly suited for studying early stages of phenotypic adaptations and related genomic consequences. Theory predicts a selection-maintained "syngameon" phase in early stages of species-flock formation, with ecologically distinct but genetically weakly differentiated emerging species. The lack of complete reproductive isolation might lead to novel combination of traits under selection and thereby increase evolution of phenotypic diversity. Here, we test whether the incipient adaptive radiation of "sharpfin" sailfin silversides (Atheriniformes: Telmatherinidae: *Telmatherina*) endemic to the ancient graben-lake Matano in Central Sulawesi (Indonesia) fulfills predictions of a "syngameon" complex, with focus on individual fitness consequence of phenotypic variation. The comparatively small but phenotypically diverse species flock of sharpfins shows fine-scaled variation in traits relevant to foraging. Previous studies suggested ongoing geneflow among different *Telmatherina* morphospecies, and presence of individuals with character combinations intermediate to the morphospecies recognized. We analyzed individual fitness consequences of phenotypic variation likely relevant to trophic resource exploitation, based on fitness proxies and a comprehensive random sample of sharpfins taken from 154 locations distributed equally around Lake Matano' shoreline and genotyped the same fish using multilocus AFLP markers. Bringing these data together, we generated phenotypic and genotypic fitness landscapes of the whole sharpfin species flock. We discuss the results in the light of the "syngameon" phase hypothesis of adaptive radiation, combining both fitness landscapes.

Keywords : Adaptive fitness landscape, Sympatric speciation, Adaptive radiation



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Identification and study of fish species in Zayandehrood River, Iran (Chaharmahal va bakhtiary basin)

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Identification and study of different fish species has the important roles in rivers and restoration. Zayanderood River the second constant river and also the main source of agriculture and drinking water in Iran. 9 stations along the Zayanderood River were chosen. To cover the all study area, substations were considered as well. Fishes were sampled by electroshocker (180-270V) and cast net (13-15mm mesh). Samples were stored in 10 % formaline and transferred to laboratory for indentification. 30 morphological and merestic characteristics were used in identification. Results showed that 7 species fish belonging to 3 families: Cyprinidae, Balitoridae and Salmonidae. Cyprinidae with 93.2 % had most frequency and Salmonidae with 0.2 % had lowest frequency. 5 species of Cyprinidae including *Alburnus maculatus*, *Capoeta aculeata*, *Capoeta capoeta*, *Capoeta damascina* and *Chondrostoma regium*, Balitoridae with one species *Turcinoemacheilus kosswigi* and Salmonidae including one species *Oncorhynchus mykiss* were identified. Among the all identified species, the last one is not an endemic species of Zayanderood River. Because of fast flowing water, low temperature, low marginal pit with relatively calm water, food shortages and steep of the river.

Keywords : Zayandehrood river, Cyprinidae, Balitoridae



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Role of the transcription factor Isl1 during the development of the pancreas in zebrafish

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Type 1 diabetes is associated with autoimmune destruction of insulin cells in the pancreas, a new production of functional mature beta-cells is thus essential for glucose homeostasis. This can be achieved by understanding of transcription factors that are required for the pancreatic development. In the mouse, the LIM homeodomain gene *Islet-1* (*Isl1*) encodes an essential transcription factor that is required for the formation of all endocrine cells. In zebrafish, *Isl1* is expressed in all endocrine pancreatic cells at early stages while at later stages, its expression is only maintained in the somatostatin cells. To define the role of *Isl1* in the development of the pancreas in zebrafish, we analysed endocrine cells differentiation in the mutant *Isl1*. We show a severe reduction of all hormones in the pancreas at early stages. However, the reduction of glucagon and insulin expression seems transient. Indeed, at later stages, the glucagon and insulin expression is reduced but not as strongly as at early stages while for somatostatin, the strong reduction is still observed at later stages. These results show that the mutant *Isl1* seems to recover the capacity to initiate the glucagon and insulin cells differentiation while the somatostatin cells remain under the dependency of *Isl1* during the pancreatic development. On the basis of our data, we propose that *Isl1* is required for the differentiation of all endocrine hormones at early stages while at later stages, *Isl1* is only important for the formation of somatostatin cell. This suggests that the differentiation of glucagon and insulin cells at late stage is under the dependency of another homeodomain transcription pancreatic factor we still have to identify.

Keywords : Zebrafish, *Isl1*, Pancreas



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Oral

Brown trout (*Salmo trutta* L.) population structure in small streams of White Sea basin, Russian European North

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White Sea brown trout (*Salmo trutta* L.) was chosen as object of analysis due to the fact that the populations are among the least disturbed by human activity. There are no artificial breeding and no stocking domesticated fish. White Sea brown trout is an object of tourist and sportive angling only and therefore main anthropogenic influence might be overfishing and changing environment. Three small populations from Svyatoy stream, Vorob'ev stream and small river Nil'ma of the Velikaya Salma straight (White Sea basin) were investigated. Distances between mouths are less than 15 km. All populations have similar environment conditions. Only one spawning site was found for each stream. Nil'ma brown trout population inhabits the stream sympatrically with Atlantic salmon (*Salmo salar* L.). Chosen populations differ in fishing degree. Svyatoy stream is situated in nature protected area. In the mouth of Nil'ma River there is situated village, so this population is hardly influenced by catching. Vorob'ev population compared to two others has medium degree of fishing. We used old scale samples for temporal differentiation of populations. We analyzed samples from different years beginning from 1992 by microsatellite loci. Length, weight and age of each fish were measured. Total 282 fishes were investigated. Exact tests for genetic differentiation revealed significant differentiation in all pairwise comparisons between samples from different populations. The number of alleles detected at each locus varied between two and four. Two populations showed temporal stability. But significant differences in allele frequencies were found in Nil'ma population samples of different years. Hybrids of trout and salmon were caught in this river. We might suppose that Nil'ma effective population size decreased below critic value needed for stable population structure, due to overfishing and decreasing spawners Allelic richness and gene diversity in all studied populations were remarkably low compared with genetic variability at the same microsatellite loci observed in other brown trout populations. The analyses reveal strong genetic differentiation among populations separated by <15 km (θ_{ST} 0.067). Populations of Svyatoy and Vorob'ev streams live in natural habitat with low fishing whereas they have the same low genetic variability and allelic richness as Nil'ma population. Thus, we suggest that the most important factor causing high genetic differentiation and low genetic variability in populations of Velikaya Salma straight are genetic drift and founder effect in small populations.

Keywords : Brown trout, Population structure, Microsatellite



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Mitogenomic phylogeny of Myctophiformes (Neoteleostei)

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Lanternfishes of the family Myctophidae is the most abundant fish group in the open ocean with about 250 species distributed worldwide from epipelagic layers down to a depth of approximately 2000 meters. Together with the poorly diversified family Neoscopelidae (Blackchins with 6 species) they constitute the order Myctophiformes. Lanternfishes show taxa-specific photophore patterns (bioluminescent light organs) and this attribute has proven useful in reconstructing phylogeny. Osteology and larval ontogeny mostly corroborate phylogeny from photophores although no molecular data has been employed. Myctophid mitochondrial genomes show high levels of gene order rearrangements compared to other vertebrate groups. Many of these rearranged gene orders and associated non-coding regions are clade defining in Myctophidae. This phylogenetic study utilizes complete mitochondrial genomes from 42 myctophiform taxa. Results from DNA sequences and unique gene order rearrangements are mostly congruent with previous morphological studies based on photophores, osteology and larval ontogeny. However, the phylogenetic position of *Notolychnus valdiviae* and some tribal relationships within the subfamily Lampanyctinae show incongruence to morphology.

Keywords : Myctophiformes, Mitogenomics



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Ecology - Fish conservation

Oral

Eel attacks – a new tool for assessing European eel (*Anguilla anguilla*) abundance and distribution patterns with gillnet sampling

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Because of complex life cycle and cryptic behavior, European eel (*Anguilla anguilla*) is difficult to monitor. During many years of gillnetting in Dutch and Czech freshwaters we were registering characteristic involutions of gillnet netting with a chewed up fish inside. We concluded that these involutions were the result of eel attacking fish caught in gillnets and called them eel attacks. The most frequently attacked fishes were young individuals of abundant species (*Perca fluviatilis*, *Sander lucioperca*, *Rutilus rutilus* and *Osmerus eperlanus*) and small sized species (*Gymnocephalus cernua*). Eel positively preferred pikeperch and negatively selected roach and smelt. Eel attacked fishes in gillnets exclusively during the night, most probably after midnight. When we compared abundance of eel attacks in gillnets with abundance of eel recorded by active gears (beach seining and trawling), we found highly positive and significant correlation (Spearman's R 0.690). Eel attacks were not distributed homogeneously within studied reservoirs, geographical areas and years. Eel attack abundance was higher in benthic in comparison to pelagic habitats. Numbers of eel attacks were higher in Dutch than in Czech reservoirs, which corresponded to a general decline of eel densities with distance from the sea. Abundances of eel attacks also declined significantly in the period 1998 – 2008. The study showed that eel attacks can be successfully used as a simple and nonintrusive tool for monitoring eel abundance using gillnets. Gillnets are widely used in fish monitoring and hence gillnet effort performed across whole Europe has a great potential in eel abundance assessment.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Poster

Morphological investigation of the brain of different populations of threespined sticklebacks

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Threespined sticklebacks (*Gasterosteus aculeatus*) are among the most widespread fish in the world. It is believed that the different populations are in the process of evolving into adaptive radiations. The stickleback is therefore a promising model to study changes in brain morphology associated with speciation. This study analyses different populations of stickleback that show well known differences in behaviour and morphology. This study investigates possible differences in brain morphology and histochemistry among these different populations. Cryostat sections were stained for NADPH-diaphorase, acetylcholine esterase, and with Nissl and myelin stains and volumes of different brain areas were measured. The first question is to what extent variations are present within populations. Morphometry of brain sections stained with Nissl stains revealed some variations especially in the size of the telencephalon, hypothalamus, and cerebellum. The distribution of NADPH-diaphorase and acetylcholine esterase, however, was very similar and reproducible. Differences between populations are apparent mainly in the size of acousticolateralis areas and related fibre tracts and in the cerebellum. Pronounced differences were observed especially between freshwater lake populations and migrating salt water fish. Our results show that even at the population level changes in brain morphology can be detected that may contribute to ongoing speciations.

Keywords : *Gasterosteus aculeatus*, Brain morphology, NADPH-diaphorase



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Oral

Zebrafish (*Danio rerio*) behavioral analysis : a new tool in toxicological assays

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While most of toxicological assays focus on lethality, teratogenicity, analysis of pollutant effects at sublethal doses may improve pollution effect knowledges. As zebrafish was recently used to test off target drug effects in particular by following behaviour for example for schizophrenia treatments. Pollutant is a major critical problem for aquatic ecosystems preservation that will require the analysis of acute and sublethal doses for single molecules, in combination and in their original and metabolic form. A zebrafish behaviour analysis was developed to allow aquatic pollutant effect screening, based on larvae response to light stimuli, assessing various important aquatic pollutants as metals, insecticide, pesticide and psychotropic molecules. Measurement of activity (%) and active or mean velocity (mm/s) and calculation of various data provide a complete overview of pollutant effects on aquatic fauna behaviour, improve the toxicological description of aquatic pollutants and could be extended to large scale screening of compounds. Principal component analysis (PCA) were performed on calculated values and profiles associated to various aquatic pollutants were compared providing efficient data to intend to index the pollutant effects and bringing to light correlation between compounds or pollutants groups. Zebrafish locomotion assays using this method offer a sensitive, rapid and powerful tool in pharmacological screening as described previously but also during toxicological assays.

Keywords : Zebrafish, Toxicology, Behavior



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Transcription factor *Egr1* during pituitary development in *Danio Rerio*

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We show that the *sox4b* gene is expressed in the pituitary anlagen starting at 24hpf and later in the entire head region including the pituitary. At 48hpf, *sox4b* mRNA colocalizes with that for thyroid stimulating hormone (*tshb*), glycoprotein subunit a (*gsua*) and the Zn finger transcription factor *Gata2a*. Loss of *Sox4b* function, using morpholino knock-down or expression of a dominant negative *Sox4* mutant, leads to a drastic decrease in *tshb* and *gsua* expression and reduced levels of *gh*, while other anterior pituitary gland markers including *prl*, *slβ*, *pomc* and *lim3* are not affected. *Sox4b* is also required for expression of *gata2a* in the pituitary. Knockdown of *gata2a* leads to decreased *tshb* and *gsua* expression at 48hpf, similar to *sox4b* morphants. Injection of *Gata2a* mRNA into *sox4b* morphants rescued *tshb* and *gsua* expression in thyrotrope cells. Finally, *sox4b* or *gata2a* knockdown causes a significant decrease of gonadotropin expression (*lhβ* and *fshβ*) at 4dpf. The anterior pituitary gland is composed of different cell types, each expressing specific hormone genes such as *pomc*, *prl*, *gh*, *lh* and *sl*. The latter four require the presence of the *Pit1* factor for their expression, several other genes are essential for various steps of zebrafish anterior pituitary development. However, many questions still remain open and more factors are clearly required to understand the entire genetic control system of pituitary development. The *Egr1* (early growth response) transcription factor, containing three DNA-binding zinc finger sequences, is involved in many developmental and adult processes. In zebrafish, its mRNA is first detected in adaxial cells of the lateral mesoderm, in specific brain areas starting at 21hpf and subsequently increasing in distinct domains of the central nervous system. In mouse, disruption of *egr1* expression leads to fertility problems, due to a diminished or complete lack of expression of the gonadotropin subunit *lhβ*. In addition, somatotropes in KO mice present abnormal cytological features and are reduced in number, consistent with their decreased *Gh* content. We study the function of *egr1* in zebrafish pituitary development. We show that *egr1* is expressed in the pituitary from 48hpf and, at 72hpf *egr1* mRNA localizes in the anterior domain of *pomc*, *prl* and *pit1* expression. Loss of *Egr1* function, using morpholino knock-down or an *egr1* mutant revealed a specific role for *Egr1* in *lh* and *gh* expression, similar to mouse. In addition, this factor acts in other pituitary hormone genes, such as *slβ*, *pomc* and *prl* around 72hpf while other pituitary markers (*gsua*) were not affected. In conclusion, the *egr1* expression pattern is different in zebrafish from mouse; it plays similar activating functions for the expression of *gh* and *lhβ* in pituitary, but an additional repressive role for *pomc* and *prl* expression.

Keywords : *Egr1*, Pituitary, Zebrafish



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Poster

Deleterious effects in *Oncorhynchus mykiss* gills after acetaminophen acute exposure : histology, detoxification mechanisms and oxidative damage

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The pharmaceutical acetaminophen (N-acetyl-p-aminophenol) is widely used in human medicine as an analgesic and antipyretic drug. In fact, it is one of the most over-the-counter (non prescription) drug sold. In some European countries, concentrations up to 6 $\mu\text{g L}^{-1}$ of acetaminophen can be found in sewage treatment plants. Such high values cause concern due to the adverse effects on non-target species and potential ecological consequences. The assessment of oxidative stress in different non-target species has been used as indicator of adverse effects in contaminated aquatic ecosystems. To test the effect of acetaminophen in aquatic ecosystems, an acute exposure (96 hours) with *Oncorhynchus mykiss* (rainbow trout) was performed, in order to evaluate the enzymatic and histological effects in fish gills. The experiment was carried out under laboratory controlled conditions, and involved one control (unexposed) group, and 3 different acetaminophen concentrations (0.05, 0.5 and 5 mg L^{-1}). A total of 15 animals were used in each concentration with 5 animals in 3 replicates per concentration. After the exposure period, the animals were sacrificed, and one branchial arch was removed for histological analysis and the remaining portion of gill tissue was preserved in liquid nitrogen for the performance of the enzymatic study. A quantitative evaluation of the gills architecture was performed. Lipoperoxidation (TBARS) levels and glutathione S-transferases (GSTs) enzymatic activity were also determined. Significant differences were observed among different concentrations and the control group for both tests indicating potential occurrence of oxidative stress in animals exposed to higher concentrations of acetaminophen (5 mg L^{-1}). In addition, there were a significant decrease of the distance between secondary lamella (ID) and one increase of secondary lamella width (SLW) when compared to control animals, although no significant difference was detected in the respiratory area of gills. This set of results suggests that the presence of acetaminophen in water is directly linked to the increase of oxidative stress levels and histological changes in fish gills.

Keywords : Acetaminophen, Gills, Biomarkers



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

An invasive species reverses the roles in a host-parasite relationship between bitterling fish and unionid mussels

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Fishes are often part of host-parasite relationships and these are frequently characterized by coevolutionary dynamics of parasite adaptations to exploit their host, and counter-adaptations in the host to avoid the costs imposed by parasitism. While fish are typically the hosts being parasitized, there are notable exceptions. An example is a unique reciprocal host-parasite relationship between European bitterling fish, *Rhodeus amarus*, and European unionid mussels. Bitterling lay their eggs into gills of live mussels and, in turn, mussel larvae parasitize fish. The European bitterling colonized most of Europe relatively recently and parasitize all sympatric European mussels, which are evolutionarily naive and have not evolved strong defences (egg rejection) against bitterling parasitism. The parasitic larvae of European mussels are unable to utilize the bitterling, although readily parasites most other European fishes. Hence, the European bitterling is a parasite of unionid mussels. We studied how an invasive mussel species can affect such coevolved relationship. The Chinese pond mussel, *Anodonta woodiana*, recently colonized European freshwaters from the region of high abundance and diversity of Asian bitterling species where it evolved strong adaptations against parasitism by many bitterling species. We found that European bitterling behaviourally responded to *A. woodiana* as to a potential host, but failed to use it properly for oviposition (one population) or used it but all the eggs were lost due to rejections by the mussel (second population). Another experiment revealed that parasitic larvae of *A. woodiana* can develop on the European bitterling successfully. Hence, *A. woodiana* effectively reversed the host-parasite relationship between the bitterling and mussels. We discuss potential long-term consequences on population dynamics of the European bitterling.

Keywords : Parasitism, Cyprinidae, Non-native species



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ethology

Oral

The effect of social environment on mating tactic of male Endler's guppy (*Poecilia wingei*)

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Phenotypic plasticity in mating behaviour can be beneficial if the relative benefits of the particular mating tactic differ across social environments. In female-biased populations males are predicted to invest more effort into courtship and advertisement of their qualities. In male-biased environment, advertisement may be costly and time-consuming and males are predicted to switch to alternative mating tactics, such as sneaking. It is not clear whether individuals respond directly to actual conditions or if they are affected by their past social experience. The aim of our study was to test the effect of different sex ratios on male mating tactic of Endler's guppy (*Poecilia wingei*). First, sexually naive males of the standardized age were allowed to mate with females and aspects of their mating behaviour (e.g. number and duration of sigmoid displays, copulations, gonopodial twists and gonopodial thrusts) were recorded. After this trial, a half of test males were housed in a tank with another male and one female (male-biased sex ratio) and the second half with two females (female-biased sex ratio). One month later, mating trials were repeated. Males from female-biased environment reduced the number of the gonopodial swings and gonopodial thrusts, likely due to absence of sperm competition in their treatment. However, they also decreased their courting rate, perhaps due to a lack of mating competition with other males. Our data show that individual reproductive behaviour of male Endler's guppy is plastic and can be affected by social environment.

Keywords : Alternative mating tactic, Social environment, *Poecilia wingei*



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ethology

Poster

Migration of perch *Perca fluviatilis* L. and bream *Abramis brama* (L.) in the Rimov Reservoir

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The presented study focused to migration and movements of perch *Perca fluviatilis* L. and bream *Abramis brama* (L.) within the canyon shaped Řimov Reservoir, Czech Republic. The main emphases were given to i) movements during spawning season, ii) reproductive homing, and iii) migration between spawning and feeding grounds. The method of the study was based on mark and recapture approach. Individuals of both species were captured and marked during their spring spawning (total number of marked fish – 7 780 perch and 6 726 bream). Recaptures of marked individuals were carried out in two periods – spring (total number of recaptured marked fish – 1 587 perch and 819 bream) and summer (20 perch and 242 bream). The study was performed in three consecutive years 2009-2011. Data were processed separately for species, sexes and different size groups.

The results revealed that: i) Perch movement during the spawning season was relatively low with 80 % of recaptures (recaptured marked individuals) located on the marking locality. Size dependency was found, the smallest perch (100-125 mm SL; fish of age 1+) having less intensive movement than larger perch (> 125 mm SL; older than 1+). Bream movement was more intensive than perch with only 51 % of recaptures located on the marking locality. Size dependency of bream movement was also found but only in case of bream males (no effect of size to movement of bream females was found). Contrary to perch, bream males of smaller size (230-300 mm SL) had more intensive movement than larger males (> 300 mm SL). ii) High tendency for reproductive homing was found for perch, 52 % of recaptures were caught on the same spawning ground the next spawning season. No size- or sex-specific differences were found in reproductive homing of perch. In case of bream, reproductive homing was sex dependent. Bream females had higher tendency for reproductive homing than males, 67 % vs. 34 % of recaptured females and males, respectively, were caught on the same locality during the next spawning season. iii) Migration between spawning and feeding grounds could not be tested in perch due to low numbers of recaptured individuals during the summer. Bream displacement from spawning ground was relatively high only 27 % of recaptured bream were caught in the marking locality and 33 % in localities adjacent to the marking locality. No size- or sex-specific differences in this migration were found in bream. It can be concluded that both species have species specific-movements in conditions of the canyon-shaped reservoir that are partly driven by sex and size of individuals.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

BOSS, Biological Object Search Service : an overview of the architecture and features of the FishNet2 search engine

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On April 22, 2010 an explosion on the British Petroleum Deepwater Horizon Oil Platform resulted in the release of large quantities of crude oil into the northern Gulf of Mexico. The ability of ecologists and other scientists to assess the impacts of the spill on the Gulf of Mexico ecosystem depends critically on the availability of baseline data on the composition and structure of biotic communities in the region under natural conditions. Natural history museums have the ability to provide much of this information as they contain data on biological resources spanning hundreds of years to the present. The FishNet2 network is a collaborative effort among fish collections around the world to share and distribute data on specimen holdings. Over the past year a number of developments have been made to address the needs of acquiring baseline data from FishNet2 in response to such temporally & geographically defined events as the BP Oil Spill. Specifically, we have improved upon the data harvesting architecture, added geospatial query capabilities, improved result summaries, made significant changes to the UI and produced an API to facilitate third party integration. The underlying architecture for FishNet2 has been generalized as the Biological Object Search Service allowing us to create instances applicable to other taxonomic networks. HerpNet2 is an example of such an instance utilizing the same architecture.

