

Societas Europaea Herpetologica – SEH
Deutsche Gesellschaft für Herpetologie und Terrarienkunde – DGHT

SEH European Congress of Herpetology & DGHT Deutscher Herpetologentag



Luxembourg and Trier, 25th to 29th September 2011



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Presenters

Societas Europaea Herpetologica, SEH (www.seh-herpetology.org), and Deutsche Gesellschaft für Herpetologie und Terrarienkunde e.V., DGHT (www.dght.de), in collaboration with the National Museum of Natural History, Vertebrate Department, Luxembourg (www.mnhn.lu) and Trier University, Biogeographie Department, Trier, Germany (www.biogeographie.uni-trier.de/index.php?id=2528).

Venue

Neumünster Abbey, 28, rue Münster, L-2160 Luxembourg (**Salle Robert Krieps** and **Salle Edmond Dune**), and the National Museum of Natural History, 25 rue Münster, L-2160 Luxembourg, (**cafeteria, ground floor**), all time, except 28th September (whole day): Trier University, Campus II, Behringstraße 21, D-54296 Trier-Petrisberg (**Audimax HS 11-13**). See program for details.

Conference office

Sunday (25th September): National Museum of Natural History, 25, rue Münster, L-2160 Luxembourg, (foyer), 15:00-19:00 hrs.

Monday, Tuesday and Thursday (26th, 27th, 29th September): Neumünster Abbey, 28, rue Münster, L-2160 Luxembourg; Salle Robert Krieps (foyer), during the conference.

Wednesday (28th September): Trier University, Campus II, Behringstraße 21, D-54296 Trier-Petrisberg (old chapel, room K101), during the conference.

Emergency?

In case you feel it is necessary please contact us via mobile phone:

Luxembourg: +352 – 691 554 346 (Edmée Engel).

Trier: +49 - 151 - 284 069 43 (Stefan Lötters).

Poster session

National Museum of Natural History, 25, rue Münster, L-2160 Luxembourg (**ground floor**), Monday, 26th September, 17:45-19:00 hrs.

What – where – when – who?

SEH OGM

Neumünster Abbey, 28, rue Münster, L-2160 Luxembourg (**Salle Robert Krieps**), Tuesday, 27th September, 16:45-18:45 hrs.

SEH Intern council meeting

National Museum of Natural History, 25, rue Münster, L-2160 Luxembourg (**Salle Découverte**), Sunday, 25th September, 17:00-19:00 hrs.

SEH Internal meeting of Conservation Committee

National Museum of Natural History, 25, rue Münster, L-2160 Luxembourg (**cafeteria**), Monday, 26th September, 19:00-21:00 hrs.

SEH Internal meeting of Mapping Committee

National Museum of Natural History, 25, rue Münster, L-2160 Luxembourg (**Salle Découverte**), Monday, 26th September, 19:00-21:00 hrs.

Welcome party, get-together and others

See program or contact conference office.

Bus leave (Trier day)

Please note that on the day at Trier University (Wednesday, **28th September**), there will be a transfer leaving at **08:00 hrs** from: 9, place de la Gare, L-1616 Luxembourg (front to the local post office). Please be on time!

Local Organizing Committee

Edmée Engel, National Museum of Natural History Luxembourg; **Franz Gassert**, National Museum of Natural History Luxembourg; **Stefan Lötters**, Trier University & DGHT; **Silvia Macina**, DGHT; **Myriam Simon**, National Museum of Natural History Luxembourg; **Michael Veith**, Trier University.

Additional staff

Pascal Aachen, National Museum of Natural History Luxembourg (MNHN); **Cindy Anders**, Trier University; **Kerstin Bidinger**, Trier University; **Luigi Cipriani**, MNHN; **Corinne Colles**, MNHN; **Elsa Duarte**, MNHN; **Guy Eicher**, MNHN; **Btissam El Filali**, MNHN; **Jan O. Engler**, Trier University; **Geneviève Faber**, MNHN; **Katharina J. Filz**, Trier University; **Noël Fischbach**, MNHN; **Alexandra Geilen**, Trier University; **Jérôme Herr**, MNHN; **Ute Herrmann**, Trier University; **Isabelle Keller**, MNHN; **Nora Lisa Krutz**, Trier University; **Alessandro Luziotti**, MNHN; **Michael Mayer**, Trier University; **Andreas Mendt**, DGHT; **Patrick Michaely**, MNHN; **Bernadette Michel**, MNHN; **Valentin Mingo**, Trier University; **Corrado Modica**, Trier University; **Anibal Nogueira**, MNHN; **Kamila Nowak**, Trier University; **Michel Possing**, MNHN; **Julia Rautenberg**, Trier University; **Daniela Rössler**, Trier University; **Elena Rudolf**, Trier University; **Frank Schmoetten**, MNHN; **Lisa M. Schulte**, Trier, University; **Ulrich Schulte**, Trier University; **Norman Wagner**, Trier University; **Philine Werner**, Trier University; **Katharina C. Wollenberg**, Trier University; and the whole staff of the MNHN building.

Scientific board members

Salvador Carranza, Consejo Superior de Investigaciones Científicas, Barcelona, Spain; **Ylenia Chiari**, University of Montpellier 2, France; **Mathieu Denoel**, University of Liège, Belgium; **Edmée Engel**, National Museum of Natural History Luxembourg; **Trenton W.J. Garner**, Zoological Society of London; **Franz Gassert**, National Museum of Natural History Luxembourg; **Richard Griffiths**, University of Kent, UK; **Spartak Litvinchuk**, Russian Academy of Sciences, St. Petersburg, Russia; **Stefan Lötters**, DGHT & Trier University, Germany; **Russell Mittermeier**, Conservation International; **Andrew Storfer**, University of Washington State, Pullman, USA; **Simon Stuart**, IUCN SSC; **Zoltan T. Nagy**, Royal Belgian Institute of Natural Sciences, Brussels; **Miguel Vences**, University of Braunschweig, Germany; **Michael Veith**, Trier University, Germany.

DGHT-Nachzuchttagung

Immediately after the international scientific herp congress, from Friday to Sunday (30th September to 2nd October), the DGHT-Nachzuchttagung will take place at Trier, a herpetocultural conference with focus on keeping/breeding herps in captivity and watching them in the wild (conference language is German). Visitors of the SEH European Congress of Herpetology/DGHT Deutscher Herpetologentag are welcome to attending this meeting. Please contact the conference office.

Welcome to the SEH European Congress of Herpetology & DGHT Deutscher Herpetologentag

From 25th to 29th September 2011, the National Museum of Natural History Luxembourg (MNHN) and Trier University will host this special international meeting uniting two leading conferences in European Herpetology.

The **SEH European Congress of Herpetology** is held every two years in different European countries since 1979; this will be the 16th meeting. **Deutscher Herpetologentag** is equivalent to the annual meeting of the German herpetological society DGHT, taking place the 47th time this year. This will be the first joint meeting of these two important societies, an extraordinary milestone meeting in European Herpetology.

Not only two societies but also two congress venues! Most of the meeting will take place at Neumünster Abbey cultural centre next to the National Museum of Natural History in Luxembourg. Key note lectures and symposiums will take place during one day at Trier University at Trier-Petrisberg. Transfer on the Trier day is provided of course. However, please make sure to be on time! For bus leave see “What – where – when – who?”.

Scientific presentations include three lectures on topics of general interest by invited speakers and three key notes on current topics by invited speakers to which each a minisymposium is dedicated. Apart from these special lectures and key notes, a wide array of scientific talks (more than 60) will be given in parallel sessions. We have tried to group them and know that this is not absolutely satisfying in all cases. Also the scientific program does include more than 60 poster presentations – do not miss the poster session, as there will be no parallel program.

Besides scientific presentations, some social events will take place including the welcome party, opening ceremony and get-together. The last mentioned is dedicated to introduce you to some local culture. Other occasions to learn more about the region and its history include sightseeing tours in both Luxembourg and Trier; for those who are interested more in science, we offer a guided tour through the museum and a bat trip, as for herps it may be too late in the year.

If you have any further need of information, please contact the conference office or do not hesitate to contact any of the staff members (indicated by colored name tags).

At the point of writing these lines, we counted 251 registrations from 37 countries. We welcome all of you and hope that you will enjoy this extraordinary meeting!

Luxembourg and Trier, September 2011

Local Organizing Committee

Sunday – Monday – Program

Sunday, 25th September 2011			
15:00-19:00	Registration (MNHN, Foyer)		
17:00-19:00	Intern council meeting SEH (MNHN, Salle Découverte)		
19:00-21:00	Welcome party (MNHN, cafeteria)		
Monday, 26th September 2011			
08:00-09:30	Registration (MNHN, Foyer)		
	Luxembourg, Neumünster Abbey Salle Robert Krieps		
09:30-10:15	Opening ceremony C. Corti, President SEH, S. Lötters, Vice-President DGHT, G. Bechet, Director National Museum of Natural History, F. Gassert, Local Organizing Committee		
	INVITED TALK chair: F. Gassert		
10:15-11:00	M. Vences: Advances in integrative taxonomy and perspectives for automated species inventories: examples from herpetology		
11:00-11:30	Coffee break (MNHN, cafeteria)		
	Luxembourg, Neumünster Abbey Salle Robert Krieps	Luxembourg, Neumünster Abbey Salle Edmond Dune	
	ALL HERPS: MISCELLANEOUS 1 chair: D. Cogălniceanu	ALL HERPS: MISCELLANEOUS 2 chair: C. Corti	
11:30-11:45	R.W. Murphy & Y.-P. Zhang: Starting the global initiative to barcode amphibians and reptiles	M.A.L. Zuffi, L. Allegranti, V. Casu, C. Giannelli, O. Lanzoni, S. Marino, F. Messina & F.D. Nardi: Size and age related sexual dimorphism and functional asymmetries in the Ruin lizard <i>Podarcis sicula</i> from Tyrrhenian coastal areas (NW Italy)	

Program – Monday

11:45-12:00	R. Creemers, E. Goverse & J. van Delft: Detection and eradication of invasive herpetofauna species in the Netherlands	J. Bourke, W. Böhme & T.C.M. Bakker: Sexual dimorphism in Darwin's frogs (<i>Rhinoderma darwinii</i>)	
12:00-12:15	J. Carr: Application of IUCN's 'Species Vulnerability to Climate Change Assessment Framework' to European reptiles	Y. Itescu & S. Meiri: The island rule in turtles	
12:15-12:30	K. Mebert: The Dice snake, <i>Natrix tessellata</i> : biology, distribution and conservation of a Palaearctic species – a synopsis on the new volume in Mertensiella book series	V. Mashkarayan, M. Arakelyan, D.J. Harris & M.A. Carretero: Genetic diversity of <i>Testudo graeca</i> in Armenia and Nagorno Karabakh Republic	
12:30-14:00	Lunch break (Restaurant Melusina)		
	AMPHIBIAN CONSERVATION chair: R. Griffiths	REPTILE ECOLOGY AND POPULATION GENETICS chair: G.F. Ficetola	
14:00-14:15	R. Rannap, K. Suislepp & A. Lõhmus: Impacts of artificial drainage on amphibian breeding sites in hemiboreal forests	A. Strugariu, Ş.R. Zamfirescu, I.E. Popescu, I. Rosca & I. Gherghel: Preliminary data on the feeding ecology of the critically endangered Moldavian meadow viper (<i>Vipera ursinii moldavica</i>)	

14:15-14:30	R. Zollinger, R. de Nooij & A. Spitzen: The natterjack toad: creating space by giving space, a management plan	S.R. Zamfirescu, A. Strugariu, O. Zamfirescu, I. Gherghel & T. C. Sahlean: Activity pattern and microhabitat selection in <i>Vipera ursinii</i> from two different eastern Romanian ecosystems
14:30-14:45	W. de Vries & E. Govers: Combining amphibian monitoring with schooling in southwestern Spain	E. Argaña & N. Sillero: GIS and GPS application for the study of home ranges of sympatric Iberian lizards
14:45-15:00	R.E. Lloyd & D. Lermen: Current European biobanking activities for amphibian conservation – where we are and where to go	S. Scali, R. Sacchi, M. Azzusi, S. Daverio, T. Oppedisano & M. Mangiacotti: Homeward bound: which factors influence the homing ability of the Common wall lizard <i>Podarcis muralis</i> ?
15:00-15:15	M. Mediani, S. Fahd & J.C. Brito: Amphibian biodiversity hotspots in Morocco: conservation priorities	V. Gomes, A. Kaliontzopoulou & M.A. Carretero: Habitat use of congeneric lacertids in sympatry: testing for interspecific and sexual trends
15:15-15:30	R. Veen, L. Riviere, R. Dohogne, S. Bogaerts & R. Snep: Dig and dump: a cheap and simple method for population revitalisation in <i>Bombina variegata</i>	F. Gassert & A. Hochkirch: Genetic diversity of the Common wall lizard (<i>Podarcis muralis</i>) populations at their northern range margin

Program – Monday

15:30-15:45	A.R. Di Cerbo, M. Dino, S. Milesi & C.M. Biancardi: Long term monitoring of yellow-bellied toad populations in Italy	U. Schulte, A. Hochkirch & M. Veith: Hybridization between native and introduced populations of the Common wall lizard (<i>Podarcis muralis</i>) at the northern range margin	
15:45-16:00	S. Canessa, A. Arillo, F. Oneto, D. Ottonello & S. Salvidio: The decline of the Apennine yellow-bellied toad in Italy: conservation of an endangered amphibian between science and politics	L. Russell & T.J.C. Beebee: The effects of landscape on the population genetics of the sand lizard <i>Lacerta agilis</i> in the southern United Kingdom	
16:00-16:30	Coffee break (MNHN, cafeteria)		
	ALL HERPS: DISTRIBUTION MODELLING & CLIMATE CHANGE chair: D. Rödder	ALL HERPS: POPULATION GENETICS chair: S. Steinfartz	
16:30-16:45	P. de Pous, J. Carr & W. Cheung: Climate change and European reptiles: from large-scale spatial range shift projections towards a more realistic assessment of species responses	J.S. Hauswaldt, C. Angelini, E. Benavides, M. Gehara, A. Polok & S. Steinfartz: The genus <i>Salamandrina</i> (spectacled salamanders) from Italy: phylogeography and population genetics	
16:45-17:00	G.F. Ficetola, A. Bonardi, R. Sindaco & E. Padoa-Schioppa: Remoteness and richness of reptile communities in the Western Palaeartic	V. Zwahlen, K. Mebert, P. Golay, J.-C. Monney, T. Durand, G. Thierry, T. Ott & S. Ursenbacher: Color polymorphism and population genetic in the asp viper: is local selection stronger than gene-flow?	

17:00-17:15	E. García-Muñoz & M.Á. Carretero: "ECO-SCIENCE": Influence of climate change on the adverse effects caused by pesticides, using amphibians as a model. First results	O. Mettouris, A. Augustinos, K. Anagnostopoulou, P. Kornilios & S. Giokas: Population ecology and genetics of two syntopic newt populations (<i>Ichthyosaura alpestris veluchiensis</i> and <i>Lissotriton vulgaris graecus</i>) at a temporary pond in southern Greece	
17:15-17:30	N. Sillero & E. Argaña: Past, present, and future biogeographical patterns of Iberian herpetofauna	J.-P. Vacher & S. Ursenbacher: Genetic structure of populations of the Smooth snake, <i>Coronella austriaca</i> Laurenti, 1768, in Alsace, France	
17:30-17:45	F. Martínez-Freiría & J.C. Brito: Patterns of morphological variation in <i>Vipera seoanei</i> : using GIS and ENM for elucidating biogeographical scenarios across the Iberian Peninsula	J. Vörös, K. Szabó, I. Kiss, S. Schweiger & D. Jelic: Genetic structure of <i>Salamandra salamandra</i> in the Carpathian Basin	
17:45-19:00	Poster Session (MNHN, ground floor)		
19:00-21:00	SEH Conservation Committee (internal meeting) (MNHN, cafeteria)		
19:00-21:00	SEH Mapping Committee (internal meeting) (MNHN, Salle Découverte)		
19:00-21:00	Sightseeing tour Luxembourg		
19:00-21:00	National Museum of Natural History: guided tour		
19:00-24:00	Bat trip near Mayen		

Program – Tuesday

Tuesday, 27th September 2011			
	Luxembourg, Neumünster Abbey Salle Robert Krieps		
	INVITED TALK chair: Jos Kielgast		
09:00-09:45	R. Griffiths: Ex-situ programmes for amphibians: conservation or cosmetic surgery?		
09:45-10:00	A. Bauer on Seventh World Congress of Herpetology, Vancouver 2012		
	Luxembourg, Neumünster Abbey Salle Robert Krieps	Luxembourg, Neumünster Abbey Salle Edmond Dune	
	TROPICAL HERP DIVERSITY chair: A. Channing	WORKSHOP SEH CONSERVATION COMMITTEE	
10:00-10:15	Z.T. Nagy, C. Kusamba, L. Lokasola, J. Kolby & J. Kielgast: Survey of the reptile fauna in the Congo basin	Open session on herpetofauna monitoring in Europe	
10:15-10:30	J. Kielgast, Z.T. Nagy, C.Z. Kusamba, A.L. Lokasola & S. Lötters: Reed frog diversity in the green heart of Africa		
10:30-11:00	Coffee break (MNHN, cafeteria)		
11:00-11:15	S. Lotzkat: Deciphering reptile diversity in western Panama	Open session on herpetofauna monitoring in Europe (continued)	
11:15-11:30	M. Solé & I. Dias: Diversity patterns along an elevational gradient in “Serra Bonita”, southern Bahia, Brazil: an amphibian hot-point inside a hot-spot		

11:30-11:45	O. Hawlitschek: Herpetofauna of the Comoros: integrative taxonomy, phylogeography and conservation	Open session on herpetofauna monitoring in Europe (continued)	
11:45-12:00	L.F. Toledo, I. Sazima & C.F.B. Haddad: Anuran defensive strategies		
12:00-13:30	Lunch break (Restaurant Melusina)		
	REPTILE CONSERVATION chair: A. Stumpel	EVOLUTIONARY BIOLOGY chair: A. Storfer	
13:30-13:45	A. Reshetnikov, I. Chikhlyayev, A. Fayzulin, A. Kirillov, A.r Kuzovenko, E. Protasova, M. Skomorokhov, & S. Sokolov: Food and parasite interactions between native semi- aquatic snakes (<i>Natrix tessellata</i> and <i>N. natrix</i>) and the alien fish <i>Perccottus glenii</i>	R. Hendrix, B. Schmidt, M. Schaub & S. Steinfartz: Habitat dependent evolution of long versus short distance dispersal in an adaptively diverging salamander population	
13:45-14:00	B. Halpern, D. Brankovits & T. Péchy: Reintroduction of Hungarian meadow viper (<i>Vipera ursinii rakosiensis</i>)	G. Velo-Antón: Genetic drift and rapid evolution of viviparity in insular fire salamanders (<i>Salamandra salamandra</i>)	
14:00-14:15	M.J. Amaral, M.A. Carretero, R.C. Bicho, J.C. Sánchez- Hernandez, F.M. Guarino, R. Valente, A.M.R. Faustino, A.M.V.M. Soares & R.M. Mann: Lacertid lizards as bioindicators of pesticide exposure and toxicity in agricultural areas	K.C. Wollenberg, I.B. Wang, R.E. Glor & J.B. Losos: Recurrent convergence in axes of diversification in Hispaniolan trunk- ground anoles (<i>Anolis cybotes</i> species complex)	

Program – Tuesday

14:15-14:30	J. van Delft & A. van Rijsewijk: Embedding single-species conservation into an ecosystem approach: conservation of the Smooth snake in a southern province of the Netherlands	M. Arias-Villarraga, R. Randrianiaina, K.C. Wollenberg, D. Metzler, F. Glaw & M. Vences: Analysis of the morphological evolution of mantellid frogs from Madagascar (Mantellidae): a possible case of adaptive radiation	
14:30-14:45	P. Pafilis, K. Sagonas & E.D. Valakos: The impact of grazing on lizard populations from East Mediterranean islets	S. Reinhard & A. Kupfer: Life history and parental care strategies of caecilian amphibians	
14:45-15:15	Coffee break (MNHN, cafeteria)		
	REPTILE SYSTEMATICS 1 chair: A. Bauer	AMPHIBIAN ECOLOGY 1 chair: B.R. Schmidt	
15:15-15:30	O. Zinenko, N. Stümpel, B.S. Tuniev, A.G. Bakiev, L.F. Mazanaeva, O.V. Kukushkin, T.I. Kotenko, A. Strugariu, T. Duisebaeva, R.W. Murphy, N.L. Orlov, N.B. Ananyeva & U. Joger: Phylogeny of small European vipers	W. Hödl: Multimodal communication in anurans – news from Borneo, India and Austria	
15:30-15:45	M. Rajabizadeh, U. Joger & G. Nilson: Review of new findings in taxonomy and distribution of <i>Vipera</i> (s.l.) of Iran	T. Goldberg, E. Nevo & G. Degani: Amphibian larvae in various habitats at the southern border of their distribution	

15:45-16:00	S. Freitas, A. Perera, D.J. Harris, M. Arakelyan, F. Danielyan, C. Corti, Ç. Ilgaz, F. Ahmadzadeh, E. García-Muñoz & M.A. Carretero: Mingling among the <i>Darevskia raddei</i> complex	D. Cogalniceanu, P. Szekely, D. Szekely, D. Roşioru & C. Miaud: Reproductive ecology of the Eastern spadefoot toad <i>Pelobates syriacus</i>	
16:00-16:15	M. Barata : Extreme genetic diversity in <i>Atlantolacerta andreanskyi</i> : another mountain cryptic species complex?	J. Riemann, S. Ndriantsoa, M.-O. Rödel & J. Glos: Habitat fragmentation and frogs: how is species richness and functional diversity in hyper-diverse amphibian communities affected?	
16:15-16:30	P. Kornilios, E. Thanou, P. Lymberakis & S. Giokas: Phylogeography of the four-lined snake with the use of mtDNA markers and comments on its subspecific taxonomy	D. Dick: Spawning site selection of anurans in a dynamic floodplain	
16:30-16:45	E. Mizsei & B. Üveges: Confirming the presence of <i>Vipera ursinii</i> <i>graeca</i> in Albania with regards of a new locality – preliminary results	J. Crnobrnja-Isailovic, S.B. Curcic, D. Stojadinovic, N. Tomasevic-Kolarov, I. Aleksic & Z. Tomanovic: Size- and sex-dependent variation in diet of <i>Bufo bufo</i> from Serbia	
Luxembourg, Neumünster Abbey, Salle Robert Krieps (200)			
16:45-18:45	OGM SEH		
19:00-21:00	Sightseeing tour Luxembourg		
19:00-21:00	National Museum of Natural History: guided tour		
19:00-23:30	Wine cellar visit in Trier		
19:00-24:00	Bat trip near Mayen		

Program – Wednesday

Wednesday, 28th September 2011			
8:00	Bus transfer from Luxembourg to Trier (please note that the busses will leave on time) See „What – where – when – who?“		
	Trier University, Campus II, Audimax HS 11 + 12		
9:00-9:05	Welcome Note: M. Veith		
	KEY NOTES TO MINISYMPOSIA chair: M. Veith		
09:05-09:55	Y. Chiari: The long and short of turtle evolution		
09:55-10:45	S. Carranza: Phylogeography and evolution of the reptiles and amphibian around the westernmost Mediterranean Basin		
10:45-11:10	Coffee break (Trier University, Campus II)		
11:10-12:00	T.J.W. Garner, J. Bielby, J. Bosch, R. Farrer, F. Clare, D. Henk, S. Walker, S. Bovero, G. Sotgiu, G. Tessa, C. Angelini, M. Favelli & M. Fisher: The Ecology and evolution of <i>Eatrachochytrium dendrobatidis</i> in Europe		
12:00-12:15	J. Garcia Moreno: Introduction into the Amphibian Survival Alliance, an IUCN-led initiative		
12:15-13:30	Lunch break (Trier University, Campus II)		
	Trier University, Campus II, Audimax HS 11	Trier University, Campus II, Audimax HS 12	Trier University, Campus II, Ausimax HS 13
13:30-16:30	Minisymposium: PHYLOGEOGRAPHY OF EUROPEAN HERPS chair: S. Carranza	Minisymposium: TURTLE BIOLOGY chair: Y. Chiari	Minisymposium: AMPHIBIAN PATHOGENES chair: T.W.J. Garner
13:30-13:45	D. Guicking, U. Joger & M. Wink: Phylogeography of <i>Natrix</i> spp.	M. Vargas-Ramírez, H. Stuckas, O.V. Castaño-Mora & U. Fritz: Extremely low genetic diversity and weak population differentiation in the endangered Colombian river turtle <i>Podocnemis lewyana</i> (Testudines: Podocnemididae)	E.A. Courtois, J. DevilleChabrolle, P. Gaucher, M. Dewynter, J. Chave & D. Schmeller: Initiation of a long-term study of amphibian species in French Guiana: Project and first results from the Nouragues station

13:45-14:00	S. Bogaerts, F. Pasmans, D. Donaire, M. Biricik, A. Almasri, R. Alonso & S. Carranza: Fire in the Near East: phylogenetics and biogeography of the Near East fire salamander, <i>Salamandra infraimmaculata</i>	R.S. Sommer & Uwe Fritz: When the pond turtle followed the reindeer: effect of climate change on vertebrate diversity in Northern Europe at the end of the Ice Age	J. Bourke, T. Ohst, K. Busse, H. Werning, Y. Graeser, W. Böhme & J. Plötner: Chytrids in Chile
14:00-14:15	B. Wielstra & P. Arntzen: The postglacial interchange of two <i>Triturus</i> newts	V. Khabibullin: Local level as a weak link in wildlife conservation system: <i>Emys orbicularis</i> (L., 1758) in South Urals as an example	U. Tobler & B.R. Schmidt: Individual level and population level effects of amphibian chytridiomycosis
14:15-14:30	A. Krug & H. Proehl: Phylogeographic population structure of European Tree frogs (<i>Hyla arborea</i>) in Germany and adjacent areas	H. Seligmann: Frameshifted chelonian mitochondrial genes code for additional proteins in presence of antisense antitermination tRNAs and the special case of <i>Lepidochelys</i>	F. Pasmans, M. Muijsers, F. Vercammen, P. Van Rooij, K. Baert, F. Haesebrouck & A. Martel: Treatment of chytridiomycosis using antibacterial compounds: Columbus' egg?
14:30-14:45	A.-L. Ferchaud, S. Ursenbacher, L. Luiselli, D. Jelić, B. Halpern, Á. Major, T. Kotenko, J. Crnobrnja-Isailović, L. Tomović, I. Ghira, Y. Ioannidis, V. Arnal & C. Montgelard: From South to North: mitochondrial markers reveal an unexpected colonization route for vipers of the <i>Vipera ursinii</i> complex in the Palearctic region	G. Velo-Antón: Turtle carapace anomalies: the roles of genetic diversity and environment	A. Spitzen – van der Sluijs, A. Martel, C. Hallmann, W. Bosman, T. Garner, P. van Rooij, R. Jooris, F. Haesebrouck & F. Pasmans: <i>Batrachochytrium dendrobatidis</i> is a widespread pathogen in the Netherlands and in Belgium
14:45-15:15	Coffee break (Trier University, Campus II)		

<p>15:15-15:30</p>	<p>V. Helfer, C. Salamin, C. Miaud & L. Fumagalli: Mutive localized cryptic lineages in southern Alps – a revised phylogeography of the Alpine salamander (<i>Salamandra atra</i>)</p>	<p>M. Vamberger, H. Stuckas, D. Ayaz, L.F. Mazanaeva, H.G. Kami, A.A. Aoufi & U. Fritz: Phylogeography and population genetics of <i>Mauremys caspica</i> (Testudines: Geoemydidae)</p>	<p>A. Martel, C. Adriaensen, S. Bogaerts, F. Haesebrouck & F. Pasmans: Identification of a novel genus of Chlamydiales reveals high prevalence in invasive exotic bullfrogs (<i>Lithobates catesbeianus</i>) and association with disease outbreaks in captive urodelans (<i>Salamandra</i> sp. and <i>Neurergus</i> sp.)</p>
<p>15:30-15:45</p>	<p>L. Russell & T.J.C. Beebee: The effects of landscape on the population genetics of the sand lizard <i>Lacerta agilis</i> in the southern United Kingdom</p>	<p>S. Böhm: Habitat usage and short-term movements in the Twist-necked Turtle (<i>Platemys platycephala</i> Schneider 1792) during the late rainy season in the Nouragues Reserve, French Guyana</p>	<p>S. Reinhard, K. Hoffmann, K. Voigt, L. Olsson & A. Kupfer: Rhizomucormycosis in caecilian amphibians</p>
<p>15:45-16:00</p>	<p>M. Pabijan & M. Vences: Phylogeography of the arid-adapted Malagasy bullfrog, <i>Laliostoma labrosum</i> (Cope, 1868)</p>	<p>M. Raemy, M. Cheylan, Z. Owen-Jones, C. Faurre, U. Fritz, S. Ursenbacher: Hybridization between <i>E. orbicularis</i> ssp. in an old natural and a young artificial contact zones</p>	<p>Concluding and closing remarks by the chair</p>
<p>16:00-16:15</p>	<p>N. Stümpel & U. Joger: Phylogeny and phylogeography of Near and Middle East vipers (<i>Daboia</i>, <i>Montivipera</i> and <i>Macrovipera</i>)</p>	<p>J. Lourenco, J. Claude, N. Galtier & Y. Chiari: Dating the origin of the Testudinoidea</p>	

Wednesday – Program

16:15-16:30	Concluding and closing remarks by the chair	Concluding and closing remarks by the chair	
16:30-20:00	Sightseeing Trier (guided tour)		
20:00-23:30	Get-together (Trier University, Campus II, K101 (old chapel))		
23:30	Bus transfer from Trier to Luxembourg		

Program – Thursday

Thursday, 29th September 2011			
	Luxembourg, Neumünster Abbey Salle Robert Krieps		
	INVITED TALK chair: E. Engel		
10:00-10:45	A. Storfer: Landscape genetics: Insights into amphibian ecology and evolution		
10:45-11:00	SEH Mapping Committee & SEH Council: A map of maps of European amphibian and reptile distribution: First step towards a new European atlas		
11:00-11:30	Coffee break (MNHN, cafeteria)		
	Luxembourg, Neumünster Abbey Salle Robert Krieps	Luxembourg, Neumünster Abbey Salle Edmond Dune	
	AMPHIBIAN ECOLOGY 2 chair: S. Lötters	ALL HERPS: PHYSIOLOGY chair: P. Lymberakis	
11:30-11:45	M. Denoel, B.D'Hooghe, E. De Pauw, P. Kestemont, J.P. Thome & G.F. Ficetola: Making more with standard ecotoxicological tests: Using sets of behavioural markers to test the effect of Endosulfan on amphibian tadpoles	S. Jordan & C. Nowack: Show me yours – I'll show you mine! Lectin histochemical comparison of the olfactory epithelia of <i>Bombina orientalis</i> (Discoglossidae) and <i>Xenopus muelleri</i> (Pipidae)	
11:45-12:00	M. Cvijanovic, A. Ivanovic, N.T. Kolarov & M. Kalezic: Do closely related Crested newt species diverge in larval development?	A. Zagar, N. Osojnik, A. Vrezec & M.A. Carretero: Does presence of con- or hetero-specific male influence preferred body temperatures of two sympatric lacertids? The case of <i>Podarcis muralis</i> and <i>Iberolacerta horvathi</i>	
12:00-13:30	Lunch break (Restaurant Melusina)		

	AMPHIBIAN ECOLOGY 3 chair: K.C. Wollenberg	REPTILES: MISCELLANEOUS chair: S. Ursenbacher	
13:30-13:45	A. Channing, A. Schmitz & M. Burger: Genetic history and advertisement call variation in Dainty frogs (<i>Cacosternum</i>)	E. García-Muñoz, M.Á. Carretero, A. Kaliontzopoulou, V. Gomes, D. Carneiro, N. Sillero, F. Jorge, C. Rato N. & R. Ribeiro: Beyond preferred temperatures. Towards an integrated approach to lacertid ecophysiology under an evolutionary framework	
13:45-14:00	L.M. Schulte, S. Lötters & M. Veith: The smell of death: How poison frogs recognize their offspring's enemies by means of chemical cues	G. Vimercati, M.A.L. Zuffi & J. Nocchi: Areas of thermal activity in a wild population of the Moorish gecko <i>Tarentola mauritanica</i> from central Italy	
14:00-14:15	E. Twomey: Sexual selection in the mimic poison frog <i>Ranitomeya imitator</i>	M. Arakelyan & F. Danielyan: Syntopic populations of <i>Darevskia biparental</i> species in Armenia and Nagrono-Karabakh	
14:15-14:30	I. Starnberger, D. Poth, S. Schulz, M. Vences & W. Hödl: Multimodal signaling in African Reed frogs: an explorative approach for investigating a complex behavior	P. Wagner: Out of the blue: a preliminary review of the African blue-headed agamas (Agamidae: <i>Acanthocercus</i>)	
14:30-15:00	Coffee break (MNHN, cafeteria)		

	AMPHIBIAN ECOLOGY 4 chair: M Denoel	REPTILE SYSTEMATICS 2 chair: Z. Nagy	
15:00-15:15	I. Meuche, K.E. Linsenmair & Heike Pröhl: How many frogs do you have to kiss to find a prince?	A. Miralles, R. Vasconcelos, A. Perera, D. J. Harris & S. Carranza: An integrative taxonomic revision of the Cape Verdean skinks (Squamata, Scincidae)	
15:15-15:30	R. Manenti, G.F. Ficetola, M. Anghileri & F. De Bernardi: Salamandra salamandra breeding in subterranean habitats: local adaptations or behavioural plasticity?	V. Gvozdik, A. Crottini, J. Moravec, A. Romano, R. Sacchi & D. Jandzik: Another slow-worm species (<i>Anguis</i> , Anguidae) revealed south of the Alps	
15:30-15:45	E.T. Krause, S. Steinfartz & B.A. Caspers: Poor nutritional conditions during the early larval stage reduce risk-taking activities of Fire salamander larvae (<i>Salamandra salamandra</i>)	A.M. Bauer, M.P. Heinicke & T.R. Jackman: Phylogenetic relationships of the Gekko and Gehyra groups of geckos (Squamata: Gekkota: Gekkonidae)	
15:45-16:00	F. Crovetto, A. Romano & S. Salvidio: Comparing two non-lethal methods for dietary studies in salamanders	Y. Bucklitsch, W. Böhme & A. Koch: Systematic and evolutionary implications of monitor lizards' (Varanidae) scale structure using scanning electron microscopy (SEM)	
	Luxembourg, Neumünster Abbey Salle Robert Krieps		
16:00-16:15	Closing remarks Wolfgang Böhme		

Abstracts of talks by invited speakers in alphabetical order

R.A. Griffiths

Ex-situ programmes for amphibians: conservation or cosmetic surgery?

The contribution of ex-situ programmes to conservation is diverse. Ex-situ activities can comprise captive breeding and reintroduction, research on captive animals relevant to wild populations, public education and the generation of funds. Equally, the contribution that each of these components can make to a wider species recovery programme can vary enormously – some programmes may be almost entirely field-based, with a small head-starting component; others comprise large-scale captive-breeding facilities that contain self-sustaining populations. Their small body size, high fecundity, low maintenance requirements and ‘hard-wired’ behavioural repertoires make amphibians better subjects for conservation breeding programmes than many ‘higher’ vertebrates. However, as many species face complex threats that are not easily neutralized, the likelihood of successful reintroduction may be low. In particular, emerging infectious diseases present significant challenges to traditional ex-situ population management. Although zoos and aquaria are high-profile promoters of amphibian conservation, they support relatively few amphibian programmes compared to their involvement with other taxa. Nevertheless, ex-situ programmes for amphibians can represent good value for money in terms of conservation impact relative to the investment of resources. Although most species of amphibians bred in captivity are not species of conservation concern, several threatened species have been successfully reintroduced to the wild following ex-situ population management. Balancing in-situ and ex-situ approaches in amphibian conservation requires engagement with political, economic and social – as well as biological – issues, and remains a challenge to the successful delivery of conservation goals.

A. Storfer

Landscape genetics: Insights into amphibian ecology and evolution

Landscape genetics has rapidly emerged as a discipline that combines tools from landscape ecology, spatial statistics and population genetics to understand how landscape features influence gene flow and fine-scale population structure. Amphibians are particularly good candidate for fine-scale landscape genetics studies, given their often limited dispersal abilities and restricted geographic ranges. Because amphibians are also in global decline, many species are also targets for conservation and management. Landscape genetics studies can help researchers identify barriers to dispersal and gene flow, as well as landscape features that facilitate gene flow, particularly those that are cryptic or counterintuitive. These data can

help with design of nature reserves and/or maintenance of corridors that maintain population connectivity and thereby genetic diversity. Our work has largely focused on landscape genetics of amphibians in Western North America, with a variety of unexpected insights into amphibian ecology and evolution. For example, Coastal tailed frogs were surprisingly able to re-colonize the Mt. St. Helens volcanic blast zone within a generation, specifically through naturally regenerating habitats as opposed to human-assisted recovery areas. Further, although tailed frogs were thought to have strong stream-associated dispersal, dispersal routes generally occurred over land, making corridors a higher priority than maintaining stream buffers during timber harvest. Contrary to our predictions, rivers and grassland shrub habitat actually facilitated gene flow in blotched tiger salamanders, likely due to periodic flooding and post-fire habitat regeneration, respectively. Among giant salamanders, gene flow varied throughout the geographic range of Cope's giant salamander, lending caution to extrapolating from one part of a species' range to another. These examples will be discussed in detail, along with a discussion of future directions for landscape genetics studies.

