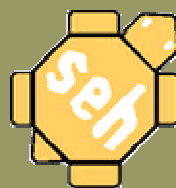
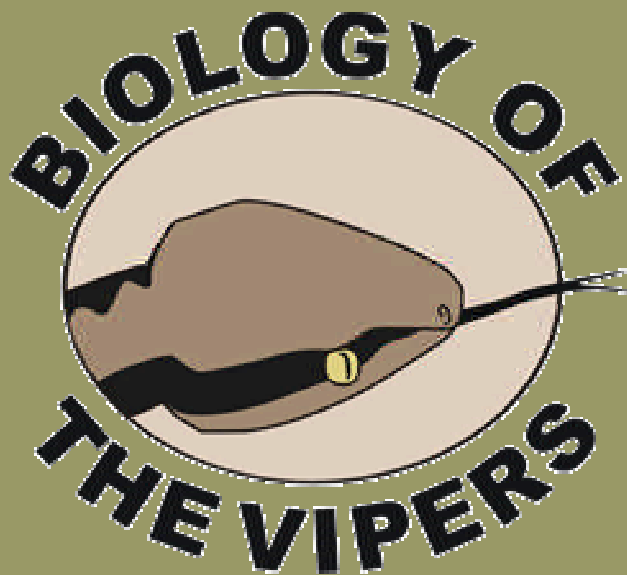
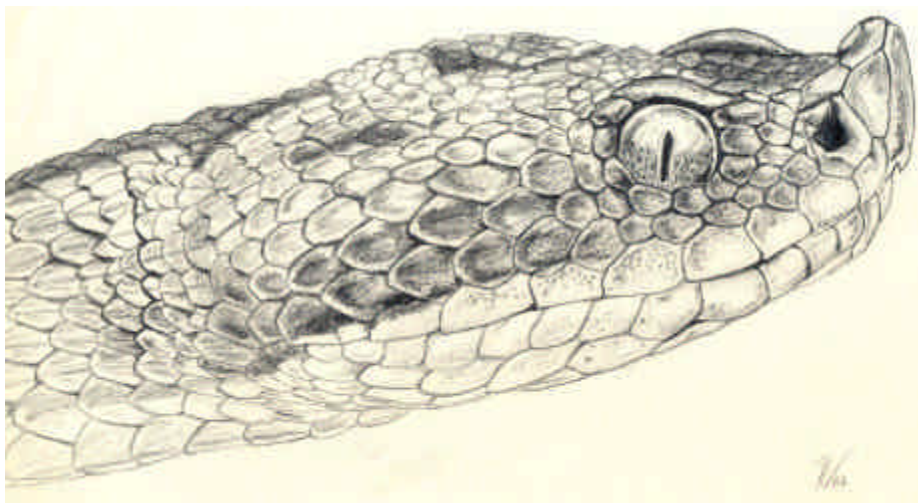


2ND BIOLOGY OF THE VIPERS CONFERENCE

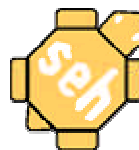
24-27 September 2007
Porto, Portugal



2ND BIOLOGY OF THE VIPERS CONFERENCE



PROGRAMME AND ABSTRACTS



24-27 September 2007
Fundação Dr. António Cupertino de Miranda
Porto - Portugal

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2nd Biology of the Vipers Conference, Porto (Portugal), 24-27 September 2007.

Abstract Book.

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LEGAL DEPOSIT

September 2007

WELCOME

Dear Participants,

Eighteen years ago, a conference on pitvipers held at the University of Texas at Arlington, resulted in the publication of the highly acclaimed “Biology of the Pitvipers” (1992, Selva). Later, in May 2000, Sweden hosted a very successful conference on vipers, which also resulted in a magnificent publication, the “Biology of the Vipers” (2002, Eagle Mt. Publ.). These conferences were both so scientifically stimulating and pleasurable that we felt that it was about the right time to propose another conference. Thus, back in 2006, our group decided to suggest Porto as the venue for the second conference and found a warm support from the SHE Council and numerous researchers. With a feeling of responsibility, the CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos (Research Centre in Biodiversity and Genetic Resources) is now very happy to host the 2nd Biology of the Vipers Conference.

Our group, mostly composed of young, enthusiastic Portuguese students developing their MSc and PhD theses at CIBIO (some in viper biology), reinforced with the contribution of foreign researchers, will be at your disposal in the different organisation tasks. The University of Porto, the Fundação para a Ciência e Tecnologia (FCT), Parque Nacional da Peneda-Gerês (PNPG), and several private institutions including Fundação Luso-Americana para o Desenvolvimento (FLAD), Fundação Dr. António Cupertino de Miranda, Chimaira Verlag, Brill Publishers, Sogrape Vinhos, Porto Turismo and the Comissão de Viticultura da Região dos Vinhos Verdes, among others, are providing the necessary economic and material support. All of them make this event possible.

So, we welcome you most cordially and hope that the conference in our city will be scientifically successful, intellectually stimulant and personally enjoyable, so we wish.

José C. Brito and Miguel A. Carretero
(The Organizing Committee)

GENERAL INFORMATION

Venue

The 2nd Biology of the Vipers Conference will be held at:
Fundação Dr. António Cupertino de Miranda (Cupertino Miranda Foundation),
Avenida da Boavista, 4245. PT-4100-140 Porto (Portugal)
Tel.: (+351) 226101189; Fax: (+351) 226103412; Site: www.facm.pt

Registration

The registration desk is situated at Cupertino Miranda Foundation.

It will be open:

- Monday 24, September: 8:30-19:00 h;
- Tuesday 25 and Wednesday 26, September: 9:00-19:00 h;
- Thursday 27 September the desk will be closed (excursion).

Updated information and eventual changes in the programme will be posted in a board be near the registration desk.

Participants are expected to pay their fees in cash upon arrival if they have not done it previously. They will also be asked to book the excursion and to register for the farewell party.

Full registration includes:

- admission to all sessions;
- congress bag and tourist information;
- programme and abstract book;
- cruise in river Douro and visit to Porto Wine cave

Accompanying persons may participate in the cruise in river Douro and the visit to Porto Wine caves.

Meals

For lunch, Cupertino Miranda Foundation has a convenient restaurant which participants are encouraged to use. Several other restaurants are available in the surroundings. For dinner, the city has plenty to offer.

Please visit: <http://www.portoturismo.pt/index.php?m=3&s=5>

Transports

Please visit: <http://www.portoturismo.pt/index.php?m=3&s=8>

http://webpages.icav.up.pt/pessoas/herpmeeting/Herpmeeting_home.htm

Changes in the programme

Eventual changes will be announced in the information board next to the registration desk.

Congress photo

A picture of all participants will be available in the congress website for download.