Keywords : Fishnet, Herpnet



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Fish isotopic niche concept : a case study with the Atlantic sabretooth anchovy

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This work proposes the new concept of isotopic niche for fish species that modify its ecological trophic rule as a function of the ontogenetic development. The idea is to represent a species ecological rule in terms of stable carbon and nitrogen signatures, using a single number, taking into account the ontogenetic change in food consumption and the effects of growth and mortality in the species biomass at any age. The model species, *Lycengraulis grossidens* (Spix & Agassiz, 1829), presents ample distribution along the western Atlantic, using estuaries as nursery grounds and inhabiting both fresh and coastal waters. Carbon (C^{13}) signatures were taken from 46 animals with total length ranging from 4.9 to 22.6 cm. Samples were taken at Pinguela lagoon (29.27° S; 50.19° W) in November/2009 and March/2010. Population parameters were all estimated from the www.Fishbase.org life history tool, considering a maximum length of 23.5 cm (TL) and maturity length of 8cm (TL). Assymptotic length (L_{∞}) was estimated as 24.7cm, the growth constant (K) as 0.27, a natural mortality rate (M) of 0.59, and a life-span of approximately 10 years. Parameters of the weight/length relationship were estimated from a sample of 1478 individuals, with proportionality coefficient (a) estimated as 0.0033 and allometry coefficient (b) as 3.29. The model is developed as follow. First, consider a fish population that presents a survival by recruit following a power function: (1) $P_t = e^{-0.59 \cdot t}$; where: P_t = proportion of the population surviving to age t (years). Animals will growth following a regular von Bertalanffy growth model: (2) $L_t = 27.7 \cdot (1 - e^{-0.27 \cdot (t-0.4)})$; where: L_t = average total length at age t (cm). The weight/length relationship follows a power function: (3) $W = 0.0033 \cdot L^{3.29}$; where W = weight (g); L = total length (cm). Biomass by recruit (B_t) result from merging equations 1 to 3: (4) $B_t = (e^{-0.59 \cdot t}) \cdot (0.0033 \cdot (27.7 \cdot (1 - e^{-0.27 \cdot (t-0.4)})^{3.29})$. Isotopic signature may follow complex patterns through the ontogenetic development. For *L. grossidens* the pattern for ^{13}C followed a logarithm curve: (5) $d^{13}C_t = 3.29 \ln(L_t) - 29.38$; where: $d^{13}C_t$ = isotopic signature at age t ; $L_t = 27.7 \cdot (1 - e^{-0.27 \cdot (t-0.4)})$. The relative isotopic impact of an age group into the community depends on its age-specific isotopic signature and its abundance as biomass. Considering the life cycle, the compound impact of a species can be achieved as follow: (6) $d_b^{13}C = \int_0^{10} [d_t^{13}C(t) \cdot B_t(t)] dt / \int_0^{10} B_t(t) dt$; where \int is the definite integral from age 0 to the maximum lifespan of the species, 10 for *L. grossidens*. Integrals were solved using Maple Software. Arithmetical approximation for $\int [d_t^{13}C(t) \cdot B_t(t)] dt$ is equal to -303.57 (from $t=0$ to 10). Numerical solution for $\int B_t(t) dt$ is 14.87. Then, the balanced isotopic signature for the species ($d_b^{15}N_t$) is -20.42 (-303.57/14.87), which corresponds to the expected ^{13}C signature for an animal of 14.2 cm.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Protein expression profiles in European eel (*Anguilla anguilla*) exposed to perfluorooctane sulfonate; combining *in vitro*, *in vivo* and *in situ* approaches

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Since the 1980s, the stocks of European eel have been declining in most of their geographical distribution area and they are now considered below safe limits for population survival. Many factors can be attributed to this decline such as pollution by xenobiotics. The aim of this research project was to develop a multi-biomarker approach to set up an evaluation and monitoring tool for assessing the health state of eels. The strategy consisted in assessing protein expression profiles (PEPs) in post-nuclear fraction of peripheral blood mononuclear cells (PBMC) exposed *in vitro* to PFOS, before *in vivo* and *in situ* validations of biomarkers. The first step of this approach was to find out PEPs from *in vitro* PFOS exposure. PBMC culture from eel was used to test the *in vitro* toxicity of this compound. Exposure time and two sub-lethal concentrations were chosen to avoid cell mortality (48h exposure at 10 µg/l and 1 mg/l). PBMC were isolated from blood by centrifugation over a Ficoll/Hypaque gradient. After *in vitro* contaminations, the post-nuclear fraction was isolated. Two-dimensional differential in-gel electrophoresis (2D-DIGE) was performed on 24 cm, pH 4-7 IPG strips and the results were analysed with DeCyder software. The identified differentially expressed proteins have been categorized into diverse functional classes, related to cell structure, protein folding (e.g. protein disulfide isomerase) and signal transduction (e.g. 14-3-3 protein epsilon) for instance with some proteins never found in proteomic studies. The second step of the approach was *in vivo* contaminations of eels. Yellow eels were exposed to environmental waterborne PFOS concentrations (0.1 and 10 µg/l) during 28 days and a similar proteomics analysis was performed on PBMC. Finally, eel samplings from three Flemish rivers with graded levels of PFOS contamination were conducted in order to validate the previous results. Common protein spots that were affected by PFOS exposure in *in vitro*, *in vivo* and *in situ* investigations will be identified and potentially used as future biomarkers of PFOS contamination in eel.

Keywords : Lymphocytes, Proteomics, Biomarkers



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Age and growth Of *Phycis phycis* (Linne, 1766) in the gulf of Tunis

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The age of fish in a population is fundamental to most of the questions fishery biologists attempt to answer about that population. The aim of this study was to report the parameters of the weight-length relationship and to estimate the age and growth of *Phycis phycis* (Linnaeus, 1766) in Gulf of Tunis. A sample of 272 specimens of *P. phycis* was collected from the landings of the small-scale artisanal fisheries between September 2007 and June 2010. The total length (TL) ranged from 14 to 55.5cm and total weight (TW) from 45 to 1779g. Length-weight relationship were described by allometrically positive for the females ($TW = 0.0083 * TL^{3.0703}$), males ($TW = 0.0063 * TL^{3.1471}$), and both sexes ($TW = 0.0082 * TL^{3.0759}$). No significant differences were found between males and females (ANCOVA, $p = 0.426$). Symmetry between the right and left otolith was compared. The relation between the total length (TL) of fish and the weight of the otolith (Wo) did not show a significant difference between the right ($Wo = 0.12 TL - 0.163$) and left otolith ($Wo = 0.11 TL - 0.124$) (ANCOVA, $p > 0.05$). The relationships between otolith radius and otolith weight with age, showed that there are no significant differences between males and females (ANCOVA, $p > 0.05$).

The growth parameters for females ($TL = 73.43 (1 - e^{-0.158 (t+1.709)})$), males ($TL = 67.51 (1 - e^{-0.168 (t+1.993)})$) and combined sexes ($TL = 65.73 (1 - e^{-0.135 (t+2.025)})$) were estimated. The females, reaching $L_{\infty} = 73.43$ cm, grew faster than the males, which did not exceed 68 cm. Moreover, the females have the higher predicted asymptotic weight ($W_{\infty} = 4446.08g$) compared to the males ($W_{\infty} = 3603.20g$). Consequently, the index of performance from growth (Φ) (cm/an) of the females ($\Phi = 2.929$) was higher than the one of the males ($\Phi = 2.883$).

Age estimation in gadiform fish has been known to present some difficulties due to otolith thickness, which in most species requires special processing methods so that growth increments become visible.

Keywords : *Phycis phycis*, Age, Otolith



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

DNA barcoding for identifying neotropical fishes : high molecular diversity in the genus *Astyanax* (Characiformes, Characidae)

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The Neotropical freshwater fish fauna is the richest in the globe. Among the 15,000 freshwater species nearly 6,000 are found in this region, being that this number could be higher due to the existence of many undescribed species. One of the most representative Neotropical orders is Characiformes, exclusively composed by freshwater fishes and with more than 2,000 species. The family Characidae is the most speciose in Characiformes covering over 1,100 valid species divided in 170 genera, of which 260 species were described in the last ten years. Despite efforts in studies of phylogenetic relationships in this family, their relationships remain uncertain, where 90 genera (>620 species) are allocated as incertae sedis and many of them have their monophyly questioned. One of these genera is *Astyanax*, with 137 valid species. Only one review so far treated the genus as a whole and some recent studies suggest that *Astyanax* is a polyphyletic group. Inside of this context we analyzed 22 nominal species and others specimens only identified at genus level using DNA barcoding, in a total of 575 sequences. The specimens are distributed throughout Brazil, Peru and Venezuela. The sequences were aligned with the program MUSCLE and a dendrogram was generated by Neighbour-joining using the Kimura 2P model in MEGA 5. Results show that there are at least 60 groups, with many nominal species allocated in different groups, indicating possible species complexes in this genus. Two groups "*fasciatus*" and "*scabripinnis*" showed little divergence inside of each one, with less than 2 % of divergence. Furthermore, there is evidence of wide geographic distribution for *A. altiparanae*, described as endemic to the Upper Parana basin, but here also found in coastal basins of the state of Rio Grande do Sul. The genetic distance within groups ranged from 0 to 1.45 %, with an average of 0.275 %. Regarding the distances between the groups, these numbers ranged from 0.9 to 31.9 % with an average of 13.2 %. These results are in agreement with the literature for freshwater tropical fish, except the average distance between the groups that are either slightly larger in *Astyanax*. The large number of groups, given the number of species analyzed, reveals a high molecular diversity, implying the need for reevaluation of the morphological identification of specimens and taxonomic revision of the genus, which is considered very complex among experts. Financial support: FAPESP, CAPES, CNPq.

Keywords : Cytochrome c oxidase subunit 1, Molecular identification, Biodiversity



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

**Genetic identification and distance between
Chalcalburnus chalcoides and *Vimba vimba persa* in
Southern part of Caspian sea**

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In this study the genetic identification and distance between two species, *Chalcalburnus chalcoides* and *Vimba vimba persa* in Southern part of Caspian Sea by using microsatellite markers were obtained. 15 dorsal and pectoral fin of *chalcalburnus chalcoides* and 15 samples of *Vimba vimba persa* were collected and stored in pure ethanol. Genomic DNA was extracted by Phenol-Chlorophorm method and Quantity and quality of extracted DNA was determined using 1 % Agarose electrophorus. DNA was used for PCR amplification of 10 microsatellite loci. The amplifications were run on 6 % Polyacrylamid electrophorus. The present study showed that 7 out of 10 markers were polymorphic. Based on Gene Alex software, genetic identification and distance among species were studied and genetic distance dendrogram were showed by TFPGA software. The result revealed that the highest and lowest genetic distance between these two species were 81 % and 42 % and the highest and lowest Fst was 0.08 at a significance level of $P \leq 0.05$.

Keywords : Microsatellite, *Chalcalburnus chalcoides*, *Vimba vimba persa*



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Phylogenetic analysis of Otothyrinae (Siluriformes: Loricariidae) with emphasis in Hisonotus based in molecular evidences

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The goal of the present study is to improve our knowledge of the phylogenetic relationship of members of the subfamily Otothyrinae. For that we use a Bayesian phylogenetic method to test the relationships among 50 representative taxa within Otothyrinae, using 2810 bps of two mitochondrial and one nuclear gene. *Hemipsilichthys gobio* and *H. papillatus* were used to root the phylogeny. Additionally samples of Hypoptopomatinae, Neoplecostominae, Loricariinae and Hypostominae were included in the analysis as outgroups. Our results showed that Otothyrinae is monophyletic. We analysed 18 species of *Hisonotus* and the results showed that it is polyphyletic, as well as the genus *Pseudotothyris*. All other genus of Otothyrinae analysed (*Corumbataia*, *Epactionotus*, *Eurycheilichthys*, *Microlepidogaster*, *Otothyris*, *Otothyropsis*, *Parotocinclus*, *Rhinolekos* and *Schizolesis*) are monophyletics. Based on these results we suggest some fundamental changes in the Otothyrinae taxonomy to reflect the monophyletic groups inside it that will help in further studies in this amazing catfish group.

Keywords : Molecular systematics, Cascudinhos, DNA



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Evolutionary and biogeographic history of the subfamily Neoplecostominae (Siluriformes : Loricariidae)

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Morphological and molecular studies of the family Loricariidae have revealed that many of the relationships among its members have yet to be resolved. The main objective of the present study is to improve our knowledge of the evolution of this highly adapted species rich group of catfishes and determinate the origin of its clades. For that we use a number of different phylogenetic methods to test relationships among 52 representative taxa within Neoplecostominae using 4676 bp of mitochondrial and nuclear DNA. Our results show that the subfamily Neoplecostominae is monophyletic, including *Pseudotocinclus* and originated 36.9 MYA (95% HPD: 22.3-52.1). Within Neoplecostominae, we recognized tree lineages. The first one (clade A) is composed of part of *Pareiorhina* and *Pseudotocinclus* distributed for both eco-regions (interior and littoral). The second (clade B) is composed of *Isbrueckerichthys*, *Pareiorhaphis*, *Kronichthys* and the species *Neoplecostomus ribeirensis* almost exclusive to littoral. The third (clade C) is composed of all species of the genera *Neoplecostomus*, except *Neoplecostomus ribeirensis*, part of *Pareiorhina* and a new genus. The clade A originated 29.5 MYA (95% HPD: 17.4-42.1). The ancestral lineage of *Pseudotocinclus tietensis* dispersed from littoral to interior drainages 8.6 MYA (95% HPD: 2.7-15.4) and *Pareiorhina* sp. 1 9.5 MYA (95% HPD: 3.0-17.0). Results of Lagrange and molecular clock analysis suggest that the origin of clade B and C is 26.7 MYA (95% HPD: 15.4-38.1) and that during that time there was an ancestral dispersal event of a clade C species from littoral to interior drainages. Within clade B more recent lineages also dispersed from littoral to interior drainages: the ancestor of *Pareiorhaphis vestigipinnis* 3.8 MYA (95% HPD: 1.0-7.3), the ancestor of *Isbrueckerichthys* sp. 1 4.8 MYA (95% HPD: 2.3-7.8), the ancestor of *I. cf. calvus* 5.9 MYA (95% HPD: 2.9-9.5) and the ancestor of *I. alipionis* 10.6 MYA (95% HPD: 5.5-16.5).



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ancestral dispersal events were reconstructed from the interior to littoral drainages between 3.5-24.0 MYA: ancestral node of new genus and species 2 24.0 MYA (95% HPD: 13.3-34.5), new genus and species 1 6.2 MYA (95% HPD: 2.3-11.2), ancestral node of *Neoplecostomus* sp. 11 3.5 MYA (95% HPD: 1.6-5.5), the ancestor of *Neoplecostomus microps* and *N. espiritosantensis* 10.2 MYA (95% HPD: 4.7-16.5). Thus, considering our Lagrange results we observed more dispersal events of Neoplecostominae lineages from littoral to interior drainages (six events) than interior to littoral (four events). Also, we hypothesize that head water captures and marine regressions have shaped this patterns of distribution within the subfamily Neoplecostominae throughout distinct basins of southeast Brazil.

Keywords : Biogeography, Catfish, Freshwater



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Evolutionary diversification in an endangered biodiversity hotspot: the Southeast Asian peat swamp forest fish fauna

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The Southeast Asian peat swamp forests (PSF), found in the Sundaland biodiversity hotspot, are waterlogged forests that grow on a layer of dead plant material. Although PSF are one of the most threatened ecosystems, virtually nothing is known about the patterns and processes of evolutionary diversification of their endemic fauna and flora. PSF are characterized by a unique, vastly stenotopic freshwater fish community, that is adapted to highly acidic black waters (pH as low as 3) and that comprises many miniature taxa and narrow range endemics, many of which have only been discovered in recent years.

Objectives: To use a multigene, molecular systematic approach to investigate the biogeography and phylogeography of selected stenotopic PSF fish clades.

Material and Methods: In order to provide a temporal time frame of PSF fish diversification, relaxed molecular clocks were reconstructed in BEAST and maximum likelihood inferences of geographic range evolution were conducted with Lagrange.

Main Results: Divergence among PSF fish lineages shows different and complex temporal and spatial patterns compatible with either Miocene-Pliocene fragmentation of the Sunda block or eustatic fluctuation throughout the Pleistocene connecting the different Sunda land masses through palaeo drainages.

Conclusions: Our molecular results identified several instances of unrecognized diversity among the studied PSF fish clades highlighting the need for urgent conservation of this unique and highly threatened ecosystem.

Keywords : Freshwater biogeography, Molecular phylogeny, Sundaland



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Oral

Lethal and sublethal toxicity of nitrites and phosphates : Effects on gills and behavior of *Skiffia multipunctata* (Goodeidae) fry

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Fish of the Goodeidae family represent an important part of Mexico's biodiversity. This group includes 21 genera and 45 species distributed exclusively in the central part of Mexico. However, the high density of human population in this part of the country and the important agricultural and manufacturing industry have provoked high levels of contamination, which affect mainly the aquatic ecosystems. These factors have led several goodeids to be considered in a critical state of conservation. Two common contaminants in water bodies are nitrites and phosphates, both participating in water eutrophication: The goal of the present study was to evaluate their effects on mortality, behavior and gill histology of the goodeid *Skiffia multipunctata* (threatened conservation status according to Official Mexican Law). We tested several concentrations of nitrites (0.0, 0.016, 0.028, 0.049, 0.085 and 0.15 mg/L) and phosphates (0.0, 0.13, 0.32, 0.88, 1.1, 1.41 and 2.4 mg/L) in fry of 1.5 month of age (three repetitions per concentration, 10 fish each one). With mortality data we calculated the concentration that kills 50% of population (LC₅₀). These were 0.064 and 13.2 mg/L for nitrites and phosphates at 24 and 96h of exposition, respectively. The sub lethal toxicity of both toxics affected gills, causing inflammation and fusion on secondary lamella and an increment in the number and size of chloride cells. Higher concentrations and longer expositions resulted in earlier gill degeneration. For behavior tests, two sub lethal concentrations of each toxic and a control without toxic were used (n=15 fish per treatment). We recorded (VCR) the preferred position in the water column and the feeding response during 15 and 25 days, twice a day (NO₂ and PO₄ respectively). Fish of the control group (without toxic) preferred the middle of the water column and were significantly more active during feeding; while the fish exposed to the toxics swam closer to the surface and ate less. This information will help us know the minimal water quality (NO₂ and PO₄ concentrations) necessary to maintain this species under laboratory conditions and to plan future repopulations in the original habitat.

Keywords : NO₂ and PO₄ toxicity, Goodeidae, Behavior



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Biological parameters of megrim, *Lepidorhombus whiffiagonis* (Walbaum, 1792) (Osteichthyes : Scophthalmidae) from the eastern Adriatic Sea

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Biological parameters of megrim collected in the eastern central Adriatic by commercial bottom-trawls were analysed. Monthly random samples, ranging from 9.0 to 35.9 cm in total length (TL) were collected from January to December 2006; with a total of 1118 specimens (538 males and 580 females) measured. The overall sex ratio was 1:1.07 in favour of females, and was close to the expected 1:1 sex ratio ($p > 0.05$). Allometric parameters of b values varied during the year; positive allometric growth was noted from November to May while in other months isometric growth was observed. In the yearly sample, the b values for males (3.16), females (3.21) and sexes combined (3.18) showed that growth of megrim was positively allometric. The GSI reached maximum values in January and minimum in June. The condition factor was lowest after spawning (June) and highest at the recovery phase (September). Otolith rings reading defined seven age classes, ranging from 1 to 7 years, including a very high proportion of individuals 2 years old. The von Bertalanffy growth parameters were, males: $L_{\infty} = 41.16$, $K = 0.152$, $t_0 = -1.39$ years; females $L_{\infty} = 44.76$, $K = 0.166$, $t_0 = -1.07$ years; sex combined: $L_{\infty} = 55.05$, $K = 0.104$, $t_0 = -1.61$ years. The fishing mortality ($F = 0.60$) and exploitation rate ($E = 0.61$), revealed a high fishing pressure on the stock in studied area.

Keywords : Megrim, Biology, Adriatic Sea



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Integration of fish fossil data into phylogenetic
and comparative studies

Oral

Fossils fishes and phylogenomic analyses

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Total evidence studies (integrating morphological and molecular datasets), although fairly common during the early stages of molecular phylogenetics, have now become quite rare in systematics. Even rarer are studies that integrate molecular data with morphological datasets that include extant and fossil taxa. During the past couple of years, however, new studies have shown that Bayesian phylogenetic methods are robust to large amounts of missing data and can be successfully used to analyze multilocus DNA matrices in combination with morphological datasets integrating extant and extinct taxa (e.g., Wiens et al 2010, *Syst. Bio.*). In this talk we will present the results of the first combined analyses of molecular and morphological datasets (including fossils) for three important groups of teleosts: the Tetraodontiformes, the Acanthuroidei and the Scombroidei. We will show how the inclusion of the fossils affects the relationships among extant taxa, and its importance for dating studies. The development of new programs that can use fossil taxa in combined analyses has the potential to revolutionize both our understanding of the fish tree of life, and reverse the long-standing decline in morphological studies.

Keywords : Phylogenomic, Fossil, Molecular clock



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Oral

Phylogenetic trends in the evolution of the telencephalon in lower vertebrates

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Numerous studies have already assessed the relative size of brains in different vertebrate groups. Many of those studies also measured and compared selected brain regions, i.e. mainly sensory input regions, to reveal sensory specializations and functional adaptations to specific habitats, ecology and behavior of the animal. The varying sizes of the telencephalon in different vertebrate species give rise to speculations whether size is related to higher cognitive functions, large sensory input areas and/or particular social behaviors. In mammals, there are detailed studies on the evolution of different areas within the telencephalon that give information on the relative volume of limbic, olfactory, and cortical areas. Studies at this level are lacking in non-mammals and particularly in anamniotes. We examined the telencephalon of selected representatives of different vertebrate groups, especially ray finned fishes, to get an overview of phylogenetic trends in the evolution of the telencephalon. In several species of elasmobranchs and many ray finned fishes, information is already available on the relative size of the telencephalon and the olfactory bulb (OB). Generally, elasmobranchs have fairly large telencephali, but sizes vary. This is similar in teleosts, where also large differences exist in the size of the telencephalon. Surprisingly, however, it was never directly tested to what extent the size of the telencephalon correlates with the size of the OB. Based on the proportion of the size of the OB to the rest of the telencephalon we found great differences, ranging from the squirrelfish with a huge telencephalon and a very small OB to sturgeons where the OB can be even bigger than the rest of the telencephalon. For example in *Anguilla*, the relative size of the telencephalon is quite high and in the range of cichlids, but this can be explained by an enlarged olfactory system and a reduced visual system. Surprisingly, *Polypterus* has one of the largest telencephali of all actinopterygians, but the OB/telencephalon ratio is in the range of *Anguilla*, *Salmo*, and *Esox*. Several groups have a large telencephalon and a very small OB suggesting that other sensory modalities are increasingly dominating telencephalic functions. Among them are osteoglossiforms, surgeonfish, and squirrelfish, all of which show an elaborate histological differentiation of some telencephalic areas independent of the size of the OB. This suggests that in these groups cognitive functions located in the telencephalon rely more on visual and/or acoustic information than on olfaction.

Keywords : Telencephalon, Cognition, Morphology



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Invited speaker

Fishes, do they ever come back?

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We are facing an on-going decline in freshwater fishes in most parts of the world. While water quality is improving in many rivers, fish habitats are further destroyed by urbanisation, channelisation, infrastructure and hydropower. Compiling Red Lists and designate protected areas are important but not sufficient to maintain and restore fish populations. Although already 18 % of the EU territory is protected by Natura 2000 sites and a number of restoration projects have improved local habitat conditions the on-going habitat destruction nullifies conservation and restoration efforts at larger scale. In order to reverse this process, new concepts have to be developed and implemented in river basin management. We need a better causal understanding of pressure-impact relationships to develop more effective mitigation and restoration strategies. By detangling the effects of multiple stressors and identifying tipping points more targeted pressure-specific programmes of measures (PoM) sensu WFD shall be developed. These PoMs have to consider the spatial configuration of metapopulation, migratory pathways within and among populations, reproduction and nursery hot spots and shifted baselines due to climate change. This more holistic approach is essential to re-establish key functions and processes of fish populations.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Poster

The sheepshead minnow *Cyprinodon variegatus* as a marine vertebrate model for investigating endocrine disrupting effects of triclosan

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Zebrafish (*Danio rerio*) has been a prominent model in toxicology. This freshwater species present many advantages both in identifying endpoints of toxicity and in elucidating mechanisms of toxicity. However, marine toxicologists lack such omnipotent model displaying similar advantages to zebrafish: small size, rapid breeding, and easy maintenance. We propose here the use of the sheepshead minnow *Cyprinodon variegatus* to define thyroid-disrupting effects of triclosan during pre-hatching development. Three females and two males were placed in each of the three breeding chambers designed for this experiment. More than 300 eggs were collected over three days and maintained in seawater with triclosan concentrations at 0, 100 ng.L⁻¹, and 100 µg.L⁻¹. Exposure of larvae to triclosan lasted until hatching. After hatching (six days post-spawning), 5 larvae per condition were placed in Bouin's fixative for brain and thyroid histology. Length and body mass were measured. The body was frozen at -80°C to determine muscle thyroid hormone levels (T3 and T4), using radio-immunoassay techniques. Hatching success, *in vivo* observations, gross observation, thyroid hormone levels, histology will be determined and discussed in the framework of whether or not triclosan may alter thyroid metabolism during pre-hatching period of the sheepshead minnow.