M. Vences

Advances in integrative taxonomy and perspectives for automated species inventories: examples from herpetology

The past 20 years have seen exciting new developments in the field of taxonomy, and amphibians and reptiles have served as important model groups to develop various new techniques and concepts. One of the most influential developments although thus far largely neglected in Europe is the “General Lineage Concept” of species proposed by K. de Queiroz. According to the GLC there is general agreement among all species concepts as to what species are: independently evolving lineages at the population level. Species concepts of the past cease being conflictive but instead are now merely complementary criteria for species delimitation. This theoretical advance has allowed developing an integrative approach to taxonomy in which different characters or sets of characters are combined to obtain more rigorous species hypotheses. Implicit application of such “Integrative Taxonomy” combined with increased exploration of remote tropical regions has led to an enormous acceleration of species discovery and description. Especially the initial screening of molecular differentiation plays a key role, although such DNA barcoding should not be used as sole argument for erecting new species. The possibility to provide at a much faster pace more rigorous species hypotheses opens perspectives for a complete inventory of Earth's largely unknown biodiversity, but the new bottleneck is the Linnean shortfall: taxonomists are unable to provide scientific descriptions and assignment of Linnean names at the same pace as new candidate species are being discovered and delimited. Promising approaches to automated species delimitation and description are being proposed but are not yet sufficiently reflecting the complex biological reality of species.

Abstracts of talks in alphabetical order by first author

M.J. Amaral, M.A. Carretero, R.C. Bicho, J.C. Sánchez-Hernandez, F.M. Guarino, R. Valente, A.M.R. Faustino, A.M.V.M. Soares & R.M. Mann

Lacertid lizards as bioindicators of pesticide exposure and toxicity in agricultural areas

Lizards are among the least studied groups in ecotoxicology, and despite a recent increase in the number of studies, there is still a lack of knowledge regarding their response to environmental contamination. In Europe, lacertid lizards have been identified as potential model species for reptile ecotoxicology. The main question of our project was to assess if highly abundant lacertid lizards belonging to the genus *Podarcis*, could be used as bioindicator of pesticide exposure and toxicity in agricultural areas. To achieve this end, we used a three-stage tiered approach. The first tier took the form of a field survey to document both exposure and population endpoints of lacertids occurring in areas of intensive pesticide and usage and areas of negligible pesticide usage. The second tier was a mesocosm study in which naïve lizards were exposed to pesticides in a controlled experiment. Finally, the third tier included a laboratorial approach to the effects of one of the most common insecticides used worldwide, chlorpyrifos. We assessed pesticide impact using a comprehensive set of endpoints applied at different levels of biological organization, including behavioral, physiological, biochemical and histological biomarkers. The field work confirmed the difficulty of differentiation between the effect of contaminants and other (local) factors at the population level but our results suggest a difference in the metabolic activity between animals from reference and exposed locations. Animals from exposed fields seem to be in worst body conditions and in a deficitary energy balance when compared to animals from the reference locations. The results of the mesocosm study validated the correlative data obtained in the field survey. While the laboratory approach showed that environmentally relevant dosages of chlorpyrifos can affect *P. bocagei*. According to our data, *P. bocagei* seems to be a suitable indicator of sub-lethal exposure to pesticides.

M. Arakelyan & F. Danielyan

Syntopic populations of *Darevskia* biparental species in Armenia and Nagrono-Karabakh

Range overlap between species even at local scales is a defining trait in the biogeography of the Caucasian rock lizards of the genus *Darevskia*. Syntopy between populations of two biparental species is remarkable, especially when they are parental contributors of parthenogenetic species. The detailed analyses of such contact zones revealed that when biparental species *D. valentini* and *D. nairensis* are in syntopy, no hybrid forms arise. This is likely due to their different

reproductive periods. In contrast, the biparental *D. raddei* and *D. portschinskii* often produce hybrids, and the parthenogenetic species *D. rostombekovi* is also found in low numbers in the same sites which suggests that they are an occasional result of hybridization. Three sympatric zones between *D. raddei* and *D. portschinskii* are known for Armenia, Nagorno-Karabakh Republic (NKR) and Azerbaijan. Likely, the reproductive isolation between *D. raddei* and *D. portschinskii* is not complete which is contributing to reticular evolution. The hybridization events between syntopic *D. raddei* and *D. portschinskii* produce lizards with intermediate scalation and coloration characters when compared to allopatric populations. Among 207 lizards from Northern Armenia 59 (28.5%) *D. raddei* and 53 (25.5%) of *D. portschinskii* displayed intermediate morphology, 6 (2.86%) were parthenogenetic *D. rostombekovi* and 4 (1.93%) triploid hybrid females *D. raddei* × *D. rostombekovi*. Of 20 lizards with intermediate morphology 53 eggs and 35 young were obtained; 12 of young were similar to *D. rostombekovi* according to their external morphology. Among 143 lizards collected in another syntopic locality with *D. raddei* and *D. portschinskii* in NKR, 24 were hybrid females of uncertain morphological ascription. Among 66 *D. portschinskii* 18 individuals displayed modified morphological characters similar to *D. raddei* while among 43 *D. raddei* 14 individuals show morphologies close to *D. portschinskii*. Therefore, the successful combination of parental species with low reproductive isolation may be considered as the main factor explaining the origin of parthenogenetic species. For next steps of reticulate evolution, the combination of biparental and parthenogenetic species is required. Namely, in the sympatric zone of biparental *D. raddei* (40% of lizards) and parthenogenetic *D. rostombekovi* (35%), *D. armeniaca* (20%) and *D. dahli* (5%), triploid hybrids arise only between *D. raddei* and *D. rostombekovi* (18 hybrid males and 6 intersexes with both hemipenises and oviducts found). *D. raddei* from this locality showed polidiosis and coloration approaching *D. rostombekovi*.

E. Argaña & N. Sillero

GIS and GPS application for the study of home ranges of sympatric Iberian lizards

Few studies have analyzed spatially the home ranges of small lizards, namely in the Iberian Peninsula. We studied the home ranges of two Iberian lacertids (*Podarcis bocagei* and *P. hispanica*) in a sympatric situation. Fieldwork was performed in a small area (Moledo beach, 0.8 ha) in the North-West of Portugal, situated within an urban area, limited by buildings, stone walls and small fields of traditional agriculture. The study area is characterized by four stone walls, and a small beach area with rocks and vegetation. Both species are in strict sympatry and present high densities. We captured 76 lizards of both species, and the exact position was georeferenced with a professional Trimble GPS (horizontal error lower than 50 cm). We collected morphological measures, as well as tissue and blood samples; we marked the lizards with colored inks and release them in the same place of capture. We followed marked and unmarked lizards during seven days, making random paths around the stone walls and the beach. By visual contact and without recapture them, we recorded lizards' positions with the GPS and collected other information such as species, sex, age, social interactions, environmental temperature, humidity, and substrate temperature. We calculated the home ranges of marked individuals with minimum convex polygons (MCP), within a Geographical Information System. We analyzed

the relationships between males and females of different species and their movements. We recorded a total of 774 individuals of *Podarcis bocagei* (339 females and 435 males), of which 236 were marked, and 243 individuals of *Podarcis hispanica* (126 females and 117 males), of which 72 were marked. Preliminary results showed movements among distant walls and overlapping of female home ranges with the home ranges of several males.

M. Arias-Villarraga, R. Randrianaina, K. Wollenberg, D. Metzler, F. Glaw & M. Vences

Analysis of the morphological evolution of mantellid frogs from Madagascar (Mantellidae): a possible case of adaptive radiation

The rapid diversification of species from a single ancestor is usually associated with adaptive radiation. The anuran family Mantellidae, with more than 200 species and endemic to Madagascar and the Comoroan island of Mayotte may represent one of those examples. In this project, morphological, molecular and statistical approaches were used to investigate the ecology, the evolution and the systematics of this family of frogs. Almost complete information about larval morphology, molecular phylogeny and ecological characteristics was available for mantellid frogs. Specific adult morphology data and comparative studies including phylogeny, morphology and ecology were missing. The aim of this thesis was to assemble a dataset for the adult morphological characters (Munich Zoological Collection) and to test through a comparative analysis the following questions: (1) Are morphological changes in adult and larval stages coupled? (2) Is there a correlation between evolutionary rate changes in adult and larval morphology? (3) In a phylogenetic framework, is there a correlation between adult morphology and ecological parameters that would characterize the evolution of the Mantellidae as an adaptive radiation? The results showed uncoupled morphological changes between adult and tadpole morphology, despite the probable correlation between the rates of change for adults and tadpoles. The correlation between ecological variables and morphology on adults, suggest a preliminary evidence for adaptive radiation in the family Mantellidae.

M. Barata, S. Carranza & D.J. Harris

Extreme genetic diversity in *Atlantolacerta andreanskyi*: another mountain cryptic species complex?

Atlantolacerta andreanskyi is a very enigmatic lacertid lizard that, according to the most recent molecular analyses, may belong to the tribe Eremiadini. It is a mountain specialist, restricted to areas above 2500 m of the High Atlas Mountains of Morocco with apparently no connection between the different populations. In this respect, the situation in *A. andreanskyi* is similar to an archipelago, with the different “islands” being represented by mountaintops. As a result of this scenario, a very high level of genetic differentiation is expected between the different populations, although it is not clear how the Pleistocenic glacial cycles might have affected this species. In fact, the relatively large and apparently disjunctive range of *A. andreanskyi*

with populations occurring on isolated mountains suggests it may not be a single species. In order to test these hypothesis 137 specimens of *A. andreanskyi* were sampled from 5 different populations across the distribution range of the species (431 Km). A total of 2 gene fragments from mitochondrial DNA (12S, ND4) and 5 gene fragments from nuclear DNA (Pdc, Acm4, Cmos, Rag1, MC1R) were amplified. The results of the molecular analyses clearly show that all the populations analyzed present a very high level of genetic differentiation for the mitochondrial markers used and are also differentiated at the nuclear level. The taxonomic, biogeographic and evolutionary implications of these findings are discussed.

A.M. Bauer, M.P. Heinicke & T.R. Jackman

Phylogenetic relationships of the *Gekko* and *Gehyra* groups of geckos (Squamata: Gekkota: Gekkonidae)

The “*Gekko* group” has traditionally has included the arboreal and rupicolous Asian and Pacific gekkonid genera *Gehyra*, *Hemiphyllodactylus*, *Gekko*, *Lepidodactylus*, *Luperosaurus*, *Perochirus*, *Ptychozoon*, and *Pseudogekko*. Using multiple nuclear and mitochondrial genes, we show that these genera do not form a monophyletic group, but rather fall into two well-supported clades. The *Gekko* clade includes the diverse genera *Gekko* and *Lepidodactylus* as well as the gliding geckos, *Ptychozoon*, which are nested within the genus *Gekko*, and *Pseudogekko* and *Luperosaurus*, which are nested within *Lepidodactylus*. The close relationship of *Luperosaurus* to *Lepidodactylus* from Vanuatu and the Solomon Islands is particularly surprising given the superficial similarity of *Luperosaurus* to both the genus *Gekko* and *Ptychozoon*. Several geographically coherent species groups are evident in the genus *Gekko*. Previously morphologically-defined groups within *Lepidodactylus* are not recovered. The other “*Gekko* group” genera constitute a separate clade with *Gehyra* (35 species) as sister to *Hemiphyllodactylus* and *Perochirus* as sister to this pair. Within *Gehyra*, three geographically discrete clades are recovered, respectively concentrated in Asia, the Pacific islands, and Australia. Ancestral area analyses suggest that *Gehyra* originated in Asia, with a single colonization of Australia occurring in the mid-Cenozoic. This date places the time of *Gehyra* colonization prior to those of other Australian gekkonid geckos, but after the near-endemic pygopodoid geckos, a Gondwanan relictual group.

J. Bourke, W. Böhme & T.C.M. Bakker

Sexual dimorphism in Darwin’s frogs (*Rhinoderma darwinii*)

Most anurans exhibit some type of sexual difference in morphology or coloration that allows males and females to be readily distinguished, but in many cases, the functional significance of these differences is not well understood. We studied Darwin’s frogs and found variation in body size, microhabitat use, dorsal pattern and body coloration within and between sexes. Males showed a higher variability than females, which were mainly brown and of the most common pattern. Males also exhibited exclusive patterns (complete green and stained) and colour (green). Furthermore, males showed differences in microhabitat use, dorsal pattern and

body coloration between different reproductive stages. Brooding males a higher variability than non-brooding males, and occurred at higher temperatures and humidity than calling males. The results suggest that *R. darwinii* shows environmentally induced phenotypic plasticity in body colour and dorsal pattern, due to differences in microhabitat use between the sexes and different male reproductive stages. This ecological differentiation may be responsible for differences between the sexes and male reproductive stages, but sexual selection may also be involved as suggested by the higher variability of brooding males.

Y. Bucklitsch, W. Böhme & A. Koch

Systematic and evolutionary implications of monitor lizards' (Varanidae) scale structure using scanning electron microscopy (SEM)

Monitor lizards (Varanidae: *Varanus* spp.) are a relatively small group of squamate reptiles, which comprise the largest living lizards of the world. Being mainly carnivorous, monitor lizards are the top predators in most environments they inhabit. In Africa, Asia and Australia, monitor lizards inhabit a variety of different ecosystems from deserts to rainforests. They show specific ecological and morphological adaptations and can be strictly terrestrial, semi-aquatic or arboreal. Across all recognized subgenera of the genus *Varanus*, scale shape and structure were analyzed using scanning electron microscopy (SEM). Results show that a micro-ornamentation (ultradermatoglyphics) as seen in various squamate groups is not present in monitor lizards. Only in few, albeit unrelated, monitor species the dorsal scales exhibit a specific honeycombed micro-structure. The ecological meaning of this micro-structure, however, is unknown. Nevertheless, scale shape and extent of granula allow identification of single species, even among closely-related monitor species such as the *V. indicus* species group. In addition, the systematic affiliation of *Varanus spinulosus*, a rare monitor species from the Solomon Islands with a unique scale structure, is discussed in the light of current hypotheses about its phylogenetic position within the Varanidae. Due to its unique scale structure, in combination with other morphological evidence, a monotypic subgenus for this monitor species seems justified.

S. Canessa, A. Arillo, F. Oneto, D. Ottonello & S. Salvidio

The decline of the Apennine yellow-bellied toad in Italy: conservation of an endangered amphibian between science and politics

The Apennine yellow-bellied toad *Bombina pachypus* (Bonaparte 1838), a small anuran endemic of peninsular Italy, has suffered a marked decline throughout its range in the last thirty years and is now listed as “Endangered” in the IUCN Red List. Small scale studies and local reports have suggested several possible causes, including habitat loss (particularly ephemeral

wetlands), infection by *Batrachochytrium dendrobatidis* and collection by poachers. However, we are still far from a complete understanding of the problem, and therefore the conservation measures undertaken so far have been tentative at best. In the region of Liguria, at the north-western limit of the species' distribution, the species is rapidly disappearing. A captive breeding program, aimed at reintroduction, was started in 2008. In spite of considerable effort, so far few results of conservation value have been achieved. It is arguable that a better knowledge of the species' ecology, as well as optimised monitoring and management plans, would improve the chances of success: further investigation is needed in this sense, which in turn will require more time. Nonetheless, the scientific needs must be balanced against a range of other factors, while the allocation of funding to the project has been targeted at a political level. The yellow-bellied toad is now used by politicians as an example of "wasted" taxpayers' money, in a climate of growing hostility against environmental protection in Italy. Ecology, conservation and politics appear to contrast each other, while herpetologists try to define the actions needed to save the species from extinction. In this talk, we present the results of a study (partly funded by the SEH) which tries to determine the ecological requirements of this amphibian as well as its population dynamics, and suggest a number of possible actions that could prove useful in the near and long-term future.

J. Carr

Application of IUCN's 'Species Vulnerability to Climate Change Assessment Framework' to European reptiles

The International Union for Conservation of Nature (IUCN) has recently developed methods to assess the relative vulnerability to climate change impacts of species within a given taxon, known as the 'Species and Climate Change Vulnerability Assessment Framework'. These methods have been developed in response to the recognition that the globally recognised process of 'Red Listing™' does not adequately assess species' risks associated with climate change impacts, as well as the fact that the commonly practised 'climatic envelope modelling' approach does not take into account the biology and ecology of each species individually. The framework itself recognises three dimensions of a species' vulnerability to climate change impacts: 'Exposure', 'Sensitivity' and 'Low Adaptability', and allows categorisation of each species' vulnerability based on a score obtained within each. 'Exposure' quantifies projected climatic changes within a species current range based on up-to-date future climatic projections, while the remaining two dimensions use a combination of expert knowledge and published literature to identify taxon-specific traits that may increase climate change vulnerability, and to conduct species-level assessments against each. In this current project, the aim is to develop a modified, reptile-specific version of this framework and to pilot it on all European reptile species. This process will allow identification of taxonomic and geographic subsets of the focal group that are at an elevated extinction risk due to climatic changes, and will provide the groundwork for the assessment of species from other geographic areas. At this stage, we are requesting the contribution of herpetologists, with a good knowledge of one or more European reptile species, for the purpose of conducting assessments based on the modified framework and/or reviewing existing assessments to ensure accuracy and validity.

A. Channing, A. Schmitz & M. Burger

Genetic history and advertisement call variation in Dainty frogs (*Cacosternum*)

The genus *Cacosternum* occurs from Ethiopia to the southern tip of Africa. Dainty frogs, like many other small amphibians, have few external morphological characters that enable species to be identified with certainty in the field and especially in collections. Advertisement calls vary in this group, and we map calls on to a molecular phylogeny, to investigate call variation and species boundaries. The phylogeny is based on mt and nuc DNA sequences. The study indicates the presence of cryptic taxa even within well-known species. The evolution of advertisement calls in this group is discussed.

D. Cogalniceanu, P. Szekely, D. Szekely, D. Roşioru & C. Miaud

Reproductive ecology of the Eastern spadefoot toad *Pelobates syriacus*

We studied the reproductive effort and output in an Eastern spadefoot toad population from the Danube Delta Biosphere Reserve (Romania), at the northern limit of its range, during two consecutive years (2010 and 2011). In this species the males are larger than females in size, but not in weight. Age of adults ranged between 3-6 years. The percentage weight loss in females averaged 27.5 ± 5.4 (range 23-41), while males lost only a smaller fraction of weight of 4.0 ± 2.8 (range 0-10). The decrease in weight in females is proportional with size, larger females losing more weight than smaller ones. Initial weight of the females was a good predictor of the number of eggs deposited ($R^2 = 0.96$). Egg size and egg number were not significantly correlated to female size or weight loss.

R. Creemers, E. Govere & J. van Delft

Detection and eradication of invasive herpetofauna species in the Netherlands

Introductions of herpetofauna species are considered to be a major threat to indigenous amphibian and reptile species. In the Netherlands recent introductions of Italian crested newt (*Triturus cristatus*), American bullfrog (*Lithobates catesbeianus*), agile frog (*Rana dalmatina*) and Siberian ratsnake (*Elaphe schrenckii*) resulted in the settlement of viable and persisting populations. Effects on indigenous herpetofauna species may vary from hybridization (*T. cristatus* * *T. cristatus*), competition for resources like food and basking spots, predation and the transmission of diseases. In the Netherlands the recorded invasive species are still in an early stage of the colonization process and therefore eradication efforts are expected to be highly effective. Early warning systems for American bullfrog were developed in cooperation with Belgian counterparts. Eradication of the bullfrog population started in 2011 and the first results

will be presented, as well as the key-factors for successful eradication. Monitoring of Italian crested newt started in 2011 to determine the population size and the hybridization rate. Risk assessments and eradication programs are carried out in cooperation with stakeholders (local authorities, citizens, RAVON and the Invasive Species Team). The success of the eradication efforts is not only a methodological issue but is also based on effective communication strategies. Developing monitoring and early warning systems as well as risk assessments are urgent since success of eradication is determined by early detection in monitoring networks and early warning systems.

J. Crnobrnja-Isailovic, S. B. Curcic, D. Stojadinovic, N. Tomasevic-Kolarov, I. Aleksic & Z. Tomanovic

Size- and Sex-dependent variation in diet of *Bufo bufo* from Serbia

We analyzed the diet composition of adult Common Toads (*Bufo bufo*) from Serbia to test for correlation between adult body size and prey size, and to check existence of sex-based food niche partitioning in adults, due to the pronounced sexual size dimorphism in this species. Prey items were found in 142 preserved adult specimens of the Common Toad deposited in the collection of the Department of Evolutionary Biology of the Institute for Biological Research in Belgrade, Serbia. These toads were collected throughout the entire season in 3 consecutive years for an extensive study of sexual size dimorphism and life history variation. The sampling area was restricted to the foothills of Mountain Avala near Belgrade, in the vegetational zone of sclerophyllous oak forests. Analysis revealed that European Common Toad feed most frequently on insects, e.g., Coleoptera and Hymenoptera (Formicidae) in almost equal proportions. A number of other invertebrate taxa were included in the diet, though in frequencies less than 0.1. The results suggest that the Common Toad is neither a feeding generalist, nor myrmecophagous specialist, as bufonids were proclaimed to be. In depth analysis of sample from Serbia revealed absence of correlation between toad body size and number of prey ingested, but significant positive correlation between toad body size and prey size, high overlap of dietary preferences and concordance of distribution of various prey types between males and females. Furthermore, males consumed small prey items in significantly higher proportions than females, while the opposite was found for mediumsize prey, which suggests possible dietary niche partitioning in prey size rather than in taxonomical composition.

F. Crovetto, A. Romano & S. Salvidio

Comparing two non-lethal methods for dietary studies in salamanders

Conservation and animal welfare concerns may arise when the diet of amphibians has to be analysed in food-web or auto-ecological studies. Since its first application on amphibians (Fraser, 1976. Ecology, 57: 238-251), stomach flushing has become a widely-used and non-

lethal alternative to dissection. However other non-lethal methods, such as faecal analysis, may be used to study amphibian diet. In this study, we compared the information obtained through stomach flushing and faecal analysis from the same individuals of the European cave salamander *Speleomantes strinatii*. After performing stomach flushing in the field, thirty-one cave salamanders were kept at constant humidity and temperature to obtain faecal samples. Prey items were identified by the same researcher under a stereomicroscope, using identification manuals and reference collections. There were no differences in the number of taxa or in the number of prey items, but Simpson's diversity and equitability indexes calculated from stomach flushing were significantly higher in comparison to those obtained from faecal analysis. Moreover, Pianka's index ($O_{jk} = 0.58$) suggested a relatively low overlap between the two samples. This is the first study comparing stomach contents and faeces from the same individual salamanders. Results show that the information obtained from these two methods is different. Stomach flushing is more informative and should be preferred, in particular when specific relationships between salamander predators and their invertebrate prey have to be investigated.

M. Cvijanovic, A. Ivanovic, N. Tomasevic Kolarov & M. Kalezic

Do closely related Crested newt species diverge in larval development?

Exploring larval development and the pattern of size and shape changes during the ontogeny of closely related species provides an important insight into the processes that lead to the evolutionary diversification among species; for such studies the monophyletic clade of crested newts (*Triturus cristatus* superspecies) is an excellent model system. We analysed interspecific variations in the larval development by comparing larval developmental stages as well as the ontogenetic changes in body size and shape during the larval development of four crested newt species (*T. cristatus*, *T. dobrogicus*, *T. macedonicus*, *T. arntzeni*). Our results revealed significant variation in the larval developmental rate, as well as differences in the size and body shape among the analysed species. These divergences are concordant with interspecific differences in adult body form and species-specific ecological preferences. The differences in body shape that we found (wider and higher tail fin in *T. dobrogicus* and *T. cristatus*) may indicate that the body forms of larvae are subject to selection in aquatic environments, resulting in the same pattern of interspecific differences among species as in metamorphosed individuals.

M. Denoel, B. D'Hooghe, E. De Pauw, P. Kestemont, J.P. Thome & G.F. Ficetola

Making more with standard ecotoxicological tests: Using sets of behavioural markers to test the effect of Endosulfan on amphibian tadpoles

Short-term assessments of the effect of pollutants are mainly based on survival rates, providing reference values such as LC50. A variety of other sublethal biomarkers are available,

particularly in the field of behavioural ecotoxicology, but they are little used in this framework. In this study, we aimed at determining the complex behavioural responses of organisms in function of concentration and time, but also after removal of the pesticide. To this end, we used 240 amphibian tadpoles (*Rana temporaria*) placed by groups of ten in 24 tanks (days 1-4: 4 pesticide treatments: 0.5 - 0.0005 mg/l Endosulfan, 1 control and 1 vehicle-control: ethanol; days 5-8: recovery period with solvent and pesticide). We used generalized mixed models (GLMM), assuming binomial error distributions, to evaluate effects of the six treatments on the frequency of behavioural traits and survival. The six analyzed behaviours were affected by Endosulfan. Two were only displayed at the highest concentrations of pesticide: abnormal movement (swirling) and position (lying on the flank) whereas the others were differently exhibited. Particularly, exposed tadpoles moved, fed and breathed at water surface less than control tadpoles. They also remained in a more central position within their tanks. The six behavioural biomarkers detected effects for different concentrations and times of exposure. Lag effects were also found after removal of the pesticide. On the one hand, this study highlights that Endosulfan is highly toxic to amphibians at environmental concentrations in the days following introduction into water bodies. On the other hand, it shows that behavioural assessment can be done within the framework of typical LC₅₀ tests, thus maximizing test efficacy, and minimizing cost and animal use in laboratory research.

A.R. Di Cerbo, M. Dino, S. Milesi & C.M. Biancardi

Long term monitoring of yellow-bellied toad populations in Italy

Long-term studies of population dynamics are of great interest for life history theory, population ecology, wildlife management and conservation biology. The yellow-bellied toad (*Bombina variegata*) is reported to be a long-living and a long-breeder amphibian species, which uses temporary ponds or low-flow river pools as spawning sites. The reproductive success strongly depends on the availability and duration of suitable ponds, and therefore on climatic and environmental conditions. In Italy, the distribution of the species is limited to the northern regions with the western side of its range falling in Lombardy. In that region yellow-bellied toad populations are highly fragmented and relatively smaller than in other parts of its geographic range. Two monitoring programs started in Lombard Prealps on two populations living in temporary ponds (Parco dei Colli di Bergamo, PBC) and in low-flow river pools (Albino, ALB), since 1988 and 1994 respectively. During monitoring activity, the yellow-bellied toads have been captured, photographed, sexed and measured. Photos of the ventral pattern have been used for individual identification during recaptures. On the first occurrence, newly metamorphosed and young individuals have been aged (0-1 years old), while a minimum estimated age of 2 years has been assigned, at the first capture, to the sexually matured toads (SVL > 30 mm) by considering our observations and literature. Life tables, survival rates and the age-specific estimation of the minimum life expectancy of the populations have been calculated. A total of 94 yellow bellied toads (46 males, 34 females, 14 immature) were identified at the site PCB during the period 1988-2009 and 102 yellow-bellied toads (38 males, 46 females, 18 young toads) were recorded at site ALB between 1994 and 2011. In both sites, 79.8% and 67.7% of the

toads, respectively, have been recaptured at least once to a maximum of 18 years (2 males in PBC, 1 male and 1 female in ALB). Therefore these four toads were at least 20 years old at the last capture, but we can suppose they were even more aged (SVL >40 mm on the first occurrence). The estimated population size were 98 (95-108, PCB) and 112 (104-136, ALB), while the mean survival rates of adults were 82% (74-90%, PCB) and 83% (77-89%, ALB). Habitat selection, reproductive ecology and body condition index (BCI) of *B. variegata* have been also evaluated. From the quite complete overlapping results of these long term studies, we can derive that longevity, high survival rates, high site fidelity together with other physiological adaptations, like the possibility for females to lay small clutches or skip the season, are the most important factors for the survival of these small and isolated populations. BCI is almost constant during adult life, supporting the idea that longevity is associated to good health and reproductive power. Coherently to this view, the estimated residual life expectancy only tends to decrease after the 15th year. These long term studies can give important support information to the specific conservation action plans in Italy.

D. Dick

Spawning site selection of anurans in a dynamic floodplain

Temporal patterns of spawning activity and calling behaviour are already well described for European amphibian species. Beside the temporal differences in behaviour, spatial components influence spawning site selection of amphibians. Discussions and studies about meta-communities or niche patterns of amphibians increased during the last decade with increasing possibilities in modelling and statistic analyses. In Central Europe, these studies are mainly done in static landscapes and with common species but rarely in dynamic landscapes like floodplains, even though these are important primary and secondary habitats for amphibians. One reason might be that there are only few dynamic and hence natural floodplains left in Central Europe. The study presented here took place in one of the most natural floodplains in Germany, the Middle Elbe River in Saxony-Anhalt. Calling behaviour and spawning site selection of the native and threatened amphibian species *Bombina bombina*, *Rana arvalis*, *Pelobates fuscus* and *Hyla arborea* were investigated from March to July in 2010 and 2011. Habitat analyses were done with the program R to identify environmental parameters that influence presence and abundance of the species at the patchy distributed waterbodies within the heterogeneous landscape. Cluster analyses and Regression trees were used to reduce dimensions of variables and regressions were done with approaches for zero-inflated data. The results show that the species have different preferences of habitat structures e.g. in vegetation structure or water chemistry of the water bodies. Information about preferred habitat structures contributes directly to floodplain landscaping to improve amphibian habitats.

G.F. Ficetola, A. Bonardi, R. Sindaco & E. Padoa-Schioppa

Remoteness and richness of reptile communities in the Western Palaearctic

The knowledge of species distribution is largely incomplete, and known biodiversity can be particularly low in remote areas. The aim of this study was evaluating the importance of remoteness of a region in determining known species richness of reptiles. We analyzed the relationships between the richness of three major groups of reptiles (turtles, amphisbaenians and lizards), bio-climatic variables and accessibility in the Western Palaearctic. We mapped on a grid the presence records for 480 native species in the Western Palaearctic, and we used spatially explicit methods (spatial eigenvector mapping and Bayesian autoregressive models) to build regression models. For each grid cell, accessibility was measured as the average travel time to the nearest city. Reptile richness was highest in areas with wide elevation range, high average temperature and annual precipitation. Reptile richness was also associated with intermediate cover of natural vegetation, and limited evapotranspiration. Furthermore, when taking into account environmental variables, known richness was strongly related with accessibility, and decreased in the most remote areas. We identified areas where climatic features would suggest high reptile richness, but in which accessibility is low. In these areas, actual richness is probably higher than the known values. Within the study area, known reptile richness is lower than expected in the Western North Africa, in the South of the Arabian peninsula and in the Central Asia mountains. Integrating accessibility measures into ecological models can help to identify areas where focusing monitoring and conservation actions.

S. Freitas, A. Perera, D.J. Harris, M. Arakelyan, F. Danielyan, C. Corti, Ç. Ilgaz, F. Ahmadzadeh, E. García-Muñoz & M.A. Carretero

Mingling among the *Darevskia raddei* complex

Due to its geographic location, the Caucasus region connects species from three different continents in a heterogeneous landscape, creating an environment prone to the development of speciation events and multiple endemisms. Among them, the lacertid genus *Darevskia* is a group of rock lizards radiating and diversifying in the region. Among their highly polymorphic members a number of parthenogenetic forms are present result from the hybridisation between bisexual *Darevskia* species. However, the origin of these forms lacks an explicit spatiotemporal context. One of the most interesting bisexual species in the group is *Darevskia raddei* which is responsible for the motherhood of some unisexual forms, namely *D. unisexualis*, *D. uzzeli* and *D. bendimahiensis* and *D. sapphirina*). Furthermore, this species is considered conspecific to *D. nairensis* and *D. (raddei) vanensis*, two forms of unclear status which link to the parthenogenetic forms need to be clarified. This, this study aims to reach a global comprehension of the three putative bisexual taxa within of the *D. raddei* complex (*D. raddei*, *D. nairensis* and *D. (raddei) vanensis*), and their phylogenetic relationships with the parthenogenetic forms they theoretically parented. A phylogenetic analysis was conducted on samples of the *D. taddei* complex, ranging from Turkey, Armenia, Georgia and Iran. Maximum Likelihood and Bayesian methods were applied on a combination of mitochondrial and nuclear

markers. Namely, three mtDNA (cytochrome b, ND4 and 12s) and two nDNA (MC1R and c-mos) markers were used. Our results confirm that *Darevskia raddei* (sensu lato) is the proposed maternal species for at least *D. unisexualis*, *D. uzzeli*, *D. bendimahiensis*, *D. sapphirina* and *D. rostombekowi*, as already supported by previous studies. However, it does not support a genetic differentiation between the three forms described within the complex, which are to be considered conspecific. Moreover, there is reinforced evidence that the three parthenogenetic forms considered arose more than once in the history of the genus, from different lineages of the bisexual parents.

E. García-Muñoz & M.A. Carretero

“ECO-SCIENCE”: influence of climate change on the adverse effects caused by pesticides, using amphibians as a model.

First results

Over the past thirty years, climate change has produced an enormous biodiversity loss as well as a shift in species distribution ranges. Amphibians epitomize the modern biodiversity crisis, and global climate change may be directly and indirectly responsible for amphibian's decline. Although amphibians are considered less sensitive to direct temperature shifts than other groups, small changes can trigger cascade effects when thermal disturbance is combined with pollutants. Among these indirect consequences, temperature changes have been demonstrated to modify the lethal and sublethal effects of contaminants in biota. Most studies addressing the adverse effects posed by contaminants to several amphibians species have been performed at moderate, constant ambient temperature of approximately 20 °C, which is an oversimplification of what happens in the environment. In fact, there is fragmental but strong evidence suggesting that temperature induces changes in acute toxicity of chemicals. This information is essential because only the interaction between environmental factors and the ecosystem into which the pesticides are introduced will determine the real ecotoxicological implications of such pesticides. Much of the interest on amphibian global declines is currently focused on the role of pesticides as single causative factors. Now, studies as the one proposed here, exploring the interactions between climate change and pesticides contamination, will provide a better understanding of the responses of species to future environmental changes and, hence, the basis for prevention, management and mitigation measures. As a first step in this research, we studied the effects of a widespread fungicide (Carbendazim) in different developmental stages of *Bufo calamita*, a widespread amphibian, at three different temperatures. Result showed that an increase of temperature turn lethal sublethal concentration. In addition, the combined effects of temperature and chemical increase the proportion of malformed individuals. These first results, hence, support the hypothesis of synergy between contaminants and global warming. The implications of climate change on the adverse effects caused by pesticides in amphibians are discussed.

E. García-Muñoz, M.A. Carretero, A. Kaliontzopoulou, V. Gomes, D. Carneiro, N. Sillero, F. Jorge, C. Rato N. & R. Ribeiro

Beyond preferred temperatures. Towards an integrated approach to lacertid ecophysiology under an evolutionary framework

Of the variables shaping the ecophysiology of lacertid lizards, undoubtedly, temperature has been the one attracting most attention. Certainly, preferred body temperatures (T_p) are well known to correlate with several physiological optima and to carry substantial phylogenetic inertia. However, much less is known on their water ecology, although some studies in other lizard families suggest that body temperature and evaporative water loss (WI) may trade-off. Both aspects together with their evolutionary trajectories are needed to wholly understand the ecophysiology and biogeography of lacertid species. By integrating thermal and water ecology data, mechanistic models of potential species distribution could be elaborated. Here, we analyse both ecophysiological traits in the *Podarcis hispanica* species complex, a group whose phylogenetic relations have been recently assessed. For a total of 14 lineages of the complex, two laboratory tests were performed: the classic T_p experiment using a photothermal gradient; and determination of WI rates in sealed chambers. Significant differences were detected for both thermal and hydric parameters even between sympatric species. Uncorrected results for thermal and hydric traits were inversely related supporting a trade-off. However, phylogenetically distant groups deviated from the common trend recommending phylogenetic correction. The importance of these results is discussed. In the near future, models based on ecophysiology may overcome some of the limitations of correlative models, especially when making inference of causation (species interactions) and when extrapolating to novel situations (climate change).

F. Gassert & A. Hochkirch

Genetic diversity of the Common wall lizard (*Podarcis muralis*) populations at their northern range margin

The common wall lizard is warmth – loving species which is mainly spread in the northern Mediterranean area. Its northern area of circulation spreads over the north of France, Luxembourg, along the Maas in Belgium, the south of the Netherlands, scattered appearances in Germany in the Eifel area and the Rhine area as far as Bonn. North of the Alps, the common wall lizard is a typical species of wine-growing regions. In Luxembourg, wall lizards are common along river valleys, whereas the species is largely absent in central and northern parts of Luxembourg. Within its native range the species shows a clear phylogeographic structure. To reconstruct the invasion history and the genetic diversity of the populations, 311 lizards (two to thirty individuals per population) were captured by hand or by noose within 31 populations of *P. muralis* in Luxembourg ($n = 162$), Germany ($n = 17$), France ($n = 93$), Italy ($n = 12$), Croatia ($n = 9$) and Belgium ($n = 18$). We sequenced for all populations a part of the mtDNA (cytochrome *b*) and genotyped all individuals at 10 microsatellite loci. We tested our data for the occurrence of

null alleles with Micro-Checker 2.2.3 and for linkage disequilibrium with Fstat 2.9.3. STRUCTURE v 2.3.1 was used to analyse the genetic structures among subpopulations. The admixture model was used. We chose the correlated allele frequency model. A F_{ST} based AMOVA with 9999 iterations was performed in GenAlEx 6.41 with the three STRUCTURE based genetic clusters as populations. In our case 15 clusters have been generated over all 31 populations, among 7 clusters in Luxembourg. By means of the statistical methods, a separation of the North Luxembourg and the South Luxembourg populations is shown. The immigration routes are clearly demonstrated for the northern populations by means of the mtDNA data.