Posters

Authors are requested to fix their posters (100 x 150 cm) at the Cupertino Miranda Foundation in the marked panels. Fixation materials will be provided.

Oral presentations

Speakers should provide a copy of their presentations (CD or USB flash disk) at least two hours before the presentation. It should be delivered at the congress PC room and tested the proper working. No private computers will be allowed. Technical advice will be available. Oral communications will last 15 minutes maximum, with additional 5 minutes for discussion.

“Biology of the Vipers II”

The organizing committee will make all efforts to publish peer-reviewed papers presented to the 2nd Biology of the Vipers Conference, following the layout of the “Biology of the Pitvipers” (1992, Selva) and the “Biology of the Vipers” (2002, Eagle Mt. Publ.) books. The articles will be limited to 10 printed pages including tables and figures. For details including the text arrangement and the file formats, please consult the “instructions to the authors” of Amphibia-Reptilia: <http://www.brill.nl/AuthorsInstructions/AMRE.pdf>

Detailed information on the deadline for submission of the papers will be announced by e-mail after the conference.

PROGRAMME OVERVIEW

	Monday, 24 September	Tuesday, 25 September	Wednesday, 26 September	Tuesday, 27 September
Scientific Programme				
08:30	Arrival and registration			
09:30	Opening ceremony	Plenary lecture	Plenary lecture	Departure for excursion
09:50	Plenary lecture			
10:30		Coffee break	Coffee break	
10:50	Coffee break			
11:00		Session 4: Behaviour	Session 7: Distribution and Ecology	
11:20	Session 1: Systematics and Evolution			
12:00	Lunch break	Lunch break	Lunch break	Lunch
13:50	Session 2: Systematics and Evolution	Session 5: Physiology	Session 8: Conservation	
15:30	Coffee break	Coffee break	Coffee break	
16:00	Plenary lecture	Session 6: Ecology	Session 9: Workshop "GIS and Vipera"	
17:00	Session 3: Morphological Variation			Arrival from excursion
Social Programme				
18:00	Visit to Porto Wine cave	Cruise in river Douro		
20:00			Farewell party	



SCIENTIFIC PROGRAMME SCHEDULE

Monday, 24 September

08:30 – 09:30	Arrival and registration	pp
09:30 – 09:50	Opening ceremony	
09:50 – 10:50	Plenary lecture:	
	A nesting of vipers: phylogeny and historical biogeography of the Viperidae and the evolution of venom composition. W. <u>Wüster</u> , A. Barlow, N.R. Casewell, L. Peppin & C.E. Pook	8
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15:10 – 15:30	Genetic differentiation of the endangered populations of Meadow vipers (<i>Vipera ursinii rakosiensis</i> , <i>Vipera ursinii moldavica</i> and <i>Vipera renardi</i>) in East Europe. B. Halpern, T. Péchy, Á. <u>Major</u> , J.B. Kiss, S. Zamfirescu, A. Zinenko & I. Ghira	20

15:30 – 16:00	Coffee break	
16:00 – 17:00	Plenary lecture:	
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17:00 – 17:20	Multi-scale analysis of geographic patterns in morphological variation of two Mediterranean vipers (<i>Vipera aspis</i> and <i>V. latastei</i>) in the Iberian Peninsula. F. <u>Martínez-Freiria</u> , J.C. Brito, X. Santos, J.M. Pleguezuelos & M. Lizana	21
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11:00 – 11:20	A microsatellite DNA assessment of polyandry in the Caucasian viper <i>Vipera eriwanensis</i> . R.W. <u>Murphy</u> , N.I. Orlov, N.B. Ananjeva, A. Agasyan & K. Choffee	24
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	Chairpersons: X. Santos, M. Zuffi	
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	O. <u>Lourdais</u>	
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	R <u>Ajtic</u> , L. Tomovic & J. Crnobrnja-Isailovic	
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	A. Gentilli, M.A.L. <u>Zuffi</u> , F. Pupin, R. Sacchi, X. Bonnet & M. Fasola	
17:00 – 17:20	Reproductive biology in an insular Golden Lancehead, <i>Bothrops insularis</i> .	35
	S.M. <u>Almeida-Santos</u> , K.N. Kasperoviczus & O.A.V. Marques	
17:20 – 17:40	Reproductive traits of female <i>Crotalus polystictus</i> in central México	36
	K. Setser, E. Mociño-Deloya, D. Lazcano, A. Kardon & J.M. <u>Pleguezuelos</u>	
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	F. <u>Martínez-Freiría</u> , J.C. Brito & M. Lizana	
18:00 – 20:00	Social Programme: Cruise in river Douro	

Wednesday, 26 September

09:30 – 10:30	Plenary lecture: Results of the Hungarian meadow viper (<i>Vipera ursinii rakosiensis</i>) conservation program. B. Halpern, T. Péchy, K. Katona, G. Szövényi, R. Vidéki, Á. Major & R. Dankovics	11
10:30 – 11:00	Coffee break	
11:00 – 12:00	Session 7: Distribution and Ecology Chairperson: G. Nilson	
11:00 – 11:20	Niche conservatism in vipers: habitat use by sympatric species in a savanna area in south-eastern Brazil. R.J. Sawaya & M. Martins	38
11:20 – 11:40	Preliminary study of population ecology of an insular population of the Nose-horned viper (<i>Vipera ammodytes</i>) from Former Yugoslav Republic of Macedonia. B. Sterijovski, L. Tomovic, R. Ajtic & J. Crnobrnja-Isailovic	40
11:40 – 12:30	Plenary lecture: Snake Charming in Morocco: the Aissaouas and their impact on poisonous snakes J.M. Pleguezuelos	-
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13:50 – 15:30	Session 8: Conservation Chairpersons: L. Tomovic, B. Halpern	
13:50 – 14:10	Population viability analysis of a local population of <i>Vipera ursinii</i> in north-eastern Montenegro. J. Crnobrnja-Isailovic, R. Ajtic & L. Tomovic	41
14:10 – 14:30	Present state of <i>Vipera renardi</i> in Ukraine (distribution, habitats, abundance, biology, problems of conservation). T. Kotenko	42
14:30 – 14:50	Current condition and conservation status of vipers in Volga-Kama Region. A.V. Pavlov & A.G Bakiev	43
14:50 – 15:10	Ten years of adder (<i>Vipera b. berus</i>) research – results and conservation recommendations. J. Penner, M. Dehling, U. Joger, A. Zitzmann & M.-O. Rödel	44
15:10 – 15:30	How conservative is vulnerability to extinction in Brazilian pitvipers? M. Martins, O.A.V. Marques & R.J. Sawaya	45
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16:00 – 18:00 Session 9: Workshop “GIS and Vipers”

16:00 – 16:20 Deciphering evolutionary patterns and conservation units in *Vipera latastei-monticola* with Geostatistics and Geographical Information Systems (GIS). 46

J.C. Brito, B. Mendonça, X. Santos, J.M. Pleguezuelos, D.J. Harris, N. Sillero, S. Fahd & S. Larbes

16:20 – 18:00 Workshop on “GIS and Vipers: use of Geographical Information Systems for analysing evolutionary and biogeographical patterns and conservation problems – practical applications to viperid snakes”.