Keywords : Ecotoxicology, Triclosan, In vivo exposure



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

The ecological and economical effect of recreational fishing in the Eastern basin of the Mediterranean sea

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In recent years, many studies have shown a sharp increase in recreational fishing activity in the western world (USA, Europe, Australia). This increase has contradictory effects, on the one hand, recreational fishing has a significant contribution to the state's economy. On the other hand, various sport fisherman's activities Found to be destructive to the marine fauna, if they are not regulated. Unlike other countries, Israel has no regulatory or management protocols for the sport-fishing industry. Therefore, the main purpose of this study is to provide the policy-makers for the first time with information that will lead to sustainable, well-regulated, recreational fishing activities. Thorough examination of the ecological impacts and economic potential of recreational fishing, including consumer surplus and state revenues, will enable formulation of recommendations for effective regulation of this type of fishing and the prevention of irreversible environmental damage. The resulting proposed solutions are expected, therefore, to improve social welfare, both in terms of preserving an important natural resource and in economic terms.

Keywords : Fishing, Ecologic, Economic



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Poster

Microanatomy of the inner ear and hearing abilities in a cyprinodontiform fish

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Teleost fishes show an amazing diversity in hearing abilities, inner ear structures, and otolith morphology. Inner ear morphology, however, has not yet been investigated in detail within the diverse order Cyprinodontiformes. Using the Mexican freshwater fish *Poecilia mexicana* (Poeciliidae) as a model species, we analyzed the position of otoliths *in situ*, investigating the 3D structure of sensory epithelia, and examining the orientation patterns of ciliary bundles of the sensory hair cells, while combining μ -CT analyses, scanning electron microscopy, and immunocytochemical methods. Hearing abilities were measured by applying the auditory evoked potential (AEP) recording technique. *P. mexicana* occurs in different ecotypes, enabling us to compare intra-specific variability (on a qualitative basis with regard to inner ear morphology) between fish from regular surface streams and from the Cueva del Azufre, a sulfidic cave in southern Mexico. The inner ear of *P. mexicana* displays a combination of several remarkable features: The utricle is connected rostrally instead of dorso-rostrally to the sacculi, and the macula sacculi, therefore, is very close to the utricle. Moreover, the *Macula sacculi* possesses dorsal and ventral bulges. The two studied ecotypes of *P. mexicana* differed mainly in the shape and curvature of the macula lagena, the curvature of the *Macula sacculi*, and the thickness of the otolithic membrane. Both ecotypes exhibited similar hearing sensitivity though, with maximum sensitivity at frequencies between 200 and 300 Hz. Our study for the first time provides detailed insights into the auditory periphery of a cyprinodontiform inner ear as well as hearing abilities and thus provides a starting point for further research on structure-function relationships of inner ears within the species-rich order Cyprinodontiformes.

Keywords : Poeciliidae, Inner ear, Cave fish



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

How does swim bladder morphology affect hearing abilities? A case study on Asian and African cichlids.

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Several teleost species evolved rostral extensions of the swim bladder which are connected to the inner ears. A few comparative studies have shown that these morphological specializations may enhance hearing abilities. We hypothesized that reducing the distance between the swim bladder and the inner ears results in a widening of the detectable frequency range and an improvement of the auditory sensitivity at frequencies above 500 Hz. To study the effect of different swim bladder morphologies – ranging from small reduced swim bladders to ones with rostral extensions – on hearing sensitivity, we analyzed specimens of four different cichlid species. We studied swim bladder morphology by performing dissections and by making high-resolution 3D reconstructions from microCT scans, and we tested hearing abilities using the auditory evoked potential (AEP) recording technique. The species displayed (i) small swim bladders (*Steatocranus tinanti*), (ii) “normally” large swim bladders without contact to the inner ear (*Hemichromis lifalili*), (iii) swim bladders with extensions coming close to the inner ears (*Paratilapia polleni*), or (iv) swim bladders contacting the inner ears (*Etroplus maculatus*). *P. polleni*, *E. maculatus* and *H. lifalili* were able to detect frequencies up to 3 kHz but *H. lifalili* had lower auditory sensitivity at 500 Hz and 1 kHz than either of the other two genera. The highest auditory sensitivities were found in *E. maculatus*, which possesses the most intimate swim bladder-inner ear contact, whereas the narrowest detectable frequency range was observed in *S. tinanti*, which has a reduced swim bladder. However, swim bladder morphology does not in all cases predict hearing abilities as hypothesized.

Keywords : Otophysic connection, Hearing abilities, Cichlidae



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Invited speaker

Eel male energetic strategy to cross Atlantic Ocean

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European eel (*Anguilla anguilla*) has a particular life cycle (including two metamorphoses) and is supposed to cross Atlantic Ocean from European coasts to Sargasso Sea. This is a huge swimming challenge (about 6000 km) requiring a lot of energy which comes only from lipid stores because digestive tract atrophies before starting impeding feeding activity. It has been calculated that females must have lipid stores averaging 20 % of their body mass in order to be able to realize such a performance. In these conditions, swimming at the estimated speed of 0.5 BL/sec, a 80 cm length eel requires about 6 months to achieve the travel. However, if 80-100 cm is a common size for migrating female, male length never exceeds 40 cm. Consequently, even if the males start their migration sooner (about 1 month) they can meet the females for reproduction at the Sargasso sea if, and only if, they swim faster. The question is “are the eel males able to swim faster than the females?” Since several years we have performed experiments allowing to compare male and female eels in terms of energy metabolism at atmospheric pressure but also in high pressure condition which mimics the migration at depth. For the different experiments the measurements routinely used were: oxygen consumption (whole animal and mitochondria), enzymes activities, glycolytic fluxes, at rest or swimming, at different temperatures and/ or pressures. Summarizing the obtained results it appears that when compared to females, males have 1) higher aerobic capacities, 2) lower anaerobic capacities, 3) lower pressure sensitivity at low temperatures. These results suggest that males are really able to swim faster than females and probably migrate deeper. The interest to migrate at a great depth is to increase the efficiency of oxidative phosphorylation and consequently to spare substrates.

Keywords : Eel, Sex differences, Energetics



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

**Mitochondrial Genetic and Truss Network
Differentiation of Spirlin (*Actinopterygii* :
Cyprinidae) In South Caspian Sea Basin of Iran**

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The genus *Alburnoides* of the family Cyprinidae is one of the most diverse and equally complex genera of the family, and possibly the order Cypriniformes. Their phylogenetic relationships are still debated, as there is no molecular data has been used to study of this in Iran. A holistic approach, combining phenotypic and genetic methods was adopted to analyze possible population differences spirlin from selected centers in the South Caspian Sea Basin of Iran. Truss distances between 16 landmarks of 314 specimens were measured. Multivariate analysis of variance (MANOVA) was performed to investigate distinctions and patterns of morphological variations among populations. The phylogenetic relationships were determined based on 774 base pairs of the mitochondrial cytochrome b gene. The nucleotide sequences were subjected through neighbor joining, maximum parsimony, maximum likelihood methods and Bayesian inference. The mitochondrial gene tree largely supported truss network. *Alburnoides* forms three major clades. The western populations may be considered as *Alburnoides* cf. *eichwaldii* whereas Talar river populations and the eastern populations may be distinct taxa of *Alburnoides* sp.

Keywords : Spirlin, Phylogeny, Iran



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Arctic cisco (*Coregonus autumnalis*) in the eastern part of the Baltic: its evolution, current status and possibilities for preservation

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Almost all natural diversity of Coregonids in Western and Central Europe is known to belong to two complex species, i.e. vendace (*Coregonus albula* complex) and whitefish (*Coregonus lavaretus* complex). The exception is pollan (*Coregonus pollan*) from several Irish lakes, and it is a freshwater form of Arctic cisco (*Coregonus autumnalis*) dwelling in the water bodies of the Arctic basin. The utmost western stable population of anadromous Arctic cisco in Europe inhabits the Pechora River belonging to the basin of the southeastern Barents Sea. No traces of Arctic cisco have been detected in a single European sea basin between the Pechora and the British Isles so far. This fact did not provide for a satisfactory explanation of the phenomena of the origin of Irish cisco, which is conspecific to Arctic cisco. Population genetic investigation of whitefish in the eastern range of the Gulf of Finland in the Baltic Sea by 30 allozyme loci showed that local island populations in the open part of the gulf are a group of complex evolutionary origin, and Arctic cisco is one of the founders together with the whitefish. Both genetic marker characteristics and some phenotype specificities - that feature intermediate indexes between whitefish and Arctic cisco - differ the hybrid form of the isle area from the whitefish dwelling along the mainland area of the Gulf of Finland. Therefore, Arctic cisco could have inhabited Europe up to the eastern shore of the Atlantic Ocean in late Quaternary period and during the Holocene via a chain of glacier water bodies located in the water catchment areas of today's basins of the White, Baltic and Northern Seas. Emergency of spontaneous hybrids among different Coregonid species is rather frequent, but formation of a stable hybrid population between the species of Coregonidae family which phylogenetically distinct from each other is a unique phenomena. In this respect, whitefish and Arctic cisco hybrid from the eastern Baltic Sea is of great interest for studying the mechanisms of their adaptation to the environment atypical for Coregonids, since there are some reasons to assume that the whole hybrid population life cycle is limited to the brackish water of the Gulf of Finland. Significant geographic distance between the islands of the central part of the Gulf of Finland from the mainland, lack of any economic activity in adjacent aquifers and strict cross-border regime in the area of the utmost western Russian islands contribute to preservation of the unique whitefish and Arctic cisco hybrid population in that sector of the Baltic Sea.

Keywords : Arctic cisco, Whitefish, Hybrid population



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Population genetic differentiation of Russian , Persian and Siberian Sturgeon species by using mitochondrial and nuclear genetic markers

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Russian (*Acipenser gueldenstaedtii*), Persian (*Acipenser persicus*) and Siberian (*Acipenser baerii*) sturgeons - are closely related Ponto-Caspian species. Investigation of its population genetic structure is an actual task, which determines measures for conservation of these species. This study analyzed the frequency of 'baerii-like' mitotypes of Russian Sturgeons of the Volga River, the Ural River, the Caspian and the Azov Sea and Persian sturgeons from the Caspian Sea. "Baerii-like" mitotype was found in 35 % of examples of Russian sturgeon from the Caspian Sea (Volga, Ural), and in 2 % from the Azov Sea and wasn't found in the Persian sturgeons. AFLP method reveals that Caspian Russian sturgeon is closer to Persian sturgeon from the Caspian Sea than to the Russian Sturgeon from the Azov. The Siberian sturgeon (of the Ob' river) has formed a separate branch to the common Persian-Russian sturgeons' cluster. The data confirm genetic isolation of Persian sturgeon from Russian sturgeon in the Caspian Sea, but the nuclear DNA markers show that the Persian sturgeon is a young species.

Keywords : Russian sturgeon, Persian sturgeon, Population genetics



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Thyroid hormone induced heterochronies in the early skeletogenesis of Cyprinidae (Teleostei).

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Heterochronies, or changes in the developmental rate and timing leading to changes in the definitive morphology, are widely regarded as a major evolutionary mechanism. The main regulators of the developmental rate of vertebrates are thyroid hormones (TH). The pleiotropic effects of TH on ontogeny are well studied in amphibians, with the metamorphosis as the most spectacular example. TH play a key role in the teleost ontogeny, too. As in amphibians, TH contribute to the transition from larval to juvenile stage. One may propose that the alterations of TH-level may lead to heterochronies in fish. However, the effects of changes in TH-level on the development and adult morphology in fish are unclear.

We investigated the effects of artificially altered TH-level (hypo- and hyperthyroidism) on the skeletal development in cyprinids: zebrafish, *Danio rerio* (Danioninae), and large African barb, *Labeobarbus intermedius* (Barbinae). These species manifest the similar reactions to the alterations of TH-level. Some skeletal structures display no visible reactions on the alteration of TH-level and may be regarded as TH-independent or weakly TH-dependent. Other structures may be considered as TH-dependent: they change the timing of the onset and rate of the development. The hyperthyroidism usually causes the premature appearance and accelerated development, whereas hypothyroidism leads to the delayed and retarded development of TH-dependent structures. Differences in the reactions to the alteration of TH-level indicate the different TH-responsiveness of skeletal elements, and are responsible for TH-provoked changes in the sequence of skeletal elements appearance, traditionally considered as the stable species-specific feature in teleost. TH-induced changes in the skeletogenesis result in the profound consequences in fish adult morphology. The hyperthyroidism causes the decrease in the number of serial skeletal elements (infraorbital bones, pharyngeal teeth, supraneurals, hypurals, scales, fin rays), as well as the loss of some cranial and postcranial cartilages and bones. The hypothyroidism leads to the increase in the number of serial skeletal structures. Both hyper- and hypothyroidism cause changes in the shape and proportions of particular skeletal elements and their complexes. These findings suggest that genetically based alterations of TH-level may cause the heterochronies with eventual evolutionary consequences in cyprinids.

The present study was carried out within the framework of the Joint Ethio-Russian Biological Expedition (JERBE III) and partially funded by the Russian Foundation for Basic Research (10-04-00787-a) and Grant of Russian President (MK-2026.2011.4).

Keywords : Heterochronies, Thyroid hormone, Cyprinidae



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Poster

Effects of dry diet supplementation with natural food on body deformities and growth in juvenile *Carassius carassius* under controlled conditions

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Introduction: In juvenile cyprinids reared under controlled conditions intensive feeding with dry formulated diets commonly results in high incidence of body deformities. Susceptibility of cyprinids to deformities is diet- and species-related, and *C. carassius* belongs to the most prone species. In contrast to formulated diets, natural diets do not induce external abnormalities, regardless of the feeding intensity. The aim of the present study was to find out whether the incidence of spinal deformities could be lowered by means of dry diet supplementing with small amounts of a natural food.

Material and methods: Six months old *C. carassius* of initially 0.81 g BW were reared at a density of 50 fish per a 20 dm³ aquarium at a temperature of 25°C for 60 days. The experiment comprised 3 triplicated groups with the intensive feeding five times a day. In group C fish were fed solely natural food, i.e. commercial frozen chironomid larvae, and the mean daily feeding rate was 31 % of fish biomass. In group F juveniles were fed exclusively dry diet (Aller Futura, Denmark) at 2.5 % of fish biomass daily. The same intensity of the feeding with a dry diet was used in group FC. However, in this group everyday supplements of chironomid larvae were fed to juveniles in single daily doses of 6% of fish biomass.

Results: No deformities in fish appeared only in group C, whereas in group F the final share of juveniles with deformities (spinal curvatures) amounted to 64%. Supplementation of a dry diet with natural food gave significantly ($P \leq 0.05$) lower incidence of deformities (31 %). The best fish growth was recorded for the fish fed dry feed with supplements. They reached finally 4.54 g BW, whereas the respective final values for groups C and F were 3.93 and 3.78 g BW (differences significant). The final content of ash in fish body was the highest in group F (13.19 % d.m.), and the lowest in fish fed only dry diet (9.11 % d.m.). Supplements of natural food in group FC increased ash content in fish body to 9.73 %. In this group the highest was level of cholecalciferol in fish body (523 ng g⁻¹). The respective values for fish fed exclusively dry diet or natural food were 253 or 110 ng g⁻¹.

Conclusions: Daily supplementation of dry formulated diets with limited amounts of natural food can be an effective tool to counteract body deformities in fish.

Keywords : Crucian carp, Feeding, Body deformities



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ethology

Invited speaker

Noise impact on fish : disturbance and avoidance in captivity

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Underwater habitats are full of natural sounds from abiotic sources, such as wind and water flow, and biotic sources, such as chorusing fish and snapping shrimps. However, human activities elevate these ambient noise levels artificially with noise from traffic, industry, and recreational activities. The typically low-frequency anthropogenic noises can cause many different problems, among which behavioural disruption and spatial avoidance, which may yield energetic costs and become detrimental for growth, reproduction, or survival. Noise-dependent behavioural changes may also be associated with noise-dependent stress levels. Although physiological modifications are often adaptive changes to meet the energetic demands and the state of mind required for making and executing adequate behavioural decisions to external stimuli, especially exposure to unpredictable and uncontrollable noise events may yield physiological changes that deserve the label of stress. The occurrence of anthropogenic noises in natural water bodies is characterized by variety in time and they are often unpredictable and uncontrollable from the perspective of the fish. There are more or less continuous noises from vessels, pumping systems, windmill farms, and gas extraction platforms. There are also repetitive sounds from pile driving, sonar use, and seismic surveys, and very brief but loud noise bursts related to explosions. In addition, there are many noise types that are in between these temporal extremes, such as sounds generated by dredging, water scooters, boats changing gear, and general construction activities. Very few noise impact studies have addressed such temporal variety, although it likely plays a critical role in the potentially negative effects of noise on fish. We investigated the disruptive effects of continuous noise as well as noise pulses on the behaviour of captive zebrafish (*Danio rerio*) and manipulated the predictability and controllability of exposure. In the first of two experiments, we used moderate exposure levels of about 112 dB re 1 μ Pa in a single tank without acoustic escape possibility. In the second experiment, we used higher exposure levels up to 140 dB re 1 μ Pa in a double-tank system with acoustic escape possibility. The first experiment revealed that noise pulses of moderate noise level could already alter behaviour and that noise impact varies significantly among temporal exposure regimes. The second experiment revealed that noise conditions can be made distinct in two tanks connected by a swim tunnel. Frequent tunnel passages by individual zebrafish allowed testing of spatial avoidance. In conclusion, variable impact of different temporal noise exposure patterns on captive fish provides fundamental insights that may have applied value outside. Although we need more noise-impact studies including the ecological relevance and the acoustic reality of the natural world, we can be certain that fish hear and noise matters.

Keywords : Behaviour, Noise impact, Zebrafish



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

African ichthyology : recent results and challenges

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In the last decennium, a special effort has been directed by the Royal Museum for Central Africa, Tervuren in collaboration with local partners towards the study of the diversity of fishes from the Congo Basin. This was coupled with intensive collecting efforts in various parts of this huge basin, including the Lower Congo, the Inkisi, the Léfini, the region around Kisangani, the Ituri, Lake Tanganyika, the Malagarazi and the Luapula. Hence, a much more fine-grained geographic coverage is now available for many taxa. The combination of major sampling efforts and detailed morphometric studies (classical and geomorphometric) lead to the description of several new species, some of which have large distribution areas while others appear to be local endemics. This clearly illustrates that the inventory is far from complete. Larger scaled studies revealed some remarkable results. The family Hepsetidae is a case in point. For many decades regarded as a monogeneric and monospecific family, a thorough review revealed that there are actually six clearly distinct species in Africa. Furthermore, fine-grained studies revealed geographic variation that was often found to render species delineation difficult. Another challenge is represented by the discovery of a complex evolutionary history, possible involving hybridization, in some Cyprinids and Mastacembelids. Such phenomena may be more common than previously thought. These findings represent challenges for future studies on the ichthyofaunas of the large lakes as well as of riverine habitats.

Keywords : Central africa, Ichthyo-diversity



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

The diversification of Ponto-Caspian shads

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Objectives: The genus *Alosa*, commonly known as shads, comprises 16 species of predominantly anadromous fishes and belongs to one of the most commercially important families of fishes (*Clupeidae*). The Eurasian representatives of this genus may have diversified, in part, due to hydrological isolation between the Eastern Atlantic, Mediterranean, Black and Caspian Sea, but the possibility of ecological speciation was not yet properly evaluated. This is particularly the case of the Ponto-Caspian region, where eight (out of the 16) putative *Alosa* species have been described according to differences on morphological traits and ecological requirements; however, their taxonomic status, phylogenetic relationships and evolutionary history were not yet fully addressed. Hence, the main goal of this study is to assess to what extent this phenotypic diversification reflects genetic divergence at putatively neutral markers, and to what extent gene flow could have constrained such divergence, in order to get insights into *Alosa* diversification within the geographic context of the Black and Caspian Seas.

Materials and Methods: Populations of the eight nominal *Alosa* species were sampled along the Ponto-Caspian basins and screened at one mtDNA gene and 11 microsatellite loci in order to estimate their genetic variation and differentiation. Phylogenetic relationships were reconstructed under different methods and an isolation-with-migration model was applied to infer the time to divergence of the Ponto-Caspian shads and to test if gene flow was involved in the process.

Main Results: The genetic data obtained support three main genetic clades/groups that better adjust to basins (Azov, Black and Caspian Seas) rather than to currently recognized species, and point to a recent divergence most likely related with basins' isolation during the Pleistocene.

Conclusions: Although our results can suggest lack of support for some of the previously described taxonomic entities in the region, the genetic diversity found in Ponto-Caspian *Alosa* species is also compatible with an initial stage of speciation, when genome-wide divergence is still far from complete. Further research is needed to clarify if this picture holds for non-neutral loci, those directly linked to adaptation and ecological speciation, and so to understand the factors that determine how far ecologically diverging populations will progress along the speciation continuum.

Keywords : Mtdna, Microsatellites, Phylogeny



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Integration of fish fossil data into phylogenetic and comparative studies Oral

Investigating the evolution of cypriniform trophic morphology using a time-calibrated phylogeny

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Cypriniform fishes comprise over 25 % of the world's freshwater fishes and their success is likely due to adaptations associated with feeding. This diverse clade is united by several feeding novelties, including a protrusible jaw. Cypriniform jaw protrusion is used differently by species feeding in diverse trophic niches including insectivory, herbivory, and benthic feeding. Modifications to the pleisiomorphic architecture of the adductor mandibula muscle likely allowed for fine-tuning of jaw protrusion associated with these distinct trophic niches. Here we reconstruct the evolutionary history of adductor mandibula structure and trophic diversity within Cypriniformes. A molecular phylogeny was constructed using six nuclear genes and was calibrated with fossil data. Mouth position and diet data were used to characterize extant species as benthic, mid-water, and surface feeders and to test for correlations between trophic niche and architecture of the A1 division of the adductor mandibula. We coded mouth position for all species in the molecular phylogeny and adductor mandibula architecture for 59 cypriniform and 5 outgroup species, including representatives from each major clade in the order. We test hypotheses regarding both the origin of jaw protrusion in cypriniforms and subsequent diversification of jaw morphologies among the clade. Specifically, we hypothesize that benthivory has evolved multiple times and that it is correlated with multiple branches of A1. Using phylogenetic comparative methods, we also test the recently proposed hypothesis that the most recent common ancestor to cypriniforms was a benthic fish. Recently, several functional advantages have been associated with multiple branches of A1, further underscoring the muscle's importance in protruding the upper jaws toward the benthos.

Keywords : Suction feeding, Benthic fishes, Premaxillary protrusion



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Notes on reproductive behaviour of blotched picarel *Spicara maena* L. (Pisces : Centranchidae)

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The blotched picarel, *Spicara maena*, is a common and abundant fish species throughout the Mediterranean and eastern Atlantic region. During the breeding season, it forms large schools over *Posidonia oceanica* beds. Males establish nests by excavating the sediment and *posidonia* rhizomes with their mouth, while females deposit adhesive demersal eggs once the nests are prepared. Accounts dealing with *S. maena* reproductive behaviour are scarce and are lacking in many aspects, especially in any quantitative description, of their reproductive pattern. This preliminary study reports for the first time, with the quantitative data, on reproductive pattern of *S. maena* in terms of nest-building – their shape, size and density. *S. maena* were encountered at a spawning location in a cove on the SE coast of island Susac, S Adriatic, in September 2011. Observations of nests were conducted by SCUBA diving. Density of the nests was quantified along three 20 m long strip transects and for 30 nests measurements of their height, width and depth were taken. On average, the number of nest per 20 m is $x \pm sd = 39.7 \pm 4.0$. The nests are typically round to oval in shape and quite large (width: $x \pm sd = 47.2 \pm 9.1$ cm, depth: $x \pm sd = 34.3 \pm 10.2$ cm, height: $x \pm sd = 34.3 \pm 3.6$ cm). The excavated material is dislodged around the nests which are tightly packed right next to each other all over the observed *posidonia* meadow. The high density and large dimensions of nests indicate high energy expenditure devoted to preparation for reproduction by males of *S. maena*. Additional research is required in order to expand our limited knowledge of the biology and ecology of this fish species. Island Susac is an exceptional location for in situ studying of *S. maena* – the island is rather small and very remote and the distinct population of *S. maena* inhabiting its surrounding waters has only few suitable coves with *posidonia* meadows available for reproduction. Thus, here the otherwise virtually impossible task of being in the right place at the right time becomes likely and enables the rare opportunity of studying various aspects of reproductive behaviour of *S. maena*.