T. Goldberg, E. Nevo & G. Degani

Amphibian larvae in various habitats at the southern border of their distribution

A study on six species of amphibian larvae, which grew and completed metamorphosis at fourteen different breeding sites in northern Israel, was conducted over several years. The sites included ephemeral ponds (rain pools), rock pool holes, springs and a stream. Most breeding sites studied, permanent and ephemeral habitats, contained *Salamandra infraimmaculata* (family: Salamandridae) larvae, although at different periods of the year. The larvae of *Hyla savignyi* (family: Hylidae), *Bufo viridis* (family: Bufonidae), *Rana bedriagae* (family: Ranidae), *Pelobates syriacus* (family: Pelobatidae) and *Triturus vittatus vittatus* (family: Salamandridae) inhabited mainly the ephemeral ponds. Many amphibian species, especially those inhabiting unpredictable environments, exhibited phenotypic flexibility in growth rate prior to metamorphosis and the period of metamorphic climax. This adaptive strategy allows individuals to optimize the probability of successfully emerging from the larval environment. In some breeding sites, only one species was found, e.g., *S. infraimmaculata*, while in others, mainly ponds, all or some of the amphibian species native to Israel were observed. The periods, during which some of the species inhabited the pools, overlapped. In a comparison study carried out over four years, the larval size and growth rate of individuals of the same species, residing in the same water bodies, were found to be different. We propose that this difference in development may show flexibility in larval growth and development, which enable them to survive in different habitats and hydroperiods under extreme conditions at the southern border of its distribution.

V. Gomes, A. Kaliontzopoulou & M.A. Carretero

Habitat use of congeneric lacertids in sympatry: testing for interspecific and sexual trends

Among the classic dimensions of the lizard ecological niche – space, time and food – the first is considered the main one driving ecological differentiation in lacertids. Under the ecomorphological paradigm, divergent body morphologies may be expected to reflect different microhabitat preferences. At the interspecific level, sympatric congeneric forms of similar body

size but different body shape may be predicted to show at least some degree of ecological segregation. Within species, since sexual dimorphism constitutes the major dimension of morphological variation, intersexual variation in habitat use could also occur. Here, we test both hypotheses using two members of the *Podarcis hispanica* species complex, *P. bocagei* and *P. hispanica* type 1A. These two forms are closely related phylogenetically, being sister taxa, and their distributions widely overlap both at geographic and local level. However, both forms markedly differ in body shape, a pattern particularly prominent when considering the degree of head flattening, where *P. hispanica* type 1A is very flat whereas *P. bocagei* presents a much higher and rounded head. In one of these sites (Moledo, northern coastal Portugal), both forms are found in strict syntopy across a sandy area with rocks and sparse vegetation and a zone with agricultural fields delimited by stone walls. During May 2011, we performed normalised transects recording microhabitat (height to the ground, slope angle, diameter of the rock, wall height and substrate) and habitat use (percentage of bare soil, vegetation and rocks in the surrounding area - 2m) variables associated to lizard observations considering species and sex, as well as time and environmental temperature. We used factorial ANOVA, log-linear analyses and multivariate techniques to assess differences between species and sexes and to represent them on a multivariate space. Both *Podarcis* forms significantly differed in height to the ground, slope angle, diameter of the rock and wall height as well as in general habitat use. Significantly, the flattened *P. hispanica* type 1A used rocks and vegetation in similar proportions while the high headed *P. bocagei* used vegetation more frequently than rocks. Log-linear analysis also showed differences between sexes in the choice of substrate at the observation spot. The ecological differentiation observed between both forms is in accordance with the predictions made based on the ecomorphological paradigm and yields a potential mechanism that contributes to the syntopic coexistence of both forms. However, since a substantial part of the females were pregnant, further research outside of the reproductive season is still needed to confirm the ecological significance of the observed intersexual variation.

V. Gvozdik, A. Crottini, J. Moravec, A. Romano, R. Sacchi & D. Jandzik

Another Slow-worm species (*Anguis*, Anguillidae) revealed south of the Alps

Four species of legless anguillid lizard genus *Anguis* have been currently recognized: *A. fragilis* from western Europe, *A. colchica* from eastern Europe and western Asia, *A. graeca* from southern Balkans and *A. cephalonica* from the Peloponnese. Slow worms from the Italian Peninsula were assigned to *A. fragilis* based on morphology despite the fact that the region served as an important glacial refugium and speciation centre for European fauna and flora. We used mitochondrial (*ND2*, *tRNAs*) and nuclear (*PRLR*) DNA sequences to address question of systematic and phylogenetic position of the Italian slow-worm populations. Our phylogenetic analyses revealed a distinct clade in mtDNA placed on a basal position within the genus *Anguis*, sister to *A. cephalonica*. Based on deep genetic divergences in mtDNA and distinct haplotypes in *PRLR* within the genus *Anguis* we propose species level for this clade. The newly recognized species is distributed throughout the Italian Peninsula to the southern slopes of the Alps and south-eastern France. Several names are available for the new species and the nomenclatural assignment is still under debate.

B. Halpern, D. Brankovits & T. Péchy

Reintroduction of Hungarian meadow viper (*Vipera ursinii rakosiensis*)

Rough estimations were putting surviving numbers of Hungarian meadow viper (*Vipera ursinii rakosiensis*) below 500 individuals, with three major occurrences in Hungary and one recently discovered population in Romania. MME BirdLife Hungary together with relevant National Parks started a complex conservation program in 2004, supported by the Ministry of Environment and the EU LIFE-Nature fund. Viper Conservation and Breeding Centre was started with 10 adult individuals, collected from 4 different populations, and after seven successful breeding periods number of vipers reached nearly 700. First reintroduction took place in March 2010, releasing 30 snakes into a reconstructed habitat in Kiskunság National Park. Snakes were released by removing them together with their artificial burrow, at the end of the hibernation period. During regular monitoring we checked these burrows by using pipe-camera. Other amphibian and reptile species started to use these burrows sometimes together with vipers. We recorded *Triturus dobrogicus*, *Bombina bombina*, *Pelobates fuscus*, *Podarcis tauricus*, *Lacerta viridis*, *Natrix natrix* and *Coronella austriaca*. We recorded vipers 54 times during these visits, 44 times in or around these burrows. Altogether 9 individuals were identified by photos taken during these events. We found remains of one viper partly consumed by a predator. Ongoing genetic analysis of this sample may reveal identity of this snake. In late February 2011 additional 70 vipers were released in 15 burrows at the same site. We plan to continue release of snakes in new sites from 2012.

J.S. Hauswaldt, C. Angelini, E. Benavides, M. Gehara, A. Polok & S. Steinfartz

The genus *Salamandrina* (spectacled salamanders) from Italy: phylogeography and population genetics

Spectacled Salamanders (genus *Salamandrina*) belong to the oldest lineage of extant salamandrids and are endemic to peninsular Italy and are found along the Apennine chain. The northern species, *S. perspicillata*, ranges from Liguria to Campania and the southern, *S. terdigitata*, from Campania to Calabria. While morphologically the two species are extremely similar, genetically, they clearly belong to two well differentiated lineages. We used mtDNA sequences, two nuclear coding genes and ten microsatellite loci, to genotype a total of 750 salamanders from 36 populations across the range of the genus. We have conducted two approaches to estimate the timing of the split of the two species, and our estimates are in support of a more recent divergence event than previous studies have indicated. In a population from the contact zone in Campania we identified interspecific hybrid individuals. While the northern species shows indication of demographic expansion, no evidence for this was found in the southern species. We have identified a potential glacial refugium of the northern species in an area north of the Lepini mountains. With high resolution microsatellite loci, we have also been able to find genetic structure even on a small geographic scale, such as the Lepini Mountains, reflecting the results of mark-recapture studies indicating high site-

fidelity. We are comparing the phylogeographic pattern of *Salamandrina* with those of other amphibian taxa with a similar distribution range.

O. Hawlitschek

Herpetofauna of the Comoros: integrative taxonomy, phylogeography and conservation

The Comoro archipelago in the Western Indian Ocean is inhabited by a relatively highly endemic herpetofauna, which is species-poor but divers at a higher taxonomic level. We recognize 7 families with a total of 28 species, 13 of which are endemic. We assessed threat status for endemic species according to the IUCN Red List criteria in the course of the Madagascar and Comoros reptile assessment using direct measurements of the extents of suitable areas. Invasive species and habitat degradation were identified as major threat factors, and 6 endemic species were assigned a threat status. However, the degree of endemism is higher than previously thought, as we could show in integrative taxonomic studies. We present the examples of Comoroan *Paroedura* geckos and *Lycodryas* snakes and discuss the ranking of island forms as species or subspecies. The results of these studies will be used further to analyze the phylogeography of Comoran reptiles, track the colonization histories of the islands and calibrate molecular clocks.

R. Hendrix, B. Schmidt, M. Schaub & S. Steinfartz

Habitat dependent evolution of long versus short distance dispersal in an adaptively diverging salamander population

The adaptation of individuals to new or different habitat conditions can lead to adaptive divergence of populations resulting finally into ecological speciation. It is obvious that many life history traits directly linked to such an adaptation process will change, but it has been rarely addressed in how far non-obviously linked life history traits can change in the course of habitat specific adaptation. Dispersal is a major life history trait that by changing the composition of individuals in populations directly or indirectly affects the ecology and evolution of species tremendously. Although habitat structure by itself can have a strong influence on dispersal, it has been so far not investigated whether dispersal patterns change during the process of habitat dependent adaptive divergence/speciation. In order to test for this we have analysed dispersal of a terrestrial salamander population that by using different larval habitat types (streams versus ponds) has diverged into two distinct habitat-associated genetic groups. By combining mark-recapture analyses with multilocus genotypic data we can show that dispersal of adult salamanders differentiated according to habitat adaptation. Pond adapted salamanders clearly displayed long distance dispersal that fits well with an unstable and less predictable environment, whereas stream adapted individuals showed a pattern of short distance dispersal that should be expected in association with a more stable environment.

W. Hödl

Multimodal communication in anurans – news from Borneo, India and Austria

Multiple cues or signals play a vital role in intraspecific communication in many more anuran species than previously thought. Visual signals can act as an additional or complementary mode of communication in noisy habitats. Foot-flagging behavior has been observed in 15 species from 5 different families mainly living along fast-flowing mountain streams that generate a continuous broadband background noise. Studies conducted in Borneo demonstrate that the foot-flagging species *Staurois parvus* avoids acoustic interference of ambient stream noise by using call frequencies less masked by the background and utilizes accompanying visual displays to signal the readiness to defend calling sites. Recent results from India show that a further foot-flagging species *Micrixalus saxicola* from the Western Ghats displays a series of visual signals during male-male aggressive behavior. Receiver responses from acoustic- vs. multimodal playback presentations give evidence that also the vocal sac acts as a visual cue. In a less noisy but more crowded habitat in Austria, male *Rana arvalis* develop conspicuous blue body coloration during the breeding season. Behavioral experiments with blue and brown color morphs provide first evidence that the blue coloration acts as an intrasexual signal to avoid mismatch during mating similar to release calls of other anurans. These studies of multimodal signals and coloration displays give important insights into the diversity of anuran communication strategies and broaden our knowledge of factors influencing signal evolution.

Y. Itescu & S. Meiri

The island rule in turtles

Body size of animals is affected by many physiological and ecological drivers. Large body size carries some advantages (e.g. greater starvation resistance and digestion efficiency, cheaper terrestrial travel) but small body size has its own advantages (e.g. fast heating rates). It is often claimed that small animals get larger and large animals get smaller on islands. The centralizing tendency of body size in island populations relative to mainland populations is commonly known as the “island rule”. Body size patterns are thought to be stronger on small and remote islands by limiting resources as well as the number of predator, competitor, and prey species. In recent years some studies challenged these hypotheses. The mechanisms that are driving the island rule in particular, and size evolution on islands in general are also hotly debated. In reptiles, the island rule was previously studied in snakes and lizards. Size in these groups seem to evolve differently, with snakes following the rule, while lizards reverse it (size becomes more extreme on islands). Lomolino (2005) included an unpublished dataset of turtles in his analysis of the island rule in all terrestrial amniotes, showing they follow the expected pattern, and claimed a general rule for vertebrates. His data were never subsequently published. Size evolution in relation to isolation and area were never studied in turtles. We collected literature data on mean carapace length (CL) and maximum carapace length (MCL) of 274 turtle species. Twenty four of these are endemic to islands. Our data encompass all turtle families and all genera that hold both continental species and insular endemic species. We tested whether

the Island rule applies in turtles by comparing the mean CL and mean MCL of insular and continental species both within genera (11 genera with both insular and mainland species) and between sister clades. The results run opposite to the predictions of the island rule, with a reduced major axis regression of island vs. mainland body size having a slope steeper than one. Gigantism in turtles on islands (e.g. Galapagos, Aldebra) is well known. It seems that such insular giants are “pushing” the slope of the regression upwards. Fossil, oceanic island turtles likewise show no tendency towards dwarfism. The absence of large predators from such islands seems to have either driven the evolution of large body size, or relaxed selection pressure for small size for turtles. Alternatively, large size may have favored dispersal to oceanic islands, and thus represents a founder event. We question the generality of the island rule, and suggest that similar selective agents can lead to different results in different taxa and on different islands.

S. Jordan & Ch. Nowack

Show me yours – I’ll show you mine! Lectin histochemical comparison of the olfactory epithelia of *Bombina orientalis* (Discoglossidae) and *Xenopus muelleri* (Pipidae)

Both frogs investigated, *Bombina orientalis* and *Xenopus muelleri*, possess three distinct olfactory organs. As commonly known, in frogs the sense of smell is located in subdivided nasal cavities. The uppermost or principal chamber incorporates the main olfactory organ, while the vomeronasal or Jacobson’s organ is located within the lowermost chamber, the cavum inferius. The additional (third) olfactory system of Pipidae such as *X. muelleri*, the so called *middle chamber epithelium* (MCE), is also relatively well-known, as frogs of the genus *Xenopus* are often used as model organisms. The MCE is located – as its name implies – within the middle chamber. Surprisingly, in members of anuran groups other than Pipidae (as for example *B. orientalis*), another third olfactory epithelium is found – the *recessus olfactorius* (RO). The RO is located at the frontal bottom of the principal chamber, often within a pit or groove. This area is also referred to as the *recessus ventromedianus cavi principale* by some authors, but in general the organ remains unnoticed and therefore very few information is available. One essential unanswered question is how the RO and the MCE are related. Morphological data indicate that the two organs might be homologous structures (Helling 1938), whereas developmental studies conducted by Paterson (1951) point into the opposite direction. The aim of the presented work was to gain new data regarding the characteristics of the RO of *B. orientalis* with the aid of lectin histochemistry. A second step includes the comparison of these findings with data descending from the MCE of *X. muelleri*. The lectin DBA (*Dolichos biflorus* agglutinin) was used to stain transverse paraffin sections through the nose of specimens from both genera in order to compare the staining patterns of the olfactory epithelia. The resulting data were analyzed with respect to the possible homology of RO and MCE. References: Helling, H. (1938). Das Geruchsorgan der Anuren, vergleichend-morphologisch betrachtet. Z. Anat. Entwicklungsgesch., 108, 587-643. Paterson, N. F. & E. Hindle (1951). The nasal cavities of the Toad *Hemipha carvalhoi* Mir.-Rib. and other Pipidae. Proc. Zool. Lond., 121, 381-415.

J. Kielgast, Z.T. Nagy, Ch.Z. Kusamba, A.L. Lokasola & S. Lötters

Reed frog diversity in the green heart of Africa

Amphibians are a globally species-rich group with most of its diversity associated with rainforests. The Congo basin in Central Africa harbours the world's second largest tropical rainforest and a wide variety of other habitats from inundated swamp forest to savannah-shrub land mosaic. However, its amphibian fauna is astonishingly among the least explored worldwide. It is expected that this "green heart" of the continent is species-rich with both widespread taxa and regional endemism including yet undiscovered species. We have begun working in the area with particular focus on the systematics of Reed frogs, genus *Hyperolius*. This monophyletic group of arboreal frogs is distributed across a broad range of habitats throughout sub-Saharan Africa and it is currently the most species rich genus on the continent. *Hyperolius* taxonomy is far from trivial as intraspecific variation in diagnostic characters is high and frequently exceed interspecific variation. As a result of this, many names and potential synonyms have been coined by early workers. Distinctive to the Congo basin a large fraction of the known taxa here have only been mentioned in original descriptions based on few preserved specimens. We apply an integrative approach including morphology, DNA barcoding, phylogeny and life history traits (in particular bioacoustics). Here, we report on the discovery of new species and how we treat some of the available names. Moreover, we discuss patterns of polymorphism in some species and preliminary analyses of species distributions. Finally we outline challenges for on-going research and perspectives for future herpetological biodiversity studies in the area.

P. Kornilios, E. Thanou, P. Lymberakis & S. Giokas

Phylogeography of the four-lined snake with the use of mtDNA markers and comments on its subspecific taxonomy

Elaphe quatuorlineata, commonly named as the four-lined snake, is a European species with weak affinities to other European *Elaphe* representatives and a close relationship to Asian ones. It occurs in Mediterranean and sub-Mediterranean zones in much of central and south Italy, excluding Sicily, and in the southwest Balkan region, including a number of Adriatic, Ionian and Aegean islands. It is an uncommon species with a fragmented range, and is listed as Near Threatened by the IUCN since it is considered to be in significant decline. Except for the nominotypical subspecies, several other ones have been described from the Aegean islands: *E. q. muenteri* (Cyclades islands), *E. q. parensis* (island of Paros) and *E. q. skyrensis* (island of Skyros). So far, few data from molecular analyses have been presented for this species in order to evaluate its intraspecific genetic diversity and the subsequent taxonomic implications. Additionally, its biogeography has not been thoroughly studied despite (a) its distribution in the Italian and Balkan peninsulas that have possibly acted as biodiversity refugia and seem to include several subrefugia and (b) the distributional gap between the two peninsulas, and (c) the intense paleogeographical and paleoclimatic history of the Aegean that has been demonstrated as a biodiversity hotspot for reptiles, hosting several endemic species or evolutionary lineages. In this study, more than 50 *E. quatuorlineata* specimens, representing

almost all of the animal's geographic distribution and recognized subspecies, were used and partial sequences of two mitochondrial (*cytb* and *CO1*) markers were targeted. The historical biogeography of this species was assessed with the phylogenetic analyses of Maximum Likelihood and Bayesian Inference and the molecular-clock based estimation of divergence times. Moreover, the validity of the subspecific taxonomic status of *E. quatuorlineata* is discussed.

E.T. Krause, S. Steinfartz & B.A. Caspers

Poor nutritional conditions during the early larval stage reduce risk-taking activities of Fire salamander larvae (*Salamandra salamandra*)

Environmental conditions experienced early in life have been shown to significantly affect growth trajectories at later stages in many vertebrate species. Amphibians typically have a biphasic life history, with an aquatic larval phase during early development and a subsequent terrestrial adult phase after completed metamorphosis. Thus, the early conditions have an especially strong impact on the future survival and fitness of amphibians. We studied whether early nutritional conditions affect the behavioural reaction of fire salamander larvae (*Salamandra salamandra*) before completion of metamorphosis. Fire salamander larvae reared under rich nutritional conditions were heavier and larger, displayed better body condition overall throughout the first three month of life and metamorphosed earlier compared with larvae raised under poor nutritional conditions. Specifically, we tested whether larvae reared under these different conditions differed with respect to their risk-taking behaviour and activity. We found no differences in the activity of larvae with respect to their experienced early food conditions. However, larvae reared under poor nutritional conditions hid significantly more often in a risk-taking test than larvae reared under rich food conditions. This increase in shelter-seeking behaviour might be an adaptation to reduce the risk of larval drift or an adaptation to compensate for physiological deficits in part by appropriate behavioural reactions. Our results indicate that environmental conditions, such as food availability, may lead to different behavioural strategies.

R.E. Lloyd & D. Lermen

Current European biobanking activities for amphibian conservation – where we are and where to go

Biobanking (or Genome Resource Banking) is recognised as an essential and integral part of the IUCN Amphibian Conservation Action Plan (Gascon et al. 2007). With Approximately one-third of the 6,260 amphibian species assessed to date described as critically endangered, endangered or vulnerable; biobanks, containing e.g. germplasm (sperm and eggs), embryos, somatic cell lines, and tissue, are a second line of defence against species extinction (Pukazhenthi & Wildt 2007). Biobanks have huge potential to serve as a resource for research (e.g. samples can be

used to assess the current genetic diversity of a population, Ryder 2005) and, in association with assisted reproduction techniques, reproduction (e.g. sperm can be used to reintroduce genes periodically to maintain the genetic diversity of a population, Watson & Holt 2001). In 2008, a nascent committee, the Amphibian Ark Biobanking Advisory Committee, was formed to facilitate the establishment of amphibian biobanks; the sampling and cryopreservation of amphibian biomaterials; and to advise the wider conservation community which biobanking methodologies are available, where training in such methodologies can be obtained and where samples can be deposited. To this end, the aim of this talk is to give a European overview of (1) the biobanking initiatives underway and the wide-range of methodologies available (from the most practical/technologically feasible to the less so) and (2) places where training in biobanking methodologies can be obtained and samples deposited. References: Gascon, C., Collins, J. P., Moore, R. D., Church, D. R., McKay, J. E. and Mendelson, J. R. III (eds). 2007. Amphibian Conservation Action Plan. IUCN/SSC Amphibian Specialist Group. Gland, Switzerland and Cambridge, UK; Pukazhenthi, B. S., Pelican, K., Wildt, D. 2007. "Genome Resource Banking" in Gascon, C., Collins, J. P., Moore, R. D., Church, D. R., McKay, J. E. and Mendelson, J. R. III (eds). Amphibian Conservation Action Plan. IUCN/SSC Amphibian Specialist Group. Gland, Switzerland and Cambridge, UK: 38-39; Ryder, O. 2005. Conservation genomics: applying whole genome studies to species conservation efforts. *Cytogenetic and Genome Research*, 108: 6-15; Watson, P. F., Holt, W. V. 2001. Cryobanking the genetic resources. *Wildlife Conservation for the Future?* Taylor & Francis, London, UK.

S. Lotzkat

Deciphering reptile diversity in western Panama

Over the past decade, the list of reptile species occurring in Panama has experienced a considerable increase, which is still ongoing. Most recent additions derive from discoveries along the Cordillera Central in the western part of the country, due to the herpetological exploration of more and more localities within this rugged mountain chain. Thus, new material has become available to approximate also the less obvious aspects of squamate diversity in this region. While some of the new species' rather obvious distinctiveness has merely been overlooked in the past, the bulk of them are either unlikely to be encountered in the field (e.g., secretive snakes) or difficult to distinguish, such as cryptic lineages within certain species groups (especially anoles) exhibiting little morphological differentiation. Based on own field studies and ongoing research, I present case studies elucidating the picture we have gained so far concerning the relationships and distribution of some of these "challenging" taxa.

R. Manenti, G.F. Ficetola, M. Anghileri & F. De Bernardi

Salamandra salamandra breeding in subterranean habitats: local adaptations or behavioural plasticity?

Most of studies on amphibians occurrence in caves focus on obligate cavernicoles, while the active use of subterranean habitats by epigeal *taxa* is less studied. The salamander *S.*

salamandra usually breeds in epigeal streams, but in karstic areas underground springs are often used as breeding habitat. Although there is evidence that the species achieves metamorphosis in underground environments, there are not detailed studies on development, behavior and breeding success in these habitats. The aim of this study was assessing whether salamander populations breeding in underground habitat show behavioral adaptations to these environments, and whether cave populations have better predation ability in underground conditions. We studied 30 salamander populations breeding in underground and epigeal streams in Northern Italy. First, we regularly surveyed larval development in four underground sites. In seven caves we recorded weight and total length of larvae at the initial and final period of metamorphosis, and compared them to larvae reared under outdoor conditions. Second, we performed a behavioural experiment about prey detection and capture. We collected larvae from 20 different underground springs and from 20 neighbouring epigeal streams. Larvae were reared under two different conditions: 10 from caves and 10 from streams were raised in underground conditions (an ancient draining gallery provided by the Monte Barro Regional Park), while 10 from caves and 10 from streams were raised under outdoor conditions. Larvae were fed with living chironomid larvae. For each larva, at the collection moment and after a month of raising, we recorded under total darkness two measures of predation performance: time of the first head turning toward the prey and frequency of prey capturing. In underground environments, larvae require more than 1 year to reach metamorphosis, and metamorphose at a significantly larger body size, compared to those grown under outdoor conditions. Both epigeal and hypogean larvae were able to detect and capture preys. In the darkness, most of larvae used an active widely foraging mode. Larvae born in underground springs captured preys with higher success than those born in outdoor conditions, while we did not detect differences for head movements. Acclimatization to underground conditions did not improve predation performance. Our results show the plasticity of *S. salamandra* larvae to successfully prey and grow in caves. The higher foraging performance of larvae born in underground conditions suggests that also behavioural adaptations to the cave environments are possible.

V. Mashkarayan, M. Arakelyan, D.J. Harris & M.A. Carretero

Genetic diversity of *Testudo graeca* in Armenia and Nagorno Karabakh Republic

Preliminary research indicates strong geographic trends in the morphology of *Testudo graeca* across Armenia and the adjacent Nagorno Karabakh Republic (NKS) but it remains unclear to what extent such variation corresponds to evolutionary units. Here, we use mtDNA (Cyt-b marker) to assess the phylogeographic relations of *T. graeca* based on 30 samples from different populations from Armenia, NKR. Results indicated three phylogeographic units. The first corresponds to *T. g. armeniaca* from SW Armenia having 0.7% divergence from the rest of populations from southern Armenia and NKR, *T. g. iberica* from north of Armenia. Within the latter, two subgroups were detected, differing 4.5-5% respectively from *T. g. armeniaca*. Although our results suggest that the specimens from NKR at Araks River Valley are closely related to *T. g. armeniaca*, instances of gene flow from *T. g. iberica* confirm contact zone between *T. g. armeniaca* and *T. g. iberica* previously recognized by their morphometric data.

F. Martínez-Freiría & J.C. Brito

Patterns of morphological variation in *Vipera seoanei*: using GIS and ENM for elucidating biogeographical scenarios across the Iberian Peninsula

Vipera seoanei is an endemic Iberian viper with Euro-Siberian affinity (pelias clade). It is distributed in Northern third of Iberia and populations in the south-western range of its distribution are isolated in mountains. It is a very polymorphic species with two subspecies (*V. seoanei seoanei* and *V. seoanei cantabrica*) and five coloration patterns described in the 1980's. Recently, it has been recognised as an endangered species by habitat alterations caused by current Global Warming. However no conservation planning has been initiated. Indeed, since past century, no study has focused on biogeographic patterns at Iberian scale, which is totally necessary for planning optimised conservation strategies. This study analyses preliminary morphological variation of the species using contemporary tools such as Geographical Information Systems (GIS) and Ecological Niche-based Models (ENM) for elucidating biogeographical patterns across the Iberian Peninsula. Twenty quantitative traits, including eight biometric (e.g. snout-vent, head or jaw length) and twelve pholidotic (e.g. number of ventral, subcaudal or periocular scales), from 315 specimens from all Iberia were analysed with geostatistics. Morphological traits were tested for sexual dimorphism and then, were interpolated by kriging in the GIS ArcMap 9.3 software in order to generate surfaces of morphological variation. Surfaces of morphological variation were combined with Spatial Principal Components Analysis (SPCA). SPCA maps were used to identify putative morphological differentiated groups with the Iso Cluster (IC) and Maximum Likelihood Classification (MLC) functions of the ArcMap. Discriminant Function Analysis (DFA) was used to test the identified putative morphological differentiated groups. Then, localities for each morphological differentiated group and 9 uncorrelated eco-geographical variables were combined in the Maxent 3.3e to identify ecological factors related to the distribution and areas for the potential occurrence of morphological groups. Three biometric (e.g. tail length) and two pholidotic traits (e.g. number of subcaudal scales) presented sexual dimorphism and thus, were separated by sexes. Surfaces of morphological variation showed clines west-east oriented for four biometric (e.g. jaw length) and five pholidotic traits (e.g. number of ventral or intercantal plus intrasupraocular scales). SPCA for the first and second components explained the 63.2 and 15.8 % of the variance, respectively. IC and MLC were asked for clustering from two to seven groups but DFA only supported the identification of two morphological groups: group 1, located in central-east Galicia, western Asturias, western León, western Zamora and north-central Portugal, and group 2, located in the rest of the area. ENM were robust ($AUC > 0.88$) and predicted potential areas of occurrence accorded to the observed distributions of the two groups. The distributions of both groups are related to different (e.g. Isothermality, for group 1, and Annual Precipitation, for group 2) and similar (e.g. Precipitation of Warmest Quarter) climatic factors; when similar, different profiles in the response curves were observed for both groups, suggesting allopatry. Biogeographical patterns are discussed under the context of geographic isolation during the Pleistocene climatic oscillations and the current intraspecific systematic of the species. Molecular studies are needed to compare with morphological patterns and recognize the intraspecific structure of *V. seoanei*.

K. Mebert

The Dice snake, *Natrix tessellata*: Biology, distribution and conservation of a Palearctic species – a synopsis on the new volume in Mertensiella book series

The semi-aquatic, mainly piscivorous dice snake (*Natrix tessellata*) is one of the few snake species that naturally occurs on three continents: Europe, Asia, and a little in Africa. Across this vast range, the snake inhabits a large variety of water bodies from freshwater channels, rivers, lakes, swamps to brackish lagoons, and even sea water, including offshore islands. It colonized mountain streams up to 2800 m as well as wadis (oases) in deserts and semi-arid areas. A new and comprehensive volume in the Mertensiella book series by the DGHT presents the status quo of knowledge of this truly palearctic species. More than 120 authors/researchers have contributed a total of 57 articles and one DVD, relating to 25 countries and touching some more. Topics include aspects about conservation projects and national distributions, surprising and newly discovered populations and larger range expansions, population dynamics, ecology, genetic and morphological variation, radiotelemetry studies, interspecific competition, inbreeding effects, hybridization, fossils, parasites, behavioral aspects, e.g. mass mating, fatal hunting methods, predation, common and unusual diet. Fascinating snippets from various contributions are packed into a colorful and interesting presentation to enlighten the magnitude of biological aspects and variability within this versatile species.

M. Mediani, S. Fahd & J.C. Brito

Amphibian biodiversity hotspots in Morocco: conservation priorities

The amphibians constitute a remarkable component of the vertebrate fauna on a worldwide scale. They are currently undergoing massive and global population and species declines because of several factors, such as habitat loss and fragmentation but probably also because of the global climate changes. In addition, amphibians are regarded as excellent indicators of environmental quality and support formulating conservation measures. With only 13 of the 106 amphibian species of the Mediterranean Basin, Morocco has the highest rate of endemic species (30.7%) of all countries bordering the Mediterranean. However, the proportion of endangered species (38.5%), according to IUCN criteria, is very high and renders particular care to the Moroccan amphibian community. Data on the distribution of amphibian species were collected along two decades of field missions over the country (N = 2830 observations) and represented in a Geographical Information System. Areas of probable occurrence for each species were estimated using maximum entropy modelling. This work presents cartographic maps with the distribution of total species richness, of endemic species, and of endangered species. Suitable areas for each species were quantified, allowing the identification of critical conservation areas. Biodiversity hotspots of amphibians in Morocco are located and comprised areas with high number of conservation priority species (endemics, rare and endangered). Priority conservation areas are mostly located along the Rif and Atlas mountains.

O. Mettouris, A. Augustinos, K. Anagnostopoulou, P. Kornilios & S. Giokas

Population ecology and genetics of two syntopic newt populations (*Ichthyosaura alpestris veluchiensis* and *Lissotriton vulgaris graecus*) at a temporary pond in southern Greece

Population ecology and genetic studies are essential for assessing the status of the globally declining amphibians, especially in habitats at risk. Therefore, we studied two sympatric newt species, *Ichthyosaura alpestris* and *Lissotriton vulgaris* in Helmos mountain, Peloponnese, Greece, during their breeding season. Individuals of both populations return each year to breed in an isolated temporary pond that is filled with water usually from January to late August-early September, depending on the weather conditions. We performed a mark-recapture experiment during the 2010 breeding season. Animals were captured in the water and marked with PIT-tags, measured for length and weight and then released. Tissue samples were extracted for genetic analyses. Ground and water temperature was recorded for the duration of the study. We used program MARK to fit the POPAN formulation of Jolly-Seber models to the mark-recapture data and estimate population parameters, such as population size, apparent survival and probabilities of entry into the pond. Water and ground temperature were used as covariates in the analyses in order to determine their effect on the above parameters. Measurements of length and weight were used to investigate for inter- and intra-population variability. Microsatellite DNA analyses were performed to assess the genetic structure of the two populations. Population size estimates were 306 individuals for *L. vulgaris* and 1032 individuals for *I. alpestris*. Male: female ratios were 2:7 and 1:1 respectively. Due to sparseness of data, models were fitted to the *I. alpestris* data only. The probabilities of individuals entering the pond in each sampling interval were greatly affected by the mean minimum ground temperature for that interval. The percentage of individuals entering the pond varied with time, but was roughly the same for both sexes. Apparent survival of males was lower than that of females probably due to the fact that males spend less time in the pond. Comparisons of mean body size and weight of individuals caught in each sampling occasion showed that in *I. alpestris* larger and heavier individuals were in the pond early in the breeding period. As the period drew to its end, smaller and lighter individuals comprised the sampled population. This was not observed in *L. vulgaris*. Genetic analyses revealed reduced levels of genetic variation relative to other conspecific populations, particularly for *L. vulgaris*, suggesting that genetic bottlenecks might have occurred, and call for specific conservation measures.

I. Meuche, K.E. Linsenmair & Heike Pröhl

How many frogs do you have to kiss to find a prince?

Female frogs have often been shown to exhibit preferences for certain male traits. However, very little is known about behavioural rules females use when searching for mates. We investigated mate sampling tactics in the territorial strawberry dart-poison frog (*Oophaga*

pumilio). We found no evidence that females compared males by visiting and courting them. Instead females mated with the closest calling male irrespective of his characteristics (e.g. acoustic and physical traits). Additionally for the first time we conducted playback experiments in the natural home ranges of receptive females to test their preferences for several call parameters: high vs. low call rate, high vs. low dominant frequency, near vs. far distance between female and speaker. Females preferred the nearest speaker as well as low frequency calls, but did not discriminate between low and high call rates. We also showed that distance differences between female and certain males counteracted the existing preference for low frequency calls. These results in combination with our behavioural observations in the field suggest that the distance to potential mates is the crucial criterion for mate choice in female strawberry poison frogs. We discuss our results in terms of benefits and costs of mate sampling.

A. Miralles, R. Vasconcelos, A. Perera, D.J. Harris & S. Carranza

An integrative taxonomic revision of the Cape Verdean skinks (*Squamata*, *Scincidae*)

A comprehensive taxonomic revision of the Cape Verdean skinks is proposed based on an integrative approach combining a phylogenetic study pooling all the previously published molecular data, new population genetic analyses using mitochondrial and nuclear data resulting from additional sampling, together with a morphological study based on an extensive examination of the scalation and colour patterns of 516 live and museum specimens, including most of the types. All Cape Verdean species of skinks presently recognised, formerly regarded as members of the genera *Mabuia* Fitzinger, 1826 and *Macrosцинus* Bocage, 1873 are considered as members of the Cape Verdean endemic genus *Chioninia* Gray, 1845. The new phylogeny and networks obtained are congruent with the previously published phylogenetic studies, although suggesting older colonization events (between 11.6 and 0.8 Myr old), and indicate the need for taxonomic changes. Intraspecific diversity has been analysed and points to a very recent expansion of *Chioninia delalandii* on the southern islands and its introduction on Maio, to a close connection between *Chioninia stangeri* island populations due to Pleistocene sea-level falls and to a generally low haplotypic diversity due to the ecological and geological characteristics of the archipelago. Three new consistent morphological synapomorphies supporting two of the four main clades of the genus have been identified. The complex taxonomic status of *Euprepes fogoensis* O'Shaughnessy, 1874 has been resolved and a lectotype has been designated for this species; *Chioninia fogoensis nicolauensis* (Schleich, 1987) has elevated to species rank, whereas *Chioninia fogoensis antaensis* (Schleich, 1987) is now regarded as a junior subjective synonym of *C. fogoensis*. Additionally, one new subspecies of *Chioninia vaillanti* and two of *Chioninia spinalis* have been described (*Chioninia vaillanti xanthotis*, *Chioninia spinalis santiagoensis* and *Chioninia spinalis boavistensis*) and a lectotype has been designated for *Mabuia spinalis* Boulenger, 1906.

E. Mizsei & B. Üveges

Confirming the presence of *Vipera ursinii graeca* in Albania with regards of a new locality – preliminary results

The meadow viper (*Vipera ursinii*) has a fragmented distribution across Europe. It has been detected on many locations of the Balkan-peninsula too (Croatia, Bosnia-Herzegovina, Serbia, Montenegro, Macedonia, Greece), but little is known from the Albanian populations. No survey was made until now, to map the distribution and to assess the habitats of the meadow viper in Albania. Until 2006 only the presence of *V. u. macrops* was documented from this country based on anecdotal faunistic records or occasionally collected and observed specimens, but in that year Hungarian scientists found a meadow viper in the Nemereçke-Mountains of Albania. This specimen was later identified as *V. u. graeca*, and was recognised as a new subspecies of the Albanian fauna. Unfortunately the identification was based on photographs and so only a handful of characteristics could be used. Here we confirm the original identification, by presenting detailed information about the pholidosis of another 7 specimens (4 males, 3 females) and 2 shed skins, found in 2010 and 2011, using generally accepted taxonomic characteristics. We also present a hitherto unknown habitat on the Lalucit Mountains, where 3 males of the 7 specimens have been found.