N. Sillero, X. Santos & J.C. Brito

The workshop will deal with spatial representation of species distribution and geographical variation (morphology and genetics) and includes:

- 1.- Exporting records from databases and GPS devices to GIS and dealing with projection systems;
- 2.- Obtaining accurate and ready to use environmental data from Internet sources;
- 3.- Preparing environmental data for predictive modelling: delimiting the study area; transforming data from vectorial to raster format; obtaining derived variables from the original dataset;
- 4.- Obtaining interpolation surfaces of geographic variation of morphological and genetic traits (Kriging);
- 5.- Extracting spatial variation patterns: Spatial Principal Component Analysis;
- 6.- Deriving habitat suitability models for species occurrence with ecological modelling tools (ENFA and MAXENT).

20:00 Social Programme: Farewell party

Thursday, 27 September

09:30 – 17:00 Field excursion

09:30 Departure of field excursion to the Peneda-Gerês National Park (PNPG).

11:30 Field visit to the “Mata de Albergaria”, a Portuguese Biogenetic Reserve of the PNPG, where *Vipera latastei* can be found.

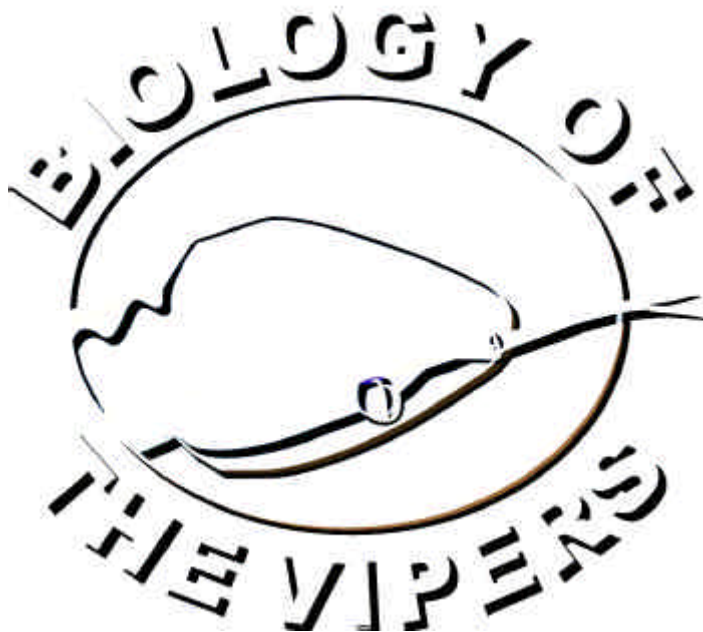
15:00 Departure from the National Park.

17:00 Arrival to Porto.





PLENARY LECTURES



Monday, 24 September
09:50 – 10:50

A nesting of vipers: phylogeny and historical biogeography of the Viperidae and the evolution of venom composition

Wolfgang Wüster, Axel Barlow, Nicholas R. Casewell, Lindsay Peppin & Catharine E. Pook

School of Biological Sciences, University of Wales, Bangor LL57 2UW, Wales, UK. w.wuster@bangor.ac.uk

The Vipers comprise the clade of venomous snakes with the most sophisticated venom delivery system, and many of the world's most medically important venomous snakes. Approximately 270 species belonging to around 40 genera (depending on author) are currently known, with a combined distribution encompassing all continents except Australia and Antarctica. Four basal groupings are traditionally recognised within the vipers: the Crotalinae and the Viperinae include the vast majority of described species, whereas two genera, the monotypic Asian *Azemiops* and the African night adders (*Causus*, six species), are often classified as separate subfamilies. In this presentation, we will use molecular phylogenies at two different taxonomic levels to explore facets of the evolutionary history of the vipers. Despite intense recent research interest in viperid phylogeny, the evolutionary relationships between the four major groups of vipers remain inadequately understood due to a lack of a comprehensive analysis of the entire family. Here, we use sequences of four mitochondrial genes sampled across the entire family to explore the phylogeny of the Viperidae. Our data confirm *Azemiops* as the sister taxon of the Crotalinae, whereas *Causus* is nested within the Viperinae. Phylogenetic relationships within the Viperinae remain poorly resolved. We use the phylogenetic tree obtained from these analyses, coupled with molecular dating methods, to reconstruct the biogeographical history of the Viperidae. At a lower taxonomic level, we use a phylogenetic tree obtained for the saw-scaled or carpet vipers (*Echis*) to test causal hypotheses for the evolution of venom composition. The role of natural selection for different prey items in influencing the evolution of venom composition has been hotly debated in the literature. Saw-scaled vipers represent an ideal model system for studies of the causes of venom evolution: clinically significant differences in venom composition are well documented, and different species of *Echis* differ radically in their diets, some species feeding heavily on scorpions, whereas others are almost entirely restricted to a vertebrate diet. Here, we present data on the lethality of different species of *Echis* to scorpions, and changes in gene expression between different species. Mapping changes in diet, venom composition and activity, and toxin gene expression onto the phylogeny of the saw-scaled vipers allows the testing of causal hypotheses for the documented variation in venom composition in this genus.

*Monday, 24 September
16:00 – 17:00*

Biodiversity and nature conservation in vipers

Göran Nilson

Göteborg Natural History Museum, Box 7283, 40235 Göteborg, Sweden.
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The family Viperidae is represented in a majority of habitats around the world. Some wide ranging taxa are locally abundant while other taxa are narrow endemics and have a more restricted occurrence. Globally several of these are represented in the biodiversity 'hot spots' that has been defined on most continents. Amongst others, regions in South America, Southeast Asia and central Asia are important viper biodiversity hot spots. Such areas should come into focus when considering nature protection. Vipers may be more exposed than other organisms by being venomous and in many regions followed by a disadvantageous reputation and aversion. Some obvious threats against vipers can be focused upon. Change of habitats is a prime factor by destroying the structure of the biota and changing the ecosystem in ways that most species cannot manage. Activities like agriculture, mining or dam constructions are such affects. Collecting of rare vipers for antivenin production purposes a similar problem locally. Research with descriptions and information of delicate localities can as well result in large scale collecting for the pet trade. It is of importance that the herpetological community acts according to these needs. When necessary, debates should be initiated in regional media and societies. Practical efforts could be initiated locally when possible. The snake tunnels on the island of Milos in Greece are such examples. Buying of land if possible, like in the Pusta of Hungary, for habitat protection is another example. Scientific research and studies of vipers are of key importance for our understanding of the ecology and biodiversity, which in turn are essential knowledge for saving populations of endangered vipers.