Keywords : Reproduction, Spawning, *Spicara maena*



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Endocrine cells ontogenesis in zebrafish

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Endocrine cells of the digestive tract include pancreatic cells clustered in the islets of Langerhans and the enteroendocrine cells, scattered throughout the digestive epithelium. Notch pathway plays a crucial role in endocrine cell fate determination and mediates cell fate decisions. The goal of this project is to decipher the molecular cascade triggered by Notch signaling that controls the endocrine cell differentiation in the digestive system. The targets of Notch signaling are usually members of the bHLH family and more precisely of the Achaete scute-like (Ascl) family or of the atonal related proteins (ARP) family. In this study, we searched for all ARP and Ascl factors expressed in the endocrine lineage of the pancreas and of the gastrointestinal tract in zebrafish. A phylogenetic tree of this ARP/ascl family allows us to identify fourteen of those factors in the zebrafish genome. We synthesized the antisense probes for all these factors and analyzed their expression profile by whole mount in situ hybridization. We also performed double fluorescent in situ hybridization to determine precisely where these factors are expressed. The role played by some of these bHLH in endocrine cell fate determination is studied by loss of function experiments using either mutants or morphants. We are presently studying in detail the phenotypes of these mutants and morphants and this will be presented on the poster.

Keywords : Zebrafish, Digestive tract, Endocrine cells



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

What makes a successful invasion? Case study of the Indo-Pacific threadfin bream, *Nemipterus randalli*, Russel 1987 in the Eastern Mediterranean.

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Identifying the characteristics of a successful invasive species is a crucial aim in invasion biology and management. Some of the species that enter the Mediterranean with the continuous influx of Indo-Pacific biota have proliferated rapidly and established large and widespread populations. First reported in the Mediterranean in 2006, Randall's threadfin bream, *Nemipterus randalli*, is one such species, much favored by the local bottom-trawl fishing industry. In this study, we monitored the integration of *N. randalli* within the local ichthyofauna during 2008-2012, gathering data from 27 bottom-trawl surveys along the Israeli and Turkish coasts, and examining more than 26,000 specimens. The population explosion of *N. randalli* along the Israeli coast and its establishment along the Turkish coast took place during 2008-2009. Its relative proportion in the Israeli samples rose to more than 25 % in number and biomass of total trawl catch. We found that the largest fish occur at 40 m depth and the smallest at 120 m. More than 83 % of the specimens were caught at night, and their recruitment occurs in early winter. These findings contrast its congeners' daytime foraging behavior in the Indo-Pacific Ocean, as well as contrasting the general knowledge regarding ontogenetic depth gradient of many fish species. Moreover, winter recruitment of *N. randalli* implies summer as the spawning season, as opposed to the late winter/early summer spawning season for most of the indigenous benthic fishes. In light of the above, we suggest that the criteria for a successful invasive species include: (1) the assortment of biological and ecological traits that an alien species carries from its origin; and (2) the plasticity to adjust to conditions in the newly invaded territory. Based on our findings, *N. randalli* indeed possesses these criteria: (1) as an original summer spawner, it benefits from a long reproductive season in the Levant, especially with the increasing SST; and (2) by having juveniles residing in deeper water and shifting its feeding diurnal behavior it may reduce predation risks and inter-intra specific competition. Investigating the population dynamics of *N. randalli* in the Mediterranean since its arrival has enabled us to study real-time marine biological invasion. For this reason, further studies on this subject will be highly informative.

Keywords : *Nemipterus*, Invasion



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Phenotypic effects resulting of the reorganizations in rDNA of the hybrids roach (*Rutilus rutilus L.*) and bream (*Abramis brama L.*)

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Genome evolution happened by the mutations leading to changes of nucleotide sequence DNA, structural reorganizations of parts of a genetic material and quantitative changes genome. Interspecific hybridization raises variability of natural populations, can play role of "supplier" of evolutionary material (Darevsky, 1974). Roach and bream (Cyprinidae) can be model objects for study of processes of reorganization genomes of the crossed species. The size genome bream exceeds of genome roach in 1.5 times, but the number of chromosomes at these species equally, therefore increases of DNA quantity can occur by of accumulation repetitious DNA. Repetitious DNA play role in the organization of structure of nucleus, in interaction of chromosomes and expense changes of their number influence at the phenotype. Revelation of possible effects is made by the analysis of inheritance species-specific ITS1 fragments rDHK at hybrids F1, F2, Fb in experimental crossings between roach and bream. It is found and confirmed by test cross elimination ribosomal genes of one of the parental species in part of the first generation of interspecific hybrid at the gastrula stage. As a rule, the paternal ITS1 fragment was eliminated; however, one specimen lost the maternal ITS1 at the "embryo before hatching". It is shown, that reorganizations of rDNA of the first generation of hybrids are characteristic not only for somatic tissues, but also for cells generative ways, stably inherited and influence at phenotype. Morphological feature of hybrid female AR5 with elimination ITS1 bream differed from sibship and was closer to reciprocal hybrid RA, than to AR with two parental ITS1 fragments. The analysis of values of morphological character of the investigated groups of underyearling backcross from test cross of female AR5 with males of both species has revealed similarity of offspring from crossing ARxA with RxA and from crossing ARxR with RxA according to character: I, Db, Ab, Vc. Such integration can be consequence of elimination ribosomal genes bream at hybrid female AR5 that has influenced on the formation of own morphotype and morphotype of its offspring. The multigene family rDNA is subjected mechanisms of the concerted evolution through gene conversion and unequal crossing-over (Li, 1997), that gives plasticity at genome. Observed phenotypic effects and the phenomenon elimination most probably results from the necessary homogenization of homologous paired structures of highly species-specific rDNA genes during coordination of the functioning of the genomes of different species at a stage initiation nuclear genome a hybrid embryo.

Keywords : Phenotype, Hybridization, Elimination



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Estimating the minimum ecological flow downstream the Gadouras dam (Rhodes Island, Greece), for conserving the local *Ladigesocypris ghigii* population

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The requirements for the minimum Ecological Flow downstream of water abstraction schemes comprise a critical concept for the preservation of ecologically significant aquatic communities, which nowadays is promoted by considerable national and international legislation frameworks. In Greece, minimum Ecological Flow is usually estimated using a fixed proportion of the average summer discharge in the target river, without taking into account local hydrological and biological characteristics. Gadouras stream is the most important surface water body on Rhodes Island (Greece) and hosts the most important population of the endangered, endemic fish *Ladigesocypris ghigii* (Cyprinidae). In recent years a big dam was constructed on this stream, posing a threat to the local *L. ghigii* population. In the present study, the minimum Ecological Flow downstream the Gadouras dam was estimated, utilizing hydrological monitoring and experimental techniques. The natural variability in flow conditions (that existed in this section of the stream before the dam's construction) and the biological requirements of the fish were also taken into consideration. *L. ghigii* is naturally adapted to the semi-arid intermittent flow conditions of the island, by surviving in small remaining refuge pools at the high of the dry period. Unfortunately, the construction of the Gadouras dam has caused acute deterioration of the habitat conditions downstream of the dam, as all water has been used to fill the dam and no Ecological Flow has been provided. This was because the Ecological Flow, initially estimated in the respective Environmental Impact study, was set too high and not considered realistic by the dam's water managers. In the current study, various water management practices and Ecological Flows from the Gadouras dam were tested, to identify and evaluate the hydrological effects on the downstream section of the stream. The relationship between the outflow from the dam, the natural water losses and the water level in the stream were determined and new requirements for the minimum Ecological Flow calculated. The revised Ecological Flow levels do not exceed 10% of the initially proposed Ecological Flow and are therefore considered acceptable to the dam's managers. The implementation of the revised Ecological Flow has been initiated and positive effects on the fish that inhabit the section of the stream downstream of the dam are expected.

Keywords : Ecological flow, *Ladigesocypris ghigii*



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Role of large river tributaries in conservation of species diversity of fishes at the regulation of their runoff and damming

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Regulation of river runoff by damming is one of the types of human impacts upon natural ecosystems. In some cases, it has conditioned irreversible processes influencing various aspects of fish biology. Fish species composition of water reservoirs is sometimes significantly different from the initial one, mostly due to anadromous, semianadromous and rheophilous fish species, which have found favorable environmental conditions in large tributaries and small rivers of water reservoirs' basins. We have analyzed and compared species structure of trawl catches in the Rybinsk and Gorki water reservoirs over the last few years and fish fauna composition of rivers flowing into these waterbodies. Rybinsk reservoir Prior to creation of this water reservoir, river Volga was inhabited by 38 fish species. However, after damming (1941-1942) number of fish species dropped to 27 due to rapid decrease of abundance and even complete disappearance of a number of anadromous, semianadromous and rheophilous fish species (Kulemin, 1944). Number of fish species has increased to 29 when vendace *Coregonus albula* (L.) and smelt *Osmerus eperlanus* (L.) have penetrated into the water reservoir from Lake Beloye (Vasil'ev, 1950). At present, there are 18 fish species from 9 families inhabiting open stretches of the reservoir according to the trawl catches. Some rheophilous species have adapted to living in the littoral zone of the reservoir, inhabiting the river mouths. Fry of chub *Leuciscus cephalus* (L.), asp, ide, dace *Leuciscus leuciscus* (L.) and riffle minnow *Alburnoides bipunctatus* Bloch. This evidences for the fact that there are self-reproducing populations of these fish species. Sterlet sturgeon as well as Volga undermouth *Chondrostoma variable* Jakowlew is found in the Mologa River. Stable populations of grayling *Thymallus thymallus* L. are found in Mologa basin rivers. Gorki water reservoir Prior to creation of this water reservoir, river Volga was inhabited by 30 fish species (Kojevnikov, 1957). Analysis of contemporary trawl catches shows presence of 19 fish species. Also, there are data on the presence of spawning grounds of chub and dace in the rocky grounds in the riverbed part of the reservoir (Lysenko, 1990). 11 more fish species were found in the middle and small rivers flowing into the reservoir. The majority are typical rheophilous species. Almost all of them were quite abundant and encountered along the entire Upper Volga basin. Therefore, Volga's tributaries have played a major role in the conservation of this river's fish fauna genetic pool.

Keywords : Tributaries, Fishes, Conservation



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Estimation of morphometric characteristics of the only confirmed record of *Pristis pectinata* Latham, 1794 in the Adriatic Sea

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Pristis pectinata Latham, 1794 is the only representative of the order Pristiformes in the Adriatic Sea. It is a globally distributed but rare species and it is on the ICUN Red List of Threatened Species. The only confirmed record of smalltooth sawfish in the Adriatic Sea dates to 1901 and the sawblade of this specimen is preserved in the Split Natural History Museum. Based on the total length of this sawblade, 34 morphometric measurements were calculated. Considering that the sawblade is about a quarter of the total length, the Adriatic specimen was 323 cm long. Other morphometric characteristics were calculated according to known percentage values of total body length. The results obtained will be used for the construction of a life-size model, which will be added to the ichthyological collection of the Dubrovnik Natural History Museum. As smalltooth sawfish are critically endangered globally, and considering that it is probably extinct in the Mediterranean Sea, there is a need to better acquaint the public with this little-known species.

Keywords : *Pristis pectinata*, Adriatic Sea



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Effect of alternating magnetic fields on selected parameters of perch (*Perca fluviatilis* L.) sperm motility

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Sperm derived from 9 spawners, was stored separately in test-tubes inside an isothermal chamber at constant temperature, prevailing on the spawning ground (10° C). The containers with sperm in it, before start of experiments, every 24 hours from the time of harvesting the sperm, were exposed to a 30-minute to an alternating magnetic field of intensity 1 and 10mT (sine wave, 50 Hz). The control setting was placed in a natural magnetic field. During analysis, sperm was diluted using activator (water). The various parameters of sperm motility were examined using a Nikon Eclipse 50i microscope and camera with a computer system for sperm motion analysis (CASA). Linear velocity (VSL) of perch sperm, shortly after collection, in the control sample, averaged 46.3 $\mu\text{m/s}$, the same value was registered for sperm exposed to alternating magnetic field of intensity 10mT (46.7 $\mu\text{m/s}$), a slight decrease in speed occurred in the sample exposed to a magnetic field of intensity 1mT, and was 30.6 $\mu\text{m/s}$. After 48 hours of experiment, movement of sperm in the control sample completely stopped. In the sample under magnetic field of intensity 1mT, after 48 hours the VSL value was 43.0 $\mu\text{m/s}$, and for samples in field of intensity 10mT was 16.0 $\mu\text{m/s}$. The highest noted sperm curvilinear velocity (VCL), shortly after collection of the sperm, was registered when spermatozoa were subjected to alternating magnetic field of intensity 10mT for 30 minutes - 76.9 $\mu\text{m/s}$, this was 69.7 $\mu\text{m/s}$ in the control sample. The lowest value of VCL, 45.9 $\mu\text{m/s}$, was registered under a magnetic field intensity 1mT. After 48 hours of experiment, sperm curvilinear velocity under a magnetic field of intensity 1mT was 57.6 $\mu\text{m/s}$ and was 30.6 $\mu\text{m/s}$ under 10mT. No movement was registered in the control sample. In the control sample the percentage mobility, MOT, after collection of sperm was 40.0 %, while the percentage of mobile sperm under alternating magnetic field of intensity 1 mT was 36.6 %, and 38.5 % under 10mT field. After 48 hours MOT in the sample under alternating magnetic field of intensity 1mT was 16.0 %, and 2.3 % in 10mT field. For the control sample, just like in VCL, no movement was registered. From above data it can be concluded that in the case of alternating magnetic field of intensity 1mT, applied for 30 minutes after collection, all tested sperm mobility parameters registered the lowest values, but under a magnetic field intensity of 10mT, there was a marked increase in VCL velocity. After 48 hours, when no more movement could be observed in the control setting, alternating magnetic field, intensity 1mT, caused the value of linear motion in this variant to rise to level comparable with that registered shortly after collection of sperm and prolonged sperm motility. A similar phenomenon was also observed in the assessment of sperm VSL and MOT parameters. Hence the process could be used in fish breeding as a means of temporary storage of sperm.

Keywords : Fish, Magnetic field, Sperm motility



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Effects of a generated magnetic field on viability of sea trout (*Salmo trutta m. trutta* L.) spermatozoa and the process of egg fertilization

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The numbers of two-habitat fish species of the salmon family (Salmonidae) that enter Polish waters to spawn has decreased recently. The problems mostly concern endangered species that are often included in reintroduction and conservation programmes. One of them is sea trout (*Salmo trutta m. trutta*). Successful fertilization, indicated by the number of eggs fertilized, results partly from sperm viability. This study was an investigation of the effects of a generated magnetic field on spermatozoa motility and the process of egg fertilization of sea trout. Gametes (eggs and sperm) were collected from three female and five male adult sea trouts caught in the estuary of the River Rega. The samples from each specimen were put in separate tubes kept in isothermal containers similar to that in natural conditions. Spermatozoa from an individual fish were exposed to a generated magnetic field of 1.0 mT or 10mT for 24 hours. Motility of sperm was recorded as the percentage of motile spermatozoa in a sample (MOT). Sperm diluted to 1:500 was activated in tap water. A drop (5 μ l) of dilution was placed in a Makler chamber and the number of motile forward-moving spermatozoa was counted every 5 seconds until no forward progression in an observed area was seen. Observations were made using a Nikon Eclipse 50i microscope equipped with a Basler A312fc camera, computer-assisted sperm analysis (CASA) system and negative phase contrast optics for use with a Sperm Class Analyzer[®] (Microptic). After 24-hour exposure to the generated magnetic field the sperm was used for fertilization of eggs. In the control, sperm exposed only to the natural geomagnetic field for 24 hours was used for fertilization of eggs. Fertilized eggs were then incubated at a stable temperature $5 \pm 0.2^\circ\text{C}$ in large (0.5 dm³) glass crystallizing dishes. The average amounts of motile spermatozoa (MOT) after exposure to a generated magnetic field of 1.0 mT and 10 mT were 7.3 % and 2.4 %, respectively. In the control, MOT was between 13.5 % (immediately after sperm collection) to 0.7 % after 24 hours exposure to the geomagnetic field. Fertilization of eggs averaged 48.4 % and 49.0 % after exposure of sperm to magnetic fields of 1.0 mT and 10 mT, respectively.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

In the control, average egg fertilization immediately after sperm collection was 42.0 % and after 24 hours exposure to the natural geomagnetic field was 17.4 %. Egg fertilization was significantly greater with the sperm exposed to the generated magnetic field than in the control. The data show that sea trout sperm exposed to a generated magnetic field for a short term retains viability at a level similar to that occurring in nature. The quality of sperm decreased during its exposure *in vitro* to the natural geomagnetic field. These data have some practical significance. They indicate a technique that may be used for retaining sperm viability, thus affecting the quality of the fry, success of reproduction, reintroduction and restoration of the species.

Keywords : Fish, Magnetic field, Spermatozoa



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Genetics

Oral

High-throughput sequencing to study cell differentiation in Zebrafish

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The loss of pancreatic insulin-producing cells (β -cells) is a hallmark of diabetes and more knowledge is needed to find alternative treatments. Thus, it is crucial to identify regulatory genes specifically expressed in this pancreatic cell subtype and involved in its differentiation. In the present study, the main pancreatic islet was dissected from transgenic TG (insulin: GFP) zebrafish adults under fluorescence stereomicroscope and β -cells were selectively recovered by FACS with high purity (about 98%). Illumina RNA-seq was used to analyze the transcriptome of beta cell. About 20 millions sequence reads from a paired end sequencing assay were obtained. These reads were assembled into transcripts, aligned on the zebrafish genomic sequence (DanRer7) using TopHat software (<http://tophat.cbcb.umd.edu/>) to find splice junctions and Cufflinks (<http://cufflinks.cbcb.umd.edu/>) for transcript assembly and FPKM (fragments per kilobase of exon per million fragments mapped) estimation of each transcript. Examination of regulatory genes previously known to be expressed in β -cells such as *pdx1*, *hlxb9/mnx1*, *pax6b*, *neuroD*, *isl1*, *insm1*, as well as the homeobox gene *Hopx* and the Hdac histone deacetylase 9, both recently detected in human β -cells, were detected well represented in our sequencing, while examination of transcription factors known to be expressed in the other pancreatic cell types (*i.e.* *ptf1a*, *mnr2a*, *arx*, *sox9b*) could not be detect, confirming the high purity of our starting β -cell preparation. These studies helped us to indentify novel regulatory genes expressed in β -cells which could be crucial for the differentiation of these cells. Functional studies, such as injections of morpholinos in zebrafish eggs, will be performed to determine the role of these factors.

Keywords : Pancreas, B-cells, RNA-seq



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Marine life-history according to environmental variations in amphidromous Gobiidae : temperature effect on dispersal and populations connectivity

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Context: Amphidromous species have complex life cycles characterised by a pelagic marine growth phase. Spawning happens in freshwater, and larvae drift downstream to the sea, after hatching. After few months as pelagic larvae, individuals return to freshwater and then experience a metamorphosis into juveniles. The pelagic phase plays a fundamental role, as it allows larval dispersion between fragmented freshwater settlement sites. The Pelagic Larval Duration (PLD) is often considered as a proxy of dispersal abilities: shorter PLD would suggest limited dispersion capacities and a restricted distribution range. The PLD of amphidromous species is longer than that of most marine demersal species, and a significant PLD variability has been observed between and within species. In amphidromous species, the environmental factors influencing the PLD are poorly known. Among marine fishes, temperature, food availability and seasonal conditions are often found to influence the larval traits. Understanding these mechanisms is fundamental when developing management tools, particularly in the case of amphidromous gobies; their post-larvae are indeed subjected to a heavy fishing pressure.

Objective: This study aims to characterize the variations of pelagic life traits according to environmental conditions of both amphidromous Gobiidae inhabiting on Reunion Island: *Sicyopterus lagocephalus* (widespread) and *Cotylopus acutipinnis* (endemic).

Materials & Methods: We used otolith analysis of post-larvae to describe the relationships between PLD, growth patterns and marine conditions (Sea Surface Temperatures & Chlorophyll a), over three consecutive years.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Main results: For both species, the PLD and the larval growth rate varied seasonally. Larvae living in high sea water temperatures exhibited a more rapid growth and shorter PLDs than those living in cool water temperatures. The chlorophyll a concentration lesser influenced the larval growth rate. Larval growth and PLD differed in reaction norms depending on the species and was shorter and less variable for the endemic species.

Conclusion: We suggest that the timing of competency acquisition to recruit is mainly influenced by oceanic conditions. Seasonal variations of temperature could affect the dispersal potential of larvae and might induce intermittent connectivity among distant populations. In global warming context, the populations' connectivity could be affected, due to reduced PLD in respond to elevated temperatures. We suggest that widespread species, exhibiting high plasticity of PLD, are more subject to a reduction of populations' connectivity. However, others ecological processes that affect population dynamics are expected to change due to climate change, which might affect persistence of both endemics and isolated populations.

Keywords : Amphidromous species, Marine life-history, Environmental condition



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Vicariance events and phylogeny of Iranian inland *Aphanius* species

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Introduction: Plate tectonics and geological processes have strongly influenced the present day landscape of the Iranian plateau since the closure of the Tethys about 23 Ma ago. However, the implication of these geological events has not been fully explored with regard to the diversification of Iranian freshwater fishes. This is particularly interesting with regard to the Iranian inland species of *Aphanius* Nardo 1827 (Cyprinodontiformes), currently represented by six endemic species that have been formally described.

Objective: We test whether the high diversification of *Aphanius* in Iran is linked to vicariance events due to Neogene and Quaternary orogenic events and changes in mountain topography, which resulted in changes of the drainage systems.

Material and Methods: We have analyzed the geological history of southern and central Iran based on literature data, and the speciation processes based on our molecular phylogenies of Iranian inland *Aphanius* species.

Results: A first split probably happened > 10 m.y. ago within the Iranian inland *Aphanius* species. This split led to the divergence of the present-day *Aphanius* vladkovi and an ancient *A. isfahanensis* clade. It is followed by the divergence of the present-day *A. isfahanensis* from the remaining ancient *A. farsicus* clade by 5 m.y. ago. A final diversification represented by star like radiation took place during the Quaternary and led to the divergence of four additional endemic species. A noticeable feature of the diversification of the endemic *Aphanius* species in Iran is their high genetic divergence, which is coupled with a lack of clear variation in morphology. In addition, a higher divergence in otolith morphology than in the morphology of the fish body occurs.

Conclusion: The evolution patterns of *Aphanius* are characterized by different rates of divergence in morphological, otolith and molecular characters. We suggest that these patterns are linked to the similarity of the individual environments and intra-species communication, apart from the vicariance events. It is likely that additional *Aphanius* species may be present in remote areas of Iran, especially in the Zagros and Alburz Mountains.

Keywords : Cyprinodontidae, Biodiversity, Zagros Mountains



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

“Same same but different”: Otoliths of *Aphanius dispar* (Teleostei, Cyprinodontiformes)

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Introduction: The Arabian killifish *Aphanius dispar* (Rüppell, 1829) is the most widespread *Aphanius* species and probably represents a species complex. Otolith morphology and otolith morphometry are well known to represent species-specific characters for teleost fishes. Additionally, otolith characters can be used as a tool to determine the taxonomic state and understanding the zoogeographic history of a given population. In the case of *A. dispar*, previous studies on the otoliths have revealed clear morphogeographical variation between inland populations, most likely due to isolation of populations and subsequent genetic divergence.

Objective: Do otolith variation also appear between coastal populations of *A. dispar* populations, which are normally interconnected by gene flow due to migration of fish or larvae drift along the coast? If so, what would be the implication with regard to the taxonomy and zoogeographical history of the respective populations?

Material and Methods: Otoliths of *A. dispar* from coastal habitats in Oman were analysed and compared with other coastal and inland populations. Methods include qualitative and quantitative otolith studies and statistical analyses.

Results: Morphogeographical otolith variation appears both in coastal and inland *A. dispar* populations. In particular, a gradual trend of otolith variation is present from East (Gulf of Oman) to West (Persian Gulf of southern Iran).

Conclusions: *A. dispar*, which is originally a coastal species, possesses a high potential for adaptation to new and ecologically different environment. This capability is an important factor for its diversification. We suggest that the gradual trend of otolith variation from East (Gulf of Oman) to West (Persian Gulf of southern Iran) indicates the zoogeographical history of the present-day *A. dispar* populations. We conclude that study of differences in otolith morphology and morphometry is appropriate to recognize distinctive populations within species complexes that are difficult to understand based on other morphological approaches.