R.W. Murphy & Y.P. Zhang

Starting the global Initiative to barcode amphibians and reptiles

The International Barcode of Life project (iBOL) seeks to obtain short DNA barcoding fragments from major groups of species. Many initiatives currently exist and these include global efforts for fishes, birds, mammals, but not amphibians and reptiles. To this extent, the barcoding of amphibians and reptiles is lagging far behind the other vertebrate groups. The project seeks to efficiently identify (1) areas for future research efforts and (2) biogeographic patterns, amphibian larvae, as well as for validating species identities for the Genome 10K project and conservation and forensic studies, among many other applications. The sequence data may be used in phylogenetics and taxonomy, although this is not a primary goal. Some technical issues, such as primer mismatch, are now resolved. The coordination of the effort will be accomplished by committee, and regional and taxonomic experts are sought as group coordinators. Protocols and recommendations will be set by committee. This will include, for example, sampling strategies (number of individuals/site or species; voucher requirements; etc.) and the lag time following sequencing before public release of the data. The Kunming Institute of Zoology will offer free barcoding services in support of this effort and this may involve the use of the facilities by researchers willing to gather their own data.

Z.T. Nagy, Ch. Kusamba, L. Lokasola, J. Kolby & J. Kielgast

Survey of the reptile fauna in the Congo basin

In the spring of 2010, a large interdisciplinary expedition was conducted in the Democratic Republic of the Congo. Four field sites between Kisangani and Bumba were surveyed along the Congo mainstream as well as at the tributaries Lomami, Aruwimi and Itimbiri. Approximately 750 amphibian and reptile specimens were collected, and tissue samples were taken for genetic analyses. We used a DNA barcoding approach to assist this survey of the reptile diversity in the Congo basin. DNA barcoding was applied for species delineation complementing morphological identification. Furthermore, we analyzed intraspecific diversity and tested the possible isolating effect of large rivers on reptiles. We confirmed that the 180 reptile samples investigated belong to >50 species. Reptile species proved to be well diverged and easy to delineate using DNA barcode sequences while intraspecific variation is generally low. Remarkable intraspecific divergence was only found in skinks and in some snakes, notably in scoleophidians. This observation indicates that rivers do not significantly hamper reptile radiation in many cases across Central Africa.

P. Pafilis, K. Sagonas & E.D. Valakos

The impact of grazing on lizard populations from East Mediterranean islets

The practice of free-range goat grazing in islets is common throughout Mediterranean Sea with well-documented consequences on plant communities. In the case of lizards grazing has been reported to alter vegetation providing less cover from avian predators, increasing thus predation risk. In this study we focused on the impact of grazing on populations of the Skyros Wall lizard (*Podarcis gaigeae*), an endemic lacertid of Skyros Archipelago (Aegean Sea, Greece). Our aim was to detect and assess possible direct and/or indirect effects on several features of lizards' overall biology. Five biotopes (three islets and two localities from Skyros Island) that differ in the duration and intension of grazing were included in the project. For a time-window of six years we realized monthly samplings during spring and summer (reproductive period of *P. gaigeae*) and recorded invertebrate population densities, lizard ectoparasites prevalence, presence and density of sea gulls and lizard population densities. As expected, grazing had a strong negative influence on plant communities. The restriction of vegetation impoverished considerably invertebrate populations, decreasing thus food availability for lizards, which feed mainly on insects. Furthermore it resulted in a serious degradation of the biotope quality since lizards in islets use plants as shelters or thermoregulation sites. Ectoparasite loads (ticks and mites) were higher in places where goats were present in large numbers for long periods. Goat activity disturbs sea gulls that normally nest on remote islands. Islets where grazing was continuous hosted few or even none breeding pair. Since sea gulls support in terms of energy many islets of Skyros Archipelago through marine subsidies, the devastation of their breeding colonies affected negatively small insular ecosystems. Finally, population densities of lizards were higher in biotopes with no grazing (Diavates islet and the dunal ecosystem of Palamari at Skyros Island) and much lower in places with intense grazing.

Ph. de Pous, J. Carr & W. Cheung

Climate change and European reptiles: from large-scale spatial range shift projections towards a more realistic assessment of species responses

Climate change has affected and changed the global biodiversity throughout the earth's history and species have adapted to novel conditions. Current climate change is however occurring much faster than past changes, and many studies have identified climate change to be among the most important threats to biodiversity. Climate change is expected to have major impacts on natural populations and has been shown to alter species' physiology, distribution, phenology and behaviour. Moreover, climate change is expected to have stronger effects on species with ectotherm physiology, restricted ranges, specific habitat requirements and limited dispersal capabilities. Although reptiles have coped with rapid dramatic climate changes in the past (e.g. Late Pleistocene) several studies have recently predicted or observed major population declines and extinctions across many regions and taxa. Although there have been several studies on the effects of climate change on European herpetofauna, these studies used either a small fraction of Europe (e.g. Iberian Peninsula) or a coarse resolution (e.g. 50 x 50 km) in combination with outdated taxonomy. Hence, there is at current no region-wide assessment of the effects of climate change on reptiles although this is highly preferable as a basis framework for spatial conservation prioritization studies and other conservation measures. This project aims to (1) build a distribution database of European reptiles on a 10 x 10 km resolution, (2) determine the effects of future climatic conditions (2050 and 2080) on contemporary ranges of European and Mediterranean reptiles using forecast species distribution models (climate envelope models) and expert-based dispersal scenarios, (3) assess species turnover across the region, and (4) to integrate this information with the IUCN's Red Listing and Climate Change Vulnerability Assessment Framework (CCVF).

M. Rajabizadeh, U. Joger & G. Nilson

Review of new findings in taxonomy and distribution of *Vipera* (s.l.) of Iran

A brief review on new findings about Taxonomy and distribution of three genera of vipers of Iran including Genus *Vipera* Laurenti, 1768; Genus *Montivipera* Nilson et al, 1999 and Genus *Macrovipera* Reuss, 1927 have been summarised. Of genus *Montivipera*, morphological analysis confirm that three full species, *Montivipera raddei* Boettger, 1890 in north western Iran, *Montivipera latifii* Mertens, Darevsky and Klemmer, 1967 in central Alborz mountains and *Montivipera kuhrangica* Rajabizadeh, Nilson and Kami, 2010 in kuhrang region of central Zagross occur in Iran. but in east of distribution range of *Montivipera raddei*, a subspecies, *Montivipera raddei albicornuta* Nilson & Andren, 1985, occur in Zanjan valley. As well in southern range of the species, a morphologically different population but closely related to *Montivipera raddei* occur which further studies is necessary to determine taxonomic rank of it. Of genus *Macrovipera*, although the subspecies *Macrovipera lebetina obtusa* (Dwigubsky,

1832) is widely distributed in Iran, occurrence of the subspecies *Macrovipera lebetina cernovi* (Chikin et Szczerbak, 1992) in north eastern Iran is confirmed. morphological comparison of the subspecies reveals that *Macrovipera lebetina cernovi* has bigger head scales than *Macrovipera lebetina obtusa* and so lower number of scales on head, around eye and on suprocular is observed in *Macrovipera lebetina cernovi*. Of genus *Vipera*, new findings shows that *Vipera ebneri* Knoepffler and Sochurek, 1955 occur in central and western Alborz till south of Sabalan mountain and *Vipera erivanensis* (Reuss, 1933) is distributed in north of Sabalan mountain till Iran and Armenia border.

R. Rannap, K. Suislepp & A. Lõhmus

Impacts of artificial drainage on amphibian breeding sites in hemiboreal forests

Artificial drainage is widely used to increase timber production and improve its quality in northern boreal and temperate forests, but its impact on biodiversity remains largely unexplored. Amphibians are particularly dependent on forest wetland qualities to complete their complex life cycles. We explored the supply of water bodies, their occupancy by amphibians, and persistence during the larval period comparatively in drained and natural forest plots in two years in Estonia. The water bodies in drained plots were more abundant but less diverse and of generally lower quality than in natural plots; however, the ditches were favoured by newts. In the dry spring of 2009, water bodies were used more frequently in natural than in drained plots, while in the typical spring of 2010, several natural depressions appeared in drained plots and the frequency of use of water bodies did not differ between natural and drained plots. However, most natural depressions used for breeding in drained plots dried out before tadpole metamorphosis; such drying was not observed in natural plots. Thus, by profoundly changing natural hydrology, intensive large-scale forest drainage reduces the variety of water bodies and the quantity and quality of amphibian breeding sites. Moreover, we suspect that, at least in some years, temporary water bodies in drained areas function as ecological traps for amphibians. We suggest that, where possible, intact wet-forest areas with remaining natural hydrology should stay undrained. In areas already drained, breeding sites for amphibians can be provided by creating depression-like enlargements to some ditches.

S.Reinhard & A. Kupfer

Life history and parental care strategies of caecilian amphibians

Reproductive strategies in amphibians include oviparity and viviparity, lentic and lotic or terrestrial breeding. Although most species do not provide care for their offspring, the diversity of parental care strategies provided by a minority of amphibians still exceed the variety known in other vertebrates. Diverse and complex parental care strategies are widespread among caecilian amphibians, encompassing egg-guarding to passive feeding of young, i.e. several

species are known to provide offspring with highly nutritious maternal skin. We follow parental care and skin-feeding in laboratory populations of the viviparous *Geotrypetes seraphini* during a successful breeding program and summarise the evolutionary patterns of life history strategies of caecilian amphibians.

**A. Reshetnikov, I. Chikhlyayev, A. Fayzulin, A. Kirillov, A. Kuzovenko,
E. Protasova, M. Skomorokhov, & S. Sokolov**

Food and parasite interactions between native semi-aquatic snakes (*Natrix tessellata* and *N. natrix*) and the alien fish *Perccottus glenii*

The diets and helminth compositions of two semi-aquatic snakes (dice snake *Natrix tessellata*, grass snake *N. natrix*) and a recently introduced invasive alien fish rotan *Perccottus glenii* were investigated. In an isolated lake, the piscivorous dice snake feeds mainly on rotan since its introduction and the subsequent elimination of native fish. Both studied snakes obtained a parasitic tapeworm from rotan. Therefore, the native snakes and the invasive fish demonstrate strong direct (consumption of fish by snakes) and indirect (transmitting parasite species) interspecies interactions. Thus, in the ecosystem inhabited by semi-aquatic snakes, the invasive fish rotan replaced the eliminated native fish in food web and became part of the parasite system that included the native snakes. This is the first report with analysis of the indirect interactions between the invasive alien Far-Eastern fish *P. glenii* and native European reptiles.

J. Riemann, S. Ndriantsoa, M-O. Rödel & J. Glos

Habitat fragmentation and frogs: how is species richness and functional diversity in hyper-diverse amphibian communities affected?

Fragmentation is a process that may lead to the loss of biodiversity, i.e. to species-depleted communities in fragments. However, the effects of the loss of species may well go beyond the change in community properties of the animal groups in question (e.g. community structure) but may affect various ecosystem properties as well as ecosystem functioning. Hence, a fragmented landscape represents an appropriate system to study general community-ecosystem dependencies. In our study we aim at understanding how patterns of amphibian diversity depend on fragmentation related properties of amphibian habitat such as forest fragment size and isolation, and how local extinctions depend on functional components of diversity, food web properties, morphological traits of frog species and their phylogenetic distance. Our study is currently conducted on frog communities in the Ranomafana area of Eastern Madagascar, a montane rainforest ecosystem. This region has an outstanding amphibian species richness with 100+ frog species including a wide variety of ecologically diverse frog species. We will present the concept of our study and first results on species and

ecological (functional) diversity of these hyper-diverse amphibian communities.

L. Russell & T.J.C. Beebee

The effects of landscape on the population genetics of the sand lizard *Lacerta agilis* in the southern United Kingdom

The sand lizard *Lacerta agilis* reaches the western edge of its range in the where it is restricted to habitats on sandy soils and consequently has a limited and patchy distribution. This has left the sand lizard particularly vulnerable to the effects of habitat loss and fragmentation and the species has suffered significant declines. Sand lizards were sampled from a number of sites within the species' UK stronghold of Dorset and genotyped at 15 microsatellite loci. Individual populations were identified using Bayesian assignment methods. Populations exhibited relatively high levels of genetic differentiation over small geographical distances and differentiation patterns could not be explained by isolation by distance. The effect of the landscape on genetic population structure was investigated at a fine scale in two scenarios: across a series of isolated/fragmented sites separated by natural and artificial barriers to dispersal; and, within a large area of forestry plantation where small patches of suitable habitat are present among larger areas of less suitable habitat. Remotely sensed habitat data was used to create a resistance surface and least-cost path analysis was used to explain genetic population structure within both scenarios.

S. Scali, R. Sacchi, M. Azzusi, S. Daverio, T. Oppedisano & M. Mangiacotti

Homeward bound: which factors influence the homing ability of the common wall lizard *Podarcis muralis*?

To test the homing ability of *Podarcis muralis*, we conducted an experiment in two different areas of Northern Italy during 2009 and 2010. The first study area (Cesano Maderno: CSM) is a wall surrounding a city park with a linear and very simplified habitat; the second one (Castelseprio: CSS) is an archaeological park in a natural area including stone walls remains, open areas and woods. The lizards were captured by noose, measured, photographed and marked with dorsal paints for individual recognition and then translocated at increasing distances (50-100-150-200 m). We considered a lizard successfully homed when we sighted it within 20m from the capture site. We translocated 491 lizards, 203 from CSM (132 males and 71 females) and 288 from CSS (145 males and 143 females) using cloth bags that did not allow the lizards to use landmarks to find their way back home. Data were analysed by means of GLM, using return as dependent variable, sex, distance, season (reproductive: March-June; post-reproductive: July-September), regenerated tail (regenerated/intact), study site as fixed factors and SVL and morph as covariates. Since, *P. muralis* is a polymorphic species (white, yellow and red coloured bellies and hybrids), we speculated that its polymorphism could be based on a two alleles system and we evaluated the morph as the number of y (ny) and r (nr) alleles for

each individual (e.g., a red individual was coded as 2r/0y, a white-red individual as 1r/0y). In this scenario, we used these codes as covariates in the analysis. *P. muralis* was able to home, since 56.7% of CSM lizards and 35.1% of CSS lizards successfully returned to their original home-range. The optimal model obtained by GLM extracted distance, study site, ny, and SVL as significant variables. Homing ability was inversely correlated with distance, but grows as lizard size and ny increase. Homing success was significantly higher in the CSM site than in CSS site, while no effect was found for sex, season, regenerated tail and nr. The lizards can successfully home when they are translocated up to 50m, but their homing ability rapidly decreases at longer distances. The effect of size could be explained by territoriality, because smaller individuals could have not established yet their territories or they could have lower quality territories and the risk of facing a long travel to home could be too high. The number of y alleles seems related to alternative reproductive strategies highlighted during previous studies: yellow lizards behaves as territorial individuals and they could be more motivated to return to their territory resources with respect to other morphs. Habitat complexity negatively affects homing ability and lizards can return more easily to their home-ranges when they can use visual cues in a linear habitat.

L.M. Schulte, S. Lötters & M. Veith

The smell of death: How poison frogs recognize their offspring's enemies by means of chemical cues

Parental care is a common strategy among vertebrates to assure successful reproduction. Especially anuran amphibians have evolved a remarkable diversity of reproductive methods, often associated with parental care such as egg guarding and tadpole transport. Among the most derived strategies are those of the Neotropical poison frogs (Dendrobatidae). In these frogs parents deposit tadpoles singly into different phytotelmata (small water bodies that form in plant leaf axils). The exploitation of these small pools is advantageous as it lowers the risk of predation, but it is more costly because of limited resource availability. Additionally, poison frog larvae are often cannibalistic, so the identification and avoidance of conspecifics represents an adaptive behaviour for these amphibians. Here we report that parental *Ranitomeya variabilis* frogs are able to recognize the presence of tadpoles in phytotelmata without invoking visual or physical stimuli, but are able to accurately determine the presence of tadpoles via chemical cues. Furthermore, it appears that these frogs can distinguish between different kinds of cues, produced by tadpoles of different species. We tested the response of the frogs to tadpoles cues of different poison and non-poison frog species, either predatory or non-predatory. While the conspecific cannibalistic tadpoles were strongly avoided by the frogs, tadpoles of other species (except of one) were not avoided (or were even preferred) for tadpole depositions, but were avoided for egg depositions. Current research is focused on the identification of the specific chemical cues produced by tadpoles that elicit responses in adults. Current experiments involve changing the cues chemically (for example using polar or non-polar passive filters) and seeing if this influences deposition decisions made by adults.

U. Schulte, A. Hochkirch & M. Veith

Hybridization between native and introduced populations of the Common wall lizard (*Podarcis muralis*) at the northern range margin

The Common Wall Lizard (*Podarcis muralis*) represents one of the few reptile species that have successfully colonized regions in north-western Europe far outside their Mediterranean native range. DNA barcoding revealed that 85 introduced populations stem from eight geographically distinct invasive evolutionary lineages. Although the high phenotypic variability in colour pattern of wall lizards at both the intra-specific and intra-population level might lead to a delayed recognition of introductions and little awareness of the problem of introgression in conservation management, there is increasing evidence of introductions at the native range margin of the species in south-western Germany. In order to infer the level of potential hybridizations in contact zones of alien and native lineages, we analysed a combination of maternally (mtDNA; cytochrome *b*) and bi-parentally inherited molecular markers (13 microsatellite loci). A total of 316 wall lizards from five mixed populations as well as one native and one pure introduced reference population were analysed. Based upon model-based clustering methods our results suggest a rapid genetic assimilation of native populations through strong introgression of introduced Italian lineages. We also found a positive relationship between genetic diversity and the number of source populations. This high genetic diversity might be caused by the introduction of founders from different native populations from the Apennine Peninsula, which is a hotspot of the species' genetic diversity. High levels of intraspecific admixture may have promoted the invasion success of mixed populations. Nevertheless, introduced pure-bred populations with a low number of founders also retained rather high levels of genetic diversity like native populations and no evidence for a genetic bottleneck was found. The extent of introgression within artificial hybrid populations suggests that introductions of non-native lineages are threatening the genetic integrity of native populations at the northern range margin through a rapid creation of hybrid swarms.

N. Sillero & E. Argaña

Past, present, and future biogeographical patterns of Iberian herpetofauna

The biogeographical patterns in species density of herpetofauna have been analysed in the Iberian Peninsula recently, but only for the present time. Therefore, we want to analyse how biogeographical patterns change from the past to the future, in order to determine if biogeographical regions have changed along time, as well as the species chorotypes. Also, we measured expansions and retractions in species distributions and identified possible areas of refugia in the past and in the future. The study area was the Iberian Peninsula only, that is, excluding the Balearic Islands, and other islands outside the continental platform. The study included all the species of amphibians (28) and reptiles (45) considered in the Atlas of Portugal and of Spain. We calculated the realized niche model of each species using Maxent

method. Current models were projected to two past climatic scenarios (last glacial maximum and last interglacial period) and to three future climatic scenarios (2020, 2050, and 2080). All climatic variables for past, current, and future scenarios were extracted from Worldclim series, at a spatial resolution of 10 x 10 km. The realized niche models were transformed in habitat suitability maps (presence/absence maps) using an standard threshold, specific to each species. Expansions and retractions in the species distributions were analysed using a Geographical Information Systems. We used a Hierarchical Cluster Analysis with Jaccard's index as association measure to determine species chorotypes. Possible refugia areas in the past and in the future were identified by overlapping past and future models with the current model. We present here preliminary results on the evolution of the biogeographical regions and species chorotypes of the Iberian Peninsula, from the last interglacial period until the year 2080, and discussed how the climate change influence them.

Societas Europaea Herpetologica (SEH) Mapping Committee and SEH Council

A map of maps of European amphibian and reptile distribution: first step towards a new European atlas

Since the publication of the first and thus far only comprehensive distribution atlas of the European herpetofauna in 1993, almost two decades have passed. In this period, the increase of knowledge on the amphibians and reptiles of Europe has been enormous. Intensive regional and national mapping efforts have been undertaken, new species were discovered and described, and the taxonomy of numerous other species has changed. It is clear that a new European atlas is an urgently needed tool for conservation and research on the European herpetofauna. As a first step towards such an atlas, the SEH Mapping Committee and SEH Council, and some external researchers, have teamed up and compiled all georeferenced distribution data available thus far from published national mapping efforts and from other publically available data sources, plus numerous unpublished data for some geographic regions. We will present the “map of maps” that has been produced by this procedure, and some analyses that were based on the acquired data. These include species richness and endemicity analyses but especially are focused at highlighting areas in Europe for which recent distributional data are still missing and where future mapping efforts should thus be supported.

M. Solé & I. Dias

Diversity patterns along an elevational gradient in “Serra Bonita”, southern Bahia, Brazil: an amphibian hot-point inside a hot-spot

We characterized amphibian species richness, abundance and changes in community composition along an elevational gradient in the “Serra Bonita” Private Natural Heritage Reserve in southern Bahia, Brazil. Visual and acoustic active search, as well as captures using pitfalls with drift fences, were performed at four different altitudes (250, 450, 650 and 850

m). Six transects of 100 m and twelve pitfalls were installed at each elevation and sampled once per month during one year. Using multiple regressions we assessed whether the community composition, richness and abundance were related to 11 environmental variables. We sampled 2270 frogs belonging to 44 species from 12 families. Species richness was highest in the extremes of the gradient (250 m and 850 m), thus resulting in a U-shaped richness pattern. Along the gradient we observed an increase in the proportion of arboreal, direct developing and stream dwelling species towards higher altitudes, and a proportional decrease in terrestrial species and those that use ponds to reproduce. The lack of suitable breeding sites, lower physiological stress and differences in structural complexity of the forest may explain this pattern. The composition and abundance of amphibians was best explained by the presence of bromeliads and trees with a circumference between 5-40 cm. Additional fieldworks were undertaken to sample breeding ponds inside the 2000 hectare large reserve, resulting in additional 35 amphibian species, thus totalizing 79 species for the area. “Serra Bonita” can be considered a hot-point for amphibians inside the hot-spot of the Brazilian Atlantic Rainforest, revealing the second largest amphibian diversity for this biome, including several endemic or recently described species.

I. Starnberger, D. Poth, S. Schulz, M. Vences & W. Hödl

Multimodal Signaling in African Reed frogs: an explorative approach for investigating a complex behavior

During calling the vocal sac serves anurans as an air reservoir, in minimizing the loss of sound energy and in distributing calls omnidirectionally. The vocal sac’s role beyond acoustics had been overlooked for some time. The diversity in vocal sac coloration and shape found in different species is striking and recently its visual properties have gained vast attention. Males of many reed frog species (Anura: Hyperoliidae) have a prominent colorful gular patch on their vocal sac, which is very conspicuous once the vocal sac is inflated. To date, the function of this gular patch is completely unknown. In a pilot study undertaken in Uganda we found strong evidence that the gular patch is a gland producing volatiles emitted while calling. Furthermore, the coloration of vocal sac and gular patch might be species specific and serve as visual signal components in calling males. First results of an explorative study integrating histology, histochemistry, spectrometry and behavioural experiments to investigate signal modalities and their role in intra- and intersexual communication will be presented. We propose that hyperoliid frogs use a complex combination of acoustic, visual and chemical signals in species recognition and mate choice.

N. Stümpel & U. Joger

Phylogeny and phylogeography of Near and Middle East vipers (*Daboia*, *Montivipera* and *Macrovipera*)

Daboia, *Macrovipera* and *Montivipera* constitute typical elements of Near and Middle Eastern snake fauna with numerous species. The current knowledge is inadequate to explain

biodiversity, speciation and evolutionary history of this group. For this purpose we sequenced three mitochondrial genes (Cytb, COI, ND5) to reconstruct a robust phylogenetic framework. The samples of almost 200 specimens included multiple populations of all known taxa. Nuclear sequences (BACH1, RAG1) were added in a partial dataset. Our data support the monophyly of the Asiatic genera *Macrovipera* and *Montivipera*, which together are the sister group of the Afro-Asiatic genus *Daboia* while *Eristicophis*, *Pseudocerastes* and *Vipera* are phylogenetically more distant. *Daboia* is into a clade composed of the North African *D. mauritanica* and the Levantine *D. palaestinae*, and an oriental clade with *D. russelii* and *D. siamensis* which has been isolated for a longer time period. Within *Montivipera* our data identified two geographical lineages: the *raddei* group with the nominal species *raddei*, *albicornuta* and *latifii* and their western counterpart with all remaining *Montivipera* lineages. The *raddei* group is characterized by very low genetic distances, indicating their historically young radiation. Within the *xanthina* group, *M. bornmuelleri* and *M. wagneri* are well differentiated genetically, whereas in *M. albizona* and *M. bulgardaghica* lineage sorting has remained incomplete. On the other hand the considerable nucleotide divergence between several lineages of *Montivipera xanthina* indicates a long lasting geographical fragmentation. The populations of the blunt-nosed-Vipers (*Macrovipera*) split into four major mtDNA lineages. Island populations from Cyprus and the Cyclades are nested within those from the Turkish south coast and have a common ancestor. Another cluster represents the subspecies *turanica* and contains samples from Middle Asia. Specimens from Trans Caucasus, Anatolia, the Levantine coast, and West Iran belong to the subspecies *obtusa*. A recently discovered population from south Iran is clearly placed at the base of the *lebetina* radiation. This endemic population might be the relict of a common *Macrovipera* ancestor and represents a new ancestral species. A phylogeographical reconstruction identifies possible radiation centres and gives a temporal-spatial scenario of the evolution of these vipers.

A. Strugariu, Ş.R. Zamfirescu, I.E. Popescu, I. Rosca & I. Gherghel

Preliminary data on the feeding ecology of the critically endangered Moldavian meadow viper (*Vipera ursinii moldavica*)

The meadow viper (*Vipera ursinii*) is one of the most threatened reptile species in Europe and this status has attracted many ecological studies throughout its range, some of them also focusing on various aspects of feeding ecology. The Moldavian meadow viper (*Vipera ursinii moldavica*) is the easternmost subspecies of *Vipera ursinii*, being endemic to Eastern Romania. Although several ecological studies have been conducted in the past on some of its populations, there is no published data regarding the feeding ecology of these highly threatened populations. Herein, we present the first data on the feeding ecology of these populations and discuss our results in the light of previous similar studies. Fecal samples were collected from specimens caught in the field and examined for incompletely digested prey items. Although forced regurgitation has been a widely used method for studying stomach content in snakes, the method we applied is less invasive and thus preferable over the former one when such a threatened species is involved. Our results indicate that Moldavian meadow

vipers forage almost throughout the year (except for the first weeks after emergence from hibernation and the last weeks prior to hibernation) in all of the studied populations. The specimens from the populations from north-eastern Romania (Romanian Moldavia) fed predominantly on common field crickets (*Grillus campestris*), with lizards (*Lacerta agilis*), rodents (Microtidae) or other orthopterans being rarely observed in the samples. The specimens from the Danube Delta population presented a much wider trophic spectrum with a higher diversity of insect taxa (Coleoptera, Heteroptera, Hymenoptera, Orthoptera) as well as a constant presence of lizards (*Lacerta agilis*) in the samples.

L.F. Toledo, I. Sazima & C.F.B. Haddad

Anuran defensive strategies

Among vertebrates, defensive behaviours have been reviewed for fishes, salamanders, reptiles, birds, and mammals, but not yet for anuran amphibians. Although several defensive strategies have been reported for anurans, with a few exceptions these reports are limited in scope and scattered in the literature. This fact may be due to the lack of a comprehensive review on the defensive strategies of anurans, which could offer a basis for further studies and insights on the basic mechanisms that underlie these strategies, and thus lead to theoretical assumptions of their efficacy and evolution. Here we review the present knowledge on defensive behavioural tactics employed by anurans, add new data on already reported behaviours, describe new behaviours, and speculate about their origins. A total of 30 defensive behaviours (some with a few sub-categories) are here recognised. The terminology already adopted is here organized and some neologies are proposed. Some of the behaviours here treated seem to have an independent origin, whereas others could have evolved from preexistent physiological and behavioural features. The role of predators in the evolution of defensive behaviours is still scarcely touched upon and this overview adds data to explore this and other evolutionary unsolved questions. Funding: FAPESP, CAPES, CNPq

E. Twomey

Sexual selection in the mimic poison frog *Ranitomeya imitator*

Understanding mechanisms that promote population divergence has been a central topic in evolutionary research and is key to our understanding of speciation and global biodiversity. In several examples of Müllerian mimicry, where two or more toxic species resemble each other, a single species is known to resemble more than one model species. This situation would seem to provide a good scenario for speciation: as populations diverge to resemble different models, both pre-mating and post-mating isolation could evolve. *Ranitomeya imitator* is a species of poison frog from central Peru which is involved in Müllerian mimicry with 4 other species of poison frogs. There are four primary mimetic morphs of *R. imitator*, each of which occurs in different geographical regions. We conducted mate choice experiments on four populations (representing two morphs) to determine whether frogs preferred to mate with their own

morph. Furthermore, we designed the study in such a way as to test for reproductive character displacement, that is, whether strength of mate preference (if any) was increased in areas where these two morphs are sympatric. With the exception of one population, we were unable to detect significant mate preferences in *R. imitator*. Furthermore, there was no evidence that the strength of preference was enhanced where these morphs were sympatric. Current research is focused on testing mating preferences on additional color morphs, and using alternative methods for measuring mating preferences.

J-P. Vacher & S. Ursenbacher

Genetic structure of populations of the Smooth snake, *Coronella austriaca* Laurenti, 1768, in Alsace, France

Alsace is a region located in North-Eastern France that displays a high level of habitat fragmentation mainly due to a very dense road network and intensive agriculture. The goal of our study was to measure the impact of fragmentation on the smooth snake, *Coronella austriaca*. Though the species has a large distribution in the region, its actual conservation status is yet to be known. We therefore chose to characterize the effect of fragmentation on the species by studying the genetic structure of populations. The sampling protocol included 12 localities distributed in the different natural regions found in Alsace: mountains, foothills and plain. The distance between the two most distant sites was 80 km. Smooth snakes were found either by sight or with artificial shelters. DNA samples were collected through buccal swabs and exuviae. In order to avoid double sampling, the pileus and neck of each snake was photographed, enabling individual recognition on the field. A total of 108 smooth snakes were sampled in 2009 and 2010. We performed several analyses in order to characterize the genetic structure of populations with 9 microsatellites markers already described for the species (Bond *et al.* 2005). The results are quite unexpected. Indeed, we did not find any genetic differentiation between populations. The mean global F_{ST} value is 0,07. Analysis of genetic structure was also conducted at an individual level by trying to regroup individuals in homogeneous clusters (at the Hardy-Weinberg Equilibrium) using a Bayesian method implemented in STRUCTURE. This approach failed to find differentiation following previously defined populations, as well as any kind of regrouping. Our analysis have neither revealed isolation of populations through distance. Finally, we performed a spatial autocorrelation test which shows that individuals share parental relationship between them up to a distance of about 3 km. Globally, the smooth snake seems to be a rather mobile snake in the region. These results indicate that the dispersal rate should be rather high between population units in order to maintain a sufficient gene flow or that the populations are big enough to avoid any kind of genetic drift. The smooth snake might use corridors made of natural and artificial habitats and microhabitats as railways, roadsides and the miscellaneous elements that are found around these infrastructures (under-road tunnels, concrete boxes along railways...). This shows that the creation of corridors does not seem to be a priority in terms of conservation for the species right now, but rather the management and restoration of habitats and microhabitats. References: Bond J.M., Porteous R., Hugues S., Mogg R.G., Gardner M.G. & Reading C.J. 2005 - Polymorphic microsatellites markers, isolated using a simple enrichment procedure, in the threatened smooth snake (*Coronella austriaca*). *Molecular Ecology Notes*, 5: 42-44.

J. van Delft & A. van Rijsewijk

Embedding single-species conservation into an ecosystem approach: conservation of the Smooth snake in a southern province of the Netherlands

The Smooth Snake (*Coronella austriaca*) is listed as an endangered species in the Netherlands, as well as in many other parts of north-western Europe. To counteract this decline, a “Smooth Snake Platform” was set up, consisting of all relevant stakeholders in the province of Noord Brabant, namely nature managers (even neighbouring Belgians), estate owners, municipalities, water boards and volunteers. This was the outcome of a provincial species protection plan that RAVON had published in 2006 after close collaboration with the stakeholders. The plan resulted in tens of kilometres of nutrient-poor verges being created in coniferous woodland, thus connecting heathland habitats of the snake that had become isolated. Furthermore, in order to connect isolated populations and to improve and enlarge current habitats, tens of hectares of heathland and raised bog were cleared of encroached shrubs and trees and tens of hectares of agricultural land were transformed into nutrient-poor habitats. Besides these relatively large-scale measures, there has been focus on the broad implementation of best practice habitat management. Here, measures comprise fine tuning in the form of piles of logs, branches and turves in raised bogs. In addition, the normally orderly Dutch land managers were made aware of the importance of leaving dead wood on the forest floor and on heathland, and of allowing bramble shrubs to develop as well as patches dominated by *Molinia* and *Deschampsia*. The major part of the many proposals to enhance the snake habitats have now been implemented. In nature management in the Netherlands, a shift is taking place from a single-species approach towards a multi-species, ecosystem approach. Therefore, in this plan other rare and endangered species of heathland and raised bog were also taken into account. Since 2009, to evaluate the effect of the management that had been carried out, a multi-species monitoring has been carried out by volunteers investing some seventeen working days a year! This has led to tens of observations of Smooth Snakes. The results show that the new corridors are being used and that the piles of logs, branches and turves are rapidly being colonised by gravid females. Other endangered species benefiting from the new management are *Caprimulgus europaeus*, *Gryllus campestris*, *Carterocephalus palaemon*, *Zootoca vivipara* and probably even the extremely rare spider *Eresus sandaliatus*. This broad conservation approach engaging all parties, paying attention to more than one species, and bringing together all knowledge on all species and their habitat management, has turned out to be very successful for both the Smooth Snake as well as other fauna and flora.

R. Veen, L. Riviere, R. Dohogne, S. Bogaerts & R. Snep

Dig and dump; a cheap and simple method for population revitalisation in *Bombina variegata*

The Yellow bellied toad, *Bombina variegata*, has experienced local extinctions and population declines in western and north-western parts of its distribution range. It is strongly protected

by the Habitats Directive, but conservation and protection of its habitat by designation of sites alone does not help. In many countries conservation programmes have been set up to save this species with different results. In ten years of active conservation testing different measurements the senior author has developed a new, simple, practical, cheap but most of all very effective method of revitalising declining populations in rural areas based on creating non-permanent breeding habitats which are tailor made to all requirements of *Bombina variegata*.

G. Velo-Antón

Genetic drift and rapid evolution of viviparity in insular Fire salamanders (*Salamandra salamandra*)

Continental islands offer an excellent opportunity to investigate adaptive processes and to time microevolutionary changes that precede macroevolutionary events. We performed a population genetic study of the fire salamander, *Salamandra salamandra*, a species which displays unique intraspecific diversity of reproductive strategies, to address the microevolutionary processes leading to phenotypic and genetic differentiation of island and mainland populations. Our study shows high genetic differentiation and the absence of gene flow among populations, except between the large and admixed interior populations. We find no support for island colonization by rafting or intentional/accidental anthropogenic introductions, suggesting that rising sea levels were responsible for isolation of the island populations approximately 9,000 years ago. This study provides evidence of rapid genetic differentiation on island and coastal populations, suggesting a rapid evolution of viviparity driven by climatic selective pressures on island populations, geographic isolation with genetic drift, or different combinations of these factors. Our study of viviparous island populations in early stages of divergence and ovoviviparous mainland populations will help to better understand the microevolutionary processes involved in rapid phenotypic shifts.

G. Vimercati, M.A.L. Zuffi & J. Nocchi

Areas of thermal activity in a wild population of the Moorish gecko *Tarentola mauritanica* from central Italy

Behavioural and ecological patterns of activity in wild Moorish gecko are still poorly known (Frankenberg, 1978; Gil et alii, 1994; Arad et alii, 1996; Carretero, 2008): we focused our research on diurnal thermal profiles. A quite large population of *Tarentola mauritanica*, living on the antique walls of our museum (NW Tuscany, 15 km East from coastal line), has been studied in past years to describe sexual dimorphism and body size characteristics (Atzori et al., 2007; Zuffi et al., 2011, in press). In order to collect large thermal data set, without capturing and stressing individuals, we preferred to detect thermal data using a laser pointer from short distance (e.g. 3-4 m). Geckoes were studied in 2010 from March to October, from 09:00 am to 18:00 pm (all day period, ADP), on average once a week, and from 11:00 am to 1:00 pm and from 3:00 pm to 5:00 pm twice a week (hourly periods, HP). We recorded 2172 thermal data, on 852 adults,

1080 juveniles and 240 newborns. Main observation frequency is in May, June and September. During ADP, the strongest correlation is between gecko activity (e.g. gecko on the wall, outside crevices), average temperatures and photoperiod. Body temperatures (e.g. dorsumT) of adults are significantly higher than in subadults and juveniles (28.5, 26.1 and 24.4 °C respectively, $P < 0.01$ to 0.005). Morning activity temperatures are lower than those recorded in the afternoon. Dorsal coloration varies during the day time, having basically two patterns, dark in the morning and bright in the afternoon. Despite average temperatures were similar between bright and dark patterns (26.8 and 26.7 °C), their distribution is quite different. During HP, adults have always higher preferred temperatures than juveniles and, in autumn, than newborns. Morning temperatures are significantly lower than afternoon temperatures. Average and median temperatures of bright vs dark coloration does not vary significantly, while distribution of recorded temperatures has a different pattern (one mode vs two modes; difference in kurtosis), suggesting a different behavioural pattern. Temperatures of geckos found inactive (hidden) vs active on the wall vs active on artificial nests are significantly different (Kruskal-Wallis test, $P < 0.001$).