Tuesday, 25 September
09:30 – 10:30

The spectacular natural history of insular cottonmouth snakes

Harvey B. Lillywhite

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Cottonmouth snakes (*Agkistrodon piscivorus conanti*) inhabit Florida's Gulf coast islands, which provide important nesting refugia for colonial wading birds. A large rookery is present on Seahorse Key, where cottonmouths are entirely terrestrial and scavenge on dead fish that are dropped or regurgitated by thousands of nesting birds. This resource is available for >6 months of the year and supports a very dense snake population. Telemetry studies demonstrate that snake home ranges are comparatively small (0.1 ha) beneath the rookery, but are larger (> 1ha) elsewhere on the island where resources are less abundant and less concentrated (e.g. invasive rats). Near the rookery, heterosexual pairs of cottonmouths can be found in close association year-round and occasionally forage together nocturnally. The male characteristically leads the female, defends her from other intruding males, and remains in attendance while she ingests fish. Elevated head displays repel subordinate males and also establish dominance when several snakes converge on the same carrion while foraging. Cottonmouths appear not to feed on colonial wading birds, but they do consume dead passerines that appear during "fallouts" when numerous individuals appear on the island when weakened by headwinds during migration. Snakes also forage on dead fish washed ashore in the intertidal zone where they also consume incidental plant material. The behaviours of these insular pit vipers are unusual, especially in social contexts related to population density and ephemeral resources. The biology of these snakes further suggests a theoretical scenario for the evolutionary transition from terrestrial to marine environments.

Wednesday, 26 September
09:30 – 10:30

Results of the Hungarian meadow viper (*Vipera ursinii rakosiensis*) conservation program

Bálint Halpern¹, Tamás Péchy¹, Krisztián Katona², Gergely Szövényi³, Róbert Vidéki⁴, Ágnes Major⁵ & Róbert Dankovics⁶

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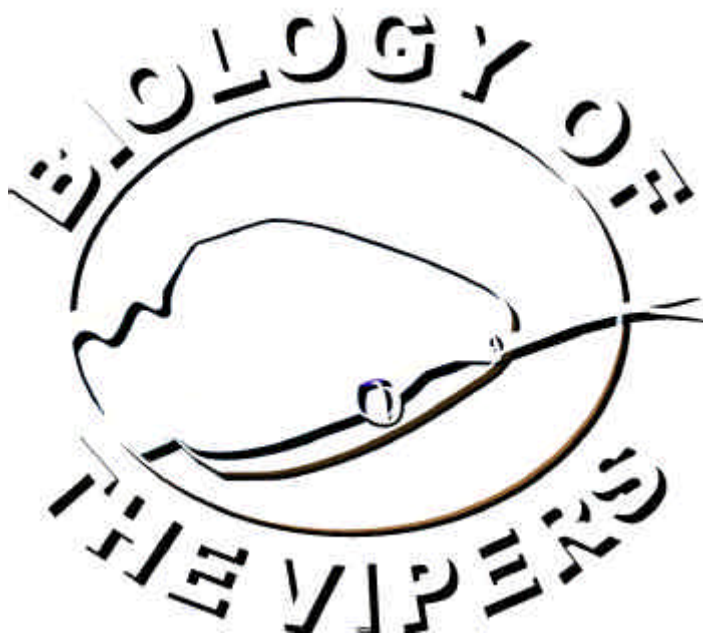
6 - Savaria Museum, Kisfaludy S. u. 9., 9700, Szombathely, Hungary.
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Recent populations of this small venomous snake are very small and isolated from each other. There are two major occurrences in Hungary: two populations in North-Western Hanság region, and eleven populations on the Great Plains between river Danube and Tisza, in the so called Kiskunság region. There is also one recently discovered population in Romania. Rough estimations put its surviving numbers below 500 individuals. MME BirdLife Hungary with Kiskunság and Duna-Ipoly National Parks started a complex program to establish the background of preserving this unique subspecies for the future. The four-year program, started in 2004, is funded by the Ministry of Environment and Water Affairs and the EU LIFE-Nature fund. The program consists of four major pillars: habitat reconstruction, monitoring and related studies, publicity campaign and the start of the Viper Conservation and Breeding Centre. Grassland reconstruction on 17 ha area targeted those tree plantations that probably robbed the species from safe hibernating places, and created a barrier between two recent populations. A detailed management plan was prepared in order to direct the difficult process of turning false acacia and pine plantations into sandy pastures. There are already certain parts with clear signs of repopulation by species from the grassland. Monitoring of recent populations is trying to describe recent habitats with objective parameters, and to prepare guidelines for their management. Vegetation of all viper habitats was mapped. We are collecting data along transects, selected on recent viper habitats. We regularly observe characteristics of vegetation, availability of hiding places and density of prey items, like Orthopterans, lizards, rodents. We try to evaluate results according to previous management of these sites and

recent viper occurrences. The active protection of a venomous snake can be difficult to accept for the general public; therefore we are using every opportunity to overcome this problem. We organised public forums and press conferences at the start of the project to inform locals and the wider public. We produced leaflets, brochures and information boards about the program and the species. We started the official website (www.rakosivipera.hu), with regular updates. Experts feared that some isolated populations due to their size are unable to grow whilst the best management effort either and their reinforcement is inevitable in order to keep them. The Viper Conservation and Breeding Centre started with 10 adult individuals, collected from different populations. The minimised predation and maximised food abundance provided by the Centre's semi-natural conditions results higher recruitment rate than in wild populations. Since the start of the Centre we had three successful breeding periods resulting in its recent state of altogether 105 vipers. We already had the first female breeding, which was originally born in captivity. First genetic tests show that offspring's have higher genetic variability than their parents, a good sign for the future. Regular veterinary support is provided under the umbrella of a successful cooperation with Budapest Zoo. Also in the frame of this cooperation, the Zoo have set up a prey-breeding facility, in order to be able to breed huge numbers of crickets, serving as main food source for the vipers. Operation of the Centre is supervised by the so called Hungarian Meadow Viper Conservation Council, created from experts and policy makers, by Nature Conservation Authority. We plan to reintroduce the first group of vipers in the upcoming years.



ORAL COMMUNICATIONS



Monday, 24 September
11:20 – 12:00

Session 1: Systematics and Evolution

What is a “Venomous” snake?