Keywords : Otolith morphology, Cyprinodontidae, Taxonomy and zoogeography



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Integration of fish fossil data into phylogenetic and comparative studies Oral

Archaeozoology and aDNA analysis document the former occurrence of sturgeon in the North Sea

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Although sturgeon was once widespread in Europe and occurred in all major rivers, the fish is currently extinct in most European countries. Until recent, this sturgeon was assumed to be the European sturgeon *Acipenser sturio* Linnaeus 1758, since this was the only species considered to be indigenous in Western Europe. However, archaeozoological and genetic research on archaeological sturgeon remains and museum specimens has indicated the historical presence of another sturgeon species, the Atlantic sturgeon *A. oxyrinchus* Mitchill 1815, in the Baltic region and along the French Atlantic façade. A new project has been initiated to determine which sturgeon species historically occurred in the North Sea through a combined morphological and molecular analysis on sturgeon remains from archaeological excavations in Belgium, the UK and The Netherlands, as well as on modern museum specimens. Preliminary results from the morphological research will be presented, indicating a possible presence of *A. oxyrinchus* in the North Sea.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Poster

Structural organization of the nucleolus in different fish species

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The nucleolus is a distinct subnuclear domain present in all eukaryotic cells. Though the nucleolus is considered today as a multifunctional domain, its primary function is ribosome biogenesis. Transcription of ribosomal genes, maturation/processing of ribosomal RNAs and assembly of rRNAs with ribosomal proteins all occur within the nucleolus. We have shown at the ultrastructural level that there are primarily two types of nucleolar organization: nucleoli containing three components in amniotes and two components in all other eukaryotes (Thiry and Lafontaine, 2005). In recent report we made the additional and surprising, finding that both types of nucleolar arrangement are found among living reptiles, viz. a bicompartmentalized nucleolus in turtles and a tricompartmentalized nucleolus in lizards, crocodiles and snakes (Lamaye *et al.*, 2011). However, though the nucleolus is well characterized in tetrapods, it has been so far much less studied in fishes.

In this work, we examined the fine structure of the nucleolus in different species of fishes belonging to six families of fishes (Cyprinidae: *Barbus barbus*, *Cyprinus carpio*, *Dania rerio*; Cobitidae: *Cobitis taenia* ; Salmonidae: *Oncorhynchus mykiss* ; Clariidae: *Clarias gariepinus* ; Chamichthyidae: *Chaenichtys rhinoceratus* ; Nototheniidae: *Notothenia rossii*). Using cytochemical (AgNOR proteins) and immunocytological (DNA, nucleolin, fibrillarin) markers, we showed that in these fishes only one type of nucleolus is present: a bicompartmentalized nucleolus. This latter organization occurs regardless of the species, the tissue, the developmental stages or the physiological states analyzed. The results are compatible with the view that all the fishes have a bipartite compartmentalization of the nucleolus.

Lamaye F., Galliot S., Alibardi L., Lafontaine D. and Thiry M. Nucleolar structure across evolution: the transition between bi- and tricompartmentalized nucleoli lies within the class Reptilia. *J. Struct. Biol.* 2011, 174: 352-359.

Thiry M. and Lafontaine D. Birth of a nucleolus: the evolution of nucleolar compartments. *Trends Cell Biol.* 2005, 15: 194-199.

Keywords : Nucleolus, Ultrastructure, Fish species



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Ecology - Fish conservation

Oral

Genetic differentiation of European grayling (*Thymallus thymallus* L.) In the Kama river as reflection of special features of the species expansion

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The goal of this work is to investigate the genetic variability and the degree of differentiation of European grayling dwelling in the spawning tributaries of the Kama River. The Kama is the largest tributary of the Volga - 1800 km long with the catchment area of 507000 km² – located at the eastern border of the species habitat. Over 70000 tributaries flow into the river, and some of them are home to European grayling. By using the analysis of 36 allozyme loci, 21 samples of grayling from different Kama tributaries were studied. The samples were subdivided into 3 clusters. Two of them comprise the Belaya River populations (the largest tributary of the Kama). The third cluster was made of graylings from other large spawning tributaries and small rivers flowing independently into the Kama. Genetic differences between the samples were within the range of $D_N=0,001-0,051$. One should highlight that the biggest differences ($D_N=0,038-0,051$) were detected between the graylings inhabiting the rivers that formally belong to the common basin of the Belaya River. This is comparable to the differences between the populations from geographically remote areas, such as between the populations from the rivers Pechora, Mezen and Northern Dvina. High value of the differences detected and the nature of the distribution of variability by separate allozyme loci (AAT-3*, AAT-4*, IDHP-3*, LDH-A*, LDH-C*) allow assuming that isolation and genetic differentiation among various grayling groups in the Kama basin could have taken place much earlier than the last glacier regression. Graylings could have penetrated the Kama basin also from several isolated refugia during the postglacial period. Complex Kama grayling population genetic structure detected during the study implies special approach to conservation this species in the river system in question. Special attention should be paid to local populations or groups of populations that make the largest input into biologic (including genetic) species diversity.

Keywords : European grayling, Genetic structure, Conservation



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Phenotypic plasticity of jaw morphology as a response to diet in cichlids: suction versus biting

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The explosive radiation of cichlids in the East-African Lakes is considered an important model system for evolutionary research. To explain their very high rates of speciation several hypotheses have been suggested. The decoupling of the oral and pharyngeal jaws is considered their most important key innovation, but recently it has been found that several other factors may also play a role in their adaptive radiation. Local adaptive responses, resulting from phenotypic plasticity, may allow cichlids to rapidly adapt to environmental changes during their lifetime and through processes like genetic assimilation such a response has the potential of becoming a heritable trait. We investigated phenotypic plasticity in response to different feeding modes in two cichlid species from Lake Victoria: *Haplochromis piceatus*, a suction feeder and *H. fischeri*, a biter. We raised groups of specimens of both species on food with the same nutritional quality, but different physical characteristics, simulating different feeding modes: (1) suction feeding from the water column, (2) scraping food and (3) biting on hard pellets. To visualize the plastic response we performed a geometric morphometric analysis of head morphology and we also compared feeding performance based on morphological proxies (theoretical bite force, KT ,...). Furthermore we focused on the lower jaw, one of the most important elements in the oral apparatus. Based on micro-CT scans we compared ossification patterns and analysed shape differences using 3D morphometrics. To some degree, the observed morphological variation between treatments seemed to be related to improving the imposed mode of feeding.

Keywords : Geometric morphometrics, Cichlidae, Phenotypic plasticity



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Microsatellite-based genetic variability of common carp (*Cyprinus carpio* L.) populations in Croatia

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Common carp (*Cyprinus carpio* L.) is economically important species for the aquaculture of Croatia. Fish farmers try to certify their stocks as genuine Croatian product; therefore, the information on genetic diversity of these hatchery stocks is urgently required in order to sustain the quality of the broodstock. Sport fishing of common carp in open waters is often based on stocking from fish farms. Hence, the hybridization of feral populations becomes an increasing problem. The aim of our study was to explore genetic variability within and among five hatcheries and five feral populations from different Croatian regions using microsatellite DNA, a hyper-variable molecular marker. Fifteen microsatellite loci of 243 individuals from 5 hatchery and 5 feral populations have been analysed. A total number of 148 alleles were recorded across loci ranging from 6 at MFW12 and MFW17 to 20 at MFW20. However, the mean number of alleles per locus was remarkably low: from 2.2 in hatchery population Našice to 7.4 in feral population of the river Danube. Pairwise F_{ST} values (0.136-0.424) were significant ($P < 0.01$), demonstrating differentiation among populations. Markov chain method test showed that all the populations deviated from HWE ($P < 0.05$). After sequential Bonferroni correction only the Vrana lake was in HWE in all the loci but MFW20. Only the loci MFW9 and MFW29 were in HWE in all the populations. The factors that may result in genetic divergence and significant reduction of the observed heterozygosity were discussed. AMOVA results for 10 populations indicate that percentage of the variation among populations was 5.62 %, which is lower than the variation within populations (61.26 %). Genetic differentiations among 10 populations, as well as among feral and hatchery populations were both significant. In comparison to hatchery stocks higher genetic variability of the feral carp populations has been found. This is particularly important in the light of the global threat to the feral carp population. As five hatchery stocks of common carp have an important status in Croatian aquaculture, our results on genetic variability within/among them and the relationships among them can provide new background of knowledge in the population conservation and breeding programs.

Keywords : *Cyprinus carpio*, Microsatellites, Croatia



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Poster

Effect of cortisol on growth and first sexual maturity in Nile tilapia juveniles, *Oreochromis niloticus*

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When fish experience periods of stress, they try to maintain their homeostatic state through biologic and physiologic responses. Primary responses imply the activation of catecholaminergic system and the Hypothalamus-Pituitary-Interrenal (HPI) axis which leads to the rapid release of stress hormones, such as cortisol, the main corticosteroid in teleosts. A previous study showed the stimulating effect of cortisol on oocyte development. The aim of this study was to assess if cortisol, through alimentation, induces an early or delayed first sexual maturity in Nile tilapia, *Oreochromis niloticus*. Eight batches in duplicate were allocated in eight 250 l aquaria until D36 post-fertilization (pf) and then transferred to 300l tanks in recirculating system (27°C). Two batches were fed with normal food (control) and the six other were fed with increased concentration of cortisol (50; 250; 500 mg/kg of food) from D30 to D50. Fish were fed at the maximal ratio (from 6.5 % at D30 to 2.8 % at D72). Every 14 days, growth parameters were controlled. At D64, 10 gonads from each batch were sampled and fixed in Bouin's fluid for further histological observations and oocytes diameters measurement. Blood were sampled on 10 fish per batch at D64 and D78 in order to assess plasma level 11-ketotestosterone (11KT) and oestradiol (E2) by RIA. At the end of the experimental period, juveniles fed with cortisol showed a slight (non-significant) lower SGR (6.1; 4.2; 4.0 % for the 50, 250 and 500 mg/kg batches respectively) than control batch (6.8 %). A significantly lower mean body weight was also observed among treated juveniles (10.0; 5.9; 5.2g for the 50, 250 and 500 mg/kg batches respectively) compared to control ones (17.3g). Moreover, cortisol-fed juveniles showed significantly lower oocyte diameters (7.8; 6.8; 6.4µm for the 50, 250 and 500 mg/kg batches respectively) than the control batch (8.7µm). Nevertheless, significantly higher GSI were observed among juveniles fed with cortisol (0.4; 0.5; 0.8% for the 50, 250 and 500 mg/kg batches respectively). Parallely, sexual steroid dosages showed that juveniles fed with cortisol had lower plasma 11KT (3.48; 2.82; 2.54ng/l for the 50, 250 and 500 mg/kg batches respectively) and E2 (0.69; 0.78; 0.65ng/l for the 50, 250 and 500 mg/kg batches respectively) production than control ones (4.56 and 1.02ng/l for 11KT and E2 respectively). Our results show that cortisol has a direct effect on growth and sexual maturity in Nile tilapia juveniles, with a decrease of growth and oocyte development and lower sexual steroids production.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Oral

Hatching time effect on the biochemical composition and energetic content of pike *Esox lucius* larvae

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Objective: Hatching is a major turning point from both ecological and behavioral points of view, yet it has little significance from morphological and physiological aspects. Indeed, hatching both within and among species is neither correlated with a fixed developmental stage nor is associated with qualitatively important morphological or physiological changes. In this study, we further explored the possible differences concerning biochemical composition and energetic content for pike larvae hatching at different times since some morphological differences have already been found between early, mid and late hatched larvae in a previous study.

Materials and methods: Based on two egg batches obtained from a single fertilization (one female with one male), three groups of larvae corresponding to three hatching times (HT1, HT2 and HT3) were made. For each hatching time, sampling of 30 larvae were realized in triplicate at subsequent days during the entire endogenous feeding period, *i.e.*, up to the total yolk sac resorption: at hatching D0, D3, D6, D9, D12 and D15 post hatching. The temperature was maintained at $12 \pm 0.5^\circ\text{C}$ during both the entire incubation and the larval rearing. Dry weight, ash, protein and energetic content were determined from elemental composition.

Main results: At hatching, body tissues of early hatched pike larvae were less important (dry weight 0.25 mg ind^{-1} HT1 vs 0.32 mg ind^{-1} HT3 ; $p < 0.05$), less energetic (5.98 J. ind^{-1} HT1 vs 8.46 J. ind^{-1} HT3 ; $p < 0.05$) with less protein content (0.17 mg ind^{-1} HT1 vs 0.22 mg ind^{-1} HT3; $p < 0.05$) but the yolk was more important (dry weight 1.44 mg ind^{-1} HT1 vs 1.33 mg ind^{-1} HT3; $p < 0.05$) and more energetic ($38.55 \text{ J. ind}^{-1}$ HT1 vs $36.29 \text{ J. ind}^{-1}$ HT3; $p < 0.05$) with a higher protein content (0.98 mg ind^{-1} HT1 vs 0.90 mg ind^{-1} HT3; $p < 0.05$) compared to the larvae hatched at the end of the hatching period (HT3). Complete yolk resorption occurred between days 9 and 12 post hatching and was more rapid for late hatching (HT3) larvae.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

During this period, the bodies of early hatched larvae continued to grow and tissues still retained protein from the yolk. As a consequence, the tissues of early hatched larvae became significantly heavier (at day 12: 1.16 mg ind⁻¹ HT1 vs 1.03 mg ind⁻¹ HT3; $p < 0.05$) with a higher energetic content (at day 12: 29.30 J. ind⁻¹ HT1 vs 26.34 J. ind⁻¹ HT3; $p < 0.05$) compared to late hatched larvae.

Conclusion: Our results showed that hatching time acts strongly on the biochemical composition of newly hatched larvae and probably on their metabolic efficiency during endogenous feeding period. Early hatched larvae hatch at a developmental stage different from late hatched ones and take a longer time period to pass from a developmental stage to another.

Keywords : Bioenergetics, *Esox lucius*, Hatching



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Ecology - Fish conservation

Poster

Assessment of the fish communities in large Croatian rivers based on the artisan fishermen and anglers' data

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Fishermen, both recreational and professional, go fishing every day, all the year round. Therefore, their catch data, if accurate, are extremely valuable when assessing the state of the fish communities, particularly of the species in demand. We studied and compared the data obtained for the two biggest Croatian rivers, the Danube and the Sava, in the areas where both types of fishing are allowed, from 2005 to 2010. The catch per unit effort (CPUE) was calculated as kg of fish caught by fisherman in one year. The average weight of the most important species was also compared. Generally, total CPUE was higher in the Danube than in the Sava river for both, professional (1585±206kg; 899±398kg), ($p < 0.05$) and recreational (14.12±2.74kg; 13.25±3.51kg), ($p > 0.05$) fishermen, respectively. The highest proportion of a single species in the professional total catch (in kg) in both rivers occupies the bream (*Abramis brama*) – less in the Danube (22.90±2.65 %) than in the Sava (38.80±11.22%), ($p < 0.05$). Similarly, the bream occupies lower proportion in the recreational catch in the Danube (13.78±2.93%) than in the Sava (15.02±2.77 %), ($p > 0.05$). The average bream in the professional catch in the Danube was heavier (1.02±0.15kg) than the one in the Sava (0.82±0.16kg), ($p > 0.05$). However, the highest proportion in the catch as a group, occupy allochthonous species – grasscarp (*Ctenopharingodon idella*), bighead (*Aristichthys nobilis*), silver carp (*Hypophthalmichthys molitrix*) and Prussian carp (*Carassius gibelio*). In the professional catch, these fishes compose 27.39±7.96 % in the Danube and 12.19±20.15 % in the Sava ($p > 0.05$), while in the recreational catch 34.22±4.15 % in the Danube and 27.99±10.93 % in the Sava ($p > 0.05$). There were lower variations of the total and single species parameters in the Danube than in the Sava river proving the Danube to be a more stabile habitat. On the contrary, the Sava river is smaller with many strong inflows in this section that can significantly influence the annual changes of the fish fauna and almost without backwaters rich with fish. Comparing the relationship of professional and recreational CPUE of the total catch inside both rivers during the investigating years, very slight linear regression was found ($r = 0.339$ for the Danube and $r = 0.105$ for the Sava river; $p > 0.05$). This only indicates that the catch of both groups reflects the changes of the fish fauna in the similar way. The trends of CPUE for both types of fishing during the investigated years did not show significant decline either of total catch nor the catch of any of the investigated species.

Keywords : Danube, Sava, Ichthyocenosis



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Spatial and environmental factors of fish biodiversity in the Ionian Sea (Mediterranean Sea)

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Diversity indices are used to assess the environmental status of exploited marine ecosystems and temporal changes due to environmental or anthropogenic factors in the Eastern Ionian Sea (Mediterranean Sea, Greece). Number of fish caught during the summer bottom trawl surveys MEDITS for the period 1998-2008 were used. For each station five diversity and evenness indices, i.e., Hill's N0 (species richness), N1 (exponential of Shannon H') and N2 (inverse of Simpson index), and two diversity indices based on taxonomic distinctness (Δ^* and Δ^+) were calculated. Furthermore, the values of these indices were related to environmental (salinity, temperature), spatial (depth, longitude, latitude), temporal (year) and fishing (fishing effort) factors using Generalized Additive Models. Model selection was based on the deviance explained and the Akaike Information Criterion. In general the combined effect of the factors considered here explained a substantial part of the sampled biodiversity (36 % – 68 %). Geographical coordinates (the interaction of longitude with latitude) explained most of the deviance of biodiversity estimates, which varied locally and didn't show any specific spatial pattern. The values of the most commonly used indices decreased with increasing depth, however two peaks were observed at around 300 and 600 m depth. Indices based on taxonomic distinctness fluctuated showing a tendency to increase with increasing depth, possibly due to the higher abundance of elasmobranchs in deeper waters. Temperature was found to affect only Δ^+ , while a (positive) temporal trend was revealed only in the case of species richness. Fishing effort and time (year) didn't seem to significantly affect diversity patterns; however this may be related with the short time series examined here. The effect of spatial and environmental factors on community metrics is common in several ecosystems and is related to habitat preferences of the species/community. Further exploration on some components of the community (e.g. elasmobranchs) and additional metrics may help highlight the impacts of the environment and fishing on fisheries resources and provide important information for management.

Keywords : Diversity indices, GAM's, Mediterranean Sea



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Ecology - Fish conservation

Poster

Seasonal changes of species occurrence, abundance and diversity in Neretva river delta (Croatia) fish populations

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The river mouth environments (estuaries, deltas), as areas of marine and freshwater dynamic contact have a high biological productivity and supports a wide faunal diversity. This area performs a crucial role in the life-cycle of many fishes. Fish assemblages there are very complex and varied, composed of true estuarine, amphihaline or euryhaline species. The Neretva river delta is among the biggest river mouth environments in the eastern Adriatic Sea and has been recognised as significant in Mediterranean area for its species richness and high degree of endemism of freshwater fishes. Moreover, it is noteworthy that several new fish species have been described from this drainage basin during the last decade. The aim of the present work is to provide an initial reference document on the specific composition of its fish assemblage. Eighty-two fish species representing 32 families were recorded in the Neretva river delta area. Sixty-nine of them (84.14 %) were estuarine and near-shore marine species, while 13 were freshwater species (15.85 %). The Atherinidae was the most abundant family (67.89 %), followed by Mugilidae (23.32 %), while Sparidae (1.14 %), Labridae (1.82 %) and Gobiidae (0.96 %) were under-represented. However, Gobiidae represent the most diverse family followed by Sparidae, Mugilidae and Soleidae. Young-of-the-Year fishes (Y-O-Y) in the littoral zone of the investigated area comprises a highly diverse fish community composed of 68 species representing 28 families. Moreover, more than 65 % (44 species) of the Y-O-Y species caught are among the species that form the main targets for commercial fisheries in the southern Adriatic. This fact emphasises the importance of the delta shallow water habitats as a nursery ground for the fish. Five most abundant species included euryhaline (*Atherina boyeri*, *Pomatoschistus marmoratus*, *Liza saliens*, *L. aurata*, *L. ramado*). *A. boyeri* was the dominant species throughout the whole sampling period, but the highest relative abundance was recorded for *Liza saliens* in August-September period (69 %). The highest species richness was observed in August with 31 species and the lowest in January with only 8 species. Collected species showed marked seasonal patterns of occurrence with the majority of each usually being caught within two month periods. Species richness and to even greater extent the total abundance of fish, underwent consistent seasonal trends and were found to increase during the warm seasons of the year (summer and autumn) following the water temperature fluctuations. These changes were largely attributable to a sequential immigration and emigration of different species, particularly estuarine-dependent marine species and also partially driven by variations in water temperature as well as salinity of freshwater discharge from the river.

Keywords : Estuaries fish, Neretva river delta, Seasonality



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Poster

Evidence for an auditory space map in the midbrain *Torus semicircularis* in teleost fishes

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The *Torus semicircularis* (TS) is a prominent structure in the midbrain of fishes, and is a major recipient of secondary sensory information from lateral line and auditory systems, and – if present – the electrosensory system. The organization of the torus semicircularis has been investigated only in a small number of species. Using Nissl stained material, we studied the cytoarchitecture of the TS in over 20 species representing several major groups of teleosts. We found the central part of the TS (TSc), which likely receives auditory input only, to vary in size across species. This part is especially large in groups that are known to communicate acoustically or may use acoustic information for orientation. These include tetraodontiforms, cichlids, anabantoids, holocentrids, and others. In other fish that do not vocalize, the TSc is very small (*i.e.* goldfish).

Many of the neurons in this central part contain the enzyme NADPH-diaphorase and are thus probably using nitric oxide (NO) as a neurotransmitter. Using NADPH-d histochemistry, which results in golgi-like staining of neurons within the TSc, we were able to describe its morphology and intrinsic organization in more detail in a chichlid, *Thorichthys meeki* and several gouramis (*Anabantoidei*).

Following tracer injections into the mesencephalic tectum of *T. meeki* and a gourami (*Trichopsis vittata*), we were able to show tectum projecting cells in the TSc and evidence for a topographic organization within this projection. Since the TSc receives auditory input, we hypothesize that an auditory space map is present here. We are currently substantiating our data pool and hope to propose a correlation between the size of the TSc and auditory spatial resolution just like visual spatial resolution is indicated by the size of the tectum opticum.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

Morphological constraints in resurgent haplochromine cichlids: the battle between escape performance, vision and oxygen uptake

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The cichlids of Lake Victoria are a textbook example of adaptive radiation which makes them an interesting model to study evolution. The dramatic ecological changes in the lake during the past three decades provide a unique opportunity to study environmental effects on cichlid morphology. Some of these environmental changes were increased predation by Nile perch, decreased water clarity and lower dissolved oxygen (DO) concentrations. As a result, the majority of the haplochromine species disappeared, but some species recovered. These resurgent species were forced to adapt morphologically to the environmental changes. Through morphological analyses at three year intervals, this study shows how several species adapted their body shape, eyes and gills. Head volume and eye size decreased during the 1990s, while the gill surface increased during the same period compared to the late 1970s. Although a decrease in head volume and an increase in gill surface seem to be adaptations to the increased predation pressure and decreased DO levels in the 1990s, a decrease in eye size in a turbid environment seems contradictory. Though these fish gave up their resolution by decreasing the angular density of the double cones, the photopic sensitivity (double cone size) remained unchanged. These results imply that the haplochromines decreased their head volume, and increased their gill surface at the cost of their eye size, but maintained their photopic sensitivity. These complex morphological changes occurred in less than a decade. Whether these changes are due to phenotypic plasticity and/or natural selection will be discussed.

Keywords : Evolutionary morphology, Functional ecology, Morphological trade-off



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ethology

Oral

Inter and intraspecific variation in a morphologically static cichlid lineage from Lake Tanganyika

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In comparison with the species flocks of lakes Malawi and Victoria, the taxonomy of the estimated 250 species of Lake Tanganyika cichlids is relatively well known. The endemic genus *Tropheus* Boulenger, 1898, consist of highly stenotypic rock dwellers, whose limited capacity for dispersal gave rise to over a hundred colour morphs. Notwithstanding their high chromatic and genetic differentiation, their morphology has been reported to have remained static. This hypothesis of morphological stasis was investigated in *T. duboisi* Marlier, 1959, a basal *Tropheus* species that shows only minor differences in colour pattern and is less stenotypic than its congeners. The results, however, showed significant morphological differentiation between geographically isolated populations.