J. Vörös, K. Szabó, I. Kiss, S. Schweiger & D. Jelic

Genetic structure of *Salamandra salamandra* in the Carpathian basin

The fire salamander (*Salamandra salamandra*) seems to be a common species in Central Europe. Previous studies discussing the biogeography of the species did not analyse populations from the Carpathian Basin, although the region has importance in zoogeography of many vertebrate species. In Hungary the fire salamander occurs in several isolated populations in the low elevation mountains, and in the last few years significant new populations have been discovered. One of these new populations was found in the Buda Hills (in the outskirts of Budapest) from where the species was thought to be extinct for about 100 years. The aim of our study was (1) to reveal the genetic pattern of the nominotypical subspecies in the Carpathian Basin (2) to determine the origin of the isolated populations in Hungary (3) to infer the population genetic structure of the newly discovered Buda Hills population. We examined 16 populations from Hungary, Austria, Slovakia, Romania and Croatia. One mitochondrial DNA fragment (D-loop) and ten variable microsatellite loci were analysed. With the mitochondrial DNA we found no variation within the studied populations. Analysing the microsatellites Structure and Geneland revealed four different groups representing a Western clade (Austria, Croatia and Western Hungary), a Northern Carpathian clade (Slovakia and the Hungarian populations from the Northern Mountain Range) and an Eastern Carpathian clade (Romania and the easternmost Hungarian population from Zemplén Mts.). The Population Graphs analysis showed that the Buda Hills population belongs to the Northern Carpathian group, but still represents a separate clade owing to its extremely low genetic variation. The habitat of this small population has become isolated in the last 100 years from the main distribution range of the species, which may have resulted in population bottleneck. It represents the lowest allele frequencies among the studied populations, and has no private alleles.

W. de Vries & E. Govere

Combining amphibian monitoring with schooling in southwestern Spain

In 2011 an amphibian monitoring program was developed for Sierra Norte Natural Park in southwestern Spain. The program was developed by a cooperation between association AMBOR and Fundation RAVON, after five years of surveys on distribution of species and habitats. The designed method combines the collecting of data to follow the development of the amphibian populations and their habitats, with the education and training of local volunteers, while the involved herpetologists guarantee a high quality and reliability of results. The data is collected such that the results can be incorporated in the national Spanish monitoring program (SARE). 116 sites were selected for monitoring twice per year, distributed over nearly all the territory of the natural park (177.000 hectares). From the most vulnerable species minimum 40 known localities with presence of the species were included; from other (national or regional) red data book species that are included on the annex IV of the European habitat directive a minimum of 20 known localities were included; and from the more common species at least 10 sites. 20 sites of each of the more important aquatic habitats for amphibians were included and at least 10 sites from other important or threatened habitats. During two weekends 30 to 40 volunteers executed the surveys including day and night visits to 18 areas and nearly all sites. Each group had an amphibian field guide, nets, torches, foto-aquaria and waders, and by photos the presence of the species was documented. Groups consisted of one experienced herpetologist, one local person that knew the areas and sites and one or two other interested persons (mainly biology students). The combination of these persons made it possible to register amphibians but also create a stimulating and educative environment in which all participants could learn and exchange. Nearly all participants observed all species for the weather conditions were favorable. The positive climatic conditions for amphibians in the winter 2010 to 2011 made it possible to initiate the monitoring program with very positive results in terms of amphibian observations. The complications that were met were mainly on an organizational level, such as organizing the authorizations for sampling amphibians and access private properties. Since a large group of enthusiastic volunteers was created, the continuation of the monitoring is guaranteed.

P. Wagner

Out of the blue: a preliminary review of the African blue-headed agamas (*Agamidae: Acanthocercus*)

Lizards in the genus *Acanthocercus* Fitzinger, 1843 are widespread in wooded savannas from northeastern to southwestern Africa (plus the southwestern part of the Arabian Peninsula). Therefore, they are an ideal group for testing zoogeographic hypotheses of arid corridor distribution colonization events of Africa. However, to test these hypotheses a clear systematic and phylogenetic framework is needed but still lacking. Most of the species occur in the nearly unexplored areas at the Horn of Africa, and therefore our knowledge about these species is sparse. Constructing a phylogeny like this requires the solution of species determination

and a good understanding of species delimitation and the diagnosing characters. In general, higher relationships of species within the genus are poorly understood as well as the relation of the genus itself to other members of the Agaminae. Especially the differences between the subspecies of *A. atricollis* Smith, 1849 and their distribution are poorly known and a review of this group is in need as they are most important to answer zoogeographic questions. In this talk a preliminary phylogeny of the genus is presented to clarify the status of *Acanthocercus* within the Agaminae and to show subsequent taxonomic consequences. Additionally, a first review of *A. atricollis* is presented including an analysis of its distribution and distribution pattern in comparison to other arid species groups.

K.C. Wollenberg, I.B. Wang, R.E. Glor & J.B. Losos

Recurrent convergence in axes of diversification in Hispaniolan trunk-ground anoles (*Anolis cybotes* species complex)

Does evolution repeat itself, or does each evolutionary instance push clades along their own unique courses? And are similar patterns of diversification recurrent over different taxonomic scales? Such scalability of convergence would indicate that the processes shaping evolutionary diversification have remained fundamentally the same throughout a clade's history, and could explain why evolutionary responses seem to be probabilistic. The evolutionary diversification of Caribbean *Anolis* lizards has become a textbook case of replicated adaptive radiation, with the same set of ecological specialists, termed ecomorphs, evolving independently on each island in the Greater Antilles. Although diversification of anoles into ecomorphs on the axes of body size and perch type can explain some of the present Caribbean anole species diversity, within-island diversification most frequently occurred within same-ecomorph clades: consequently, understanding the factors involved in within-ecomorph intra-island radiation is important in understanding the anole radiation in general, and, more specifically, whether intra-clade diversification has occurred in the same general manner as among-ecomorph diversification early in anole history. At an even lower taxonomic level of inference, one might ask whether the processes regulating geographic variation within species also follow the same rules. We investigated the role of environmental factors in the diversification of *Anolis* species on a large Greater Antillean island. We studied the geographical variation in *Anolis cybotes* to understand why diversification occurs in this widespread species, and found that different genetic groups are restricted to distinct environmental conditions. Similarly, most morphological and habitat use variation occurs among these groups. However, another component of ecomorphological variation is related to the environment independently from the genetics of populations: Morphology seems to evolve convergently and adaptively along similar environmental gradients. These found axes of recurrent genetic and morphological differentiation correspond to those observed on higher taxonomic level in anoles, which attributes an important role to these evolutionary processes in *Anolis* diversification.

A. Zagar, N. Osojnik, A. Vrezec & M.A. Carretero

Does presence of con- or hetero-specific male influence preferred body temperatures of two sympatric lacertids? The case of *Podarcis muralis* and *Iberolacerta horvathi*

Species interactions are complex processes derived from a combination of organisms' physiological predispositions and their behavioural and ecological traits combined with their spatial and temporal distribution. Understanding interspecific interactions between two lacertid species should include a multi-level approach. The focus of individual studies should interfere with each other, but the first step should be done separately. *Podarcis muralis* and *Iberolacerta horvathi* are sympatric in almost whole range of *I. horvathi*'s distribution (endemic to Southern Alps in NE Italy, S Austria and NW Slovenia and Dinaric Mountains in Slovenia and Croatia) and display overall similarity in morphometric, coloration and ecological characteristics. *I. horvathi* is more abundant at higher altitudes whereas *P. muralis* shows the opposite trend, suggesting competitive exclusion pattern. One way to understand biological processes of lacertid species on a mechanistic level is to perform experiments investigating preferred body temperatures (Tp), since the use of best basking sites could be source of competition in ectothermic reptiles. For two consecutive years we performed a comparative analysis of Tp with experiments in laboratory thermo gradients (20 -50°C; measurements at 11 hourly intervals) with specimens of both sympatric species to compare interspecific variation. *I. horvathi* selected higher Tps than *P. muralis* but mainly in spring and in the afternoon, in summer and early morning being more similar. *P. muralis* had a broader range of Tp than *I. horvathi*, suggesting it to be more eurythermic. Secondly, we investigated if the presence of conspecific or heterospecific male influences the males' Tp of both species to find out if inference interactions influence Tp. Preliminary results show that the influence of presence of con- or hetero-specific males on Tp was only evident in *I. horvathi*, but not in *P. muralis*.

S.R. Zamfirescu, A. Strugariu, O. Zamfirescu, I. Gherghel & T.C. Sahlean

Activity pattern and microhabitat selection in *Vipera ursinii* from two different eastern Romanian ecosystems

Habitat loss and direct persecution by humans are the main threats for snakes, especially venomous. *Vipera ursinii* is considered the most endangered European viper and in eastern Romania (*Vipera ursinii moldavica*) it persists through very few inland (steppic) and deltaic populations. The ecology of this subspecies is relatively poorly known. Our study aims to compare the activity pattern and microhabitat selection depending on age, sex, and female reproductive status, in steppic and deltaic meadow viper populations, data that can be used for adjusting possible conservation efforts. The study areas lie in steppe patches of continental region of the north-east of Romanian Moldavia and in the Danube-Delta, near the Black Sea coast. The steppic habitats are hill-slopes with small bluffs across, covered mostly by xerophilous grasses, whereas the deltaic one lies on the southern part of a levee and consists of a mosaic of small sandy plateaus, channels and depressions covered with psamophilous and

higrophilous grasses. We recorded and analysed several habitat characteristics in relation to the age, sex and gravidity of the vipers observed during different periods from spring to autumn, from 2008 to 2011. In spring, both in steppic and deltaic populations, the males are the first to emerge in hibernation habitats. After a couple of weeks the first females and juveniles appear. The individuals tend to cluster around the hibernation sites represented by bluffs with relatively low vegetation cover, in the steppic habitats, and by high sandy plateaus covered with tussocky vegetation dominated by *Juncus littoralis* and *Juncus maritimus*, in the delta. Both microhabitats seem to offer optimal conditions in terms of thermoregulation, food supply, and protection against predators over relatively small areas. Males generally do not feed till the onset of the reproduction, which practically commence after the emergence of females. At the beginning of summer, the vipers move diffusely through different microhabitats, except for the gravid females from the delta which continue to inhabit the elevated areas. By the end of summer, the same situation perpetuates for juveniles, adult males, and non-gravid females, whereas post-partum females begin to move through the habitat. In autumn, the vipers, irrespective of age or sex, gather towards the hibernation site. In steppic habitats the low-vegetated bluffs act like a balcony, in the sense that it supplies a flat area for basking at midday, vertical walls for basking in the morning and afternoon and borrows for sheltering. They also permit the water to flow, which allows the vipers to avoid drowning in case of heavy rain or snow melting. In deltaic habitats, floods appear to be the main factor that forces the vipers to take to high ground. Outside the flooding period, gravid females seem to prefer the high-grounded tussocks, which, unlike the densely vegetated areas uncovered by water, supply both open space for basking and shelter against overheating and predators.

O. Zinenko, N. Stümpel, B.S. Tuniev, A.G. Bakiev, L.F. Mazanaeva, O.V. Kukushkin, T.I. Kotenko, A. Strugariu, T. Duisebaeva, R.W. Murphy, N.L. Orlov, N.B. Ananyeva & U. Joger

Phylogeny of small European vipers

All known species and most subspecies of the subgenus *Pelias* (27 taxa, about 1000 samples) were studied using sequences of two mitochondrial (Cytb and COI) and two nuclear genes (Rag-1 and Bach-1). The general topology of the tree of small European vipers was similar to earlier reconstructions (Kalyabina-Hauf et al., 2004; Garrigues et al., 2005; Gvozdik et al., 2007). The number of samples and taxonomic and geographic diversity facilitated a historical biogeographic analysis and a phylogenetic testing of the current taxonomy. In the *kaznakovi* complex, no or only minor differences were detected in the mtDNA genes between *Vipera kaznakovi* and a number of Caucasian taxa (*V. magnifica*, *V. orlovi*, *V. darevskii*). However, two main lineages were distributed on opposite macroslopes of the Caucasus. *Vipera orlovi*, *V. magnifica* and some samples of *V. dinniki* clustered together with northern *V. kaznakovi*, and *V. dinniki*, *V. darevskii* and several specimens morphologically determined to be *V. lotievi* clustered together with *V. kaznakovi* from Turkey and Georgia. In the *berus*-complex *V. b. nikolskii* had a wide zone of introgression with *V. b. berus* and this was characterized by mitochondrial discordance. The South Alpine haplotype of *V. berus* crossed the Alps in the east and was found in Germany. *Vipera renardi* had unexpectedly high haplotype diversity across its range. Hotspots occurred in the Northern Caucasus and Central Asia. The main events in the evolution of the *renardi*-clade included Pleistocene genetic diversification in montane refugia

and independent transitions to lowland steppes in some recent lineages from the Northern Caucasus and the Crimea. Further problems were detected for some newly described taxa: *V. lotievi* was polyphyletic; *V. r. puzanovi* possessed a haplotype that had a wider distribution than the subspecies; *V. r. bashkirovi* and *V. altaica* hardly differed from eastern *V. renardi*. Nuclear DNA data identified cases of natural hybridization between *V. renardi* and *V. berus* in Tatarstan as well as gene flow between lineages in most cases of sympatric or parapatric species. These findings raised important questions about possible hybrid origins of some taxa and the role of hybridization plays in evolution of small vipers.

R. Zollinger, R. de Nooij & A. Spitzen

The Natterjack toad: creating space by giving space, a management plan

Species protection can easily conflict with economic interest. In the Netherlands, the presence of the strictly protected Natterjack toad often leads to conflicts. For one particular region, it is even clear that application of conservation-minded legislation is counterproductive. Therefore, a species management plan (SMP) was specifically created for this region by means of a joint planning process that included all stakeholders. The SMP is a framework for guaranteeing the long-term viability of the population of the Natterjack toad while preventing unnecessary legal procedures. As such, it has both economic and ecological advantages. Thorough ecological studies of the Natterjack toad formed the basics of the SMP, e.g. research on dispersal capacity and home-range by radio-transmitters. Both research and the process of developing and carrying out of the management plan Natterjack Toad will be presented and discussed.

M.A.L. Zuffi, L. Allegranti, V. Casu, C. Giannelli, O. Lanzoni, S. Marino, F. Messina & F.D. Nardi

Size and age related sexual dimorphism and functional asymmetries in the Ruin lizard *Podarcis sicula* from Tyrrhenian coastal areas (NW Italy)

Body size structure largely varies between sexes in *Podarcis sicula campestris* at adult stage, from 61 to 67 mm in snout to vent length and from 5 to 7.7 g in body mass ($n = 109$ females, $n = 139$ males, average values; $t_{\text{testmass}} = 11.703$, 246 df, $P < 0.0001$; $t_{\text{testsvl}} = 8.169$, 243 df, $P < 0.0001$); head size also markedly diverges between sexes, with male heads larger 20% than females (8.1 vs 10.2 mm head width at the maxillary condillies; $n = 109$ females, $n = 137$ males; $t_{\text{testcondili}} = 15.635$, 244 df, $P < 0.0001$). In a smaller intensive study area (sandy coastal site vs grassy and wooded area, 6 km apart), on 44 males and 32 females, we observed that the dorsal bright green colour apparently does not vary intra- and inter-monthly (April-June 2011); capture and recapture sessions during late May early June 2011 (pitfall traps in the sand; 6 males and 5 females recaptured a second time, 1 male recaptured a third time, on first series of 27 captures) shown no variation in dorsal markings (i.e., size and shape) on head, neck or dorsum, allowing us to recognize the individuals as first or second capture individuals. Femoral pores are 20 in

males and 19 in females (average values), and their number is significantly different between sexes (Mann Whitney U test right-sex = -4.048, $P < 0.0001$; Mann Whitney U test left-sex = -3.504, $P < 0.0001$), not between right and left thighs. Femoral pore secretion varies among males: longer, heavier and larger headed individuals show almost all femoral pores active, while smaller males have from 60 to 75% pores active (Spearman rho right pores-svl = 0.359, $P = 0.005$; Spearman rho left pores-svl = 0.370, $P = 0.003$). This could imply a differential sexual function of femoral secretion. Magnified digital images of head scales revealed growth rings and, despite the method should be validated using skeletochronology, we found a good relationship to body size (Spearman rho body mass = 0.452, $P = 0.005$, $n = 35$), showing how larger individuals are actually older ones. Older one with detectable rings is a 3.5 yrs individual, despite several large and very old individuals may reach 4 or even 5 years.

V. Zwahlen, K. Mebert, P. Golay, J-C. Monney, T. Durand, G. Thierry, T. Ott & S. Ursenbacher

Color polymorphism and population genetic in the Asp viper: is local selection stronger than gene-flow?

The asp viper (*Vipera aspis*) is a very polymorphic species, with ground color varying from light grey, dark gray to reddish brown. The subspecies exhibit different dorsal patterns which could be rhomboid (in *V. a. hugyi*), with thin to large dark blotches (in *V. a. aspis* and *V. a. francisciredi*) or with a zigzag band (in *V. a. zinnikeri*) similar to the one displayed by the adder. Melanistic individuals are frequently found in the Alps, representing locally more than 50% of the population. In addition, previous studies demonstrated that the dorsal pattern is substantially affected by abiotic factors, such as temperature or humidity (Golay, 2005). We investigated a mountain massif in the French Alps containing up to 50% of concolor individuals (i.e. showing no or greatly reduced dorsal pattern; see Mebert et al., 2011). This peculiar morph is restricted to a small area and become rare or absent 5 km away from the source population. We consequently took this opportunity to study the gene flow and the morphological differentiation at a small scale in order to understand if local selection or limited gene flow could explain this particular dorsal pattern. A total of more than 220 individuals (about 55 unicolor ones) were captured. Dorsal pattern were noted, DNA samples were taken and the results will be discussed. Golay, P., 2005. Systématique du complexe *Vipera aspis* (Serpentes, Viperidae) en Suisse. Université de Montpellier, Montpellier. Reference: Mebert, K., Zwahlen, V., Golay, P., Durand, T., Ursenbacher, S., 2011, Ungewöhnlich hoher Farb-Polymorphismus in alpinen Aspispvipern in Frankreich – Zufall oder natürliche Selektion? Elaphe 2011, 13-19.

Abstracts to key notes and related symposiums in alphabetical order by first author

S. Böhm

Habitat usage and short-term movements in the Twist-necked Turtle (*Platemys platycephala* Schneider 1792) during the late rainy season in the Nouragues Reserve, French Guyana

The twist-necked turtle (*Platemys platycephala*) is a member of the turtle family Chelidae that has a widespread distribution all over the Amazonian rainforest. Even though the species is known to science for a long time, detailed ecological studies on life history are rare. The aim of this diploma thesis project was to determine which microhabitats were used by *P. platycephala* on a spatial and temporal scale in the primary rainforest of the Nouragues Reserve, French Guyana. To monitor movements, 4 Twist-necked turtles (3 males, one female) were followed using radio-telemetry during a period of 2 weeks in 2009 and 3 weeks in 2010. Turtles radio-tagged in 2009 were using the same areas again in 2010. To determine main activity time, turtles were tracked twice a day in 2010. During dry periods turtles moved less than during days with rainfall. The turtles were frequently encountered resting under logs or in the leaf litter. Habitats used were hilly forest areas, palm swamps and temporary puddles in the forest, which were frequented after or during heavy rainfall. Permanent waterbodies were rarely used. Aquatic habitats had a mean canopy cover of over 80%, pH between 6.0 and 6.5, temperatures between 25 and 27 °C and conductivity between 30 and 50 μS^{-1} . Stomach flushings showed that amphibian eggs and larvae, worms (oligochaetes) and insects (coleopterans) were used as food items. Due to the elusive lifestyle of *P. platycephala*, sample size of animals tracked and stomach flushings was low. This and the surprisingly terrestrial behaviour and the small areas of activity indicate that the species has quite different habitat requirements than previously assumed, which suggests studies on long-term movements and further diet samples are needed. Furthermore, challenges while using GPS systems under dense forest conditions are discussed.

S. Bogaerts, F. Pasmans, D. Donaire, M. Biricik, A. Almasri, R. Alonso & S. Carranza

Fire in the Near East: phylogenetics and biogeography of the Near East fire salamander, *Salamandra infraimmaculata*

The Near East fire salamander, *Salamandra infraimmaculata*, is a poorly studied species. Our aim was to assess the phylogeographic pattern of the Near East fire salamanders. In this talk we present the results of a phylogenetic analysis based on 12S rRNA and Cytochrome b mitochondrial DNA sequences of specimens from over 30 localities including Israel, Lebanon,

Syria, Turkey and Iran. We will discuss historical views and to try to shed some light on its taxonomy, biogeography and evolution.

J. Bourke, T. Ohst, K. Busse, H. Werning, Y. Graeser, W. Böhme & J. Plötner

Chytrids in Chile

Chytridiomycosis is an amphibian disease caused by the chytrid fungus *Batrachochytrium dendrobatidis* (*Bd*) that has been clearly linked to amphibian declines on every continent except Antarctica. In Chile, we examined with histological and molecular techniques, eleven species of frogs in six localities in southern Chile, as well as in archived frogs, with a special focus in Rhinodermatidae family, which has declined in the last years and *Bd* has been suggested as the reason of *Rhinoderma rufum* disappearance. The fungus was identified in three wild populations, but not in the archived Rhinodermatidae. Our findings expand the list of *Bd* hosts to include *Rhinoderma darwini*, *Batrachyla leptopus* and *Pleurodema thaul* and the spatial distribution in Chile to include the most southern *Bd* record (Raúl Marín Balmaceda).

S. Carranza

Phylogeography and evolution of the reptiles and amphibian around the westernmost Mediterranean Basin

The Mediterranean basin has been highlighted as one of the 25 biodiversity hotspots of the planet, increasing the interest of any studies directed to understand how biodiversity is generated and maintained in this region. The Mediterranean Basin has a complex but very well known geological history that dates back to the beginning of the Mesozoic era, some 200 million years ago. During all this time, the geomorphology of the basin has changed dramatically affecting the surrounding biota, which has speciated, evolved and disappeared in accordance to the major geological and climatic events occurred in this area. As a result of its complex and, at the same time, well-known geological history, the western Mediterranean Basin has been the subject of many studies showing that marine and terrestrial barriers can have very complex effects on local faunas and that simple vicariance or dispersal approaches fail to unravel the intricacies of these. However, a combination of molecular phylogenies and molecular clocks have enabled many of the events involved to be unraveled. In some cases, the results are potentially subject to further testing using fossils and archaeological material. In this talk I will use the excellent model provided by the reptiles and amphibians of the Mediterranean Basin and molecular phylogenies to try to understand how biodiversity is generated and maintained in this interesting area of the planet.

Y. Chiari

The long and short of turtle evolution

There are currently more than 300 species of living turtles described. Major questions still remain about how these animals have evolved at both long and short timescales. For instance, at a deeper time, the phylogenetic position of the turtles within Amniotes is still unsolved and represents a much debated topic. Yet such knowledge is indispensable to our understanding of the morphological and molecular evolution of vertebrates. Amniotes includes mammals, birds, and non-avian reptiles (Lepidosauria, Crocodylia, and Testudines). Within this group turtles are placed differently depending on the type of data used (morphology, embryology, fossils, or molecular data) and the type of analyses employed. Competing hypotheses include the placement of turtles with respect to the birds and the other non-avian reptiles. In my talk, I will discuss these different hypotheses and the data supporting them. I will also present preliminary results on how transcriptomic data can shed light on this question. At a shallower evolutionary time, the morphological variation of the turtle shell represents a continuous source of interesting discoveries. The turtle shell is a complex polygenic morphological trait that serves a variety of functions besides providing physical protection (e.g., animal self-protecting, thermoregulation, locomotor performance, physiological functions, and successful mating and reproduction). Thus, the turtle shell is considered to be an important trait for individual survival and fitness. Shell shape morphological variation within and among species has been associated to sexual dimorphism as well to different performances in the above mentioned functions. In my talk, I will give an overview on the existing and currently described intra and interspecific shell shape variation and the factors that seem to explain this variation. I will also briefly present my current work on the evolution of the turtle shell in Galapagos tortoises. To conclude, I will give an overview on the current conservation status of turtles worldwide, discussing the major threats to the survival of the most endangered species in this group. I will use the Galapagos tortoises as an example to describe possible conservation strategies applied to preserve these unique animals.

E.A. Courtois, J. DevilleChabrolle, P. Gaucher, M. Dewynter, J. Chave
& D. Schmeller

Initiation of a long-term study of amphibian species in French Guiana: Project and first results from the Nouragues station

Amphibian population declines and sudden species' extinctions began to be noted at the beginning of the 1980s. Since then, efforts have been made to understand the causes of such losses. Nonetheless, even if the Neotropical Region has a greater species richness of anuran amphibians than any other region in the world, very few long-term data are currently available. Here, we propose a long-term monitoring of amphibian species of the dendrobatidae family in several places in French Guiana and to couple this with a monitoring of parameters that are known to affect amphibian populations: climate, habitat destruction, parasites and

pathogens. In particular, we will follow the occurrence of *Batrachochytrium dendrobatidis* (Bd), an emerging infectious disease which has proved widely destructive to global amphibian biodiversity. A preliminary study has been conducted in 2011 in the Nouragues reserve and showed that CMR (Capture-Mark-Recapture) along transects coupled with audio transects are the best methods for covering a wide range of Dendrobatidae species in a zone.

A.-L. Ferchaud, S. Ursenbacher, L. Luiselli, D. Jelić, B. Halpern, Á. Major, T. Kotenko, J. Crnobrnja-Isailović, L. Tomović, I. Ghira, Y. Ioannidis, V. Arnal & C. Montgelard

From South to North: mitochondrial markers reveal an unexpected colonization route for vipers of the *Vipera ursinii* complex in the Palearctic region

This study aims to elucidate the phylogeographic pattern of the *Vipera ursinii* complex; the taxonomic status of the included taxa and the age of the splitting events have been subject to debate. The objectives are to localize potential refugia and date split events in order to infer a scenario explaining the diversification of this species complex. Sequences of Cytochrome b and subunit 4 of the NADH mitochondrial DNA genes were analyzed for 125 individuals from 46 localities through the entire distribution range of the complex. The phylogeographic structure was investigated using Bayesian and Maximum Likelihood methods. Molecular dating was performed using three calibration points to infer the timing of evolution of the complex. Eighty-nine haplotypes were observed with both genes concatenated. Phylogenetic inference evidenced two main groups referring to the *ursinii* and *renardi* clades, among which several subclades were identified. Samples from Greece (*Vipera ursinii graeca*) constituted the sister taxa of both clades and appeared as the first split among the *V. ursinii* complex. Moreover, three main periods of diversification were revealed mainly during the Pleistocene (2.4-2.0 Mya, 1.4 Mya and 1.0-0.6 Mya). The present distribution of the *Vipera ursinii* complex seems to have been shaped by the Quaternary climatic fluctuations. The Balkan, Caucasus and Carpathian areas were identified as probable refugia. Our results support a South to North pattern of colonization, different from the East to West colonization previously proposed for this complex. Comparisons of mitochondrial genetic distances between taxonomic groups indicate that the taxonomic levels of the different taxa should be reevaluated within this complex in the light of new evidence.

T.J.W. Garner, J. Bielby, J. Bosch, R. Farrer, F. Clare, D. Henk, S. Walker, S. Bovero, G. Sotgiu, G. Tessa, C. Angelini, M. Favelli & M. Fisher

The Ecology and evolution of *Batrachochytrium dendrobatidis* in Europe

Batrachochytrium dendrobatidis (Bd) is now widely recognized as a major cause of amphibian declines in the Neotropics and Australia. While some cases of European amphibian mass mortality and local declines are reported, the picture that begins to emerge is that the effects

of *Bd* in Europe are not as marked as in these other two regions. In this talk, we will present findings from studies of 3 separate amphibian communities to outline some of the hypotheses why the emergence of *Bd* in Europe has not been as catastrophic as it has been in Australia and Central America. We will also present the results of a long term genomics study of the fungus and discuss how the underlying genetics of *Bd* influences disease dynamics.

D. Guicking, U. Joger & M. Wink

Phylogeography of *Natrix* spp.

The genus *Natrix* has a western Palaearctic distribution and contains three recognized species: *N. natrix*, *N. tessellata* and *N. maura*. The latter two occupy equivalent niches and virtually exclude each other in their distribution ranges, whereas *N. natrix* overlaps broadly with both other species. So far only *N. natrix* has been subdivided into subspecies. We analysed complete mitochondrial cytochrome *b* sequences of *Natrix* specimens from the entire distribution range (except *N. natrix* from the Tyrrhenian islands and North Africa) and nuclear ISSR-PCR fingerprints. Of the three main evolutionary lineages identified in *N. maura*, two occur in North Africa, the likely center of origin of this species. Different levels of genetic differentiation in the Iberian Peninsula reflect different times of isolation in the Pleistocene. Nine major mitochondrial lineages were identified in *N. tessellata*, and most of these were supported by nuclear data. The three most basal lineages comprised populations from Iran, Jordan and Egypt, and Greece, respectively. Other lineages were associated with samples from the Turkish peninsula, the Caucasus, the Aral Sea, and the easternmost part of the species' distribution range. A comparison of mitochondrial cytochrome *b* and nuclear ISSR-PCR based phylogenies shows discordance of the two data sets in the northern Turkish peninsula and the Aral Sea, suggesting possible gene flow among lineages. Evidence of post-Pleistocene range expansions was found in Europe and Middle Asia, with glacial refugia most likely located in southern Europe or on the Turkish peninsula and in the Caucasus region. *N. natrix* is the sister group of *N. tessellata*. In the European mainland, it diversified into four mitochondrial lineages, corresponding partly to described subspecies. The Iberian subspecies *N. n. astreptophora* is the sister to all the others, suggesting a western European origin of the species. The age of these lineages and possible speciation are discussed.

V. Helfer, C. Salamin, C. Miaud & L. Fumagalli

Mutiple localized cryptic lineages in southern Alps – a revised phylogeography of the Alpine salamander (*Salamandra atra*)

The evolutionary history of the endemic Alpine salamander (*Salamandra atra*) has been revisited with a sampling of 141 individuals distributed over 48 distinct locations, covering for the first time the whole species range and including all described subspecies (*atra*, *aurorae*,

pasubiensis and *prenjensis*). The results, based on three mitochondrial (totaling 2,138 bp) and nine microsatellite markers, revealed two deeply divergent lineages, largely distributed over the Northern Alps and Dinaric Alps respectively, as well as several localized lineages distributed across north-eastern Italy. This is the first time that a strongly supported evolutionary lineage is described over the whole Dinaric Alps. More interestingly, the presence of several localized and distinct shallow genetic lineages in northeastern Italy, in addition to the yet well-known *aurorae* and *pasubiensis* subspecies, suggests signs of cryptic genetic differentiation, despite few or un-differentiated external morphological traits. Altogether, our analyses put to the fore an unsuspected intraspecific genetic diversity, which is not accounted for by the current taxonomy. It denotes the important contribution of phylogeographical studies to a better documentation of within species diversity and preservation. In addition, our data support glacial survival of this long-lived species in peripheral glacial refugia in the eastern and southern range of the Alps, suggesting that survival in northerly glacial refugia is not limited to species with short generation time. Moreover, a lack of phylogeographical substructure in the northern Alps suggests a rapid leading-edge expansion toward west from an eastern Austria refugial area, closely following the retracting glaciers, suggesting a high dispersal ability of the species. All in all, this study revealed unexpected patterns of spatial genetic variation in the alpine salamander that should foster further research to investigate if the newly discovered lineages exhibit particular adaptations, and should contribute for a better understanding of the effects of climatic oscillations on taxa confined to mountain systems.

V. Khabibullin

Local level as a weak link in wildlife conservation system: *Emys orbicularis* (L., 1758) in South Urals as an example

The complex approach to wildlife conservation must work properly at all scales and levels. In reality, the conservation strategy has different efficiency at different levels: it almost always works properly at the international level, often - at the national and regional levels, but only sometimes - at the local level. At local level we (as conservation biologists) can deal with local authorities and local community. Local government: is the closest level of administration to the community; able to adapt higher level government policies to on-ground actions; manages land use planning; responsible for regulating conservation activities in local government area. Local community should be involved in threatened species recovery for the following reasons: species protection; spreading awareness; local identity; improved relationships; continuity of leadership. As part of local-oriented conservation approach, community engagement in the pond turtle recovery program may include: community involvement in on-ground works; informing and involving local landowners; a basic community education and awareness program; involving amateur biologists in recovery actions; adoption of the species as a local icon. So, it is necessary to include local approach in species conservation, otherwise the theoretically well-designed measures will remain on paper; without the support of regional and local communities and authorities, the future of *E.orbicularis* conservation programs are doubtful. The ineffective local protection of *Emys orbicularis* (L., 1758) in South Urals can illustrate this idea.

A. Krug & H. Proehl

Phylogeographic population structure of European Tree frogs (*Hyla arborea*) in Germany and adjacent areas

For several European amphibian species multiple postglacial colonisation routes have been found, sometimes resulting in hybrid zones in the areas of contact between lineages. Such areas are of particular interest for species conservation. It is essential to maintain these lineages as Conservation Units and prevent them from artificial mixture that would be caused by inadvertent displacement or resettlement projects. In order to identify the population genetic pattern of the European Tree frog in Germany, saliva and tissue samples from a total of 317 individuals from 30 populations were collected and genetically analysed by sequencing the mitochondrial gene cytochrome b (900bp) and genotyping 8 microsatellite loci. Both molecular markers indicated high molecular diversity with up to 4 Cytb haplotypes within some populations and mean expected microsatellite heterozygosity of 0.73. The distribution of Cytb haplotypes further evidenced a genetic division between northern and southern German populations. A Bayesian analysis of microsatellite data divided the study area into four major genetic groups. The discovered population structure will be discussed in reference to their importance for conservation management of this endangered species.

J. Lourenco, J. Claude, N. Galtier & Y. Chiari

Dating the origin of the Testudinoidea

The superfamily Testudinoidea is the most diverse extant clade of turtles. Thanks to its complex distribution, extensive fossil record, and the increasing amount of molecular data available, this group offers interesting opportunities for testing biogeographic hypotheses. Surprisingly, despite recent advances in the phylogeny, paleontology, and molecular dating of major turtle groups, the temporal origin of this group is still largely unknown. To address this issue, we used a comprehensive molecular dataset to perform phylogenetic and molecular dating analyses, as well as the available paleontological data to calibrate the age of the nodes in the phylogeny. The molecular dataset includes the complete mitochondrial genomes of several turtle species including the newly sequenced mitochondrial genome of four new species. Our results revealed an earlier timing for the origin of the modern Testudinoidea than previously reported, raising new questions about the historical biogeography of this group.

A. Martel, C. Adriaensen, S. Bogaerts, F. Haesebrouck & F. Pasmans

Identification of a novel genus of Chlamydiales reveals high prevalence in invasive exotic bull frogs (*Lithobates catesbeianus*) and association with disease outbreaks in captive urodelans (*Salamandra* sp. and *Neurergus* sp.)

Besides chytridiomycosis and ranavirosis, few microbial disease entities have been studied in amphibians. We describe a novel genus, containing at least two new species of *Chlamydiales* from wild, introduced bullfrogs (*Lithobates catesbeianus*) and from captive urodelans (*Neurergus* sp. and *Salamandra* sp.). Bullfrogs (*L. catesbeianus*) are considered a high impact invasive exotic species in Europe that frequently carries infectious diseases such as chytridiomycosis and ranavirosis. In this study, we identified a novel genus and species of *Chlamydiales* in bull frog tadpoles from an introduced, large population in Flanders. Identification of the novel chlamydia was based on the identification of a unique sequence of a 1474 bp 16S rRNA fragment. This novel chlamydia taxon was detected in 71 out of 100 tadpoles examined. The tadpoles examined did not show any signs of clinical disease. A second species of *Chlamydiales* was detected in captive urodelans belonging to the genera *Neurergus* and *Salamandra* based on the 16S rRNA fragment. In these species, the presence of the chlamydiae was associated with severe clinical disease, resulting in high mortality. No other causes for the disease observed were found using histopathological examination, bacterial and viral examination, including PCRs for herpesviruses, iridoviruses and chytridiomycosis. In conclusion, we describe a novel genus of *Chlamydiales* containing at least two novel species in amphibians. Although the association with clinical disease in the urodelans suggests possible pathogenicity of these taxa for amphibians, the pathogenic relevance of the novel chlamydia taxa is not clear at present. These findings emphasize the need for further research into the role of invasive amphibians in pathogen pollution.