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Historically an operational criterion have been used to categorize a reptile as venomous; simply put, a reptile was venomous if its bite resulted in relatively rapid incapacitation or death. For the last several decades there has been significant debate regarding the application of the operational criterion to the colubrid snakes, the group that includes the majority of living snakes. Most of these snakes have traditionally been described as non-venomous, though it has long been recognized that some, like the African Boomslang (*Dispholidus typus*), can fatally envenomate humans. A number of current researchers have essentially avoided this contention by abandoning the operational definition in favour of an attributional criterion for venom. To these researchers venom is recognized not by its impact following a bite, but rather by the presence within an oral gland of either: 1) chemical compounds which are structurally similar to compounds isolated from the venom of operationally-defined venomous snakes, or 2) mRNA, or post-analysis cDNA, sequences which are similar to those of operationally-defined venomous snakes, or 3) compounds capable of producing physiological responses in standardized toxinological assays. There is strong congruence between the operational and attributional criteria when applied to what were traditional viewed as venomous snakes, such as cobras or rattlesnakes. Unfortunately, for the majority of snakes, as well as other squamate reptiles, the two criteria produce discordant categorizations. This contribution will explore these two approaches and attempt to offer a conciliatory definition for “venomous.”

A molecular phylogeny of Caucasian vipers

Robert W. Murphy, Nikolai I. Orlov, Natalia B. Ananjeva, Amy Lathrop, Aram Agasyan, Iydmila Mazanayeva, Sergei Ryabov, Konstantin Shiryaev & Audrey P. Kapeleris

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The phylogenetic relationships of the Caucasian vipers were investigated using mitochondrial DNA sequences from cytochrome b, ND2 and 16S. The samples included multiple localities for many taxa, especially those having a broad distribution within the Caucasus. Some other European vipers were also included in the analysis. The evaluation included *Vipera ammodytes*, *V. latastei*, *V. aspis*, *V. seoanei*, *V. berus*, *V. sachalinensis*, *V. dinniki*, *V. ursinii*, *V. orlovi*, *V. kaznakovi*, *V. eriwanensis*, *V. lotievi*, *V. renardi*, and *V. nikolskii*. The sequence data were evaluated using maximum parsimony as well as Bayesian inference methods. Intraspecifically, incomplete lineage sorting was observed for *V. berus*, *V. ursinii*, *V. orlovi*, *V. renardi* and *V. dinniki*. This finding might also reflect the presence of multiple cryptic species or the invalidity of some taxa. The associations of the species conformed to subgeneric designations of Nilson et al. (1994). *Vipera ammodytes* was resolved as the sister group of all other *Vipera* included in our evaluations. Sequentially, the groups branched off as follows: *V. latastei* + *V. aspis*; *V. seoanei*, *V. berus*, *V. sachalinensis* + *V. nikolskii*; *V. dinniki*; *V. orlovi*, + *V. kaznakovi*; and finally *V. eriwanensis*, *V. lotievi*, *V. renardi* + *V. ursinii*.

Monday, 24 September
13:50 – 15:30

Session 2: Systematics and Evolution

First steps towards a molecular phylogeny of Near- and Middle East Mountain and Blunt-nosed vipers of the genera *Montivipera* and *Macrovipera*

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Systematic and phylogenetic relationships among species of the genera *Macrovipera* and *Montivipera* are contentious. In particular the systematics of the mountain vipers have been subject to controversy. Depending on previous authors' species concepts, populations are regarded as valid species, or as allopatric populations of one and the same species. In this study we used molecular data of the complete mitochondrial protein-coding gene Cytochrome b, to determine the phylogeny of both genera. Our data support the monophyly of *Montivipera* and the Asiatic *Macrovipera*. Within *Montivipera* two monophyletic groups were identified: the *raddei* group (with the nominal species *raddei*, *albicornuta* and *latifii*) and the *xanthina* group, containing all other known *Montivipera* taxa. The phylogenetic relationships are: (*lebetina*, ((*raddei*, *albicornuta*), *latifii*), (*xanthina*, (*bornmuelleri*, (*wagneri*, (*albizona*, *bulgardaghica*)))))). The *raddei* group is characterized by very low genetic distances, indicating their historically young radiation. In contrast the genetic distances within the populations of *M. xanthina* are higher than between other nominal species of the *xanthina* group. In all our analyses *M. xanthina* is paraphyletic. Populations from Turkish Taurus Mountains belong to a separate clade than other *M. xanthina* populations. Within the genus *Macrovipera* four genetically separated clusters exist, representing the taxa *lebetina* and *schweizeri* (Cyprus and Cyclades), *turanica* (Middle Asia) and *obtusa* (Irano-Anatolian populations) and probably a new *Macrovipera* taxon, from Iran. The extent of genetic distance between the genera *Montivipera* and *Macrovipera* is up to 13.8%.

Molecular phylogeny and quantitative trait analysis of the genus *Echis*

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A consensus on the species-level taxonomy of the medically important viper genus *Echis* has yet to be reached. Multiple similar species have been described based on weak morphological evidence and no comparison has been made with a molecular phylogeny. Given the extensive distribution of *Echis* and the known variation in venom composition between populations, a robust phylogeny is essential in order to optimise the production and selection of appropriate antivenom. Here, we use DNA sequences from the mitochondrial genes cytochrome b, NADH dehydrogenase subunit 4, 16SrRNA and 12SrRNA to reconstruct the phylogeny and quantitative trait analysis of scalation, biometric and colour-pattern characters of the genus to provide a framework for understanding their systematics. Analyses to date group the different populations of *Echis* into four distinct species complexes, the *Echis carinatus*, *E. coloratus*, *E. ocellatus* and *E. pyramidum* groups. The four species groups are not congruent with the three subgenera proposed in 1990. Two recently described species, *E. khosatzkii* Cherlin 1990 (*pyramidum* group) and *E. omanensis* Babocsay 2004 (*coloratus* group), are strongly supported as *bona fide*, monophyletic species. The exact position of other species boundaries is less certain. At this stage, there is a general lack of genetic and morphological differentiation between *E. pyramidum* and *E. leucogaster*. Genetic differentiation within the *E. carinatus* group also needs clarification, although quantitative trait analysis supports the notion that both *E. carinatus sochureki* and *E. multisquamatus* are part of a long morphological cline within *E. carinatus*, and therefore should be conspecific.



Genetic structure of the French *Vipera ursinii* populations

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The Orisini's Viper (*Vipera ursinii*) is one of the most threatened snakes in Europe. Its fragmented distribution and its specific requirements contribute to this precarious conservation status. In the western extreme of its distribution area (south-eastern France), this species is scattered in 14 populations occupying variable surface areas (between 25 and 2500 ha).

Using genetic (nuclear and mitochondrial) markers, we have investigated the genetic structure between most populations. Preliminary results showed a high degree of genetic differentiation between most populations. Furthermore, a strong geographic structure was observed with both approaches. These analyses revealed limited mitochondrial variability in all populations, whereas nuclear markers did not display a reduced genetic diversity even in small populations. One of the largest populations however, displayed a reduced genetic diversity and the possible reasons will be discussed.