Although *Tropheus* is an important model for evolutionary research, the genus' taxonomy is confused and many of its species are ill-defined. One of the long-standing problems in *Tropheus* is the relation between *T. annectens* Boulenger 1900 and *T. polli* Axelrod 1977, which is linked to the uncertainty regarding the type locality of *T. annectens*. Using both historical and recent material from the coastlines of the D.R. Congo and Tanzania and using multiple techniques, this problem could finally be resolved. For *T. duboisi*, *T. annectens*, *T. polli* as well as for other *Tropheus* species, the distributions of different morphotypes was shown to correspond more with ancient connections of shorelines, than with recent ecological barriers.

Keywords : /



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Tiny worms from tiny fishes: what (functional) genetics and parasitology can teach us about gobies and their radiations ?

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Gobiidae (gobies) is one of the most species-rich fish families. Several lineages underwent radiation. Since this is a major mechanism underlying biological diversity, gobies can be considered a prime target for research into speciation, evolution and biogeography. As the family contains many small and often cryptic species, a multidisciplinary approach is crucial to describe and understand the actual diversity of gobies. Here we present molecular genetics and evolutionary parasitology as additional tools to reach this goal. Nucleotide sequence data can indicate populations that should be managed as separate units or deserve species status. Furthermore, they can support morphological species descriptions and provide a reliable means for non-specialists to identify gobies to species level. Besides species identification, these data can help to clarify phylogenetic relationships and biogeographic affinities. In case of protein-coding genes, sequence data can shed some light on selection processes and functional adaptation to the (local) environment. A European case study concerns the sand gobies (including the smallest European freshwater fish *Economidichthys trichonis*). In terms of diversity and endemism, their freshwater stronghold is the eastern Mediterranean Basin. Indeed, its role as glacial refugium together with a dynamic biogeographic history stimulated the maintenance and diversification of this region's freshwater fauna. Many uncertainties remain regarding the taxonomy, phylogeny and biogeography of the endemic gobies. This poses urgent assessment and management difficulties, as several gobies (including, in all probability, undiscovered populations and species) endemic to the region are severely endangered as a result of anthropogenic impact. Apart from sand gobies, we will touch upon American seven-spined gobies (*Elacatinus*) and *Millerigobius*.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Both neutral (mitochondrial) and functional (opsin) genes are used for phylogeny reconstruction. In view of the rapid diversification observed in many goby radiations, including sand gobies, the genes in question might not always be able to adequately capture recent evolutionary events. In this case, data from parasites can be used, as their generally faster evolution can result in a “magnifying glass” for their hosts’ history. Our example addresses *Gyrodactylus* (Platyhelminthes: Monogenea: Gyrodactylidae) ectoparasites of sand gobies. A combined morphological (haptoral and genital hard parts) and multi-marker (ITS rDNA, Cox1, Cox2) molecular study on these flatworms helps to clarify taxonomic and biogeographic questions regarding these biologically and conservationally important fishes.

Keywords : *Gyrodactylus*, Opsins, Phylogeny



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

The inland ichthyofauna of the Phu Quoc Island : taxonomic and evolutionary aspects

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An objective: The island faunas represent unique opportunities to study both specific evolutionary trends in different groups of animals and the main features of fauna genesis. The largest Vietnamese Island, Phu Quoc, is situated in the Gulf of Thailand and belongs to remains of the ancient Phu Quoc sedimentary basin (dated from Late Jurassic to Cretaceous) together with the mountainous area between Vietnam and Cambodia. The recent island territory was isolated from the mainland about 10 thousand years ago.

Materials and methods: About 4000 fishes were collected in 46 stations of the Phu Quoc Island represented by different kinds of water bodies and habitats from 06 December 2011 to 12 January 2012. Their identification was based on different regional publications. As a total 97 species from 39 families and 13 orders of teleostean fish was identified; they were more detailed morphologically studied in the Zoological Museum of the Moscow State University.

Main results and conclusions: The analysis of fish species revealed in different water systems of the Phu Quoc Island demonstrate enough low number of true freshwater fishes (33 species); most of them are represented by cypriniform taxa (16 species). Most of fish populating inland waters of Phu Quoc Island are conspecific with freshwater fishes known from Cambodia and neighboring mainland populations or belong to species widely distributed in marine and brackish waters in the Gulf of Thailand and even in West Pacific. Only two studied species should be described as new taxa, but they also may have overlooked conspecific populations in Cambodia, similarly to *Clarias gracilentus* newly described both from the Phu Quoc Island and Cambodia (Ng *et al.* 2011). The obtained results presume the next main trends of the fauna genesis in the Phu Quoc Island: 1) the replacement of true freshwater species by more viable euryhaline fishes; 2) low effects both of the founder principle and disruptive selection; 3) the elimination of species with short-range adaptability.

Keywords : Ichthyofauna, Evolution, Taxonomy



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Morphogenetic divergence and taxonomic relations between the Mediterranean and Black Sea conspecific / congeneric populations in different fish groups

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An objective: Morphogenetic divergence of historically isolated Black Sea fish is of great interest both for the development of practical taxonomy and for recent study of gene flow among populations in the case of continuous so called "Mediterranization" of the Black Sea fauna (it means the penetration of Mediterranean organisms).

Materials and methods: Fish samples deposited in the Zoological Museum of the Moscow State University (ZMMU) and Zoological Institute of RAS, St. Petersburg, as well as craniological collection from ZMMU were used to study morphological divergence between conspecific / congeneric Mediterranean and Black Sea populations in several families - Uranoscopidae, Mullidae, Centracanthidae, Sparidae, Atherinidae, and Gobiidae. To evaluate genetic interpopulation divergence both cariological studies and molecular genetic analyses (mitochondrial *cyt b* gene) were performed by including literature data and haplotypes deposited in the GenBank. Fishes with different ecology were compared.

Main results and conclusions: The studied Mediterranean and Black Sea conspecific populations demonstrate different levels of both morphological and genetic divergences not correlated one with another and not obviously caused by any ecological features, namely pelagic or bottom eggs, larvae, and adult specimens determining their dispersion possibilities, gene flow power, and promotion to isolation. At the same time the divergence trades revealed for several species testify to inevitable recent taxonomic revision in studied fish taxa. In such a way, the results obtained indicate the absence of morphogenetic grounds for separation of the Black Sea populations of the red mullet *Mullus barbatus* into subspecies. Whereas the higher levels of both morphological and caryological divergence of the Black Sea stargazers (genus *Uranoscopus*) certainly should be treated as the basis of their separate taxonomic state. Unfortunately, to evaluate the effect of the Mediterranean gene flow in the Black Sea population diversity more ingenious genetic analysis should be developed. This problem is of the utmost interest for further investigations.

Keywords : Divergence, Taxonomy, Mediterranean



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecophysiology and Ecotoxicology

Oral

Glycolytic fluxes, a new approach to evaluate the impact of pollutants on energy metabolism in fishes

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Objective: In France pesticides are of important uses, nevertheless their impacts on the non targeted aquatic environment are not very well known. Indeed, a lot of substances are found in freshwater systems following the overland flow next to treated areas. Our objective was to develop a new approach to evaluate this impact. In this aim, we focused on the energy metabolism of ponds' fishes that constitute good integrators of the pollution of a year of production. The well functioning of energy metabolism is essential to an organism to maintain, to grow up and finally to reproduce ensuring the survival of the species. A particular biochemical method was chosen, the glycolytic fluxes technique, as it allows to measure in each sample the aerobic and anaerobic capacities of the first steps of the glycolysis. It gives an estimation of the maximal aerobic and anaerobic capacities together with the time of transition from the one stage to the other.

Materials and methods: Roaches from 4 different ponds showing different hydrodynamic characteristics and watersheds (size and percentage of culture) were chosen and sampled at the end of the year of production. Glycolytic fluxes were measured in white muscles together with Acetylcholine esterases activity. Besides chemicals (pesticides and metals), geographical and hydrodynamic characteristics were evaluated.

Main results: Roaches from the different ponds show similar aerobic capacities at the glycolytic level ($47.1 \pm 3.6 \mu\text{mol}/\text{min}/\text{g}$), but anaerobic capacities are different following sites properties. In the site presenting the highest percentage of watershed culture (85 %) and the lowest water residency time (1.5 month), anaerobic metabolism is also the highest ($1288.0 \pm 156.9 \mu\text{mol}/\text{min}/\text{g}$). It is hypothesized that this site presents the highest impact on energy metabolism. Indeed an elevated anaerobic metabolism could be interpreted as a compensation of impeded aerobic metabolism (at another level than glycolysis, probably at the respiratory chain level).



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Moreover, this site shows the lowest AchE activity (41.8 ± 3.6 U/gprot) *i.e.* the lowest transfer of nerve influx. This perturbation of the nerve transmission could be compensated by the highest anaerobic capacities and the lowest transition time from aerobic to anaerobic flux in white muscle. The high anaerobic capacities is however lower in females than in males and we hypothesized that it could be in order to preserve energy stocks as it is of particular great importance to the female gonads development. Conclusion: Glycolytic fluxes measurement appears as a good biomarker and needs to be finely characterized under laboratory controlled conditions.

Keywords : Energy metabolism, New biomarker, Roach



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Ethology

Poster

Migratory behaviour of European grayling in a one-year radiotelemetry monitoring in Arve river and its tributaries

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The European grayling (*Thymallus thymallus*) populations of the Arve River, a French-swiss tributary of Rhône River, declined in the last 40 years, as observed in most of Western Europe populations. This decrease may be mainly due to the regional economical development which led to alterations and fragmentation of the riverbed (pollutions, containment, dams building, aggregate extraction, etc.). Fish are still present in main river as well as tributaries, and five main sub-populations are known on this river. A recent phylogeographical study revealed that two of these sub-populations located in two Arve river tributaries (Nant de Sion and Menoge, geographically close to each other) were genetically different. The environment fragmentation due to human activities could explain this structure, as well as a natural breeding isolation in the tributaries because of fish behaviour (homing). To test these assumptions, a preliminary study was initiated in 2011, which aimed to describe the migratory movements of European grayling between two successive spawning seasons, and to determine the home range of both sub-populations. For this purpose, 17 spawners (mean total length: 366.18 ± 40.67 mm) were marked in spawning tributaries of Arve River with long-life external mount radiotelemetric transmitters (Advanced Telemetry Systems F1970 models, 441-days life range). Until winter, all fish were tracked once per week and their precise GPS position was noted, and then once per month until they moved again in February 2012. First results showed the co-existence of two types of migratory behaviour: sedentary fish, which stayed all year long in the spawning tributary, and migrant fish, which left the tributary to reach summer and winter habitat in the Arve River. Migrant fish covered up to 18.1 km downstream and 5.5 km upstream in Arve River, revealing a minimal 24 km home range. Individual behaviour of fish was also informative, e.g. a fish stayed 3 months in downstream vicinity of Arthaz dam, before using fish-bypass and continuing to go upstream in Arve river. This study revealed preliminary and important clues about the grayling population dynamics in the Arve River, as connectivity in Arve-tributaries system, population home range and potential dams clearing. All-year-long migratory behaviour was also described as fish were still tracked and detected in 2012 pre-spawning movement.

Keywords : *Thymallus thymallus*, Radiotracking, Migratory behavior



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

Systematics of the Freshwater Fish Diversity of Kaladan River, Mizoram, India

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Kaladan River, approximately 350 kilometres in length originates from the western face of the Chin Hills in Myanmar and flows into Mizoram, India and back to Myanmar in the Arakan (Rakhine) and finally into the Bay of Bengal near Sittwe. The river, itself a drainage, neither connected to the Ganga-Brahmaputra drainage nor to the Chindwin-Irrawaddy is expected to support highly endemic species. Ichthyofauna of the Koladyne is poorly explored. A recent collection included 45 fish species under nine families. Cyprinidae was represented by 22 species, Sisoridae by nine, Balitora and Bagridae by four each, Chandidae by two and Siluridae, Belonidae, Gobiidae and Channidae by one each. *Semiplotus modestum* (Day) is endemic to the drainage. The collection included some species occurring in the Barak and Brahmaputra basins and a number of unnamed species. Four sisorids, viz., *Glyptothorax ater*, *G. caudimaculatus*, *G. chimtuipuiensis*, *Hara koladynensis* and *Pseudecheneis koladynae*, one bagrid, viz., *Batasio convexirostrum* and one cyprinid, viz., *Barilius koladynensis*, have been recently described. Three more sisorid species and two nemacheilid are under description. The occurrence of two unnamed species of the labeonine genus *Akrokolioplax* Zhang & Kottelat, so far monotypic, with its type species, *A. bicornis* occurring in the Upper Salween (Nu Jiang in Chinese) is interesting. The study also records unnamed *Crossocheilus*-like labeonine species with rostral flap. Only a few species of the drainage have been included in the IUCN Freshwater Fish assessment and the status of almost all the species have been found to be data deficient since there are no adequate information on the biology, population and distribution of the species. Further study of the fish fauna would come out with interesting results. Detailed study on the tectonic evolution, particularly the formation of Kaladan fault that trends north-east-south-west along the Kaladan River, the river basin evolution in this region and fish species distribution and their phylogenetic relationship are wanting. It has become necessary to report the diversity and status of the endemic fish fauna for their conservation in view of the proposed projects for navigation and power generation across the river.

Keywords : Ichthyofauna, Kaladan, India



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

Evolutionary morphology

Oral

**Comparative Osteology of *Cyclopsis tentacularis*
(Cyclopteridae, Scorpaeniformes)**

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The structure of the skeleton of *Cyclopsis tentacularis*, an endemic species from the northern part of the Sea of Okhotsk, is studied for the first time. Generally, it corresponds to that in other representatives of Cyclopteridae. The differences in structure of *Cyclopsis* and of other investigated cyclopterids are both plesiomorphic and apomorphic. The plesiomorphic ones are comprised of sutural articulation of pteroticum and prooticum, spiny ray in the beginning of D2, berycoid opening in ceratohyale, bony pharyngobranchiale 2, emargination in the anterior margin of scapula, and postcoracoid opening in coracoideum. The apomorphic ones are separation of parietalia, absence of bony basibranchialia, presence of emargination in the posterior margin of supracleithrum, and reduction of several last epipleural ribs. The presence of numerous plesiomorphies does not confirm Ueno's viewpoint (Ueno, 1970) on the advanced position of *Cyclopsis* in the family Cyclopteridae. Final conclusions on the position of *Cyclopsis* in the system of Cyclopteridae and of the system of this family itself may be made only after proper investigation of the external morphology and osteology of all genera of Cyclopteridae.

Keywords : Osteology, *Cyclopsis*, Cyclopteridae



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

A complex evolutionary history in the large cyprinids from the Inkisi River basin (Lower Congo, DRC)

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The Inkisi River basin is the largest of the Lower Congo affluents. To a large extent it is well isolated from the remaining part of the Lower Congo by the Zongo and the Sanga falls (respectively ± 58 and ± 24 m height). Although at first glance morphologically quite dissimilar, the distinctiveness of the genus *Varicorhinus* from *Labeobarbus* has been questioned repeatedly (e.g. Banister, 1973), a view supported by recent genetic research (Tsigenopoulos et al., 2010). Preliminary identifications of the large size cyprinids from above the Zongo falls revealed the presence of typical *Labeobarbus* specimens (*L.*-morphotype) with fleshy lips, a narrow mouth and two pairs of well developed barbels and *Varicorhinus*-like specimens (*V.*-morphotype) with a horny lower lip and a clear cutting edge, a wide mouth and generally no barbels at all. However, in addition, various intermediate morphotypes were found. A detailed morphological study, including 30 measurements, 22 external and 9 X-ray counts has been undertaken on 37 specimens. Principal Component Analyses (PCA) on these measurements revealed that the *L.*- and *V.*-morphotypes almost exclusively differ in the typical morph-related head measurements except for the dorsal-fin base length and the dorsal-fin ray number, both of which have significantly higher values in the *V.*-morphotype. Further, both morphotypes differed significantly in lower gill raker number on the first gill arch. Finally, overall intra-morphotype variation of both types was comparable but clearly smaller than the variation within the group intermediate morphotypes. Mitochondrial COI data revealed no genetic differentiation between the three morphotypes. In contrast, a PCA of composite 48 AFLP genotypes representing 797 loci of all Inkisi phenotypes as well as some Lower Guinean taxa indicated that: (1) variation of AFLP genotypes is non-random with respect to the three morphological Inkisi phenotypes; (2) geographical proximity of collected specimens within the Inkisi contributes to the variation of AFLP genotypes; and (3) morphologically clearly different species, such as *V. robertsi*, appear to be closely related to the Inkisi-species complex. As such, phenotypic divergence in sympatry and even syntopy reveals to be correlated with genetic divergence. However, further analyses are necessary to differentiate between alternative evolutionary scenarios that may have contributed to the large cyprinid diversity in the Inkisi.

Keywords : Taxonomy, Cyprinidae, Africa



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Oral

Reproductive investment of *Nothobranchius furzeri* females along the rainfall gradient : interpopulation comparison

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The life-history theory postulates that individual fish may allocate energy into three main components (growth, self-maintenance and reproduction), and the concept of trade-offs assumes that energy invested in one component is not available for the other two. Individuals should allocate their resources to maximize their fitness, leading to differences in resource allocation among individuals, populations and species. We used an annual killifish, *Nothobranchius furzeri*, to test predictions that differences in expected lifespan affect the resource allocation. Fishes of the genus *Nothobranchius* inhabit ephemeral pools across East African savannahs. The duration of the pools depends on the length of rainy season. There is a strong gradient across the range of *N. furzeri*, from dry inland areas at a higher altitude to a humid lowland region in the proximity of Indian Ocean and this is mirrored in the time window available for completion of the life cycle among populations. In this study, we concentrated on testing differences in allocation to reproduction by females across the range of *N. furzeri*. We predicted that fish from the dry region (short expected lifespan) should invest to rapid growth, sooner onset of maturation and higher fecundity compared to fish from the wet region. In the context of life-history theory, this should result in a higher relative gonad mass in fish from dry region. We also predicted a higher number of eggs in females from the dry region, with a potential consequences for the egg size. We analysed females from nine localities belonging into four genetic metapopulations inhabiting areas along the rainfall gradient. By comparing relative weights of ovaries we found that females from the driest region invested in reproduction significantly more than in other three metapopulations. Moreover, these females also produced the highest number of eggs which were significantly smaller than the eggs of females from the wettest region. We discuss our results in the context of this extreme life history. Financial support came from CSF P506/11/0112.

Keywords : Annual killifish, Reproduction, Life-history theory



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Oral

Mesopelagic barreleye-fishes (Opisthoproctids) : Evolutionary “experiments” in eye designs

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Opisthoproctids are a group of mesopelagic teleosts that comprise seven genera including 19 species: *Opisthoproctus* (2 sp.), *Winteria* (1 sp.), *Macropinna* (1 sp.), *Rhynchohyalis* (1 sp.), *Dolichopteryx* (10 spp.) *loichthys* (1 sp.), and *Bathylychnops* (3 spp.). Their common name, barreleyes, indicates that most of them have tubular eyes, a feature they share with many other deep-sea fish. Early studies of ocular morphology have noted additional features in barreleyes such as diverticula, corneal lenses and eye-pads, the function of which were, however, poorly understood.

The recent discovery of a focussing mirror in *Dolichopteryx longipes* has lead us to review the structure of several barreleye genera and species using serial sectioning and/or MRI visualisation, and additional light and electron microscopy. *Opisthoproctus soleatus*, *Winteria telescopa*, and *Bathylychnops exilis* came from RV Discovery cruise 243 (Pl. J. Partridge), *Dolichopteryx longipes* from FS Sonne cruise 193, and *Rhynchohyalus natalensis* was collected by A. Flynn on a CSIRO cruise directed by R. Kloser, and obtained via J. Marshall.

Opisthoproctus, *Winteria*, *Rhynchohyalus*, and *Dolichopteryx* had tubular eyes, whereas *Bathylychnops exilis* had a roughly half-spherical eye. Small diverticula budding off from the main retina in the tubular eye were found in *Opisthoproctus*, and *Winteria*. *Rhynchohyalus* had a large diverticulum with a downwards-facing cornea-like window admitting light either directly onto the diverticular retina, or via a diffusing mirror on the medial wall separating the diverticulum from the main eye. The mirror contained irregular guanine crystals in cells corresponding to the retinal pigment epithelium. In *Dolichopteryx* the general eye design was similar to *Rhynchohyalus*. However, the reflecting crystals were regular and plate-like, and showed a precise orientation that focussed the incoming light onto the diverticular retina. The *Bathylychnops* eyes contained several diverticula. Some of these were budding off the main eye and seem to receive light from there. The main diverticulum faced laterally and was equipped with its own lens derived from the scleral/corneal stroma. Another diverticulum seemed to receive light via scleral light guiding “eye-pads”. The presence of ocular diverticula has also been noted in pearleyes, but the degree of their differentiation appears to be unique in barreleyes. A divergent development may be recognised, either towards mirror-based optics (*Rhynchohyalus* and *Dolichopteryx*), or towards additional lens or light-guiding devices (*Bathylychnops*). Unfortunately, the systematic position of the barreleye species and their specific modes of life are not known well enough to allow a more comprehensive analysis of these data.

Keywords : Opisthoproctids, Ocular morphology, Mesopelagic



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Comparative analysis of biometric characters of Atlantic Cod *Gadus morhua* L. from different areas of its distribution

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The material to study was collected within 1998-2006, in the area of the southern Baltic Sea (ICES III d SD 24-26, six samples), in the Sounds (III b SD 23, the Sund area, one sample), the Irminger Sea (Va - off the coast of Iceland, one sample) and the Barents Sea (II b - near the Bear Island, one sample). A total of 462 specimens were examined. The following studies were performed: morphometric (performed by two methods: conventional measurements and truss network distances) involving 40 characters of fish head and body, 14 metric characters of fish skull and four characters of swimbladder, and the age determination (by scales and otoliths reading). The objectives of the present work were to present a detailed characteristics of particular cod samples and the analysis of taxonomical status of cod populations inhabiting the southern Baltic by comparison with the cod populations from the Sounds and north Atlantic. In the samples examined the cod in the length class of 35.1-45.0 cm (constituted of 47.17 % of the all specimens studied) from the III and IV age group prevailed. Results of UPGMA analysis concerned the metric characters of fish body for particular samples showed a close similarity among all Baltic populations of cod, as well as between them and cod from the Barents Sea, while the cod population from the Irminger Sea was found to be distinct both from the Baltic and Barents Sea cod. In the case of swimbladder characters, the most distant from the most populations examined were samples from the Pomeranian Bay (southern Baltic) and Irminger Sea. The UPGMA analysis of fish skulls pointed for very close affinity between cod populations from the southern Baltic and cod from the Barents Sea, especially between cod from the Barents Sea and Kołobrzsko-Darłowskie Bank (eastern stock), and a long distance for the sample from Irminger Sea. UPGMA analysis of morphometric characters of three combined populations of the cod studied: one from Baltic Sea (six samples), one from Sounds and one from the northern Atlantic (two samples) showed the dissimilarity of Baltic populations, especially in metric characters of fish body (described with the conventional method) and metric characters of fish skull.