M. Pabijan & M. Vences

Phylogeography of the arid-adapted Malagasy bullfrog, *Laliostoma labrosum* (Cope, 1868)

The Malagasy bullfrog is a stout, terrestrial frog widely distributed in open areas of western and central Madagascar. *L. labrosum* is an explosive breeder of lentic waters with a generalized tadpole; larval developmental time is relatively short at about 1 month. We sampled 82 individuals from the entire distribution and examined mtDNA (16S and *cytB*) and 2 nuclear genes (*Rag1*, *BDNF*) and provide one of the first phylogeographical case studies of an arid-adapted, tropical amphibian. Contrary to what is known for most other Malagasy amphibians, we find that only about 2% of a 1092 bp fragment of mtDNA is polymorphic in *Laliostoma*; there is no indication for the existence of cryptic species. The most basal and divergent clade is found in southwestern Madagascar (Toliara). Another major mitochondrial break divides *Laliostoma* populations into those lying north of the Mangoky River (northern 2/3 of the island) and south of the river. The northern clade is further subdivided into two distinct groups: a haplotype-poor clade found in the extreme north of the island and a haplotype-rich central clade. Nuclear gene variation was about 10 times lower than mtDNA variation. It was also somewhat conflicting: while northern populations (Antsiranana, Ankarana) were clearly distinct in all markers, there was very little structure evident in the central and southern populations, suggesting high population connectivity. Overall we find evidence for a southwestern center of high genetic diversity in both mtDNA and nuclear loci indicative of a putative refugium during

periods of unfavorable climate, and a clearly demarcated but much less variable clade confined to the northern tip of Madagascar. A single clade with a possible northern origin has recently expanded across most of western and central Madagascar, while a southwestern mitochondrial lineage has colonized much of the southern part of the island, including sites along the southeastern coast of Madagascar. Our genetic data support a stepping stone model of gene flow resulting in population connectivity over considerable geographical distances. Despite the arid conditions prevailing across most of its range, *Laliostoma* may have a high capacity for individual dispersal.

F. Pasmans, M. Muijsers, F. Vercammen, P. Van Rooij, K. Baert, F. Haesebrouck & A. Martel

Treatment of chytridiomycosis using antibacterial compounds: Columbus' egg?

There is an urgent need for the development of safe and effective treatment protocols against chytridiomycosis in amphibians. Efficacy for itraconazole and voriconazole has been proven in the past. However, the universal use of both antimycotics cannot be advocated due to several constraints such as possible toxicity, high product prices and/or risk of contributing to the development of antimycotic resistant in human pathogens. Chloramphenicol has been mentioned to effectively cure chytridiomycosis. However, toxic side effects of chloramphenicol as known to occur in a number of vertebrate species, have not been studied yet. We studied *in vitro* antifungal activity against *B. dendrobatidis* of ten antibiotic and chemotherapeutic agents. Florfenicol and the combination of trimethoprim and sulfadiazin (TMP-S) showed *in vitro* activity against *B. dendrobatidis* with minimum inhibitory concentrations (MIC) of 0,5-1,0 µg/ml and 8,0 µg/ml, respectively. Mixed cultures of sporangia and zoospores of strains JEL423 and IA042 were killed completely after ten days of exposure to 100 µg/ml florfenicol. After 14 days of exposure to 10 µg/ml florfenicol 75% fungicidal effect was recorded. Ten days of TMP-S incubation at a concentration of 40 µg/ml as well as 8 days at a concentration of 80 µg/ml resulted in complete fungal killing. Zoospores were not 100% killed within 4 days of exposure to 10 or 100 µg/ml florfenicol or 8, 16, 40 and 80 µg/ml of TMP-S as assed using flow cytometry. Because of the apparent usefulness of florfenicol, toxicity of this compound was evaluated by exposing tadpoles of *Alytes muletensis* for 10 days to a concentration of 10 or 100 µg florfenicol /ml water. Whereas exposure to 100 µg/ml resulted in marked toxicity, no adverse effects were noticed at a concentration of 10 µg/ml. Florfenicol concentrations remained stable in bathing solution during a ten day period. In an *in vivo* trial, post metamorphic midwife toads (*Alytes muletensis*), experimentally inoculated with *B. dendrobatidis*, were treated with 10 µg/ml of florfenicol during 21 days. None of the treated animals cleared the infection. We thus conclude that, despite marked anti *B. dendrobatidis* activity *in vitro*, the florfenicol treatment used is not capable of eliminating *B. dendrobatidis* infections from amphibians.

M. Raemy, M. Cheylan, Z. Owen-Jones, C. Faurre, U. Fritz & S. Ursenbacher

Hybridization between *E. orbicularis* ssp. in an old natural and a young artificial contact zones

Hybridization has recently become an important concern for conservation genetics, as hybridization between distinct genetic groups may result in the loss of ecotypes and in outbreeding depression. Hybridization between three subspecies (*E. o. orbicularis*, *E. o. hellenica* and *E. o. galloitalica*) were investigated in an old natural contact zone (Southern France) and in a artificial pond where the three subspecies have been recently introduced (Moulin-de-Vert, Switzerland) using both mitochondrial and nuclear genes (respectively the cytochrome *b* and microsatellites). Genetic analyses revealed high and complex levels of hybridization between subspecies. Microsatellites indicated ancient hybridization between *E. o. orbicularis* and *E. o. galloitalica* in Southern France. Central and Western France populations harboured non-hybrids *E. o. orbicularis*, while South-Eastern populations sheltered *E. o. galloitalica* hybridized with *E. o. orbicularis*. In the population of Moulin-de-Vert, about 70% of the individuals were analysed as recent hybrids. Indeed, the population is presently not in Hardy-Weinberg disequilibrium ($p \leq 0.01$). These results may suggest hybridization between *E. orbicularis* ssp. in the wild and a slight gene flow on both sides of the Rhône River between *E. o. orbicularis* and *E. o. galloitalica*, suggesting that this river is not a barrier to the dispersion of this species.

S. Reinhard, K. Hoffmann, K. Voigt, L. Olsson & A. Kupfer

Rhizomucormycosis in caecilian amphibians

In contrast to the knowledge about infectious diseases such as *Chytridiomycosis* in frogs and salamanders few information is yet available about fungal infections in caecilian amphibians. Several species among the members of the subphylum Mucoromycotina are known to be opportunistic pathogens. Infections caused by the genera *Rhizopus*, *Mucor*, *Lichtheimia*, *Apophysomyces* and *Rhizomucor* do occur predominately in immunocompromised hosts and grow at elevated temperatures in axenic cultures. Laboratory populations of the caecilian amphibian *Typhlonectes natans* (Gymnophiona: Typhlonectidae) abruptly showed symptoms such as apathy and external fungal skin infection, lethal within 24 hours. Although few infections of Mucoromycotina in amphibians are known, this is the first report of an infection by a member of the genus *Rhizomucor*.

L. Russell & T.J.C. Beebee

The effects of landscape on the population genetics of the sand lizard *Lacerta agilis* in the southern United Kingdom

The sand lizard *Lacerta agilis* reaches the western edge of its range in the where it is restricted to habitats on sandy soils and consequently has a limited and patchy distribution. This has

left the sand lizard particularly vulnerable to the effects of habitat loss and fragmentation and the species has suffered significant declines. Sand lizards were sampled from a number of sites within the species' UK stronghold of Dorset and genotyped at 15 microsatellite loci. Individual populations were identified using Bayesian assignment methods. Populations exhibited relatively high levels of genetic differentiation over small geographical distances and differentiation patterns could not be explained by isolation by distance. The effect of the landscape on genetic population structure was investigated at a fine scale in two scenarios: across a series of isolated/fragmented sites separated by natural and artificial barriers to dispersal; and, within a large area of forestry plantation where small patches of suitable habitat are present among larger areas of less suitable habitat. Remotely sensed habitat data was used to create a resistance surface and least-cost path analysis was used to explain genetic population structure within both scenarios.

H. Seligmann

Frameshifted chelonian mitochondrial genes code for additional proteins in presence of antisense antitermination tRNAs and the special case of *Lepidochelys*

In the marine Olive Ridley turtle (*Lepidochelys olivacea*), the +2 frameshifted mitochondrial Cytb gene lacks stop codons, suggesting overlapping genes; other open reading frames code for unknown proteins, frameshifted sequences code for regular mitochondrial proteins, but contain many stops. Alignments between frameshifted proteins and homologues from other turtles reassign stops AGR->Gly, defining a new, overlapping genetic code for overlapping genes in *Lepidochelys*. Proteins coded by frameshifted mitochondrial genes of other turtles are homologous with the unknown proteins from *Lepidochelys*' main frame. Alignments reassign stops UAR->Trp and AGR->Lys, a chelonian overlapping genetic code for overlapping mitochondrial genes (besides *Lepidochelys*). Gene ND4 differs among two *Lepidochelys* mitochondrial genomes available in Genbank: in DQ486893, ND4 coding is normal; in NC_011516, the open reading frame codes for another protein, ND4 is coded by the frameshifted sequence including stops reassigning UAR->Trp and AGR->Lys. Simulation analyses randomly reassigning synonymous codons, conserving main frame coding, show optimization of synonymous codon usages in natural sequences for overlap coding: natural sequences align more frequently, better and for longer stretches than simulated sequences with proteins in Genbank than natural sequences. Potential for overlap translation independently of import of cytosolic tRNAs with anticodons recognizing AGR codons exists: antisense tRNAs matching stops and resembling tRNAs with the predicted cognate amino acids (Trp, Lys; Gly in *Lepidochelys*) occur in most chelonian mitochondrial genomes. Cloverleaf formation capacities of antisense tRNAs with anticodons matching UAR codons coevolve with overlapping gene numbers, confirming translational activity by antisense antitermination tRNAs recognizing stops. Some programmed frameshifts probably code for variants of the usual mitochondrial proteins, but generally, functions of the overlapping coding system remain unknown. A similar overlapping coding system exists in primates, where cloverleaf formation of antisense tRNAs recognizing stops and reassigning AGR->Arg also coevolve with detected numbers of putative

overlapping genes, with indications that the overlapping system is active under anaerobic conditions, high temperatures and/or low resource availability. Hierarchical coding between the regular main and the overlapping coding systems perhaps originated from the dual lifestyle of the presymbiotic mitochondrial ancestor. Physiological requirements perhaps caused switches between regular and overlapping genes and genetic codes in *Lepidochelys*. Convergence suggests that anaerobiosis is a main factor in this: the frameshift-coded variants of some mitochondrion-encoded *Lepidochelys* proteins resemble more homologues from salamanders than from other chelonian species.

R.S. Sommer & U. Fritz

When the pond turtle followed the reindeer: effect of climate change on vertebrate diversity in northern Europe at the end of the Ice Age

The impact of the termination of the last Glacial and the onset of the present Interglacial (Holocene) on large-scale faunal shifts, extinction dynamics and gene pools of species are of special interest in natural sciences. A general pattern of climate-triggered range expansion and local extinction of vertebrate species is known for Europe, and shows that in the modern temperate zone the main faunal change took place mainly during the Late Glacial (14,700-11,700 years ago) and Early Holocene (11,700-9,100 years ago). Based on large datasets of new radiocarbon data, we present precise temporal dynamics of climate-driven disappearance and appearance of reindeer and pond turtle in southern Sweden. These two species are significant climate indicators in Late Quaternary biostratigraphy. Our data reveal that the reindeer disappeared from southern Sweden c. 10,300 years ago, whereas the pond turtle colonized the area c. 9,860 years ago with a 450-year gap between each species. Around 5,500 yrs ago pond turtle records suddenly terminate in Sweden, some 1,500 years before the Holocene thermal maximum ended in Scandinavia and distinctly earlier than previously thought. This extinction coincides with a temporary cooling oscillation during the Holocene thermal maximum. The post-glacial range dynamics of pond turtle and reindeer are a unique model case, allowing insights into the faunal turnover of other vertebrates during the last natural global climate oscillations at the Pleistocene-Holocene transition.

A. Spitzen-van der Sluijs, A. Martel, C. Hallmann, W. Bosman, T. Garner, P. van Rooij, R. Jooris, F. Haesebrouck & F. Pasmans

***Batrachochytrium dendrobatidis* is a widespread pathogen in the Netherlands and in Belgium**

The chytrid fungus *Batrachochytrium dendrobatidis* is considered responsible for the decline in amphibian populations worldwide, being the causative agent of the disease chytridiomycosis. We conducted a retrospective study with museum specimens as well as a large scale screening

of wild populations of Dutch and Belgian amphibians for the presence of *B. dendrobatidis* infections. This screening shows that *B. dendrobatidis* is widely distributed in the Netherlands and in Belgium and infects most indigenous amphibian species. Although *B. dendrobatidis* was found in a museum specimen of *Epidalea calamita* from 1999, no mass mortalities have been observed that could be attributed to chytridiomycosis. *Lithobates catesbeianus* and *Alytes obstetricans* were significantly more infected than other species. Larvae of all species were infected significantly more than adults. Strong variation in prevalence between years was detected for some species. We suggest that *B. dendrobatidis* arrived in Europe during the late nineties of the 20th century and became endemic.

U. Tobler & B.R. Schmidt

Individual level and population level effects of amphibian chytridiomycosis

The fungal disease chytridiomycosis caused amphibian population declines on many continents. We report a summary of our research on the effects of chytridiomycosis on the midwife toad, *Alytes obstetricans*, in Switzerland. In a laboratory experiment, we could show that chytridiomycosis can cause high mortality in midwife toads shortly after metamorphosis. In contrast, when we looked at the effects of the pathogen on population trends or the distribution, including local extinctions, of the midwife toad, we found no negative effects of the pathogen on trends or distribution. Thus, while chytridiomycosis had strong effects on individuals, there were no measurable effects at the level of the population.

M. Vamberger, H. Stuckas, D. Ayaz, L.F. Mazanaeva, H.G. Kami, A.A. Aoufi & U. Fritz

Phylogeography and population genetics of *Mauremys caspica* (Testudines: Geoemydidae)

The West Asian terrapin, *Mauremys caspica*, is widespread throughout Eastern Europe, the eastern Mediterranean and the Middle East. In this study, we used 14 quickly evolving microsatellite loci and mtDNA sequences for gaining insights in its poorly known population structuring and population history. We include 41 populations from the whole distribution range (Turkey, Azerbaijan, Russia, Iran and Saudi Arabia). Previous studies used mtDNA sequences only and found a weak phylogeographic structure within *M. caspica*. However, our analyses using Bayesian algorithms showed a more pronounced geographic structuring. Migration and gene flow among a priori defined populations as well as diversity and divergence indices were also investigated. Furthermore, population demography was studied, providing important information for the conservation of this species.

M. Vargas-Ramírez, H. Stuckas, O.V. Castaño-Mora & U. Fritz:

Extremely low genetic diversity and weak population differentiation in the endangered Colombian river turtle *Podocnemis lewyana* (Testudines: Podocnemididae)

Podocnemis lewyana is an endemic river turtle of Colombia that is endangered due to anthropogenic impact. Using ten unlinked polymorphic microsatellite loci and a 691-bp-long DNA fragment corresponding to the more variable portion of the mitochondrial control region, we investigated genetic diversity and population structure throughout its range. Both neutral markers showed extremely low diversity and weak population differentiation. Our data indicate that the genetic history of *P. lewyana* has been impacted by multiple bottlenecks, local extinction, population expansion, and re-colonization since the Pleistocene. The resulting negligible differentiation pattern was most likely aggravated by the species' small distribution range. Based on weak differences in allele frequencies among populations, we suggest that three regions should be treated as demographically independent Management Units in order to preserve a maximum of genetic diversity: (1) the Upper Magdalena River Basin, (2) the Lower Magdalena + Lower Cauca + San Jorge River Basins, and (3) the Sinú River Basin. Among the Management Units, only low to moderate levels of gene flow were detected that is largely unidirectional from Management Units 1 and 3 into Management Unit 2.

G. Velo-Antón

Turtle carapace anomalies: the roles of genetic diversity and environment

Phenotypic anomalies are common in wild populations and multiple genetic, biotic and abiotic factors might contribute to their formation. Turtles are excellent models for the study of developmental instability because anomalies are easily detected in the form of malformations, additions, or reductions in the number of scutes or scales. In this study, we integrated field observations, manipulative experiments, and climatic and genetic approaches to investigate the origin of carapace scute anomalies across Iberian populations of the European pond turtle, *Emys orbicularis*. The proportion of anomalous individuals varied from 3% to 69% in local populations, with increasing frequency of anomalies in northern regions. We found no significant effect of climatic and soil moisture, or climatic temperature on the occurrence of anomalies. However, lower genetic diversity and inbreeding were good predictors of the prevalence of scute anomalies among populations. Both decreasing genetic diversity and increasing proportion of anomalous individuals in northern parts of the Iberian distribution may be linked to recolonization events from the Southern Pleistocene refugium. Overall, our results suggest that developmental instability in turtle carapace formation might be caused, at least in part, by genetic factors, although we do not discard the influence of environmental factors affecting the developmental stability of turtle carapace. Further studies of the effects of environmental factors, pollutants and heritability of anomalies would be useful to better understand the complex origin of anomalies in natural populations.

B. Wielstra & P. Arntzen

The postglacial interchange of two *Triturus* newts

Hybridization, followed by backcrossing of subsequent generations with the paternal species, can cause mtDNA to be transferred across the species boundary. Such mtDNA introgression can be asymmetric, with a ‘receiver’ species showing mtDNA typical of a ‘donor’ species over a substantial part of its range. On the Balkan Peninsula, two parapatrically distributed crested newts, *Triturus karelinii* and *T. macedonicus*, provide an example of asymmetric mtDNA introgression. Although limited genetic admixture occurs at their contact zone, the nuclear gene pools of these newts have remained isolated. Still, *T. karelinii* mtDNA has been recorded in *T. macedonicus*, at localities far removed from the contact zone. We hypothesize that ‘foreign’ mtDNA was taken up by the ‘receiver’ (*T. macedonicus*) when it geographically replaced the ‘donor’ (*T. karelinii*). According to this scenario, the contact zone between the species has shifted over time, whereas mtDNA reflects the initial position of their contact zone, before the onset of outcompetition. By conducting a comprehensive phylogeographical survey, we accurately delimit the zone of asymmetric mtDNA introgression in *T. macedonicus*. We then built ecological niche models for both crested newt species and project these on current and past climate layers. This allows us to test whether past climate change drove a species overturn in the zone of mtDNA introgression.

Abstracts of posters in alphabetical order by first author

M. Afroosheh & S.M. Kazemi

***Macrovipera lebetina cernovi* (Ophidia: Viperidae), a newcomer to Iran**

The genus *Macrovipera* Reuss, 1927 comprises four species that are distributed in Middle East countries mostly (in west border from north of Africa to Pakistan, the east border). The macrovipera fauna of Iran consist of two subspecies: *Macrovipera lebetina obtusa* Dwigubsky, 1832 that is distributed in western, northwestern, southwestern and center Iran and a doubtful species *Macrovipera lebetina cernovi* Chikin and Szczerbak, 1992, that the occurrence of this species in Iran has been reported in some references (Ananjeva et al., 2006; Rastegar-Pouyani et al., 2008) however, all of these reports base on probabilities and predictions, because its distribution has been extended to Kopet Dagh mountains (northeast of Iran), but after carrying out field work in various regions of North – and Razavi-Khorasan Provinces we report occurrence of this species in Iran according to the reliable identification key: this large snake attaining 2 meters in length. The head is large; the neck girdle is well marked. The body is massive, slightly flattened in the dorso-ventral plane, covered with keeled scales. The head is covered with small scales. Large regular shields are absent. Large supraocular shields are absent. There are 23- 27 rows around the mid-body. Subcaudal scales are arranged in two rows. This taxon normally has semidivided supraoculars, in the ring of scales surrounding the eye, the upper much larger than the others (more than or equal to the diameter of the eye), spots on the back of narrow, elongated across the body, on a ridge merge into a continuous or intermittent narrow band (Pattern of body sometimes darkbrown or melanistic black). So it can be confirmed certainly that this species has passed over Kopet Dagh Mountains, Turkmenistan, and has penetrated to the northeastern Iran. Some species were collected during the field work 2007 – 2010 and some of them were identified in collections Zoological Museum of Sabzevar Tarbiat Moallem University and Zoological Museum of Seyed Mahdi Kazemi in Qom. *Macrovipera lebetina cernovi* is found in the very diverse desert and montane-steppe biotopes. Most frequently it occurs in dry foothills, on mountain slopes with bush vegetation, rocky ravines with small streams and springs, in pistache open woodlands, on precipices in river valleys, on the banks of irrigation channels. It lives with various species like: *Naja oxiana*, *Gloydus halys caucasicus*, *Eryx tataricus*, *Eryx miliaris*, *Eryx jaculus turcicus*, *Eryx elegans*, *Dolichophis jugularis*, *Hemorrhois nummifer*, *Hemorrhois ravergieri*, *Platyceps karelini karelini*, *Platyceps najadum najadum* and *Natrix tessellata tessellata*. It goes into the mountains up to 2500 m above sea level. In these new localities a lowest altitude is about 950 m and highest one is 2700 m.

M. Afsar, B. Afsar & H. Arikan

On a new population of *Rana macrocnemis* (Ranidae: Anura) from Western Anatolia

In this study, a new *Rana macrocnemis* population recorded from Emir Mountains were investigated in terms of morphological characters. The blood-serum samples were analyzed electrophoretically with polyacrylamide disc electrophoresis. The data obtained from this new material were also compared with the relevant references.

A. Altunisik, T. Ergul, S. Gul, M. Tosunoğlu & N. Ozdemir

Age determination and some growth parameters of *Hyla arborea* (European Tree Frog) population inhabited at different localities

Body size and age of two Turkish *Hyla arborea* populations sampled at different latitudes but at equivalent altitudes (Konaklı in the Antalya region and Gelibolu in Çanakkale region) were assessed. Age was determined for 76 specimens by counting the lines of arrested growth (LAGs) in cross-sections taken from phalanges. The maximum observed lifespan was of 4 years in the Konaklı and of 5 years in the Gelibolu population. Age at maturity was estimated 2 years for both populations. The mean body size of males and females of Konaklı population was significantly smaller than those of Gelibolu population. While significant correlation was determined between body size and age in both males and females in Gelibolu population, it was determined in only males of Konaklı population. Endosteal resorption rate was found % 28 of whole Konaklı population while it was found % 50 of whole Gelibolu population.

A. Barth, M. Solé, V. de Souza Andrade & M.A. Costa

Karyotype variation in four Brazilian *Phyllomedusa* (Anura: Hylidae) species revealed by NOR banding and Fluorescent *in situ* hybridization

Phyllomedusa burmeisteri and *Phyllomedusa bahiana* are clustered in the *Phyllomedusa burmeisteri* group and separated from *Phyllomedusa rohdei* and *Phyllomedusa nordestina* which are included in the *Phyllomedusa hypocondrialis* group. These species shows a complex taxonomy. *P. bahiana* was previously considered as a sub-species of *P. burmeisteri* and *P. rohdei* shows molecular divergences and probably contains additional taxa. Karyotype features, such as chromosome number and morphology and location of rDNA sites are useful cytological characters for species differentiation. In the present study, we analyzed the rDNA regions in these four species using NOR banding and 45S rDNA *in situ* hybridization. Ten individuals of each species were sampled in different regions in the state of Bahia, Brazil. Cytological preparations followed the methodology proposed by Schmid (1978) with modifications. NOR banding technique followed Howell and Black (1980) with modifications. For Fluorescent *in situ* Hybridization (FISH) we used the HM123 probe which contains part of the rDNA 45S of *Xenopus*

laevis (Meunier-Rotival et. al 1979) labeled dUTP-Cy3. *P. bahiana* and *P. burmeisteri* showed NOR bands near the centromere in the long arm of the 8th pair. *P. bahiana* showed a heteromorphism in the NOR size. The homomorphic state, with the two short NOR bands was also observed in the population. *P. nordestina* had the NOR localized in the interstitial region of the short arm of the chromosomes. Variation in the number of NOR bands was also observed in two different populations which showed three and four chromosomes with NOR band, respectively. *P. rohdei* showed telomeric NOR and presented a variation of one to four chromosomes with NOR bands in the same population. The results from FISH analyzes coincided with the NOR banding in the four species, confirming the locations and NOR variations observed. Presence of multiples NORs are relatively common in anurans and is regarded as a derived state. The pattern of number and distribution of rDNA sites corroborated the taxonomic classification with insert *P. bahiana* and *P. burmeisteri* in the same group (*P. burmeisteri*) and *P. rohdei* and *P. nordestina* in *P. hypochondrialis* group. Support: UESC (Universidade Estadual de Santa Cruz); FAPESB (Fundacao de Amparo a Pesquisa da Bahia).

E. Başkale

Factors influencing presence and abundance of Lycian salamander *Lyciasalamandra fazilae* (Başoğlu and Atatür, 1974)

Biotic and abiotic factors have considerably affected amphibian distribution, population size, abundance and site occurrence. To investigate these variables in relation to presence and abundance of *Lyciasalamandra fazilae*, Lycian salamander, we conducted field work studies between September 2010 and May 2011 in south-western region of Anatolia where is distribution area. The collection of environmental information was conducted at microhabitat scales (1 x 1 m quadrat) for the purpose of quantifying accurately microhabitat characteristics of individual present sites, and macrohabitat scales (10 x 10 m quadrat) for the purpose of quantifying abundance of species in relation to characteristics of surrounding sites. We used Pearson's correlation coefficients to examine correlations between the variables, and the problem of multicollinearity in multiple regression analyses. The data were submitted to a multivariate analysis at microhabitat and macrohabitat scales in order to investigate the most important explanatory factors influencing presence and abundance of Lycian salamander. According to the results of statistical analysis, slope was found to be important explanatory factor for presence of Lycian salamander while, litter depth, vegetation cover and distance to urban were found to be important explanatory factors for abundance. These results were evaluated and interpreted in term of amphibian conservation and habitat management programs.

M. Biaggini, F. Contini, M. Capula, & C. Corti

Patterns of morphometric and pholidotic variation in *Algyroides fitzingeri*

Lacertid lizards are undoubtedly among the most remarkable reptiles in the Mediterranean area, especially because of their abundance and ecological prominence. Nevertheless, the investigations carried out on these reptiles have been strongly unbalanced with respect to the various taxa studied, with some species achieving the status of study models, and others being virtually overlooked. No doubt *Algyroides fitzingeri* (Wiegmann, 1834), the smallest lacertid lizard of the Mediterranean region, is one of such overlooked species. It is endemic to Corsica and Sardinia (Mediterranean Sea) where it inhabits mainly thermo-Mediterranean areas, seemingly preferring not too arid sites, where bushes, dry-stone walls, rocks and relatively dense vegetation are present. It occurs also at upper altitudes beyond the wooded zone (up to 1834 m a.s.l. on Sardinia). The ecology and morphological variation of this species are still relatively little studied. In this paper we investigated pholidotic and morphometric variation in *A. fitzingeri* to assess the possible pattern of geographic variation of the samples studied. All specimens were obtained from the collections stored in the Zoological Section "La Specola" of the Museo di Storia Naturale dell'Università degli Studi di Firenze, in the Museo Civico di Zoologia of Rome (Italy) and in the Museum und Forschungsinstitut "Alexander Koenig" Bonn (Germany). Six pholidotic characters (dorsal, ventral, collar and gular scales, femoral pores, scales number under the fourth toe) and six biometric measurements (snout-vent length, head width, h. height, h. length, front and hind limb length) were recorded on 135 adult individuals (96 males, 39 females) from several localities of Sardinia (at altitudes between 20 and 1600 m a.s.l.) and two sites of Corsica, using an electronic caliper. Statistical analyses (t-test, ANCOVA, Pearson Correlation, Residual Analysis) were performed on Sardinian specimens to test for variation between sexes and to explore whether and how altitude affects the distribution of morphometric variability. Females (Mean SVL = 37.54 mm) attained larger mean size than males (Mean SVL = 36.57 mm), although this difference was not statistically significant. When considering SVL as a covariate, females were characterized by shorter front and hind limb, and by smaller head (all head measures) than males. Moreover, females had a number of dorsal and ventral scales higher than that of males (Mean dorsal scales: males = 17.02; females = 17.66; Mean ventral scales: males = 20.28; females = 22.50). The analysis performed on altitudinal variation indicates that in males (i) the number of gular scales, (ii) front limb length and (iii) head height increase with increasing altitude. Finally, we performed descriptive statistic on Corsican specimens, because of their small sample size: the results seem to indicate that they are morphologically closely related to the Sardinian ones, but further studies are foreseen to deeper investigate these aspects.

D. Botoni, P. Kapli, C. Ilgaz, Y. Kumlutaş, A. Avci, N.R. Pouyani, B. Fathinia, P. Lymberakis & N. Poulakakis

Phylogeography of the Anatolian lizard, *Apathya* Méhely, 1907 (Sauria: Lacertidae)

Apathya is a lacertid genus occurring mainly in south-east Turkey and its adjacent regions (part of Iran and Iraq). So far two morphological species have been attributed to the genus, i.e. *A. cappadocica* (with five subspecies, *A. c. cappadocica*, *A. c. muhtari*, *A. c. schmidtlerorum*, *A. c. urmiana* and *A. c. wolteri*) and *A. yassujica*. The first of them occupies most of the genus' distribution while *A. yassujica* is endemic of the Zagros Mountains. The topology and the genetic distances retrieved from this study, reveal that *Apathya* is a highly variable genus, which comes in agreement with the high morphological variation found in previous studies. Such levels of morphological differentiation and genetic divergence often exceed those between species of other Lacertini genera that are already treated as full species, justifying our view that the genus requires taxonomical revision. The phylogeographical scenario proposed reveals that dispersal and vicariant events in Anatolia and Southwest Asia throughout the Miocene, Pliocene, and Pleistocene resulted in the present distribution of the genus under study. Key geological event for the understanding of the phylogeography of the genus is the movement of the Arabian plate that led to the configuration of Middle East specifically the formation of the mountain ranges of Turkey and Iran.

J. Brejcha, L. Jeřábková, V. Miller & M Šandera

Distribution and invasiveness of Pond slider (*Trachemys scripta*) in the Czech Republic

Pond slider (*Trachemys scripta*) is in the Czech Republic casual alien species that is attempting to reproduce. The first mention of the pond slider in our area come from 60's of the 20th century. Based on published data, verbal notices and unpublished data we put together a list of 269 records of pond slider in the Czech Republic. In 12 cases we recorded 10 or more individuals. 7 attempts of reproduction were noted. In one case, eggs were successfully artificially incubated for the period of 95 days at the 25,5°C. Data was put into a map. The main areas of occurrence are regions with warmer climate and higher residential density. Locally pond slider may affect native species of flora and fauna, but on basis of current state of knowledge it cannot be described as pest species. Sliders are found in more than 99% at a distance of 750 meters from the addressable point and altitude to 451 m above sea level. In the wild of the Czech Republic there are records of some other taxa of non-native freshwater turtles which are available on the market. There are turtles of genera *Chelydra*, *Graptemys*, *Mauremys* and *Pseudemys*. These turtles are able to survive in natural conditions of the Czech Republic for several seasons. Our goals in the near future are: A website with information not only about the possibilities for unwanted turtles, studying reproductive biology of pond slider and other monitoring and evaluation of distribution of alien freshwater turtle species in the Czech Republic. Project is supported by Museum of Nature Czech Paradise (Muzeum Přírody Český Ráj). Interim results were used for the bachelor thesis, Brejcha (2010), published in bulletin of Czech Herpetological

Society: Herpetological Informations (2009 and 2010) and provided for the global database of invasive species led by the Invasive Species Specialist Group under the IUCN.

R. Cabral, F.S. Campos, D. Brito & M. Solé

What's the effectiveness of protected areas for amphibian conservation in Brazil?

Amphibians are the most threatened vertebrate group in the world. One of the main conservation strategies to preserve threatened species is the establishment of protected areas. Currently, 32% of amphibian species worldwide are threatened and 25% are Data Deficient. We conducted gap analyses to observe if the protected areas in Brazil cover the geographical range of the amphibian populations in the country. Species range data were obtained from the International Union for the Conservation of Nature (IUCN), which were overlapped to the Brazilian protected areas, using the software ArcGIS 9.3. We evaluated 646 species of amphibians and selected only the areas with a strict protection (IUCN categories I to IV). The Brazilian territory was divided into cells of 0.5° by 0.5°. Only cells that had more than 25% of their area covered by protected areas were considered as protected. An Index of Integral Protection (IIP) was calculated for families of the unprotected amphibians in Brazil, through the number of unprotected species per family divided by the number of species of each family. Linear regressions were performed to verify if there is a correlation between these values. A total of 121 (20%) of the Brazilian amphibian species are not protected by the current protected area network. Among these, 71 (64%) are classified as Data Deficient (DD), 12 (9%) are Threatened (VU, EN, CR), 5 (3%) are Near Threatened (NT) and 31 (24%) are Least Concern (LC) according to the IUCN Red List (IUCN, 2010). The amphibian family with the largest number of unprotected species was Hylidae (33%). However the analyses of linear regression showed a high correlation between the number of non-protected species in each family with the number of species of each family ($R^2 = 0.86$; $p < 0,001$). Considering this bias, the results of the Index of Integral Protection indicated the family Eleutherodactylidae as the most unprotected amphibian family in Brazil (IIP = 0,5). Among the unprotected species, there is a large number of Data Deficient species. The absence of knowledge about species distribution may hide threatened species and makes the development of new protected areas less efficient. Species with restricted distribution are more likely not to be included in the protected areas network, as corroborated in our analysis. Assessments like this can provide the basis for systematic conservation planning, since our results alert that the creation of new protected areas is necessary.

V. Cafuta

Identification of native Slovenian snake species from poorly preserved snake sheddings – preliminary results

Snake shedding (also exuvium, shed skin, slough) represents a perfect imprint of snake's scalation. With a completely preserved shedding, a species can usually be easily determined by

using known identification characteristics (head scalation, number of dorsal scales, absence/presence of keel on scales, etc.). However, problems arise when the shedding is poorly preserved and consequently the available identification keys can not be used. The aims of this study were (1) to establish a comparative collection of snake sheddings of all 11 native Slovenian snake species, (2) to find new identification characteristics of sheddings to differentiate between these species and finally (3) to make a key for identifying native Slovenian snakes from poorly preserved snake sheddings. Most of the sheddings were collected by members of *Societas herpetologica slovenica* between 1997 and April 2011. The collection contained 348 sheddings of all the native Slovenian snake species. 300 sheddings were collected in the wild in Slovenia (86% of all sheddings), 29 sheddings in the wild in other countries (8%) and 90 sheddings were acquired from terrarium animals with unknown origin (5%). The most represented species was *Hierophis viridiflavus* (90; 25.9%), followed by *Zamenis longissimus* (46; 13.2%), *Coronella austriaca* (41; 11.8%), *Natrix natrix* (41; 11.8%), *Natrix tessellata* (29; 8.3%), *Vipera ammodytes* (25; 7.2%), *Elaphe quatuorlineata* (17; 4.9%), *Telescopus fallax* (9; 2.6%), *Vipera aspis* (3; 0.9%), *Vipera berus* (2; 0.6%) and *Hierophis gemonensis* (1; 0.3%). There were also 44 unidentified sheddings (12.6%). Only 26.7% of all sheddings were almost completely preserved (most parts of the head, body and tail intact). The preliminary results show that there are characteristic differences between sheddings of different species especially in (1) coloration, (2) number, position and size of apical stigmata and (3) shape and micro ornamentation of dorsal scales. These characteristic differences should allow to make the first key for the identification of native Slovenian snake species from shedding fragments and maybe even from sheddings of separate scales. However, it is necessary to first obtain additional sheddings to enlarge the sample size for several species with least sheddings in our collection.

D. Carneiro, E. García-Muñoz, A. Kaliontzopoulou, G.A. Llorente & M.A. Carretero

Comparative ecophysiological traits of two *Podarcis* wall lizards from NE Iberia

Differences in ecophysiological characteristics may contribute to determine habitat use and geographic range in lacertid lizards, even if a considerable phylogenetic influence has already been demonstrated, especially for thermal traits. Assessing ecophysiology in sympatric species of different origin may be particularly elucidative on the contribution of the different factors involved. Two *Podarcis* species partly overlap in NE Iberian Peninsula: *P. liolepis*, widely distributed in NE Iberia but restricted in SE France; and *P. muralis*, restricted to mountains in Iberia but widespread across the rest of Europe. Two ecophysiological tests were performed with ten adult males and females of both species. In the first one, preferred body temperatures (T_p) were measured in photothermal gradient at 10 time intervals. In the second one, the water loss (WI) rates in sealed chambers during 12 hours. Although both species did not differ in overall snout vent length, while males were longer than females in *P. liolepis*, the opposite trend was observed in *P. muralis*. Although (pregnant) females have lower T_p s, no differences between species were detected. However, *P. muralis* displayed higher WI than *P. liolepis*, in the second half of the experiment. These differences persisted even if corrected for initial body mass. These results suggest that environmental humidity and not temperature, together with

the presence of a congeneric saxicolous species, may be responsible for the restricted range of *P. muralis* in Iberian peninsula.