Cryptic genetic diversity in a widespread viper: phylogeography of the African puff adder (*Bitis arietans*)

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In recent years, phylogeographic studies of wide-ranging taxa have become one of the principal tools in our attempts to understand continental-scale distribution patterns, as well as contributing to the unravelling of the systematics of many groups of organisms. Among reptiles, the vast majority of such studies have focussed on European and North American taxa, for obvious logistic and socio-economic reasons, whereas tropical Asian and African species have been investigated much more sparingly, or only with limited geographical coverage. The African puff adder (*Bitis arietans*) is the most widespread and medically important viper on the African continent. Despite its wide distribution (sub-Saharan Africa excluding the rainforests, north-western Africa, south-western Arabian Peninsula), it has attracted little taxonomic attention, and only a single subspecies, *B. a. somalica*, is widely recognised. Here, we use sequences of several mitochondrial genes sampled from throughout the species' range to investigate patterns of genetic differentiation in *B. arietans*. Our data reveal considerable phylogeographic structure, including a number of highly distinct haplotype clades within *B. arietans*, which differ by p-distances more usually associated with interspecific comparisons. In southern Africa in particular, considerable genetic diversity is found on a small geographical scale. We compare the phylogeographic pattern found in the puff adder with those of co-distributed snake species, and discuss its possible causes.

Genetic differentiation of the endangered populations of Meadow vipers (*Vipera ursinii rakosiensis*, *Vipera ursinii moldavica* and *Vipera renardi*) in East Europe

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The *Vipera ursinii* complex involves subspecies and species living in small and fragmented populations which are highly endangered, primarily because of the destruction of their habitat. At the same time, the status and phylogenetic relationships of the species and subspecies have been under debate and re-evaluation. To get deeper insight into the differentiation of the members of the complex, we investigated 99 individuals living in 10 populations of 6 regions (two counties of Hungary, three areas of Romania and two regions in Ukraine) of *Vipera ursinii rakosiensis*, *Vipera ursinii moldavica* and *V. renardi*, this latter species considered to be taxonomically most related to lowland subspecies of *Vipera ursinii*. We analysed the genetic differences on the basis of 184 polymorphic RAPD fragments, 109 alleles of 6 microsatellite loci, and 29 morphometric characters. Multivariate analyses with molecular markers clearly separated the samples according to their origin and showed a significantly smaller genetic distance between the two subspecies of *V. ursinii* compared to their distance to the *V. renardi* samples. AMOVA values detected only 58% of genetic variability within populations, while 33% variability was revealed among regions and 9% occurred among populations of the regions. On the basis of morphological characters, the differentiation proved to be smaller than for the molecular markers. According to these results the conservation genetic plans should be based on molecular analyses. The differentiation of some mitochondrial sequences is under investigation.

Session 3: Morphological Variation**Multi-scale analysis of geographic patterns in morphological variation of two Mediterranean vipers (*Vipera aspis* and *V. latastei*) in the Iberian Peninsula**F. Martínez-Freiria¹, J.C. Brito², X. Santos³, J.M. Pleguezuelos⁴ & M. Lizana¹

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The general distribution pattern of the Iberian vipers is parapatry, but in NE Spain there is sympatry between *Vipera aspis* and *V. latastei*, where mixed populations of “true” and intermediate forms are found in syntopy. Patterns of geographic variation in 15 morphological traits were investigated in 604 specimens (354 *V. aspis* and 250 *V. latastei*) with spatial interpolation tools (*kriging*) and Spatial Principal Component Analysis (SPCA) in a Geographical Information System. At the regional scale (NE Spain, 64000 km²), for both males and females, a north-south clinal variation pattern was observed, with increasing number of apical scales (APIC) and decreasing number of ventral scales (VENT) and dorsal marks. At the local scale (High course of Ebro River, 300 km²), for both males and females, a north-south clinal variation pattern was observed, with decreasing VENT and increasing APIC. Three groups of vipers were clearly discriminated: A) *V. aspis* group (VENT males: 147, 138-160, females: 150, 136-158; APIC males and females: 2, 2 - 3) located in the northern region of the study area; B) *V. latastei* group (VENT males: 141, 132 - 151, females: 143, 131 - 155; APIC males: 4, 3 - 7, females: 5, 3 - 7) located in the southern region; C) intermediate forms group, with high level of morphological variability (VENT males: 144, 136 - 146, females: 145, 136 - 155; APIC males and females: 3, 2 - 5) located in the central region, where syntopy between *V. aspis* and *V. latastei* was observed. Regional-scale results suggest the possible occurrence of multiple hybrid zones, whereas local-scale results identify a hybrid zone where possibly gene flow between these closely-related species occurs. Funded by FCT (POCTI/BIA-BDE/55596/2004).

Morphometric analysis of the Asian pitviper *Ovophis monticola* complex

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Establishing species boundaries and relationships in the Asian pitvipers through traditional morphological methods has proven difficult and unreliable due to various factors including the prevalence of morphological convergence among genera and cryptic speciation. In recent studies, genetic analysis and multivariate morphological analysis has begun to reveal the complex relationships in this group and has lead to a great deal of reclassification in light of the new data. One of the groups which has not yet been investigated with this methodology is the genus *Ovophis*, which after removal of two species which proved to be unrelated, consists solely of species of the *Ovophis monticola* complex. These are found in montane regions across Asia from Nepal and North India to Eastern China, and Southwards through Laos, Vietnam, Myanmar, Thailand and Cambodia to Malaysia and Sumatra. Varying numbers of species and subspecies are recognised by different authorities and the ranges of these are ill defined. In this study traditional species boundaries in *Ovophis* are discussed in light of a multivariate morphological analysis of around 200 live and preserved specimens from across the range. The utility of the original diagnostic characters for the species and subspecies are discussed, and morphological variation is examined in a biogeographic context. In addition, the phylogenetic relationships between several populations have been investigated using sequence data from 4 mitochondrial genes.