Keywords : Morphometrics, Atlantic cod, UPGMA analysis



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Analysis of taxonomic position of Cod *Gadus morhua* L. from the Baltic sea based on the comparison of meristic characters

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The material to study was collected in the southern Baltic (ICES SD 23-25), in the area of Odrzańskie Bank (Pomeranian Bay - three samples), Kołobrzieszko-Darłowskie Bank, Gulf of Gdańsk, Puck Bay and in the Sund (Sounds). Eighteen meristic characters were examined. The objectives of the present work were to present a detailed characteristics of particular Baltic cod sample, the analysis of taxonomical status of cod populations inhabiting the southern Baltic by comparison with the cod populations from the Sounds and north Atlantic, as well as a trial to assess the taxonomical value of meristic characters complex allowed to determine the term of "subspecies" on the example of Atlantic cod with the statistically significant characters for *Gadus morhua* species differentiating the cod populations at the level of subspecies. Results of UPGMA, concerned the meristic characters show the following arrangement of samples examined: cod from the Barents Sea is distant, while cod from the Irminger Sea is close to the cod samples from the eastern stocks - Kołobrzieszko-Darłowskie Bank and one sample from the Pomeranian Bay. Cod from the Gulf of Gdańsk and Puck Bay are very similar, and fish from the Pomeranian Bay (second sample) and Sounds are close to them. The following meristic characters determined the affiliation of cod to the western stock: count of rays in the first dorsal fin – lower than 14, in the second one- higher than 18, anal ray count – higher than 19 (two samples from the Pomeranian Bay), whereas the count of rays in the first dorsal fin – higher than 14, in the second one- lower than 18, anal ray count – lower than 19 pointed for the eastern stock: one sample from the Pomeranian Bay, cod from the Kołobrzieszko-Darłowskie Bank, Gulf of Gdańsk and Puck Bay. Meristic characters of cod from the Sounds and two samples from the northern Atlantic, according to the available literature, are typical for the subspecies *G. morhua morhua*. Meristic characters, which were established by the discriminant analysis, are as follows: gill number counts (on two gill arches), caudal fin ray count and caudal vertebral number. The results obtained in the present work, confirmed the occurrence of two stocks of cod in the Baltic Sea: the western and eastern ones. Cod samples caught in the Pomeranian Bay belong to two stocks; therefore the Pomeranian Bay can be regarded as the area of cod mixing. To recognize the subspecies, more studies are needed in this area, with the hybrids of subspecies, collected or cultured if possible.

Keywords : Meristics, Baltic cod, UPGMA analysis



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Poster

Biomorphometric characteristics of *Rhinochimaera atlantica* Holt & Byrne, 1909 (*Holocephali*: Chimaeriformes) from the Greenland sea

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The material to study was collected within 2006-2009 (from April to November), in the area of Greenland Sea, at the depth of 1000-1200 m, as the by-catch during the commercial catches of Greenland halibut *Reinhardtius hippoglossoides* with the deep water otter trawl net (type BACALAO, mesh size of 119 mm). The specimens are deposited in the collection of Department of Hydrobiology, Ichthyology and Biotechnology of Breeding, West Pomeranian University of Technology in Szczecin, Poland. The objectives of the present work were to present a detailed characteristics of the morphometric characters, the stomach contents, hepatosomatic index and the parasite fauna of the straightnose rabbitfish from the Greenland Sea, usually found on or near the bottom of continental slopes. Eight specimens of *Rhinochimaera atlantica* were studied (five females and three males). Forty morphometric and two meristic characters (of gill arch) were examined. The gills, mouth and internal organs (stomach, intestine, liver, heart, spleen and gonads) were examined separately. Muscles were also studied. All measurements and other examinations were made on thawed material. The total length of fish covered the range from 82.3 to 130.0 cm, and weight from 1,259.0 to 5,239.3 g, respectively. Females were longer (average length TL = 113.82) than males (93.10 cm) and heavier (3,312.7 and 1,853.3 g, respectively). The biggest female (130.0 cm TL) had a broken and knitted cartilaginous rostrum. Remaining individuals had snout long and pointed, sword-like. Dental plates were smooth without rod-like internal structure. Anal fin was confluent to caudal fin. Upper margin of caudal fin was with a series of denticulations and a frontal tenaculum was short, less than eye-length in males. One female, caught in August (126 cm of TL), had two egg capsules, weighing 4.60 g each. Stomachs of the specimens studied were empty, with the one exception, where one deep-water red shrimp was found. Possibly the stomachs content was regurgitated after capture. The hepatosomatic index ranged from 11.12 to 17.97 % and was slightly higher in females (15.02 % compared to 13.85 % in males). The fishes studied hosted only one parasite species. The parasites were recorded in the spiral valve intestine of two individuals, and they belong to order Tetracystida (Cestoda). Their morphology was definitively different from the cestode species described in this host till now.

Keywords : Straightnose rabbitfish, Morphometrics, Parasites



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Genetics

Poster

Involvement of the *dhx34* gene in the development of the adenohipophysis in *Danio rerio*

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The pituitary is a small endocrine gland located below the diencephalon and forming an anatomical and physiological link between the nervous and endocrine systems to control many body functions such as metabolism, osmoregulation, reproduction and growth. The pituitary is divided into two parts: a neurosecretory, the neurohypophysis and an endocrine part, the adenohipophysis. Our study examines the surprising role of the RNA helicase Dhx34 in the development of the adenohipophysis in *Danio rerio*. Our study revealed that the decrease in expression of Dhx34 by injection of a specific morpholino leads to increased expression of prolactin, a sharp decline of growth hormone and somatolactin expression and, to a lesser extent of pro-opiomelanocortin and thyrotropin expression. In addition to decreased hormone expression, thyrotropes undergo a spatial disorganization. These results indicate that Dhx34 acts on the endocrine Pit1-positive lineages by repressing the anterior lineages and promoting the posterior lines. We also demonstrated that the number of anterior pituitary cells is not affected by the decreased expression of Dhx34. In conclusion, although this study must be pursued, we already proved that the *dhx34* gene is required for proper development of the adenohipophysis in zebrafish.

Keywords : Dhx34, Adenohipophysis, Development



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Studies of the size and structure of *Eupallasella percnurus* (Pisces, Cyprinidae) populations as a part of programme of its conservation in Poland

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Introduction: In Poland, *Eupallasella percnurus* has exceptionally high ecological status as one of the rarest and most threatened with extinction freshwater fish species, which requires active conservation measures. One of such measures is establishing new populations through single or multiple translocations of cultivated or wild individuals, originating from local populations, into suitable water bodies. Within the framework of the only one so far in the country, long-term programme of *E. percnurus* protection, carried out in Central Poland (Mazowieckie Voivodeship), four new populations were successfully established in the last decade. One of them, a population from Kowalicha village, established in 2004-2006, was monitored first in 2010. Then its total size was estimated at about 600 individuals excluding those aged 0+. The aim of the present work was to compare the size and structure of this population with two others (Guzy, Siedliszcze), both of considerably longer existence of about 50 years, in 2011. All the populations inhabit former peat excavations of similar size (0.10-0.15 ha) and depth (max. 1.0-1.5 m). Due to different surroundings, considerable differences in their basic water properties (pH of 5.7-7.6; conductivity of 60-380 $\mu\text{S cm}^{-1}$) exist.

Materials and Methods: Lincoln-Petersen (mark-recapture) method with the use of baited traps was applied to evaluate the total size of the population, its sex structure (males, females and juveniles older than 0+) and age structure. To distinguish fish sex, the studies were carried out in the spawning period (May-June). All the fish captured in the 1st catch were marked by clipping the end (2-3 mm) of their pelvic fin.

Results: For *E. percnurus* populations from Kowalicha, Guzy and Siedliszcze, a total 247, 646 and 498 individuals were caught and marked. The total size of the populations was estimated at 1518, 2192 and 2135 individuals, respectively, with strong dominance of adults over juveniles. Among mature fish, in all populations males were considerably less numerous than females (M to F ratio of 1 : 1.2-1.6). In all populations individuals at the age of three years prevailed.

Conclusions: Five years after the final fish translocation, the newly established *E. percnurus* population in Kowalicha has reached both size and structure very similar to those found for existing considerably longer populations from small water bodies in Poland. Water properties within the range recorded in our study seem to be not decisive for the size and structure of the populations.

Keywords : Lake Minnow, Populations, Protection



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Adaptive brain morphology and neuroanatomy in fishes Oral

Lateral line centers along the brain neuraxis : homologous or convergent ascending pathways in vertebrates?

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Mechanosensory and electrosensory lateral line systems are ancestral for craniates and vertebrates, respectively. The mechanosense is lost in most adult anurans and lost independently with amniotes. The ancestral electrosense is additionally lost in the ray-finned fish lineage (incl. teleosts). However, some teleost taxa acquire electroreception newly and independently (silurids, gymnotoids, mormyrids) in evolution. Ascending (lemniscal) lateral line pathways along the brain neuraxis have been reported in all taxa (lampreys, cartilaginous fishes, ray-finned fishes, and amphibians). These pathways are highly comparable up to mesencephalic levels, but are more diverse in the forebrain. A key issue is whether the diencephalic so-called preglomerular region of ray-finned fishes is developmentally arising from the dorsal thalamic histogenetic unit at the proliferative ventricle embryonically or from that of the posterior tuberculum. This is critical for determining homology of adult diencephalic relay centers. Recent progress in developmental molecular biology and behavioral studies further allows for recognition of the identity of telencephalic centers receiving lateral line input in teleosts, with the major such telencephalic area being the homologue of the mammalian hippocampus or medial pallium. Although convergently evolved, the electrosensory pathways in teleosts nevertheless reveal how patterns of synaptic large-scale connectivity in ascending lateral line pathways are re-used in phylogeny.

Keywords : Lateral line system, Central anatomy, Evolution



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Phylogeny, Systematics

Oral

The systematics of Malaysian *Puntius* and its allies (Pisces: Cyprinidae)

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The variation of criteria among authors and the discrepancies between morphological and molecular data generated a troublesome situation concerning the delimitation of the genus *Puntius*, which remains as yet unresolved. This is the first documentation on phylogenetic relationships among *Puntius* species in Malaysia integrating classical morphometrics, geometric morphometrics and molecular techniques. Morphological and phylogenetic studies were conducted on 10 Malaysian *Puntius* species and their allies obtained from five locations in Peninsular Malaysia. A total of 312 samples were analysed. The quantitative data were analysed using analysis of variance (ANOVA), Principal Component Analysis (PCA) and Discrimination Function Analysis (DFA). Results were further supported by sequencing of the cytochrome c oxidase subunit I (Cox1, 501 bp), cytochrome b (Cytb, 857 bp) and 16s ribosomal RNA (16SrRNA, 571 bp) mitochondrial genes and recombination activating gene (Rag2, 860 bp) and beta actin (β -actin, 911 bp) nuclear genes. A combination of mitochondrial and nuclear data for phylogenetic relationships analysis was conducted from 39 representative samples of *Puntius* species. The phylogeny among taxa was constructed through Neighbor joining (NJ), Maximum parsimony (MP), Maximum likelihood methods (ML) and Bayesian inference (BI). The topologies resulting from molecular analysis are the first to examine *Puntius* in a broader context and were consistent with the taxonomic hierarchy based on geometrical morphometric analyses recommending the nomenclatural change of 4 species from the other *Puntius* species in this study.

Keywords : Cyprinidae, Phylogenetic, Geometric morphometric



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Ethology

Poster

Behavioural effects of approach-avoidance motivational conflicts in Zebrafish: testing an Attentional Control Model on videotracked swimming activity

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Motivational conflicts have been thoroughly studied in birds and mammals over the last decades, but their investigation has remained anecdotic with respect to fish. However, recent researches reveal that, emotion and cognition also play a pivotal role in the expression of fish behaviour. Fish exhibit fear, long-term memory, attentional and learning capacities that are comparable with those of other vertebrates, including nonhuman primates. Thus, fish can be expected to manage motivational conflicts using cognitive similar resources. As many other teleost fishes, zebrafish (*Danio rerio*) is a good candidate to investigate the behavioural effects of approach-avoidance conflicts because of its genetic and neurophysiological proximity with "higher" vertebrates. The present study aims to determine how Zebrafish reacted to threats of different magnitude (low vs. high) following the delivery of food.

A total of 66 female wild type AB zebrafish were tested in these experiments. Eight small aquaria (illuminated 12h/day by 14w neons tube and placed in 8 white wall boxes to improve visual contrast) were used, successively to train and test single fish. Each arena was composed of two parts (24×20×8 cm & 8×20×8 cm, length×depth×width) separated by an anti-reflection pane of glass; the width of aquaria was narrow to minimise data loss during the 2-D video-tracking; the left part was the place where fish could freely move; the right part contained a threatening stimulus (low threat: a mere loop of yellow thread; high threat: a basic homemade dummy of *Xenentodon cancila*). In order to elicit approach behaviour, ZM-400 powder food was delivered through a funnel placed 40 mm away from the "dummy's area". Data were recorded on digital Sony® camera and they were analysed using the EthoVision Color-Pro® 3.1 video tracking system.



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Six groups of 11 fish each were defined. The different groups specify the stimuli presented on test day: G1-FT+: fish were exposed to food and, 15 s later, to the high threat for 30 s; G2-ØT+: no food, high threat; G3-FT-: food, low threat; etc.

The results indicate that the swimming total distance moved and turn angle mean are altered by the presence of food, its association with threat, and the magnitude of threat. Although these results can be partly interpreted in terms of fear or anxiety, we suggest that the zebrafish behaviour measured in conflict situations may require an explanation in terms of differences in attentional control on a task demands. Attention here is defined in the sense of selectively allocating cognitive resources to one aspect of the environment while ignoring other aspects. One of us has developed a model (the Anselme 's Anticipatory Dynamics Model) based on empirical evidence that attention is a limited cognitive resource, so that behavioural performance related to one stimulus depends on the amount of attentional resources allocated to another stimulus. The data are discussed in the light of this theoretical model.

Keywords : Motivational conflicts, Video-tracking, Zebrafish



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

Ecology - Fish conservation

Poster

Early development of the freshwater goby *Knipowitschia croatica* Mrakovčić *et al.* 1994 (Actinopterygii, Gobiidae)

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The larval development of the freshwater goby species, Vrgorac goby, is described under laboratory conditions. Eggs were pear shaped, 1.4 x 1 mm in size. Hatching occurred 9 to 10 days after spawning, and larvae had a mean TL of 4.27 mm, with the tail fin and all three pairs of otoliths developed and clearly visible. Hatched larvae were positively phototaxic. The mouth opened 2–3 days after hatching (DAH), with larvae feeding independently on the third day. The yolk sac was absorbed and notochord flexion began 6–8 DAH. Metamorphosis was complete at 31 DAH, and juveniles had a mean TL of 10.69 mm and moved towards the bottom of the tank to begin demersal life.

Keywords : *Knipowitschia croatica*, Larval development, Morphological characteristics



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Ecology - Fish conservation

Poster

Insight in garfish *Belone belone* (L., 1761) diet in the Adriatic Sea

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The main aim of this study was to describe and give an insight in garfish feeding habits by describing its prey and possible size-related changes in diet. Garfish, *Belone belone* (Linnaeus, 1761), is a pelagic, oceanodromous fish species largely spread in brackish and marine waters of the north-eastern Atlantic, Mediterranean and the Black Sea. Similar to other pelagic fish species garfish has migratory pattern; generally it is found in offshore areas, except during the spawning period (January – May) when its specimens migrates into coastal regions. Biological knowledge of garfish population, that inhabiting Adriatic Sea, is partial and refers only to its reproduction traits, while there are no data concerning its diet. Garfish specimens (N=211, 23.1 cm). Analysis of gut content indicated that garfish preferred feeding on animal food (94 %), while plant component found inside of garfish guts referred to pieces of brown algae (Phaeophyta) and wads of *Posidonia oceanica*. A total of 24,992 animal preys belonging to ten taxonomic groups were identified. According to presented data, copepods (56.9 %) and decapods (44.4 %) were the most frequent, while the most abundant prey items were euphausiids (59.9 %) and copepods (20.7 %). Diet composition of garfish specimens was not size related (TL-%N: $0.007 < r^2 < 0.417$; $P < 0.05$) as all examined garfish preyed mainly upon euphausiids, decapods and copepods. Fullness index decreased with garfish size (% Jr= $4.022 - 0.032TL$) but not statistically significant ($r=0,382$, $p=0,075$). Conversely to a low value of fullness index (mean \pm SD: 2.70 ± 1.84 %) quite high vacuity index was obtained (% V=31.88 %).

Analysis of gut content confirmed garfish as omnivore fish species but with a pronounce preference for animal food. Obtained knowledge of this fish trophic ecology should provide better comprehension of its functioning in an ecosystem.

Keywords : Feeding, *Belone belone*, Adriatic sea



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

Index

A

ABDISSA Belay	27
ABE Kelly	140
ABELLÓ Pere	136
ADAMSON Eleanor	1, 193
ADRIAENS Dominique	35, 153, 157, 231
AGADJIHOUEDE Hyppolite	149
AHOUANSON MONTCHO Simon	48
ALEKSEEVA Yaroslava	30
ALEXANDRINO Paulo	211
ALFARO Michael E.	86, 196
ALIABADIAN Mansour	204, 260
ALJAMAL Mohammed	2
AL-KHARUSI Lubna H.	227
AL-MAMRY Juma M.	227
ALTNER Melanie	3
AMARA Rachid	4
AMIR Aïcha	17
ANASTASOPOULOU Aikaternini	5
ANGANTHOIBI Nongmaithem	249
ANIČIĆ Ivica	232, 236
ANSELME Patrick	261
ANTOSZEK Artur	254, 255
ANTUNES Sara Cristina	180
AOKI Nana	116
APONE Fernando	65
ARNEGARD Matthew	43
ARTAMONOVA Valentina	30
ASAI Toshinobu	6
ASHIKAGA Fernando	7



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

B

BAGCI Enise	9
BALBÍN Rosa	136
BANYANKIMBONA Gaspard	11
BARBERA Carmen	136
BARBIERI Roberta	12, 217
BARDONNET Agnès	70, 89, 98, 248
BAREKE Eric	71
BARISIC Josip	50
BAROILLER J-F	13
BART Henry	14, 184
BARTÁKOVÁ Veronika	15
BASS Andrew	16
BEALL Edward	20
BEER-LJUBIC Blanka	50
BEKAS Petros	5
BELAY Abdissa	207
BELLI Mathilde	17
BENAYAHU Yehuda	200
BENTLEY Andy	184
BERNARD Benoît	18
BERTEN Laetitia	19
BETANCUR-R Ricardo	212
BETOULLE Stéphane	20, 107, 246
BETTI Eric	46
BIANCHINI Adalto	61
BIANCO Pier Giorgio	21
BIERNACZYK Marcin	220, 221
BINI Guillaume	248
BIRZAKS Janis	22
BLAISE Sébastien	107
BLAŽEK Radim	15, 23, 252
BLUST Ronny	9
BOČINA Ivana	82
BOCKMANN Flavio	65
BODEN Gert	24, 154
BODILIS Pascaline	25, 85



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

BOISTEL Renaud	157
BOJANIĆ VAREZIĆ Dubravka	26
BOLLIET Valérie	70
BOONE Matthieu	231
BORCHERDING Jost	164
BORISOV Vasily	27, 207
BORON Alicia	28
BORVIKOVA Elena	29, 30, 32, 33
BOSC Pierre	224
BOUAZIZ Ahmed	34, 141
BOUILLIART Mathias	35
BOYLE Kelly	36
BRAHMI Boualem	34
BRČIĆ Jure	120, 170
BRIEDE Agrita	22
BRITZ Ralf	1, 37, 38, 193
BRYJA Josef	15
BUI Thi Bich Hang	39
BUJ Ivana	40, 41, 80, 134, 143, 263
BURRIDGE Christopher	42
BYRKJEDAL Ingvar	175

C

ĆALETA Marko	40, 41, 50, 80, 143, 263
CAPELA Ricardo Campinho	59
CARAYON Marie	98
CARLIER Annie	107
CARLSON Bruce	43
CARNEVALE Giorgio	196
CAROSI A	93
CARPENTER Kent	56
CATINAUD Ludovic	248
CATTANEO Franck	98, 168, 248
CAUDRON Arnaud	248
CAVRARO Francesco	45
CECCONI Ambra	45



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

CECH Martin	176, 183
CHANET Bruno	46, 124
CHATER Inès	47, 187
CHATZINIKOLAOU Yorgos	111
CHEN Wei-Jen	14
CHIACHIO Marcio Cesar	190, 191
CHIKOU Antoine	48
CHILMONCZYK Stefan	20
CHRISTIAENS Joachim	157
CHRISTODOULOU Maria	49
CIGROVSKI MUSTAFIC Martina	50
ČIKEŠ KEČ Vanja	51, 264
CIVÁŇOVÁ Kristína	52
ČIZMIĆ Frane	219
CLAES Julien	53
CLEMENS Michelle	55
CLOES Marie	229
COAD B.W.	151
COELHO Rui	64, 142
COLLETTE Bruce	56
COLLEYE Orphal	57
CONDET Manon	128
CORNELISSEN Ilse	58
CORREIA Alberto	59, 180
COSTEDOAT Caroline	52
COUZIN Iain	69
COWX Ian	217
COZ-RAKOVAC Rozelinda	50
CRAW Dave	42
CURE Y.	178

D

DĄBROWSKI Jarosław	254
DA FONTOURA MARTINS Mariana	61
DALCQ Julia	122
DAMIR Naoual	141



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

DANIS Lorraine	71
DAS Krishna	199
DAUD Siti Khalijah	260
DÁVIDOVÁ Martina	23, 62, 164
D'COTTA H.	13
DEAN Mason	53
DE CROP Wannes	63
DECRU Eva	66, 67
DE FRANCO Bruno A.	64
DEGANI Gad	68
DE KEGEL Barbara	157
DELAHAUT Laurence	246
DELCOURT Johann	69, 70
DELEUZE Stéphane	81
DE LOS SANTOS-BAILON Alejandra	194
DEMEULDER Bertrand	71
DE MEYER Jens	231
DEMMER J.	58
DENOËL Mathieu	70
de PALAMINY Alix	17
DEPIEREUX Eric	71
DEPIEREUX Sophie	71
DE PINNA Mario	65
DETTAÏ Agnès	17, 46, 124
DIAMANT Ariel	215
DIEU Marc	186
DIMITRIOU Elias	217
DIRNWÖBER Markus	72
DISHMA Mayanglambam	249
DJIOTSA Joachim	73
DOBROSLAVIĆ Tatjana	219
ĐOĐO Željana	74
DOKOS John	5, 237
DONALDSON Terry J.	75
DOOSEY Michael	14, 76
DORNBURG Alex	77
DOUDA Karel	181
DOUXFILS Jessica	137



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

DRAGICEVIC Branko	78, 79, 114
DRASTIK Vladislav	183
DUFOUR Jean Louis	187
DULCIC Jakov	26, 74, 78, 79, 114, 238
DUNLOP John	53
DUPLIC A.	80

E

ECONOMOU Alcibiades N.	242
EPLER Piotr	117
ERPENBECK Dirk	94
ESMAEILI H. Reza	92, 151, 204, 226
ESNAULT Stephen	81

F

FARCY Emilie	20
FARIA Rui	211
FAUCON-MOUTON Philippe	248
FEDORENKO Leonid	211
FELIX Christophe	246
FERNÁNDEZ DE PUELLES M ^a Luz	136
FERNHOLM B.	158
FERRI Josipa	82, 120, 170
FILALI Tahar	141
FISLER Marie	124
FLASSE Lydie	173, 214
FLEISCHER Aliza	200
FONTAINE Pascal	234
FONTOURA Nelson F	83, 185
FORESTI Fausto	7, 64, 142, 166, 188, 190, 191
FORMICKI Krzysztof	220, 221
FOSTIER Alexis	71, 89
FOURNIER Michel	20
FRANCOUR Patrice	25, 84, 85
FRANKEN Johanna	147



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

FREDERICH Bruno	86, 163
FREYHOF Jörg	90
FROESE Rainer	87
FROIDBISE Sophie	261
FUJII Yota	105, 116
FUJITA Tomohiko	113

G

GALICKA Wanda	167
GALIL Bella	215
GALINOU-MITSOUDI Sofia	88
GALLUT Cyril	17, 46, 124
GARDEUR Jean-Noël	234
GARNIER Simon	69
GAUDANT Jean	94
GAUDIN Philippe	224
GAUTHRAY Ghislain	199
GAWLIK Bernd	186
GEERINCKX Tom	63
GEFFARD Alain	20, 107
GEFFROY Benjamin	89
GEIGER Matthias	90
GERMANN-ARNOLD Brigitte	169
GHAYE Aurélie	91
GHETTI L.	93
GHOLAMI Zeinab	
GHODRATNAMA Maryam	148, 189
GIKOUMI Sofia	111, 242
GIANNETTO Daniela	93
GIERL Christoph	94
GILLES André	52
GLAMUZINA Branko	74, 238
GŁOWACKI Łukasz	95, 167
GOLANI Daniel	92, 96
GOMEZ GARVIN Jaime	128
GON Ofer	127