*Y. Chiari, J. Crnobrnja Isailović, K. Poboljšaj, B. Halpern, T. Gent, C. Ayres, J-P. Vacher, B. Farkas, G.F. Ficetola, S. Salvidio, M. Raemy, M. Vamberger, S. Thienpont, S. D'Angelo, D. Ballasina, M. Barocci, A. Bonardi, L. Bottoni, L. Canalis, A. Centeno, S. Crosetto, R. Dankovics, N. D. Sabec, V. Ferri, P. Filetto, P. Genta, T.G. Molnár, M. Govedic, N. Greggio, G. Gyorffy, R. Jesu, T. Kovacs, I. Kiss, L. Luiselli, G. Mesaros, S. Masin, S. Mazzotti, F. Montanari, M. Noguer I Plana, D. Ottonello, T. Pechy, L. Sala, S. Scali, T. Somlai, G. Takacs, G. Tedaldi, S. Ursenbacher, F. Vianello & A. Zagar

* Names order is as following: 1) members of the SEH-Conservation Committee in order of contribution, 2) co-authors in order of contribution, 3) alphabetical order for equal contribution of the rest of the co-authors

European conservation projects on *Emys*

Emys orbicularis is a freshwater turtle species widely distributed in Europe. Natural populations of this species show evidence of decline throughout the species European range. This species is considered “near-threatened” based on IUCN categories and protected through the Habitat Directive and Bern Convention on European wildlife. Numerous conservation projects have been developed independently in different European countries. We here present a summary on the projects for which we collected data up to this point for France, Hungary, Italy, Serbia, Slovenia, Spain and Switzerland. Our data collection indicates that conservation efforts toward the management and protection of *Emys orbicularis* are generally not coordinated across Europe or within each country and mostly occur at a local level involving a single site or one limited area. Furthermore, these conservation projects are not equally distributed across the species range in any country. Most projects are financed by local authorities, with some cases where funding have been provided by private companies, organizations and conservation societies. Data collected so far have identified current LIFE programs involving the protection and monitoring of *Emys* in Italy, France, Slovenia and Spain. However, a search of the European Commission official database of the LIFE program using the keyword “*Emys*” indicates that from the year 2000, 21 LIFE projects took place in distinct European countries, including (beside Italy, France, Slovenia, and Spain) Hungary, Lithuania, and Latvia. Despite the benefits of coordination across Europe, exchange of information, and financial support through the LIFE program, only a few European countries, local park authorities or research institutes currently benefit from these programs. In all countries habitat disturbance and destruction due to the intensification of the agriculture and urbanisation are the primary causes of the decline of this species. Other threats include road and human killing and competition with invasive species. According to our data, ongoing conservation projects on *Emys* focus on the monitoring of the existing populations, habitat restoration - including the construction of corridors to allow migration among fragmented populations and the construction of sites suitable for the reproduction, basking and ecological needs of this species -, reintroduction of genetically compatible individuals, and monitoring of the reproduction and offspring survivorship. Most projects focus only on one of these aspects and a very few projects

also include public education and awareness rising. We feel that improved communication, information exchange and coordination among the people leading these projects would allow improving the conservation efforts across Europe. We finally address the situation of *Emys orbicularis* in the UK. Remains of this species have been found in Eastern England dating back some 5,000 years indicating that, since the last glaciation the species did occur in the UK. Occasional contemporary records of the species are presumed to be of escaped/ released non-native animals but further studies would be required to confirm the origin of these individuals. Moreover, the persistence of the species opens up the question about the relevance of conserving this species in countries that are outside its current known range.

A. Drechsler, K. Freund, S. Kuenzel, J.S. Hauswaldt & S. Steinfartz

Fast and effective development of microsatellite loci for European newts by 454-sequencing of tetra-nucleotide enriched microsatellite loci libraries

Development of microsatellite loci for non-model research organisms is still a time consuming and/or expensive endeavour, especially if the price that professional companies charge for developing microsatellite loci is considered. Next generation sequencing, such as the 454-sequencing approach, makes it now possible to sequence large genomic areas of a specific focal species at rather low costs. Here, we describe an approach that combines 454-sequencing of tetra-nucleotide enriched microsatellite loci libraries and subsequent development of microsatellites for three distinct European newt species: the crested newt (*Triturus cristatus*), the palmate newt (*Lissotriton helveticus*) and the Pyrenean newt (*Calotriton asper*). We describe the rather simple and straightforward enrichment of microsatellite loci libraries, the 454 sequencing approach and the final development of microsatellite loci that are polymorphic in the respective populations of each focal species.

A. Drechsler, D. Ortmann & S. Steinfartz

Applied conservation genetics on a strong decimated population of Crested newts (*Triturus cristatus*) in Krefeld (Germany)

In the course of restructuring the palace garden in Krefeld (Germany) the water body of the „Greiffenhorstpark” was desludged and a bentonite ground was inserted in the year 2001. During this measure 4.390 adult individuals of great crested newts (*Triturus cristatus*) were found, the largest direct evidence for a population of *Triturus cristatus* across its range still until today. From 2004-2006 a monitoring of the population of the Greiffenhorstpark showed that the formerly largest population on record shrank to less than 100 individuals. From 2008-2011 another monitoring combined with a conservation genetic approach focused also on 26 additional occurrences of crested newts in that area. On the basis of more than seven

years of monitoring and sampled 2.400 individuals for genetic analysis, this study will combine demographic aspects with population genetic data for this species to a so far non-reached level. A management plan based on insights of demographic and genetic structure should allow stabilising this former outstanding population in terms of population size.

B. El Marnisi, S. Fahd, U. Fritz & A. Khamlichi

Demography and ecology of a population of the European pond turtle (*Emys orbicularis*) from the Jbel Khizana (western Rif Mountains, northwestern Morocco) (Reptilia: Testudines: Emydidae)

The European pond turtle (*Emys orbicularis*), having a wide western Palearctic distribution range, occupies in Northern Africa only a relictual, limited range in the northern mountain ranges of the Maghreb. The species reaches its southern limit in Morocco, where records are known from the coastal region of the Atlantic Ocean, the Middle Atlas and the Rif Mts. Our study population is from a wetland in the Jbel Khizana (western Rif Mts). Studies were conducted at this site from March to June 2006. The estimated individual density of pond turtles there is about 1 individual per m². The population consists of 46% of females, 38% of males, and 16% of juveniles, with a sex ratio being slightly biased towards females (1.25 : 1). There is a pronounced size difference between the two sexes (straight-line carapacial length 124.8 ± 6.3 mm in females vs. 120.1 ± 10.4 mm in males). In adults and juveniles, a marked sexual dimorphism occurs with respect to the following characters: shell height, gular scute length, anal scute length, tail length, and weight. During the study period, no significant differences were found with respect to the activity of males and females. Our preliminary results serve as a basis for more detailed investigations, in particular regarding the conservation of the species and of its habitat. *Emys orbicularis* is an endangered species in most of its distribution range, and this is especially true for Morocco, where it is the most endangered chelonian species.

T. Ergül, A. Altunışık, S. Gül & N. Özdemir

Analyzing the population structure of *Hyla savignyi* from different altitudes in Turkey

Body size and age of two *Hyla savignyi* populations from different altitudes (Şanlıurfa 476 m and Hatay 10 m) in Turkey were analyzed. Age was determined for 105 individuals by counting the lines of arrested growth (LAGs) in cross-sections taken from phalanges. Maximum longevity was determined as 6 years for Şanlıurfa population and 5 years for Hatay population. It was found that mean body size of males are smaller than those of females for both populations. Significant correlation was determined between body size and age in males for both populations. Significant differences were found in terms of body size and age for males showing that Hatay males were significantly larger and older than those from Şanlıurfa.

Comparisons with the average size and age observed in the populations confirmed the effect of altitude in the *Hyla savignyi* populations.

A. Feldman

Drivers of snake richness differ geographically

Temperature is considered to be the most important factor affecting reptile richness. However, large scale analyses of the relationship between different climatic variables and snake species richness are scarce. Further more, Different parts of the world have unique climatic patterns, and whereas temperature might strongly influence snake richness in cold regions, in hot and dry regions (such as deserts), high temperatures may be a limiting factor. In such regions factors such as productivity and habitat heterogeneity may more strongly affect snake distribution. I studied the effect of temperature, precipitation, elevation range and environmental productivity on snake species richness in different parts of the world: Australia, North America (Mexico to Canada) and the Middle East (Israel, Egypt, Jordan and Arabia). Using AIC weights I found the best fitted model for each region. The best model for Australia included all four candidate variables, whereas the model for the Middle East excluded elevation range, and that for North America excluded precipitation. The amount of variance explained by the models differed between regions, being much higher in North America than elsewhere. The relative effects of different variables were not the same in all regions: Temperature was the single best predictor of snake richness in North America, whereas precipitation was the single best predictor of snake richness in the Middle East and in Australia. Furthermore, temperature was positively correlated with richness in Australia and in North America, but was negatively correlated with snake richness in the Middle East. Snake species richness is thus driven by different factors in different parts of the world, a point to consider when drawing inferences from global models.

M. Flecks, F. Weinsheimer, W. Böhme, S. Lötters & D. Rödder

Estimating population size of the Turquoise dwarf gecko *Lygodactylus williamsi* based on available habitat

Population size of the endangered Turquoise Dwarf Gecko *Lygodactylus williamsi* was estimated using a simple, habitat-based method. The species is endemic to a few small forest fragments in eastern Tanzania, where it exclusively dwells on *Pandanus* trees. By categorizing the vegetation and assessing *Pandanus* abundancy, the available habitats for the species were enumerated. Given that the geckos are uniformly distributed and number of specimens per *Pandanus* plant is constant throughout the range, the potential population size can be inferred from the available habitats. Our results are supported by empirical observations.

J.T. Gal, K. Szabo & J. Vörös

Effect of *Batrachochytrium dendrobatidis* on an amphibian community in Hungary

The present study aims to reveal the prevalence, intensity and abundance of the amphibian chytrid, *Batrachochytrium dendrobatidis* in an amphibian community in Hungary. The pathogen was detected first in the country in 2004 and is still present at many locations. A previous study showed high prevalence of a juvenile yellow-bellied toad (*Bombina variegata*) population in Iharkút, Magas-Bakony, in a permanent lake close to an open Bauxit mine. Our objective was to analyse this affected area and find out which species and which developmental stage is most susceptible to the chytrid fungus within this amphibian community. We also examined whether the prevalence, intensity and abundance of the pathogen differs between seasons. We examined 241 specimens of 8 taxons and found *Bd* on 26 specimens (22 *Bombina variegata* and 4 *Pelophylax sp.*), however none of them showed the clinical symptoms of chytridiomycosis. During our field work, we did not find any dead amphibians either and there was no sign of population decline. The prevalence within the entire community was 0,108. The statistical analyses showed significant difference in prevalence between juvenile *B. variegata* and *Pelophylax sp.*, indicating the first species to be more infected. Moreover, we found evidence that both the prevalence and the mean intensity was higher in the yellow-bellied toad population during the spring. Despite the fortunate fact that chytridiomycosis seems to be absent from Hungarian amphibian communities, constant monitoring of the presence of *Batrachochytrium dendrobatidis* is needed.

E. García-Muñoz

Effects of agrochemical binary mixtures on three Iberian amphibians

Agrochemicals are used to improve agricultural production and to controll undesirable plants and animals. Effects of these chemical compounds in non-target organism are difficult to evaluate, among others causes, due to the chemical interactions and/or combinations that occurs in ecosystem. Amphibians epitomize the worldwide biodiversity loss, which has been named as the “sixth mass extinction”. In addition, agrochemicals have been proposed as one of the major threat of these vertebrates. Ammonium nitrate, is one of the most commonly used fertilizers worldwide, and is known to produce negative effects on anuran tadpoles, including increased mortality, anatomical abnormalities and delayed growth and development. On the other hand, copper sulphate is used as fungicide during spring and autumn and also causes effects on survival, growth and development. Both chemicals co-occur in aquatic ecosystem where amphibian larvae are present. In this study three Iberian amphibian, was used in static toxicity tests under laboratory conditions. Effects on mortality and total length were analyzed under different combinations of both chemicals at sublethal concentrations. The concentrations used in this study are environmentally relevant, and occur in several wetlands where these species inhabit. Results showed that these amphibian larvae were high sensitive to this heavy metal exposure and sensitive to this fertilizer exposure. In addition, results obtained

in binary mixtures show the complexity of the effects, that chemicals combinations generate on aquatic organism. Furthermore, different responses were found at different exposure time and at different chemical combinations of both chemicals in mortality and length. The results obtained in binary mixture tests show the complexity of the effects that chemical combinations generate on aquatic organism.

E. García-Muñoz, V. Gomes & M. Ángel Carretero

Lateralization patterns in escape behavior are not universal in *Podarcis* lizards

Recent studies evidenced brain lateralization in ectotherms occurs and propose that the right eye/left hemisphere is involved in predatory behavior while food searching while the left eye/right hemisphere seems to control predator monitoring, making lateralized individuals able to carry out both tasks simultaneously. However, most of these studies are based on a single species (among reptiles *Podarcis muralis*), and these results are assumed as general. Here we studied the lateral component of the escape behavior in three different lineages of the *Podarcis hispanica* species complex. A total of 10 male and 10 female adults were tested 10 times using a “T” design, during two different days (five races per day). Statistical analysis was made using *Log Linear* analysis. The results showed that, although, there is lateralization in escape behavior, it varied between the studied lineages. While the first one lineage present $\approx 80\%$ of right preference, the second one present $\approx 60\%$ and the third one lineage tested showed $\approx 50\%$ of preference to the right part. Interaction between *lineage*side* was statistically significant whereas, no differences in the interactions *sex*side*, and *sex*lineage*side* were found. Result advise against generalizing results on lateralization tests and recommend broader comparative research on this topic. In addition, the possibility that the individual learning between subsequent races, of escape behavior, is discussed.

P. Geissler

Ecological comparison of two convergent species of stream dwelling lizards: *Tropidophorus cocincinensis* (Scincidae) and *Potamites ecleopus* (Gymnophthalmidae)

Among around 80 lizard species in freshwater habitats, convergent morphology has evolved in several phylogenetic lineages in the families Gymnophthalmidae, Scincidae and Varanidae. The highest diversity of freshwater lizards is observed in the neotropical and the oriental realm. Both, the genus *Tropidophorus* from South east-Asia and the genus *Potamites* from South America are distributed along small forest streams and show astonishing similarities in morphology like dorsal crests and laterally flattened tails. Only few is known about the ecological niches of this convergent lizards. In this study, ecological data of *Tropidophorus cocincinensis* DUMÉRIL & BIBRON, 1839 and *Potamites ecleopus* (Cope, 1876) are compiled from

literature as well as own field work and compared statistically. Similarity is measured according to prey utilization, microhabitat use, activity pattern, and temperature preference. Niche breaths and overlaps are calculated.

M. Gidis & I.E. Cevik

Concentrations of some heavy metals in water and sediments from some habitats of *Trionyx triunguis* in Turkey

The present status of the Nile Soft-Shelled turtle (*Trionyx triunguis*) populations of Turkey was surveyed and intensive studies were carried out at Kukurtlu Lake-Mugla, Seyhan River-Adana and Paradeniz-Mersin, which are the most important sites in Turkey. Concentrations of heavy metals (Cd, Cr, Cu, Fe, Mn, Ni, Pb, Zn) were measured in water and sediments in Kukurtlu Lake-Mugla, Seyhan River- Adana and Paradeniz-Mersin. Cd, Cr, Cu and Fe concentrations were below the detection limit in water. The mean concentrations in water were analyzed as; Pb>Mn>Ni>Zn in Lake Kukurtlu, Pb>Mn>Zn>Ni in Seyhan River and Zn>Mn>Ni>Pb in Paradeniz. Results for levels in water were compared with national and international water quality guidelines. Zn concentration was detected high in Seyhan River and Paradeniz. The mean concentrations of Cu, Fe, Mn, Pb and Zn in sediments were analyzed consequently as; 1,355; 42,41, 8,88; 0,3; 1,017 mg L⁻¹ in Lake Kukurtlu, 5,93; 88,21; 30,9; 0,186; 6,105 mg L⁻¹ in Seyhan River and 0,737; 16,26; 6,66; 0,15; 0,243 mg L⁻¹ in Paradeniz.

J. Glos, A. Strauß, R.-D. Randrianiaina, U. Struck, S. Handreck, J. Canitz & M. Vences

Assessment of trophic structure through stable isotope analysis in hyper-diverse larval amphibian communities

Indirect measures constitute the preferential methods in trophic ecology when direct analyses are either difficult to perform or to quantify (e.g., direct observations), or are not permitted by national statutes (e.g., removal experiments) or in contrast to rules of good scientific practice (i.e. dissection). The analysis of stable isotopes is a recent yet well-established and easy-to-perform method that can be used to assess a variety of relevant parameters in food web ecology. In our study on hyper-diverse larval amphibian (tadpole) communities (>20 species in a 30 m stream transect) in streams of a montane rainforest in Eastern Madagascar (Ranomafana NP) we analyze the structure of food webs using stable isotope analysis. Isotopic signatures distinguished between trophic groups of amphibians. Including isotope analyses on the syntopic invertebrate fauna and natural food sources of tadpoles (e.g., algae, organic detritus), we show that in general tadpoles are intermediate links in the aquatic food web. We highlight the trophic position and ecology of different eco-morphological groups of tadpoles and of functionally unique taxa (e.g., sand eating tadpoles). Analyzing food webs of this larval community and food webs of the adult community in the adjacent terrestrial habitat (in an ongoing study) makes the Ranomafana anuran assemblage an outstanding and excellent system to study and compare trophic structures of different life history stages and the role

of amphibians in the entire food web as both habitats are used by the same species as larvae (freshwater) and adults (terrestrial habitat).

J.E. González-Fernández

Evaluation of scientific collections: a model case, the Iberian-Balearic amphibians preserved in the natural history collections

We present a museological study of the scientific collections from an analytic perspective, overcoming the classical historical approach undertaken until now. For this purpose used the group of the Iberian-Balearic amphibians preserved in the Natural History collections. A comprehensive compilation of the information available in more than 60 collections of this group has been used as a model case to analyse the collection concept, its utility, reliability and validity. We requested information about Iberian-Balearic amphibians to 260 Institutions which probably housed these specimens into their zoological collections. We obtained positive answer from 65 Institutions. This Information allowed us to make a catalogue of the Iberian-Balearic amphibians preserved in the Natural History collections. Also we have evaluated the validity of the batracological collections and their contents as scientific tools in different research areas such as: (1) Taxonomy and Nomenclature (2) Chorology and Zoogeography (3) Ecological Biogeography (4) Biogeography, Genetics and Conservation (5) Scientific education. (6) History of the collections (7) Anatomy and Morphology (8) Evolution and Development (9) Evolutionary Chorology (10) Phylogeny and Molecular Taxonomy. We used different statistical methods to analyze the information related to collection specimens, and also the information inferred by us (for instance: UTM 10x10 Km coordinates) We made tables of results that we used to make correlations between analysed variables, to know the capacity of each variable to infer others. Finally we made several cluster analysis where the operational taxonomic units (OTUs) are each of the different Iberian-Balearic amphibian collections. In conclusion, concerning the evaluation of the zoological collections of Iberian-Balearic amphibians, the total number of the preserved amphibians in each collection is an important factor to determinate its value, but it is not the only relevant one. The collection value is influenced by other factors that aren't directly correlated with the total number of specimens, such as randomness in sample origin, inclusion of type specimens, presence of samples of tissues or DNA extracts, or the endemism of the preserved species. On the other hand, the total number of specimens is a highly correlated factor with geographic location and potential georeference. This fact is extremely interesting in light of the wide spectrum of possibilities that this geographic information offers in relation with different research disciplines. We also must to into take count other factors that influence collection quality, such as the presence of type specimens, essential for taxonomic revisions, or the preservation of samples of tissues and DNA, or the presence of stained and cleared skeletons that allow evo-devo studies. In short we can affirm that while quantity (number of specimens) is important, other factors are needed to build collection quality.

S. Gul, N. Ozdemir, B. Kutrup, A. Altunisik & T. Ergul

Systematics of Treefrogs (*Hyla*, Hylidae, Amphibia) in Turkey based on mitochondrial dna sequence

Despite previous work on the phylogeny of Palearctic *Hyla*, several problems still exist regarding systematics of *Hyla* in Turkey. The systematics of treefrogs (*Hyla orientalis* and *Hyla savignyi*) in Turkey was studied using combined mitochondrial genes (12S ribosomal RNA and cytochrome *b*) and sampling a total of 102 individuals from 51 localities. It was found that *Hyla orientalis* is represented by a single lineage, whereas *Hyla savignyi* was divided into two lineages by the mitochondrial genes, but not the nuclear gene. Also it was determined that *Hyla arborea schelkownikowi* is a junior subjective synonym of *Hyla orientalis*.

J.S. Hauswaldt, M. Höer, M. Ogielska & M. Vences

A new PCR based method to distinguish among European water frogs (*Pelophylax*)

Reliable distinction among European water frogs, *Pelophylax lessonae* (LL), *P. ridibundus* (RR) and the hybrid form *P. esculentus* (RL), is only possible using molecular characters. A number of methods are already available for accomplishing this, such as allozymes, microsatellites, and a recently published PCR-RFLP based approach. We are presenting a simple 1-step PCR based method that allows discriminating among the three taxa. We have verified the method using samples genotyped for other markers and in addition, we also sequenced two nuclear gene fragments to confirm our findings. Triploid *P. esculentus* (RRL or LLR) are even more difficult to diagnose morphologically because of the gene-dosage effects. We are currently applying the same new PCR approach (however, with a fluorescent tag) to help discriminating among diploid and the two triploid hybrid forms, and our preliminary results are looking very promising. Our new method will cut down time and expenses drastically for a reliable identification of European water frogs and most likely it will also be suitable for determining ploidy status of hybrids.

J.S. Hauswaldt, N. Westphal, M. Höer & M. Vences

Novel non-invasive DNA sampling methods for amphibians and reptiles

Non-invasive tissue sampling methods such as skin swabs allow sampling of small amphibians for which buccal swabbing is not an option. Furthermore, it allows even untrained persons to collect tissue samples. Other types of tissue, such as fecal pellets, shed skin, or dried up body remains (e.g. road kill) could be useful for studying elusive species, as well as for forensic purposes. Removal of external parasites, such as ticks, is likely to be appreciated by the host. We have tested a standard salting-out DNA extraction method on various types of non-invasive

tissue samples including: (1) buccal and (2) skin mucous swabs from European water frogs (*Pelophylax*) and newts in the aquatic stage, (3) fecal pellets from various species of anurans and squamate reptiles, (4) shed reptilian skin, (5) dried up remains of amphibians, and (6) ticks collected from lizards. A fragment of mitochondrial DNA was then amplified and compared with reference sequences. Overall, it was possible to obtain DNA from all types of non-invasively collected samples, but not every sample contained sufficient DNA and some samples did not yield quality sequence. To compare the skin mucous with the buccal swabbing method, we obtained samples from 70 amphibians collected under field conditions and compared DNA extraction and amplification success, as well as the quality of sequences. We also compare the level of contamination among samples taken from animals kept in individual containers, vs. among samples that were obtained from animals placed together in a bucket.

S. Hofman, M. Pabijan, D. Dziewulska-Szwajkowska & J.M. Szymura

Comparative analysis of mitochondrial genomes in waterfrogs of the *Pelophylax esculentus* complex

The sequences of entire mitochondrial genomes provide large and informative datasets for phylogenetic analyses at various taxonomic levels and also give insight into population-level processes such as introgressive hybridization, demography and selection. The central European water frogs *P. lessonae*, *P. ridibundus* and their natural hybridogenetic hybrid *P. esculentus* offer a unique opportunity to study mitochondrial introgression in vertebrates. The transfer of *P. lessonae* mtDNA into *P. ridibundus* individuals has occurred repeatedly across a wide geographical area in central Europe and was probably mediated by the hybridogen *P. esculentus*. We obtained the nucleotide sequences of multiple mitochondrial genomes (15376-78 bp without control regions) from all 3 taxa, including a *P. ridibundus* frog with introgressed *P. lessonae* mtDNA. The gene content and organization of all studied mitogenomes corresponds to the typical neobatrachian arrangement. Divergence between the mtDNAs of *P. lessonae* and *P. ridibundus* is high with an uncorrected *p*-distance of 11.9% across the entire mitogenome. However, the rate of nucleotide substitution depends on the degree of functional constraint with up to 30-fold differences in levels of divergence between the slowly evolving rRNA and tRNA genes and rapidly evolving protein coding genes. Uncorrected *p*-distances in protein coding genes between *P. lessonae* and *P. ridibundus* varied from about 11.3% (*COIII*) to 17.0% (*ATP8*). Amino acid substitutions were most prevalent in *ND* genes (especially *ND5*, *ND4*, *ND2*). Out of the total of 211-213 amino acid substitutions in mitochondrial protein coding genes between *P. lessonae* and *P. ridibundus*, only 25 (ca. 12%) can be classified as radical replacements (replacement by an amino acid with different physicochemical properties). However, a significantly higher number of amino acid substitutions was detected in the *ND4*, *ND4L* and *cytb* genes of *P. lessonae* (including 36% of all radical changes). Overall, despite the high divergence between *P. lessonae* and *P. ridibundus* mitogenomes, the overarching force shaping the evolution of the mitochondrial genome of *Pelophylax* is selection against deleterious change, as reflected by the predominantly neutral patterns of substitution. This may facilitate interspecific mitochondrial introgression, explaining the ubiquity of mitochondrial introgressants in this species complex. Nonetheless, a handful of radical replacements and disproportionate change in some genes of the *P. lessonae* lineage may be indicative of adaptive processes operating on

the mitochondrial genome. Additionally we propose a simple and rapid molecular protocol for determination of mtDNA type and nuclear genome composition in *Pelophylax*. We used these methods for screening 97 frogs from 30 localities across central Poland, and confirmed them by sequencing, morphological and analysis of allelic variants in LDH-B.

M. Jansen, F. Brusquetti, C.F.B. Haddad, M. Plath & M. Pfenninger

Intersexual communication and speciation in Neotropical frogs (genus *Scinax*): is mating call evolution a driver of cryptic amphibian diversity?

Cryptic species complexes in Neotropical frogs are a common phenomenon. Frogs and toads are strongly dependent on acoustic communication in various contexts, above all mate finding and mate choice. Therefore, bioacoustics plays a vital role in anuran biology, and possibly, anuran calls act as a driver in the diversification of species. The hylid frogs of the “*Scinax fuscomarginatus* species complex” offer a unique framework in which to elaborate this hypothesis. Against the background of a preliminary phylogeographic study of the closely related and morphologically very similar *S. fuscomarginatus*, *S. parkeri*, *S. trilineatus* and *S. lutzorum*, we conducted a comprehensive bioacoustic and genetic sampling of Bolivian populations of *S. parkeri* and *S. fuscomarginatus*. We analysed tissue samples from 67 tissue samples from six localities, and important material from the type locality of *S. parkeri*. The analyses of the 16S mitochondrial gene fragments suggested that two well divergent lineages are involved. The analyses of about 520 advertisement calls of 33 “call vouchers” revealed two divergent advertisement calls congruent with our molecular results. However, we found a high call variation between populations of *S. cf. fuscomarginatus* and *S. parkeri* at localities where both occur sympatric. These preliminary results suggest diversification of conspecific signals in sympatry (reproductive character displacement). Further studies are planned to study the evolution of the communication system in this species group.

R. Karamiani & N. Rastegar-Pouyani

A review of the Leopard geckos of the genus *Eublepharis* Gray, 1827 (Sauria: Eublepharidae) on the Iranian Plateau

The family Eublepharidae encompasses six genera and more than 20 species which are distributed in tropical to temperate habitats of Eurasia, North-Central America and Africa. One of the eublepharid genera is the genus *Eublepharis* Gray, 1827 which, as a vicariant group, encompasses five valid species distributed from Turkey through the Iranian Plateau to India. Three species of *Eublepharis* occur on the Iranian Plateau as follows: the leopard gecko, *Eublepharis angramainyu* Anderson and Leviton, 1966 collected for the first time from an old road between Masjed-Suleiman and Batwand, Khuzestan Province, southwestern Iran. This lizard occurs in the western foothills of the Zagros Mountains and in the upper Tigris-Euphrates basin in Iran, Iraq, northeast of Syria, southeastern Anatolia and Kara Dagh-Arsanli

of Şanlıurfa Province, Turkey. The authors recently collected specimens of this lizard from Kermanshah, Ilam and Lorestan Provinces in western and southwestern regions of the Iranian Plateau. *Eublepharis turcmenicus* was described in 1977 by Darevsky based on three specimens collected in Bakharden, Chandyr, Kopet Dag, near Ashkhabat, Turkmenistan. The panther gecko, *Eublepharis macularius* (Blyth, 1854) which is mainly distributed in Afghanistan, Pakistan and northwestern India is tentatively listed in herpetofauna of Iran based on Zarudny's record (1903) from eastern Khorasan, very close to the Afghan border. No record of *Eublepharis* has yet been addressed from the central regions of the Iranian Plateau. Distribution maps of the above-mentioned species of *Eublepharis* are given.

M.A. Kazemi, M. Afroosheh & M. Sadata Tahami

New record of Plateau snake skink, *Ophiomorus nuchalis* (Squamata: Scincidae), from a different locality

The plateau snake skink (*Ophiomorus nuchalis*) is a native lizard in Iran. There are only a few reports about its distribution, ecology and systematics status. According to the latest reports (Nilson and Andrén 1978; Mozaffari, 2010) it seems that *O.nuchalis* is distributed in Kavir National Park, a protected area between Tehran, Qom and Esfahan Provs. Nilson and Andrén (1978) noted that this species was collected under stones on almost bare gravel ground, the area is one of broken rocky mountains and alluvial plains, there was no loose sand in the vicinity of the type locality, and Mozaffari et al. (2010) found them at the bank of a dry river with clay topsoil, but in this new record a specimen was collected in Arisman village, Esfahan Prov., 33°39'N, 52°E. This locality is toward south of the last reported localities. This species has been seen in May-Jun, especially near the farms (vegetables farms like cucumber and tomato bushes). This species is nocturnal and active after sunset to sunrise, its optimum temperature is 15°-25°C, it is a fossorial species and in hot days creeps into the holes and cracks. Other lizards that coexist with *O.nuchalis* in this new locality are: *Eumeces schneiderii princeps*, *Trachylepis aurata transcaucasica*, *Ophisops elegans*, and so on. According to this record it seems that distribution area of this species is broader than we expected, it has moved to the south and to the more different locality than the past reports. It can be noted here that *O. nuchalis* can live in different localities as far seems that can adopt somewhat with environments with human activities (e.g. farms).

S. Keckeis, P. Mitteröcker & G. Gollmann

Geometric morphometrics of body shape of *Salamandra salamandra* larvae from diverse water bodies

Fire salamander larvae inhabit diverse water bodies, ranging from fast running streams to stagnant pools. In recent studies, phenotypic plasticity as well as sympatric speciation have been discussed as causes of their morphological variation. To probe the generality of patterns of adaptive change, we examined fire salamander larvae from streams and standing water

bodies in Vienna (Austria). We photographed the larvae in lateral and dorsal view immediately after capture in the field. To assess variation in body shape, we use advanced methods of geometric morphometrics.

F. König & C. Nowack

First description of a previously unnoticed intranasal gland of the Green puddle frog (*Occidozyga lima*)

In the present study we analysed the anatomy of the nasal region of *Occidozyga lima* (Anura, Amphibia), focussing on the glandular structures related to the olfactory system. For this purpose we investigated transverse paraffin sections of the frog's nose, stained with Petersen's azan. Normally, three major nasal glands are found in association to the anuran olfactory organs, namely the *glandula nasalis medialis*, the *glandula nasalis lateralis* and the *glandula nasalis oralis interna* (Gaupp, 1904). All three glands are thought to play important roles during olfaction. The *glandula nasalis medialis* is closely related to the vomeronasal organ, whereas the *glandula nasalis lateralis* opens nearby the external naris. The *glandula nasalis oralis interna* always occurs in conjunction with the recessus olfactorius, a rarely known additional olfactory organ of many frogs. In *Occidozyga lima* we were not able to find a recessus olfactorius or a *glandula nasalis oralis interna*. Instead, we observed a further, fourth intranasal gland, previously undescribed for the family Ranidae. This gland opens in the proximity of the external naris at the junction between the main cavity and the accessory nasal cavities. The staining pattern of this unidentified gland differs considerably from that of the lateral and medial nasal glands. Helling (1938) briefly mentioned a somewhat resembling glandular structure in two species of the family Microhylidae and in one species of the family Brevicipitidae, and called it the *glandula nasalis infundibularis*. If the two glands are homologue structures requires further investigation.

A. Kaliontzopoulou, V. Bandeira & M.A. Carretero

Sexual dimorphism in locomotor performance in *Podarcis* wall lizards: going multivariate

Sexual dimorphism (SD) in locomotor performance is prominent in many species of lizards. This functional pattern is related to both size and shape SD and it has been associated to sexual selection on males, related to territorial behaviour. Locomotor capacities of lacertid lizards are related to habitat variation, following ecomorphological predictions, but SD has not been extensively investigated. The few existing studies have indicated a lack of SD in this respect. We investigated SD in locomotor performance and its relation to morphological traits in a population of *Podarcis bocagei*, a species endemic to the Iberian Peninsula. We measured sprinting, climbing and clambering speed, as well as manoeuvrability, of adult male and female *P. bocagei* in a racing track. We also quantified body size and shape, including characters potentially relevant for locomotion, in the same individuals. Our results indicate that while

SD in performance is not significant when looking at each locomotor component separately, differences between sexes are significant when treating the data in a multivariate framework. This is due to differences between sexes in the trade-offs between conditions: while females are relatively stable across designs, males are fast sprinters, but suffer a visible reduction of their locomotor capacity when climbing or serpentizing. Fitting biomechanical predictions and previous observations, the morphological variables associated to locomotor performance are total body size and limb length. Our study suggests that significant, but previously unnoticed, SD may exist in locomotor performance in lacertids and remarks the importance of multivariate analyses when examining performance capacities.

A. Kosyan, M. Arakelyan & F. Danielyan

Comparison of seasonal activity and reproductions cycles of syntopic *L. agilis* and *L. strigata*

The zone of syntopy between *Lacerta agilis*, *Lacerta strigata* and *Parvilacerta parva* were discovered in vicinity of Mets Parni village, Lori Province, Armenia. 93 individuals of *L. agilis* (83.7%) and 18 of *L. strigata* (16.2%) and one lizard of *P. parva* were examined during 2009-2011. According to our observations, the season activity of *L. agilis* is shorter than syntopic *L. strigata* on month. *L. strigata* emerged from hibernation at mid-April and were active until the mid-October, while *L. agilis* left winter burrows two week after *L. strigata* at the beginning of May and disappeared into hibernation on two week earlier at the end of September. Females of *L. strigata* lay their first clutch of eggs at the end of May, whereas *L. agilis* lay the first clutch at the beginning of summer. The hatchlings of both species active till end October when the thermal conditions still favourable. Similarly, the appearance of young from winter hibernation occurs earlier than adults. Our surveys also revealed that two syntopic species possess spacial differentiation of the same slope, where in bottom of slope were met *L. strigata*, in the middle of slope were both species and on higher places near to top of slope were mainly *L. agilis*. Thus, the dates of season activity, stages of reproductive cycles as well as pattern of spacial differentiation allow to syntopic species to share resources of habitats.

M. Luznik, E.V. Buzan & B. Krystufek

Mitochondrial DNA reveals new lineage of the smooth newt *Lissotriton vulgaris* in SW Slovenia and Istria

The smooth newt *Lissotriton vulgaris* is represented in Slovenia by two subspecies, which differ in male epigamic traits. The nominal subspecies *L. v. vulgaris* is confined to the north-eastern part of the country, specifically to the Pannonia lowland, while the rest of the country is populated by *L. v. meridionalis*. The range borders of these two subspecies are not sharply defined because of frequent records of males displaying intermediate characters. A broad transition zone between these two subspecies is known from the rest of Europe, with some level of gene introgression. The aim of this study was to identify mitochondrial DNA (mtDNA)

lineages in Slovenia and to screen populations for possible gene introgression. We screened 200 tissue samples of the smooth newt from 38 localities along a south-west to north-east transect across Slovenia, including the peninsula of Istria. Analyses were performed on two mtDNA genes, ND2 and ND4. Partial genes were concatenated, which resulted in 1727 bp of high-quality sequences. Sequence analysis retrieved 49 haplotypes and only one of them was previously recorded from central Europe. Maximum likelihood (ML) phylogenetic tree reconstructions, including all newly retrieved haplotypes in addition to 67 reference haplotypes from GenBank, were performed. The ML tree retrieved four distinct clades present in the investigated area. The majority of new haplotypes were attributed to a clade with a wide geographic distribution throughout Europe. Haplotypes from this clade were very common in eastern Slovenia, and included individuals showing morphology of either subspecies, *vulgaris* or *meridionalis*. Limited to the north-eastern part of the country was another clade which was recognized in previous studies, and shown to occupy central Europe and the Balkans. Additionally, two genetically well distinguished clades, both exhibiting morphology of *meridionalis* subspecies, occur in sympatry in western Slovenia and Istria. One was previously recorded from Italy, while the second was not recognized so far. It held a well supported sister position against clades from eastern Slovenia. The newly discovered clade could have evolved in allopatry and secondarily became into contact with the Italian lineage. Our results also show that mitochondrial lineages of the smooth newt in Slovenia do not corroborate the division into two morphological subspecies, as was already recognized in previous phylogeographic research.

M. Meikl, J. Schauer, A. Gimeno, V. Helfer & R. Schwarzenbacher

Survey of Alpine- and Fire salamander populations in Austria

The Alpine Salamander, an endemic amphibian species that lives in Alpine regions across Europe, and the Fire Salamander, the best known salamander species in Europe because of its eye-catching coloration, are among threatened species in Austria because they require habitats prone to destruction by human invasions. Despite their central role in the alpine ecosystem, our academic record about their actual distribution, and most importantly, their habitat ecology is very scarce. In order to resolve this shortcoming, this project intends to use a community-based approach that allows participation and networking of scientists and people from all over Europe. Salamander observations are collected and disseminated on the webportal www.alpensalamander.eu. Besides, monitoring and genetic analyses for both species will allow us to determine adequate management units for conservation. Furthermore, the project collaborates with 30 schools to bring the knowledge of salamanders into the children's mind. The children get aware of the importance of salamanders by means of workshops, excursions and lab visits, and they learn how to protect amphibians and their environment. We believe that the protection of amphibians and their habitats is only possible by actively involving the public.