Ontogenic shift of sexual dimorphism in Meadow viper (*Vipera ursinii macrops*) from Bjelasica Mt. (Montenegro)

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Sexual dimorphism in morphological traits in adult snakes is widespread and well-documented. But, since data about sex differences in newborns and/or in subadults are scarce, it is unclear whether sex differences are set at birth or they arise post-natally. In this study, we analysed pattern of sexual dimorphism in newborns, juveniles and subadults, as well as in adult individuals of meadow viper (*Vipera ursinii macrops*) from the Bjelasica Mt. in Montenegro. Morphological data were collected for 124 newborns (born in captivity), 62 juveniles and subadults and for 96 adult individuals. By using univariate, bivariate and multivariate statistics, we analysed intergender differences in body size (snout-vent length and weight), head dimensions (head length, head width, mouth length and mouth width) as well as in tail length. In newborns, we tested inter-family differences in sexual dimorphism. Since our study was conducted during four consecutive years (2003-2006) we had opportunity to check year-to-year variation in degree of sexual dimorphism in neonatal snakes. Among newborns, sexual differences were found for body size and tail length. Interestingly, we also found significant influence of family and year-to-year variation of sexual dimorphism in neonates. In juveniles and subadults, intergender differences were found for head dimension and tail length, while in adults, sexual dimorphism was found for body size and tail length. Possible causes that might generate the revealed ontogenic pattern of intergender differences are discussed.

Session 4: Behaviour

A microsatellite DNA assessment of polyandry in the Caucasian viper *Vipera eriwanensis*

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Multiple paternity can significantly increase the effective population size of organisms. This can be a particularly important evolutionary strategy in small, isolated populations. Consequently, we investigated polyandry within six clutches of Armenian *Vipera eriwanensis*. The clutches contained from 5 to 11 embryos. A suite of 11 hyper-variable microsatellite DNA loci was developed. These loci were variable among all species of Caucasian *Vipera*, and most were variable within species. Ten of these loci were consistently resolved in the embryos of *V. eriwanensis*, of which seven loci varied within at least some clutches. As many as four alleles were expressed within any population, and in all of these cases the mothers were heterozygotic for the locus. Because the genotypes of the potential fathers were not known, we cannot reject the null hypothesis of a single breeding event for each of the clutches. Consequently, polyandry, if it occurs, may not be common in *V. eriwanensis*. The necessity of sequencing alleles to confirm their homologies was revealed at one locus that appeared to exhibit little variation. Two alleles produced identical pherograms but these masked variation. One allele had a repeat sequence of (CT)5(CA)9AA(CA)3 and the alternative allele appeared as (CT)4(CA)10AA(CA)3.

Maternal cannibalism of non-viable offspring by *Crotalus polystictus*

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We collected gravid *Crotalus polystictus* during June-August of 2004, 2005 and 2006 in Central Mexico recording 205 litters from 163 different females maintained in captivity to parturition. Production of non-viable offspring (ova and stillborn neonates) was common (45% of litters). We left non-viable neonates, as well as live siblings, together with 79 of these females for 0-72 hours, to provide females the opportunity to cannibalize non-viable offspring. Sixty five percent (51 of 79) ate some or all non-viable offspring, consuming an average of 10.7 g (13% of their postpartum mass). A single snake consumed live offspring, eating two live neonates and a stillborn neonate. Females consumed both stillborn neonates and ova in similar proportions. We evaluated factors that influenced the decision to cannibalize using logistic regression. Large females, females with proportionally large clutches, and females held captive for longer periods were more likely to cannibalize than were other females. Consumption of non-viable offspring confers energetic benefits to females, as females gain a meal when emaciated. This behaviour also confers survival benefits to both females and living siblings, because cannibalism reduces chemical cues released by rotting ova and dead neonates, which might serve to attract potential predators.

Chemical prey preferences in the ingestively naive White-Lipped Tree viper, *Cryptelytrops albolabris*

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Among venomous snakes, arboreal vipers form a distinct group which has special behavioural, morphological and functional adaptations for living in a complex three-dimensional environment of bushes and/or trees. Majority of arboreal vipers are small to medium snakes with prehensile tails which enables them to anchor themselves on branches. Although they are quite popular as pets and as objects for studying taxonomic relationships, surprisingly little is known about their ecology and behaviour. In the series of experiments, we tested chemical preferences of the newborn, ingestively naive White-Lipped Tree Vipers (*Cryptelytrops albolabris*). Sixteen animals were tested using cotton swabs smeared with eight scents: fish skin, frog skin, lizard skin and day-old mouse skin. Also, the abdominal compartment smears of each of the scent-providing animal were included in the test. All these scents may be relevant as the food odours in nature. As a negative control, we used distilled water and as a pungency control perfume diluted 1:7. The rate of tongue flicking was measured as a response to the various olfactory stimuli. Each animal was tested with eight scents + two controls. The animals were tested once daily with one scent and with the other scents/controls on the consecutive days (for 10 days). The order of presentation of the scents/controls was randomly generated for each snake. After the first series of the experiments, the snakes were fed three times in 10 – 14 day interval with day-old mice and tested again with the same number of scents/controls, 15 days after the last feeding. The results will be discussed in the light of the ontogenetic diet shifts and their relevance to the evolution of chemosensory preferences in vipers and snakes in general.

Session 5: Physiology

Skin lipids of a pit viper, *Gloydius blomhoffii* and some other Japanese species of snakes

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We have examined the skin lipids of some species of snakes in Japan, including a pit-viper, *Gloydius blomhoffii*. The purpose of this study is to locate sex pheromones of these snakes. Sex pheromones of snakes were previously only found in a New World natricine snake, *Thamnophis sirtalis* and a colubrid, *Boiga irregularis*. These species possess long chain methyl ketones, of which those of *T. sirtalis* were experimentally recognized as sex pheromones. Among the species we have examined, a natricine snake, *Rhabdophis tigrinus* possessed long chain methyl ketones similar, but not identical, to those of *T. sirtalis*. And a colubrid snake, *Elaphe quadrivirgata* possessed a series of long chain nitriles. On the other hand, *G. blomhoffii* possessed 14 saturated hydrocarbons, most simple materials among the species examined. The number of carbon in these hydrocarbons was 24-32. Although we have not yet succeeded in the attraction of males by these materials, from the similarities to methyl ketones in *T. sirtalis*, and difference among species, it is strongly suggested that these are sexually important materials.

Why do pregnant aspic vipers (*Vipera aspis*) thermoregulate so precisely? An experimental test of the optimal developmental temperature hypothesis

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Vertebrates have developed a wide diversity of parental strategies to reduce potentially deleterious impact of environmental conditions on their progeny. A growing literature suggests that early developmental influences may also have long-term consequences on offspring quality and reproductive success. Thus, improved regulation of development is considered a major driving factor in the evolution of reptilian viviparity. Still, only a few studies have experimentally manipulated the thermal environment in viviparous species to assess the long-term significance of maternally regulated developmental temperature. In the aspic viper (*Vipera aspis*) gestation is associated with major ecophysiological shifts including a dramatic reduction in food intake and activity along with an increase in thermoregulatory activities. Reproductive effort is high in this species and constraints of gestation significantly contribute to the great survival and energetic costs of reproduction. We expect such additional constraints to be balanced by significant fitness benefits, presumably related to offspring developmental quality. By implanting temperature loggers I showed that pregnant aspic vipers maintain high and very stable temperature with evidence of a precise thermal set point. Additionally, I manipulated daily thermal regimes during gestation using climatic chamber. I imposed only mild deviation from thermal regimes maintained by free-ranging females resulting in different mean temperature and time spent at the thermal set point. Live and healthy neonates were obtained in each treatment but various fitness-related variables were affected. Overall, my results largely support the optimal developmental temperature hypothesis.