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

GONÇALVES Fernando	180
GOREN Menachem	215
GOTO Akira	97
GRABOWSKA A.	28
GRIMARDIAS David	98, 168, 248
GUIGUEN Yann	71, 89
GUINTARD Claude	46
GUROVSKI Aleksey	32
GUTIERREZ-OSPINA Gabriel	194

H

HABLÜTZEL Pascal	99
HADIATY Renny K.	106
HAGENAARS An	9
HAMER Paul	59
HARALBOUS John	237
HARMON Luke	43
HARRIS Matthew	100
HASAN Saad	43
HELSEN Philippe	231
HERDER Fabian	55, 90, 101, 106, 171
HERLER Jürgen	72
HERNANDEZ Patricia	102, 212
HESS Martin	201
HOFMANN Hans	103
HOFMANN Michael	2, 55, 104, 121, 177, 197, 239
HOLLMANN Michael	43
HOSOYA Kazumi	6, 105, 113, 150
HUYLEBROUCK Jan	106
HUYSE Tine	242

I

IMSIRIDOU Anastasia	88, 132
INUI Takehiro	116
IRNAZAROW Ilgiz	155



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

J

JABLONSKA O.	28
JACINTE Mickelson	233
JADAN Margita	232
JAFFAL Ali	20, 107
JAKOVLEVA Leva	22
JASQUET Laurie	261
JAWAD Laith A.	227
JAWORSKI Andrzej	234
JEANRAY N	178
JIRKŮ Miloslav	23
JIRSOVÁ Dagmar	23
JOHNEN Nicolas	229
JOHNSON David	38
JOLLY Sabrina	107
JORIS Marine	108
JUCHNO D.	28, 229
JURAJDA Pavel	164
JUZA Tomas	176, 183

K

KACZKOWSKI Zbigniew	132
KACZMARCZYK Dariusz	109
KAJRUP Bodil	110
KALOGIANNI Eleni	12, 111, 217
KAMIŃSKI Rafał	208, 258
KAMLER Ewa	234
KANAIWA Minoru	116
KAPITANOVA Daria	112, 207
KARAIKOU Nikoleta	132
KAWASE Seigo	105, 113
KERZABI Fedja	34
KESTEMONT Patrick	18, 39, 71, 130, 135, 137, 186
KESZKA Sławomir	256
KETELAARS Henk A. M	176



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

KEVER Loïc	114
KHELOUI Hana	141
KHERCHOUCHE Aldjia	141
KIM Eun-Jin	115
KIRTIKLIS L.	28
KITAGAWA Tadao	116
KLACZAK Artur	117, 159, 160
KLOPFSTEIN Seraina	118
KNAPEN Dries	9
KOCVARA Lubos	183
KODUKHOVA Yulia	216
KOGBÉTO Marie-Josée	48
KOHOUT Jan	119
KOIZUMI Noriyuki	116
KOŠČO Ján	159, 160
KOUTRA Athanasia	88
KOUTSIKOS Nicholas E.	242
KOVACIC Marcelo	242
KOŽUL Valter	219
KRALJEVIĆ Miro	238
KRAMER Bernd	127
KRASZEWSKI Tomasz	221
KRATOCHVIL Michal	176, 183
KRSTULOVIĆ ŠIFNER Svjetlana	120, 170
KRUK Andrzej	167
KRÜTZFELDT Nils	2, 121, 239
KTARI Mohamed Hédi	47, 187
KUBECKA Jan	176, 183
KUJAWA R.	28
KULLANDER Sven	158

L

LADICH Friedrich	201, 202
LALÈYÈ Philippe	48, 125, 149
ŁAPIŃSKA Małgorzata	132
LARBUISSON Arnaud	108, 122



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

LARMUSEAU Maarten H.D.	242
LATLI Adrien	18, 123
LAUESEN Peter	35
LAUTREDOU Anne-Claire	124
LAZARTIGUES Angélique	246
LECCHINI David	19
LECOINTRE Guillaume	17, 46, 124
LEDEROUN Djiman	125
LEES Janek	126
LEFKADITOU Eugenia	5
LEGAC Florence	71
LEONARDOS Ioannis	12, 162
LEPRIEUR Fabien	162
LESKA A.	28, 229
LEVY Gal	68
LOKESHWOR Yumnam	249
LOOS Robert	186
LORANCE Pascal	237
LORENZONI M.	93
LOSSON Isabelle	261
LOUISY Patrick	25

M

MAAKE Pholosi	127
MADI MOUSSA Rakamaly	128
MAEX Margo	9
MAHE Kélig	47, 187
MAHINI A.S.	151
MAIA Anabela	129
MAINFROID Isabelle	223
MAKHROV Alexandr	30
MALAVASI Stefano	45
MALLEFET Jérôme	53
MANDIKI Robert	130, 137, 233
MANKIEWICZ-BOCZEK Joanna	132
MANSOURI Parviz	172



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

MARČIĆ Zoran	40, 41, 80, 134, 143, 263
MARKOV Martina	195
MARTIAL Joseph	73, 122, 179
MARTIN Jean-François	52
MAŠOVÁ Šárka	23
MASSART Sophie	135
MASSUTÍ Enric	136
MATHIEU Cédric	137
MATIĆ SKOKO Sanja	26, 82, 138, 213, 238
MATULIĆ Daniel	232, 236
MAYANGLAMBAM Dishma	
MAYDEN Richard	14
MCDOWALL Robert	42
MEGALOFONOU Persefoni	49
MEGHOUCHE Amine	141
MÉLARD Charles	81, 233
MELCHER A.H.	151
MELNIKOVA M.N.	139
MELO Bruno	140
MENDEL Jan	160
MENDIL Hamza	141
MENDONÇA Fernando F.	64, 142
METSCHER Brian D.	202
MEZHHERIN Sergey	211
MICHALKOVA Veronika	164
MIHINJAČ Tanja	134, 143
MILLA Sylvain	39, 130, 135, 137
MILLER Derek	43
MILLER Noam	69
MILLOT Sandie	144
MINOS George	132
MIOČIĆ-STOŠIĆ Jure	40
MIYA Masaki	14, 145, 175
MOHAMADIAN Samira	148
MOELANTS Tuur	146
MOGDANS Joachim	147
MOHAMADIAN Samira	172, 189
MOKHTARI Abbas	172



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

MONTCHOWUI Elie	149
MOORE Jon	77
MORALES Millke	142
MORANTA Joan	136
MORAT Fabien	20
MORIMUNE Toshihiko	150
MOSTAFAVI Hossein	151
MOTTA MARQUES David	185
MOTTE Patrick	108
MRAKOVČIĆ Milorad	40, 41, 50, 80, 134, 143, 263
MRDAK D.	80
MRKVICKA Tomas	183
MULLER Marc	108, 122, 165, 178, 179, 257
MUNROE Thomas	152
MUNYANDAMUTSA Philippe	153
MUSKA Milan	183
MUSSCHOOT Tobias	24, 154, 251
MUSTAFIĆ Perica	40, 41, 50, 80, 134, 143, 263
MYTILINEOU Chyssi	5, 237

N

NAGELKERKE L.A.J.	58
NAKAJIMA Jun	115
NAPORA – RUTKOWSKI Łukasz	155
NĂVODARU Ion	211
NAZARKIN M.V.	250
NEAR Thomas	77
NEO, Yik Yaw	209
NEUMANN Dirk	160
NEUTENS Céline	157
NGUYEN Thanh Phuong	39
NILSSON Dan-Eric	53
NISHIDA Mutsumi	145, 175
NKOGO ROBLES Silvia	130
NONGMAITHEM Anganthoibi	
NORÉN Michael	158



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

NOWAK Michał	117, 159, 160
NTAKIMAZI Gaspard	11
NUNES Bruno	59, 180
NZAU MATONDO Billy	161

O

ODDONE Maria Cristina	61
OIKONOMOU Anthi	162
OLIVAR María Pilar	136
OLIVEIRA Claudio	7, 64, 140, 142, 166, 188, 190, 191
OLIVIER Damien	163
ONDRACKOVA Marketa	164
ONIKURA Norio	115
ORDINES Francesc	136
OROS Mikuláš	23
ORSI Mario L	7
OSTASZEWSKA Teresa	155
OTTEN Auke BC	165
OVIDIO Michaël	161

P

PALLAORO Armin	138, 195, 238
PANSONATO-ALVES José Carlos	166
PAPADOPOULOU Konstantina	5
PAPOUSEK Ivo	62
PARMENTIER Eric	19, 36, 57, 114, 125, 144, 163
PAVLOV S.D.	139
PAZIAN Marlon	166
PEERS Bernard	73, 91, 173, 214, 223
PEKÁRIK Ladislav	119
PENCZAK Tadeusz	95, 167
PERNETTE Florence	248
PERSAT Henri	168
PETER Armin	169
PETERKA Jiri	176, 183



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

PETRIĆ Mirela	120, 170
PFAENDER Jobst	101, 171
PHARISAT André	94
PHILIPPART Jean-Claude	161
PIERRARD Marie-Aline	186
PIERRE Michaël	71
PILARCZYK Andrzej	155
PIRALI KHEIRABADI Esmail	172
PIRIA Marina	232, 236
PIRSON Justine	173, 214
PIVOVAROV E.A.	139
PLATH Martin	201
PLETTERBAUER F.	151
POLACIK Matej	15, 252
POLITOU Chrisi-Yianna	237
POMPEI Lura	93
PONCIN Pascal	70, 149, 161, 261
PONOMAREVA Ekaterina	174
PONOMAREVA Maria	174
PONTIER Jérôme	81
POPEK Włodzimierz	117, 159, 160
POULSEN Jan Y.	175
PRCHALOVA Marie	176, 183
PRIGNON Christian	81
PŘIKRYLOVÁ Iva	23
PRINZ Janine	177
PRUVOT Benoist.	178

Q

QUETGLAS Antoni	136
QUIROZ Yobhana	178, 179

R

RADTKE Grzegorz	258
RAES Martine	186



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

RAMESHORI Yumnam	249
RAMON Montserrat	136
RAMOS Ana Sofia	180
ŘEHULKOVÁ Eva	23
REICHARD Martin	15, 181, 182, 252
REICHENBACHER Bettina	3, 92, 94, 226, 227
REES Davis	175
REZUCHA Radomil	182
REZVANI GILKOLAE Sohrab	148, 189
RIHA Milan	176, 183
RIOS Nelson	184
RIVES Jacques	248
RODRIGUES Lucia Ribeiro	185
RODRIGUES Sara	180
ROLAND Kathleen	186
ROMDHANI Ahlem	47, 187
RONQUIST Fredrik	118
ROUGEOT Carole	81, 233
ROUHOLAHI Shaghayegh	148, 172, 189
ROSSINI Bruno C.	188
ROXO Fábio Fernandes	190, 191
RÜBER Lukas	1, 193
RUEDA Lucia	136
RUEDA-JASSO Rebeca A.	194

S

SAFNER Roman	232, 236
SAITOH Kenji	14
SAMARAS Dimitrios	88
SANCHEZ Wilfried	107, 246
ŠANDA Radek	41
ŠANTIĆ Mate	195
SANTINI Francesco	86, 196
SANTOS Miguel N.	64, 142
SATOH Takashi	145, 175
SCHERBENOK Yuri	230



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

SCHINEGGER R.	151
SCHLAEPPI Thomas	169
SCHLIEWEN Ulrich K	251
SCHLUESSEL Vera	197
SCHMITZ Anke	147
SCHMUTZ Stefan	151, 198
SCHNITZLER Joseph	199
SCHULTZ Doron	200
SCHULZ-MIRBACH Tanja	92, 201, 202
SEBERT Philippe	203
ŠEDIVÁ Alena	119
SEIFALI Mahvash	204, 260
SELLESLAGH Jonanthan	4
SEMENOVA A.V.	139
SECHUKOVA A.L.	139
SENDEK Dmitry	205
SENHORINI José A	7
SENOU Hiroshi	6
SERGEEV Alexey	206
SHAFIE Shafigh	172
SHAHAR Ron	53
SHKIL Fedor	27, 112, 207
SHINOHARA Gento	175
SHREIDER Maria	30
SHUBINA Elena	174
SIDELEVA Valentina G	97
SIKORSKA Justyna	208, 258
SILVESTRE Frédéric	186, 199
ŠIMKOVÁ Andrea	52
ŠKELJO Frane	120, 170
SLABBEKOORN Hans	209
SLATER Graham J.	86
SLOVACKOVA Iveta	164
SLYN'KO Yuriy	32, 33
SMEETS Hubert JM	165
SMIRNOV Sergey	27, 207
SMITH Carl	181
SMITH J.Christopher	5



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

SMUC Tomislav	50
SNOEKS Jos	11, 24, 66, 67, 125, 146, 153, 154, 210, 241, 251
SOBECKA Ewa	255, 256
SOLTANI Mehdi	148, 189
SORENSEN Laurie	86, 196
SOTELO Graciela	211
SPOZ A.	28
ŠPREM Nikica	232, 236
SPRINGE Gunta	22
STAAB Katie Lynn	102, 212
STAGLIČIĆ Nika	195, 213
STERN David	173, 214
STERN Nir	215
STOLBUNOVA Veronika	29, 216
STOUMBOUDI Maria	12, 217
STRELNIKOV Aleksandr	218
STRELNIKOVA Aleksandra	218
STRUNJAK-PEROVIC Ivancica	50
SUČIĆ Ivana	134
SUIĆ Josip	236
SULIĆ ŠPREM Jadranka	219
SWARTZ Ernst	127
SZCZERBIK Paweł	117, 159, 160
SZULC Joanna	220, 221

T

TAHERI MIRGHAED Ali	148, 172, 189
TAKESHIMA Hirohiko	175
TANG Kevin	14
TANŃSKI Adam	220, 221
TARIFEÑO Estefania	223
TÈHOU Aristide	48
TEICHERT Nils	224
TEIMORI Azad	92, 151, 226, 227
TELETCHÉA Fabrice	234



XIV European Congress of Ichthyology
Liège, 3-8 July 2012 (Belgium)

THELEN Nicolas	229
THEUNISSEN Tom EJ	165
THIEREN Els	228
THIRY Marc	229
THOMAS Marielle	246
TIČINA Vjekoslav	26
TITOV Sergey	230
TKINT Tim	153, 231
TOMKIEWICZ Jonna	35
TOMLIANOVIĆ Tea	232, 236
TOMSON Thomas	81, 233
TOPIC POPOVIC Natalija	50
TORRES Asvin P.	136
TORRICELLI Patrizia	45
TRABELSI Awatef	234
TRAUTWEIN C.	151
TREER Tomislav	232, 236
TSAGARAKIS Konstantinos	237
TSIORA Anna	132
TURAN Cemal	211
TUSER Michal	183
TUTMAN Pero	26, 138, 238

U

ULAMA Tim	239
-----------	-----

V

VALADE Pierre	224
VALLS María	136
VALOVA Zdenka	164
Van den BOSCH Bianca	165
VAN DER MEER Henny	240
VANDEWALLE Pierre	48, 125
VAN HOOREBEKE Luc	157
VANHOVE Maarten P.M.	242



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

VAN LOO Denis	157
van OIJEN Martien J.P.	105
VAN RIJSSEL Jacco C.	240
VAN STEENBERGE Maarten	241
VARI Richard	140
VASEK Mojmir	176, 183
VASIL'EVA Ekaterina	211, 244, 245
VASIL'EV Victor	244, 245
VATANDOUST S.	151
VERBRUGGEN V.	73
VERGAUWEN Lucia	9
VERHEYEN Erik	231
VERON Antoine	20
VETESNIK Lukas	62
VETESNIKOVA SIMKOVA Andrea	62
VETTIER Aurélie	246
VIGIER Laure	248
VILIBIĆ Ivica	138
VISHWANATH Waykhom	249
VOLCKAERT Filip A.M.	242
VONCKEN A.	178
VOSKOBOINIKOVA Olga	250
VOZ Marianne	73, 91, 173, 214, 223
VREVEN Emmanuel	11, 66, 67, 125, 146, 154, 210, 251
VRTILEK Milan	181, 252

W

WAGENVOORT Arco J.	176
WAGNER Hans-Joachim	253
WAMUINI LUNKAYILAKIO Soleil	251
WATERS Jonathan	42
WEISS Steven	168
WÉNON Dossa	48
WIĘCASZEK Beata	254, 255, 256
WIELOPOLSKA Magdalena	256
WILLASSEN Endre	175



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

WILEY Edwardb	76, 184
WILSON Mark	42
WINANDY Marie	165, 178
WINDHAUSEN T.	179, 257
WINKLER Kathrin	168
WITTE Frans	240
WOLNICKI Jacek	109, 208, 258
WOOD Robert	14
WULLIMANN Mario F.	259

Y

YAMAMOTO Atsuya	116
YAZDANI MOGHADDAM Faezeh	204, 260
YLIEFF Marc	70, 261
YOKEŞ Baki	215
YOKOYAMA Ryota	97

Z

ZABINSKA M.	28
ZALEWSKI Maciej	132
ZANELLA D.	50, 134, 263
ZAWADZKI Claudio Henrique	190, 191
ZOGARIS Stamatias	242
ZORICA Barbara	51, 264
ZULJEVIC Ante	213



XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

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XIV European Congress of Ichthyology Liège, 3-8 July 2012 (Belgium)

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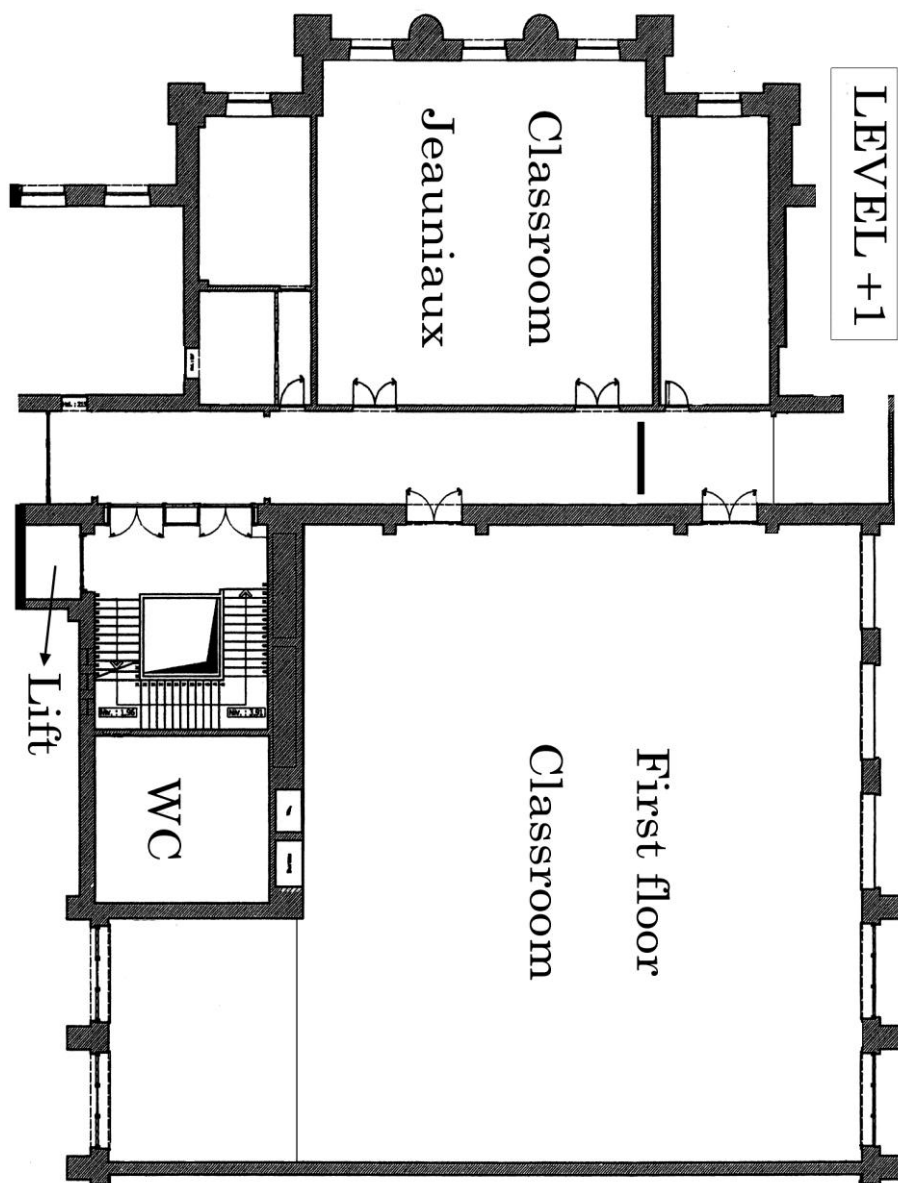


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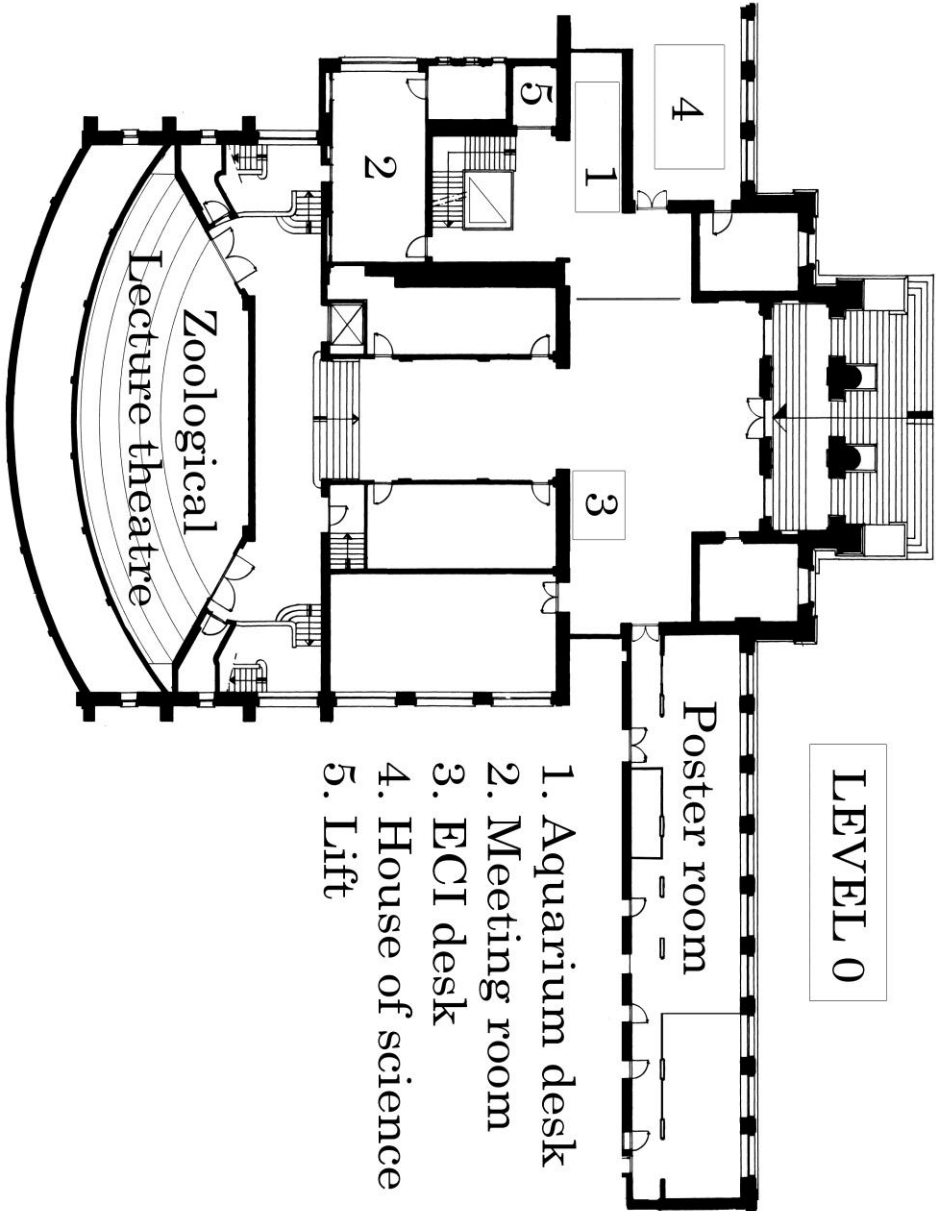


XIV European Congress of Ichthyology
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50th Anniversary