M. Mangiacotti, S. Scali, R. Sacchi, L. Bassu, C. Corti, C. Fresi, V. Nulchis & M. Grazia Satta

Do endemic and non endemic lizards compete for space? A case study from two Sardinian lacertids

Interspecific competition in contact areas is a major topic in ecological studies and it is particularly interesting when endemic are involved. The aim of this study is to analyse eventual competition between the endemic *Podarcis tiliguerta* and the autochthonous *P. siculus* in Sardinia, by comparing suitability models. Our specific aims were to detect which ecological factors affect species occurrence and to assess if niche separation follows active competition. Potential distribution was modeled using the maximum entropy method, with 12 ecogeographical variables as predictors. The models fitted well for both species (mean AUC = 0.836). The most informative variables were: anthropic areas (urban and crops), altitude, road density, edges, potential evapotranspiration (PET) and annual precipitation for *P. tiliguerta*; road density, altitude, anthropic areas, PET and annual precipitation for *P. sicula*. The Tyrrhenian wall lizard is more sensitive to habitat modification and it occurs mainly in natural and semi-natural areas, with low road and high edge densities. The habitat suitability for the Italian wall lizard is higher near intensively cultivated areas and urban patches, where PET is higher. *P. sicula* in general is the only lizard found in flat lowland areas despite being present at higher altitudes (e.g. in villages) while *P. tiliguerta* lives in more complex and natural habitats throughout the island. Only relatively small areas in Sardinia resulted suitable for both species and this result confirms that a partial niche separation between them occurs. *P. sicula* is probably favoured by anthropic activities that reduce suitable areas for *P. tiliguerta*.

Y.B. Manteifel, E.I. Kiseleva & A.N. Reshetnikov

Low molecular weight metabolite as pheromone in anuran tadpoles

It was shown, that disturbed larvae of *Rana aurora* avoid zones with increased content of conspecific excretions and ammonia, a final product of tadpole nitrogenous metabolism (Kiesecker et al., 1999). It was supposed that an increase of ammonia concentration during synchronous activation of moving activity in the dense group of tadpoles can play a role of nonspecific disturbance pheromone, promoting an avoidance of the alarm source. So, ammonia can be a simple and one-component pheromone. We studied reactions three more anuran species to solution of this substance and registered similar behaviour. For two amphibian species we determined also differential sensitivity of chemoreception. Under ammonia level lesser than 0.04 mg/l absolute threshold for the toad *Bufo bufo* larvae was < +0.2 mg NH₃/l. Differential threshold dI/I fall within the range between 400 to 500%. For the frog *Rana temporaria* larvae differential threshold at background NH₃ level 0.15 mg/l is close to 200% and at background NH₃ level 1.1 mg/l it is close to 100%. Tadpoles of both anurans have less differential sensitivity to ammonia comparing with human olfaction and taste, but it permit to use ammonia as intra- and interspecies communication mean. Thus, our data show

that probability of perception ammonia and using it as disturbance pheromone or one of its components for *B. bufo* tadpoles is restricted by waters with the background ammonia level not more than 0.4 mg/l. Perception of ammonia by *R. temporaria* tadpoles is not restricted in the all range of its possible background concentrations, that is from 0.05 to 1.1 mg/l and more. Such limits of the “operating range” corresponds to the natural conditions: the concentration of ammonia in the coastal waters of the lake Glubokoe, from which the tadpoles were collected, lay typically in the range 0.06-0.1 mg/l. The observed species differences of differential sensitivity may be explicable by ecological specifics: in contrast to *R. temporaria*, the *B. bufo* larvae have several antipredator mechanisms and should be less dependent on the response to non-specific pheromone. Communicative role of simple substances is a promising area for further study of chemical communication of amphibians and other aquatic animals. The increasing concentration of ammonia can act as chemical signal at the very different biocenological levels and significances, inducing intrapopulation, assamblage and can induce complex effects.

J.-J. Mao & Y.-C. Lai

The distribution of *Sinonatrix annularis*, *Enhydris chinensis* and *E. plumbea* in northern to central Taiwan, and an assessment of the habitats they utilize

We investigated the current status and population distribution of 3 semi-aquatic snakes, i.e., the Chinese water snake (*Enhydris chinensis*), the rice paddy snake (*Enhydris plumbea*), and the Asiatic banded water snake (*Sinonatrix annularis*) from northern to central Taiwan (Taipei, Yilan, Taoyuan, Hsinchu, Miaoli, Taichung, Changhua, Nantou, Yunlin, and Chiayi Counties). From July 2009 to December 2010, a total of 309 sample plots were selected according to their watersheds and habitat types, and floating funnel traps were set within them to sample semi-aquatic snakes. During the inventory time period, 36,621 trapping nights were conducted and 391 snakes were observed, including 306 Asiatic water snakes (*Xenochrophis piscator*), 39 rice paddy snakes, 25 Chinese water snakes, 11 many banded kraits (*Bungarus multicinctus multicinctus*), 6 buff striped keelbacks (*Amphiesma stolatum*), 1 Chinese cobra (*Naja atra*), 1 Formosan kukri snake (*Oligodon formosanus*), 1 Asiatic banded water snake, and 1 olive keelbacks (*Sinonatrix percarinata suriki*). The spatial distribution of *E. plumbea* was restricted to northern Taiwan, and showed a rather continuous pattern with the highest population density in Tamshui Township, decreasing outwards, while that of *E. plumbea* was scattered in isolated patches and decreased southwards. Of all the species, the population status of the *S. annularis* was rather critical. Overall, the population status of the 3 species were low in density and narrow in distribution patterns. Further investigation and population monitoring are crucial for the continued survival of these species. The distribution of the Asiatic water snake tends to overlap with habitats of the Chinese water snake, the rice paddy snake, and the ringed water snake, and therefore, can be used as baseline for their potential distribution patterns.

C. Matos, E. Argaña & N. Sillero

Amphibian road mortality: northern Portugal country roads as models

In recent years the landscape has been undergoing major changes through urban sprawl and its accesses, leading to an increase in fragmented natural areas. These linear structures (and its factors) interfere with various ecological processes. Collisions with vehicles are the main direct cause of animal mortality on the roads. Amphibians are the group of animals most commonly affected. These animals show higher biological susceptibility to the impact of roads. Iberian studies have shown that the roads play an important role in the degree of mortality on amphibians, but information regarding spatial patterns on causalities on roads in northern Portugal is still scarce. Mitigation measures are necessary, even knowing their use is not always effective. It is important to understand where they should be applied so their real purpose is successfully achieved. Predictive models are tools that can be used to identify hotspots in existing roads and can be used to prevent the risk of future road kills in upcoming projects. The main goals of this study are (1) to identify the levels of amphibian's road-kills in northern Portugal, and (2) to determine patterns of amphibian mortality on country roads in northern Portugal. The study area was selected within 50 km around the city of Porto, covering a total of 41 counties. This area was considered for logistical reasons but also cover most types of land uses that can be found in northern Portugal. The selection of the study area was performed in three phases: country roads selection, key habitats (CORINE) and land use selection, selection of 7 sample paths and analysis. Amphibian species records were analyzed (recorded as live or road-killed) in order to identify temporal and spatial patterns of occurrence, as well as road-killed hotspots (using GIS clustering tools). In a total of 157 km of road distributed along our study area we have found 403 amphibians. Our preliminary results show that 82% of the animals found are road-killed. *Bufo bufo* is the amphibian specie most affected with 83% of mortality and an average of 2,77 amphibians per kilometer.

I. Meuche & H. Pröhl

Behavioural strategies of competing males in strawberry poison frogs

Territoriality is a behavioural strategy essential to the breeding ecology of many species in which male reproductive success is limited by access to females. In the present study, we investigated the relative importance of female availability and pressure caused by male intruders for the regulation of territory size of male strawberry poison frogs, *Oophaga pumilio*. We show that males defended smaller territories in areas with a high female density. Only males in good body condition were able to defend small territories in areas of high female density. In contrast, intruding pressure caused by competing males was positively correlated with territory size. Our results also showed that males lowered their dominant calling frequency during agonistic interactions. Because only males in good condition were able to produce very

low dominant frequencies, the observed decrease appears to be an honest signal containing information about fighting abilities. Thus, the negative correlation between dominant frequency and mating success of males found in previous studies seems to be the result of intrasexual competition between males rather than a product of female preferences for low-frequency calls.

B. Mitterlehner, S. Hartwig, A. Maletzky & M. Kyek

Distribution, habitats and space use of the Aesculapian snake (*Zamenis longissimus* Laurenti, 1768) in the province of Salzburg (Austria)

The province of Salzburg features some patchily distributed populations of the Aesculapian snake (*Zamenis longissimus*), which is strictly protected by provincial law and is listed in Annex IV of the EU-Habitats Directive, as well as in Annex II of the Bern Convention. As the populations in Salzburg represent a part of the northern edge of the current species range, the province of Salzburg has a special responsibility for its protection. Still there is a lack of information concerning the species distribution and particularly its favoured habitat parameters. In the context of two master thesis, that started in 2010, we aim to enhance the knowledge about the distribution of *Z. longissimus* in the province of Salzburg, and gather detailed data on habitat use and home ranges of snakes in the area between Puch bei Hallein and Kuchl, southeast of the city of Salzburg. In order to find out habitat preferences, we classified different landscape categories in the investigation area, dependent on structural diversity and types of land use. We actively searched for snakes, using transect counts (length 500 m, placed equally in different landscape classes). Furthermore artificial refuges, as well as interviews with locals were used. In occupied habitats, several parameters like density of vegetation and kind of canopy were documented. Snakes were caught, measured, marked via ventral scale clipping and released in the same place. During the first field season 45 observations of *Z. longissimus* were documented and a clear preference for small-scaled cultivated landscapes and settlement areas could be shown as well as the favored vicinity to closed woodland areas. A comparably high number of observations were made on stacks of firewood. Additionally we present first data of a radio-telemetry study, carried out in 2011, to gain detailed information about home ranges, egg deposition sites and habitat use of Aesculapian snakes in our study area.

E. Mizsei & B. Üveges

Novel defensive behaviours in both sexes of *Vipera ursinii graeca* (Serpentes: Viperidae)

During our surveys in Albania to record new distribution localities of *Vipera ursinii graeca*, three specimens out of seven handled vipers displayed unusual behaviours when their morphometric characteristics were measured. Two males showed defensive hemipenis display, and one female showed a hitherto undocumented behaviour by protruding its cloacal gland and

excreting secretions. This is the first report of cloacal defensive behaviour in snakes as well as of defensive hemipenis display in the genus *Vipera*.

S. Ndriantsoa, J. Riemann, M.-O. Rödel & J. Glos

Habitat fragmentation and frogs: what is the influence of matrix quality on species richness and functional diversity in hyper-diverse amphibian communities?

Matrix habitat, i.e. the non-forested area in between patches of natural forest habitat, might have a key influence on the diversity of these forest patches as it might or might not act as a corridor for dispersal. Moreover, higher quality matrix reduces the isolation of forest patches by allowing species to expand their activities (e.g., feeding) outside of fragments, or it might be even suitable habitat *per se* for some species. In our study on hyper-diverse amphibian communities (100+ species) in a mid-elevation rainforest in Eastern Madagascar (Ranomafana NP) we analyze the composition and structure of matrix habitat in a fragmented landscape. We aim to identify important drivers of amphibian community structure in this landscape, and hypothesize that the quality of matrix habitat is one important driver. Furthermore, we analyze the suitability of different types of matrix habitat (i.e., rice fields, banana plantations, secondary vegetation) for migration of frogs between fragments, therefore influencing frog diversity in the forest fragments, and as valuable habitat for some species. We will present the concept of our study and first results on the effect of matrix quality on species and ecological (functional) diversity of these amphibian communities.

J. Nopper, Y.R. Ratovonamana, D. Rakotomalala & H. Razafindraibe

Reptile communities of Tsimanampetsotsa National Park (Madagascar) under the impact of human pressure and climatic change

In Madagascar, conservation of natural ecosystems falters at times of political instability when resources from natural ecosystems provide better (or maybe the only) income for the local people than the conventional land use systems. Within a BMBF funded project on the development of sustainable land use, we assess the reactions of reptiles as habitat specialists to various forms of habitats that vary in relation to anthropogenic or environmental impacts. The results should help to understand the effects of habitat characteristics on reptiles in ways that can be considered in future management plans.

G. Norval & J.-J. Mao

Is a biodiverse environment reducing the invasibility of the Brown anole (*Anolis sagrei*) in Taiwan?

The Brown anole (*Anolis sagrei*) naturally occurs in the warmer regions of the Americas. Since we discovered the brown anole in Taiwan in 2000, we have been studying the ecological interactions between this exotic invasive species and native fauna. To date, we have never observed any *A. sagrei* within the relative diverse secondary forest patches, located in the core area of the known area of distribution of the brown anoles in southwestern Taiwan. This study was thus done to clarify whether there is a possibility that a higher biodiverse environment is decreasing the invasibility of *A. sagrei* in this area. From October 2006 to December 2007, we conducted this study to test whether the diversity-invasibility hypothesis provides a better explanation for the absence of *A. sagrei* in the secondary forest. The study was done by focusing on the species composition inventory of the vegetation (grasses, forbs and trees), terrestrial invertebrates, amphibians and reptiles in betelnut palm plantations and the secondary forest in Santzepu, Sheishan District, Chiayi County. Twelve experimental short-fence funnel-trap units were set within this area to determine the species diversity of terrestrial invertebrates, amphibians and reptiles. Each trap was situated in the center of a 10×10 m quadrant, which was analyzed for vegetation composition and species diversity analysis. We recorded plant species, grass and forbs cover ratio, canopy cover ratio, DBH (diameter of breath height) of trees, and the stone content ratio in the soil in each quadrant. We found that the overall biodiversity, on average, were higher in the secondary forest (non-invasive area) compared to the surrounding betelnut palm plantations (invaded areas). The number of woody species, dominance, and amphibian and reptile species richness and abundance, were higher in non-invaded areas. The invaded areas only had a higher grasses and forbs cover ratio. The secondary forest harbors a larger variety of reptiles, some of which are known predators and competitor of *A. sagrei*, which may explain the absence of this species in this habitat type.

D.P. Pandey

Snakes in the vicinity of Chitwan National Park, Nepal

Chitwan National Park (CNP) is situated in south central subtropical lowlands of the inner Terai. Here, I present a checklist of snake species found in the vicinity of CNP. I recorded 32 species belonging to 23 genera and five families (e.g., two typhlopids, four boids, 17 colubrids, one viperid, and eight elapids). Of the 32 species I recorded, 16 were non-venomous species, six were mildly venomous, and 10 were venomous. *Echis* and *Daboia* were not recorded in this region, though these have been reported from other parts of Nepal in some field guide books. Based on the results, I recommend that an additional inventory of snakes be undertaken to verify the absence or existence of *Echis* and to determine distributional pattern of *Daboia* in Nepal because the identification of the distribution of venomous snake species can assist in determining regionally specific antivenin. In addition, further study of snakes in both agricultural and forest ecosystems should be carried out to document their diversity and status in Nepal, as well as snake-human encounters/conflicts.

E. Pitta, C. Kassara, S. Giokas & S. Sfenthourakis

Community structure of reptiles and amphibians on islands

The structure of natural communities is hypothesized to be determined by general assembly rules that give rise to particular patterns. One such pattern is nestedness, demonstrated when the communities of species-poor sites are subsets of those in successively richer communities. Additionally, characteristic species co-occurrence patterns may reveal species interactions or specific habitat preferences. In this work we investigate species co-occurrence patterns of reptiles and amphibians as well as the degree of nestedness of insular communities of these animals. We also investigate the influence of various factors on the dissimilarity in species composition between islands. We compiled 35 presence-absence matrices from studies that report the distribution of reptiles and amphibians on islands (9 matrices refer to amphibians, 17 to lizards and 9 to snakes). Species co-occurrence patterns are investigated using a pair-wise approach and the degree of nestedness is assessed using the NODF metric. We use partial Mantel tests to investigate the influence of inter-island distance, area and elevation on the dissimilarity of species composition between islands. Overall, species co-occurrence patterns (pair-wise interactions) are detected in just a few exceptional cases, whereas the communities of reptiles and amphibians on islands appear to be less nested than expected by chance (significant results in 14 matrices). The most important factor influencing species composition on islands is inter-island distance. Dissimilarity in species composition is significantly positively correlated with inter-island distance in almost half the matrices examined in this study.

J. Primus & G. Gollmann

Dispersal and migrations in yellow-bellied toads, *Bombina variegata*

The yellow-bellied toad, *Bombina variegata* (Anura, Bombinatoridae) is endangered in central and western Europe. So far, most population studies have been conducted either in nature reserves or in strongly disturbed habitats such as quarries, gravel pits or military areas, but few data from managed forests are available. Since 2002 we study yellow-bellied toads in Groß-Krottenbach in the Vienna Woods. The study area of about 300 ha is mainly covered by deciduous forest and is situated about 300 m to 700 m above sea level. In 2008 and 2009 a total number of 447 juveniles were registered. Fieldwork with the aim of recapturing toads from these cohorts was carried out in the summers of 2010 and 2011. Immediately after capture, the ventral colour pattern of each toad was photographed; snout-vent-length (SVL) and body mass were recorded. In 20 days of fieldwork in 2010, a total of 541 individuals were recorded, of whom 198 toads were recaptured at least once. From the juveniles first registered in 2008 and 2009 67 were recaptured at distances of up to 1850 m from the site of first registration.

A. Pupina & M. Pupins

Distribution and conservation of the Fire-bellied toad (*Bombina bombina* L.) in Latvia

Populations of fire-bellied toad existing in the territory of Latvia live on the northern border of this species' area, which is located near the southern border of Latvia, where it meets Lithuania and Belarus. Fire-bellied toad *Bombina bombina* L. is included in Appendix II of Berne Convention "Specially protected animal species". A small number of fire-bellied toad *B.bombina* on the northern border of its area has been the reason for its inclusion the List of preserved species of Latvia and in Latvian Red Data Book in the 1st category (endangered species). In our research determination of vocalizing males is one of the basic methods of detection of *B.bombina* findings. *B.bombina* count by voices was done in sunny, warm and calm weather in the time period from 10:00 till 22:00. During the researches from 2004 - 2010 five new subpopulations were documented in Latvia: Demenes, Ainavas, Spulgu, Medumu, Eglaines and two old: Ilgas, Bauska. All found *B.bombina* subpopulations lie in the South of Latvia near to Lithuania and Belarus. The part of this research has been executed owing to support of LIFE+ Project LIFE09NAT/LV/000239 "Conservation of rare reptiles and amphibians in Latvia" with the contribution of the LIFE+ financial instrument of the European Community.

M. Pupins & A. Pupina

Distribution and conservation of the European pond turtle (*Emys orbicularis* L.) in Latvia

Emys orbicularis is that species in Latvia, which dwells on the northern edge of the species distribution and the existence of which is endangered. *Emys orbicularis* is situated in the second application of Bern Convention "Convention on the conservation of European wildlife and natural habitats" and in the document Nr.396. of Latvian Ministry. As a result of human activities new factors of anthropogenic origin appear which negatively influence the *E.orbicularis* in Latvia. The oral and special pamphlet questionnaire was carried out among the Latvian inhabitants. Each case was estimated by the scale of reliability from 1 (the lowest grade) to 4 (the highest grade): 4 – the author checked it or he has a photo of a turtle; 3 – the biologist observed it; 2 – the respondent observed it – not a biologist; 1 – other person observed it. The communications (n=96) about the observation of *E.orbicularis* in Latvia were registered. 5 animals (4 adults and one subadult) were registered in 2010 in field researches. The part of this research has been executed owing to support of LIFE+ Project LIFE09NAT/LV/000239 "Conservation of rare reptiles and amphibians in Latvia" with the contribution of the LIFE+ financial instrument of the European Community.

N. Rastegar-Pouyani, R. Karamiani & E. Rastegar-Pouyani

Review on the Iranian species of *Darevskia* (Sauria: Lacertidae)

So far, seven species of the genus *Darevskia* Arribas, 1997 have been documented from Iran: *Darevskia chlorogaster* (Boulenger, 1909), *Darevskia defilippii* (Camerano, 1877), *Darevskia mostoufii* (Baloutch, 1976), *Darevskia praticola* (Eversmann, 1834), *Darevskia steineri* (Eiselt, 1995), *Darevskia valentini* (Boettger, 1892) and *Darevskia raddei* (Boettger, 1892). Based on extensive and long-lasting field work in various regions of the Iranian Plateau, taxonomy and distribution of the lacertid lizards of the genus *Darevskia* Arribas, 1997 are discussed. Some new records and a new taxonomic entity within this genus are reported. The distribution maps of all the studied species are given and a key to the Iranian species of *Darevskia* is provided.

T. Reinhardt, S. Steinfartz & M. Weitere

Linking the evolution of habitat choice to ecosystem functioning: direct and indirect effects of pond-breeding fire salamanders on the aquatic-terrestrial coupling

Shifts in the life history traits and behaviour of species can alter ecosystem functioning. In fish-free habitats, the larva of the Firesalamander (*Salamandra salamandra terrestris*) are considered the only vertebrate top-predators influencing biodiversity and the flux of biomass. Here we estimate the effects of pool-breeding fire salamanders on pool food webs and on the animal-mediated flux of matter between pools and the adjacent terrestrial habitats. Typically Fire Salamanders breed in first order streams and the pool-breeding ecotype is considered a recently evolved local adaptation. Our estimates are based on biomass data of the fauna of different vernal pools as well as data on the stomach content, growth rate and population dynamics of the salamander larvae in these habitats. Due to high mortality rates during larval phase and relatively small metamorphosis size of the pool breeding salamanders (in contrast to stream-breeders of the same species), the biomass export of metamorphosed salamanders in late summer usually falls below the biomass import. This net-import of matter and energy into the aquatic habitat is further accelerated as the salamanders consume both organisms of terrestrial origin trapped on the water surface (supporting import) and aquatic insect larvae with terrestrial adults (preventing export). All together, the adaptation of fire salamanders to breed in pools leads to strong net increases of animal-mediated import of terrestrial matter into the aquatic habitats and the community structure of macroinvertebrate food organisms. In the light of global decline and ongoing habitat destruction and fragmentation understanding on how single species can influence habitat functioning becomes of special importance, especially for amphibian species.

I. Rocha, D. Salvi & M.A. Carretero

Assessment of the origin of the Iberian populations of *Podarcis sicula* using mitochondrial markers

The species introductions already constitute one of the major threats to biodiversity worldwide. Determining the origin of such aliens is the first step to develop successful strategies of prevention and minimisation. The Italian wall lizard, *Podarcis sicula*, is a lacertid predominantly present in the central Mediterranean region, also inhabiting Sardinia, Sicily and Corsica as well as on many Adriatic islands. It frequently occurs in humanized areas, but is really fast and shy compared to other lacertids. Several scattered populations have been reported across the Mediterranean basin, namely Toulon in France, Istanbul and Marmara Islands in Turkey, Tunis and Tripoli in North Africa, and Menorca in Spain where is the dominant lizard. Experimental evidence has demonstrated behavioural interference and competitive exclusion of congeneric species and instances of hybridisation between introduced populations and other local *Podarcis* are also known. This suggests that the introduction of this species may be highly harmful for the local biota. In the Iberian Peninsula, populations of undetermined origin are currently known from three coastal populations with very contrasting climatic conditions. Namely, those in Almeria city (SE Spain) and Noja beach (Santander, N Spain) are suspected to be old (40-50 years ago) whereas that in Lisbon (SW Portugal) is a more recent (end of 90's). Here we assess the origin of all three populations using the cytochrome b gene by putting sequences generated together with those published for the species both in its autochthonous range and in other introduced populations. Results are discussed in the context of the phylogeography of the species and its invasive character.

G.M. Rosa, I. Anza, J. Conde, F. Martins, P. Moreira, R. Rebelo & J. Bosch

Chytrid fungus and the reality of Portuguese amphibian high elevation populations

In the last years, it has been recognised that the emergence of a new infectious disease, chytridiomycosis, is one of the major causes of amphibian decline and biodiversity loss at the global scale. This pathogen has been first detected in Europe less than ten years ago. By the end of August 2009, several post-metamorphic *Alytes obstetricans* were found dead on the surroundings of an artificial pond called "Lagoa do Covão das Quelhas" (1810 m a.s.l.) in the Serra da Estrela Natural Park (PNSE), Central Portugal. The similarity of this event with the mass die-offs in Peñalara Natural Park (Central Spain), lead us to suspect of a possible new chytridiomycosis outbreak. We here present new evidence suggesting that chytridiomycosis is related, not only, to the observed mortalities of *A. obstetricans* but also to the experienced recent decline of the toads' populations in the area. Some ponds/lakes in the same area and elevation range maintain different levels of chytridiomycosis prevalence. We present data on the association with the presence/ absence of predators, other amphibian species and their densities.

D. Roşioru, M. Tudor, E. Buhaciuc, P. Szekely & D. Cogălniceanu

Reproductive effort and reproductive success in the Danube crested newt (*Triturus dobrogicus*)

The reproductive effort and success were studied experimentally using 15 females of *Triturus dobrogicus* from Lake Sinoe (Danube Delta Biosphere Reserve, Romania). The average period of oviposition was 22.7 ± 5.1 days (range 13-31), and the average number of eggs deposited by a female was 306 ± 119 (range 160-489). The daily number of eggs deposited decreased in time, the higher daily deposition rates occurring during the first week. Only 38.9% of the eggs hatched. The age of the females was between 2-6 years old, the highest reproductive output corresponding to the 3 years old females. At the end of oviposition 8 females were randomly selected and injected with FSH and LH. Hormonally stimulated females continued to deposit for almost a week an average 60.5 ± 44.9 eggs/female (range 3-110), thus increasing the average number of eggs deposited by each female from an average of 299 to 368 eggs. The number of eggs deposited after hormone stimulation was negatively correlated to the initial number of eggs deposited ($R^2 = 0.47$), indicating that reproduction output is limited. There was no significant weight loss during reproduction, suggesting that a prolonged reproduction involves less effort.

U. Schulte, V. Mingo, C. Modica, M. Veith & A. Hochkirch

Reconstructing the invasion history of a thriving introduced Wall lizard population in Germany

Since the 1930's introductions of wall lizards took place in Passau, Bavaria, Germany. 80 years later this population has to be considered as the world's largest introduced wall lizard population. It has extended its range about 30 km along a railway, now trespassing the Austrian border. Using DNA barcoding, we assigned the population to a geographically distinct evolutionary lineage which can be found in southern-most Slovenia, north-western Croatia, and the eastern part of the Po Plain (so-called Venetian Clade). Morphology suggests that, in concordance with mtDNA data, the source population stems from the Bologna-Modena area. To reconstruct the invasion history of the population a total of 165 individuals were genotyped at 13 microsatellite loci. In order to investigate routes of expansion wall lizards were sampled every 5 km along a transect, covering the whole invasive range of this population. First results indicate a rapid expansion of the population.

A. Schulze & M. Jansen

When tadpoles tip the scale: larval morphology as part of an integrative anuran inventory

Cryptic diversity of Bolivian lowland frog species was revealed by the inclusion of selected anuran larvae in the course of an integrative taxonomy approach. The combination of

mitochondrial DNA (16S), bioacoustics, adult and tadpole morphology increased the number of putative units, and several lineages were proposed for further taxonomic revisions. Herein, we present some cases in which the tadpoles evidenced the classification of divergent lineages.

E. Simonov & M. Wink

Fine scale genetic structure and male-biased dispersal in a metapopulation of Halys pit viper (*Gloydius halys*)

An investigated population of Halys pit viper (*Gloydius halys*) is situated in the Novosibirsk region (Russia, West Siberia) and removed on 180-200 km from the nearest known locations. Due to the natural habitat fragmentation, *G. halys* shows here a patchy distribution, with a series of local populations along the Berd' river, where rocky habitats are available. A sample of 157 individuals from three local populations has been studied. Analysis of variability of eight microsatellite loci has revealed the existence of the fine scale (5-11 km) genetic structure at low level between all pairs of subpopulations (F_{ST} vary from 0.010 to 0.021, $p < 0.05$). Estimations of heterozygosity and inbreeding coefficients are shown no evidence for inbreeding depression. Two different tests for bottlenecks haven't found traces of historical or recent reduction in population size. Hypothesis of sex-biased dispersal has been tested using F_{IS} , F_{ST} and relatedness estimations separately for both sexes. F_{ST} and relatedness are significantly higher for females, whereas F_{IS} is higher for males, but insignificantly ($p = 0.469$). Thus, we are suggesting that males are the more dispersing sex.

I. Starnberger, P. Kamminga, V.C. Fosah & C. Nuttman

The „push-up“ as a calling posture in *Nectophrynoides tornieri* (Bufonidae)

Males of Tornier's Forest Toad, *Nectophrynoides tornieri*, were observed to perform a peculiar display posture, the 'push-up': the males raised themselves from a substrate (always a plant structure) by first stretching their fore legs into a 'sit-up' and then their hind legs to assume the position. We examined possible functions for the push-up position in manipulative behavioral experiments. In a majority of the tested males, the introduction of a conspecific male only evoked the less conspicuous sit-up display, whereas a playback of male vocalization more often triggered the full push-up position, usually followed by a vocal response. We found no association between the sit-up and the push-up display and the presence of a female *N. tornieri* near a male's calling perch. Our findings support the hypothesis that the push-up posture is a display in response to other calling males; whilst being the usual calling posture, it might also be important in visual communication.

J. Stockinger, V. Hennig & J. Glos

Amphibians under global change: adaptive strategies to mitigate the effects of climatic change in an urban landscape

Changes in land use practices and other anthropogenic pressures negatively affect biological diversity. In combination with these effectors, the predicted climatic change will further influence biodiversity in forests, aquatic systems and urban landscapes – all ecosystems will be affected. The objectives of the project KLIMZUG-NORD is to develop techniques and methods to minimize the consequences of climate change and to support the economy and society to adapt to the higher risks implicated by climate change. Our study within KLIMZUG-NORD will address the effects of climate change on amphibian communities in an urban landscape with the city of Hamburg as model system. We will analyze the role of habitat networks, and will develop a dynamic concept for nature conservation. Three approaches will achieve this goal: (1) a GIS based spatial analysis of historical and recent amphibian distributions within the greater Hamburg city area, and the development of a predictive model for amphibian distributions under a climatic change scenario, (2) field studies on amphibian habitat use along two urban-rural gradients, including an analysis of the role of habitat networks for amphibian diversity, (3) experimental studies on (larval) amphibians to test hypotheses on causal factors for climate change effects that were developed from predictive models.

A. Valdeón

Death of *Emys orbicularis* reproductive females by drowning in a drainage ditch

In a study of the biology of the European Pond Turtle (*Emys orbicularis*) in the wetland “Badina Escudera” (Villafranca, Navarre, Spain), three reproductive females with calcified oviductal eggs were detected dead in a recently constructed drainage ditch with 60-90 cm depth. The dead terrapins were found between the wetland and the nesting area, in places where the ditch rises several centimeters over the level of the water and had vertical walls of soil with no vegetation. Another one was observed exhausted in the bottom of the ditch and it was captured and revived applying the artificial respiration. The terrapin was marked with a radio tag and was released to the ditch the following morning and it was observed laying eggs successfully that night. The most probable hypothesis is that the reproductive turtles, after entering the ditch, try to get out at the closest point, without looking for better places, because of the biological pressure of the egg laying. The turtles repeating the attempt to exit the ditch at difficult places end up exhausted and they fall to the bottom of the ditch where they drown.

A. Valdeón, J.G. Campo, L. Lorente, J. Álvarez, Ó. Arribas, A. Bertolero, L. Fortuño, M.Á. Franch, J.D. Moreno, R. Regal, F. Sebastián, E. Arrechea & L.A. Longares

Current knowledge about *Emys orbicularis* in Ebro basin (Northern Iberian Peninsula)

European pond turtle (*Emys orbicularis*) is a poorly known species in Ebro basin. During the last years, their populations are being researched, especially in Navarre, Ebro Delta Natural Park, and some points of Aragón. In Navarre and Aragón the species has several healthy populations (Aragón and Gállego Rivers), but others are dramatically reduced or locally extinct (Arga river, Ebro river). In Ebro Delta Natural Park, the species only accounts with 7 confirmed autochthonous specimens, but nowadays, due to a breeding program and reintroduction project, there are more than eighty specimens in the wild. In Navarre, the knowledge of *Emys* distribution is relatively good in most of rivers and wetlands. However, in Aragón there are a lot of sites without sampling, so it is possible to discover new populations during next years. In la Rioja, there is only one recognized core which is the most upstream *Emys* population currently known in the Ebro River. Because of that, especial sampling efforts and monitoring shall be made in this region. In Navarre, the species has been found in the rivers Ebro, Aragón, Arga and Cidacos, and in several tributaries and lagoons among these basins. In Aragón, although there are records of the species in lagoons in Cinco Villas area, rivers Ebro, Gállego, Cinca, and others, nowadays, only has been researched in a few spots in these rivers, and in a group of lagoons in northeastern region. By this, new populations could appear in future samplings. In Catalonia there are a few European pond turtle populations near the Mediterranean coast, and the only one belonging to the Ebro basin is located in Ebro Delta Natural Park, although old records were scattered along the river course, witnessing a past wider distribution. Population structure of some of these populations has been analyzed. The results showed different age and sex-structure, having some of them high frequency of old animals (Villafranca, Galachos del Ebro), whereas others have high percentage of young turtles -less than 110 mm- (Gállego River, medium Aragón River's streams, Bardenas Reales), and the rest show intermediate situations (Cidacos River, Aragón River oxbows, Cinca River). In natural populations of Ebro Delta Natural Park there are few specimens and they are very old, while in the reintroduced population there are a lot of young specimens, some of them recently reaching sex maturity. Sex ratio is about 1:1 in natural populations. However, males are twice that females in Ebro Delta Natural Park reintroduced population.

A.B. Vassilieva

Heterochronies in the skeletal development in Asian tree frogs (Anura: Rhacophoridae) with different life histories

Many tropical anurans are known to be highly embryonized direct-developers, i.e. they do not possess larval stage and hatch from the eggs as completely formed froglets. Several previous researches on direct-developing frogs (mainly leptodactylid *Eleutherodactylus coqui*) had shown that their cranial ontogeny is marked by prominent heterochronic repatterning in comparison

with non-embryonized frogs. Species belonging to the Old World family Rhacophoridae show a large spectrum of developmental patterns, ranging from typical biphasic life history with feeding aquatic larva through different degrees of embryonization to true direct development. Hence, this lineage gives a good opportunity to study the influence of the life history on skeletal ontogeny in anurans. To reveal the possible heterochronies in the skeletal development in direct-developing frogs, we compared sequence and timing of vertebral, limb and skull bones formation in species with and without the larval stage. All direct-developing rhacophorids including the *Philautus* sp. (*Ph. banaensis* complex) studied here, are relatively small in adult state, that's why here we compared biphasic species of two size classes: large (*Polypedates leucomystax*, *Rhacophorus annamensis*) and small (*Chiromantis nongkhorensis*), to consider the plausible effects caused by miniaturization. Alizarin staining and clearing *in toto* was applied to the adult specimens of all species, to the tadpoles and newly metamorphosed froglets of biphasic species and to the embryos and hatchlings of *Philautus* sp.; all specimens and clutches were collected in Vietnam in 2009-2010. The sequence of overall skeletal development is found to be very similar in all biphasic species studied, with minor intra- and interspecific variations; all ossifications appear after hatching, during the larval period, metamorphosis and postmetamorphic growth. In contrast, in *Philautus* sp. the great majority of bones forms during the embryonic period, and hatchlings possess almost complete bony skeleton (excluding vomer, columella, and sphenethmoid, all present in adults). Also in this species, in skeleton formation some heterochronies are observed in comparison with biphasic rhacophorids. Thus, limb ossification starts relatively earlier, prior to the skull, but the vertebral arches ossify slightly later. However, the most pronounced heterochronic shift affects some cranial ossifications: in *Philautus* sp. the lower jaw bones (angulosplenic, dentary, mentomeckelian) form somewhat precociously than in biphasic frogs, as well as the suspensorium elements (squamosal, quadratojugal), but such endochondral bones as exoccipital and prootic appear remarkably later. The relative acceleration of jaws and suspensorium ossification was observed in some other direct-developing amphibians and can be assumed to be the evolutionary consequence of embryonization. On the other hand, the retarded (postmetamorphic) formation of vomer and columella in both *Philautus* sp. and *Ch. nongkhorensis* is probably caused by pedomorphosis. Based on the data obtained, we can conclude that heterochronies play an important role in the repatterning of the skeletal formation in evolution of amphibian ontogeny.

P. Werner

Is the Alpine salamander an alpine species?

The Alpine salamander (*Salamandra atra*) is restricted to lower montane and montane regions of the Alpine arc and the Dinaric Alps. It commonly occurs in parapatry with the Fire salamander (*S. salamandra*; a species widely distributed in central and eastern Europe) and co-occurrence is known from small contact zones in Austria and Switzerland. Based on preliminary observations, the geographic range limits of the Alpine salamander may either be associated with climatic conditions along an altitudinal gradient or be determined by biotic interactions with the Fire salamander. Due to similar resource requirements and physical advantage, *S. salamandra* may 'determine' the range of the Alpine salamander in the sense of resource competition. To identify the restricting factors for its distribution, in particular the potential role of the Fire

salamander, four approaches at different scales are employed. This presentation emphasizes the conceptual design of the running study and represents first interesting results. Species distribution models were utilized to test whether the range borders of the two salamander species are determined by climate. Within their contact zones, species-specific requirements were analyzed via site-occupancy modeling and microhabitat analyses. In order to find signs for interspecific 'avoidance' between the salamanders, olfactory preference test are being used.

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