Thermal biology of Meadow viper (*Vipera ursinii macrops*) from Bjelasica Mt. (Montenegro)

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Ectotherm tetrapods thermoregulate by adjusting habitat use and by active behavioural control and hence, thermoregulation is probably one of the most important proximate factors influencing habitat use of terrestrial reptiles, at least in temperate climates. Here we present data about thermal biology and microhabitat preferences of the population of highly endangered European Viper, *Vipera ursinii macrops*, from the Bjelasica Mt. We measured cloacal temperature, soil temperature and air temperature at 5 cm above the ground. Sample size was 251 individuals over four years of study (2003-2006), during spring, summer and autumn. We analysed adult males, adult females (pregnant and non-pregnant) as well as subadult individuals. Type of behaviour was classified as: basking, moving, resting in shade and hiding. Microhabitat type was also recorded, and classified into open, semi-open and closed habitats. Time of day and expositions were also recorded. We analysed associations among temperature, microhabitat preferences, and preferred expositions, type of behaviour and time of the day, for pregnant and non pregnant females, males as well as for subadults. Precise data about thermal biology and preferred environmental temperatures of cold-adapted meadow viper could be very important for the evaluations of influences of climatic changes to local populations. Information on habitat requirements of this highly endangered species should be central to management planning. Thus, the results of this study support the idea that the management programs can effectively conserve a species, only if such programs protect critical habitat components at suitable spatial scales.

Suboptimal thermoregulation in male adders (*Vipera berus*) after hibernation imposed by spermiogenesis

Gábor Herczeg¹, Jarmo Saarikivi¹, Abigél Gonda², Jarmo Perälä¹, Aino Tuomola¹ & Juha Merilä¹

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In ectotherms, the main behavioural option for thermoregulation is the adjustment of daily and seasonal activity to the thermal quality of the environment, while when active, ectotherms thermoregulate by shuttling in between thermally differing microhabitat patches. Here, we focused on the question whether other behavioural or physiological processes could force ectotherms to maintain activity during thermally unfavourable periods, when accurate thermoregulation is impossible irrespective of microhabitat selection. We compared the thermoregulation of male adders (*Vipera berus*) between two periods in spring when, (1) only males and, (2) also females and juveniles had terminated their winter hibernation. We found that males thermoregulated actively both in the lab and in the field. Accurate thermoregulation was only possible during the second period due to the low thermal quality of the environment. Male adders maintained lower mean body temperature in the field than in the laboratory within both periods, and in addition, their body temperature during the first period was in average 4°C lower than in the second. The thermal qualities of the natural basking sites used showed a similar pattern. We discuss the results in the context of a potential trade-off between spermiogenesis and thermoregulation, where the benefits of early spermiogenesis coupled with inaccurate thermoregulation are higher than the associated costs.

Vulnerable vipers vomit: experimental manipulation of thermoregulation & safety

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Loosing a prey represents a high energy cost for infrequent feeders such as vipers. Loosing life is certainly a higher cost. The capture and the digestion of large preys require foraging effort and specific thermoregulation; two types of behaviours that can entail significant exposure to predators. Therefore, we expect that some regulations influence the decision to hold in the stomach a prey recently acquired versus to get rid off it via regurgitation (trade-off between costs and benefits to resume digestion). In snakes, regurgitation can be provoked by natural factors, low ambient temperatures or diseases for instance, or can be the consequence of handling (stress). However, the causes for regurgitation have not been studied accurately. We manipulated the feeding status, the thermal ambiance, the occurrence of a shelter, and the level of stress (simulation of an attack by a predator) in *Vipera aspis*. As expected our results showed that low ambient temperature stimulate regurgitation. They also revealed for the first time that the presence of a shelter, the level of stress, and an interaction between these two factors are crucial. These results enable to understand why unfed snakes tend to maintain high body temperatures when no shelter is available, but remain under cold shelter when available. They also reinforce the notion that even small open-areas in natural habitats can constitute serious obstacles to snakes. Conservation plans should integrate the importance of shelters, both in captivity and for field managements.

Tuesday, 25 September
16:00 – 18:00

Session 6: Ecology

Feeding habits of an Asian pit viper, *Ovophis okinavensis*, with an enigmatic sexual difference in diet composition

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Despite the diversity and world-wide distribution of Viperid snakes, dietary information of them is largely biased to New World and European species. We examined feeding habits of a subtropical Asian pit viper, *Ovophis okinavensis*, in the northern mountain area on Okinawa Island, Ryukyu Archipelago, Japan. During a 10-years ecological survey, stomach contents of a total of 1019 snakes were examined, and a total of 461 prey items were recovered. Prey items consisted of six, one, two, five, and three species of frogs, lizards, snakes, birds, and mammals, respectively, suggesting that the snake is a dietary generalist. However, 92.9% of the total diet consisted of frogs, indicating that quantitatively the snake is considered a frog specialist. This high dependency on frogs is obviously attributable to the predominant consumption on two species, *Rana okinavana* and *R. narina*, which are explosive breeders that aggregate to breeding sites during winter. No clear ontogenetic changes in diets were observed. Prey size was correlated with snake size, but large snakes did not drop small sized prey from their diets. There were no sexual differences in the frequency of frogs in diets, but males exploited *R. okinavensis* more frequently than females. Direct field observations demonstrated that this higher *R. okinavensis* consumption by males is due to the biased appearance of males to a breeding site of this frog. The absence of females in the breeding site of *R. okinavensis*, which should be a rich food resource even for females, is unexpected, and its possible causes are discussed.



The role of prey availability in the geographic variation of reproductive output in the Iberian *Vipera latastei*

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In the Iberian Peninsula there are three viper species with allopatric distributions (*Vipera aspis*, *V. seoanei*, *V. latastei*), being *V. latastei*, the most largely distributed. In agreement to its occupancy of almost all the Iberian Peninsula, *V. latastei* inhabit very contrasted regions, from dry to rainy areas (170 - 3000 mm average annual rainfall) and from the sea level up to 3000 m altitude. Despite this apparent high tolerance to climatic conditions, *V. latastei* occurs in small and reproductively isolated populations, and there is evidence for population declines throughout its distribution range. This viper shows several characteristics that increase its proneness to extinction: very low recruitment rate, high dietary specialization and low dispersal rates, although some of them vary across its Iberian range. In the northern distribution limit, where the species contact with the other two Iberian vipers, *V. latastei* exhibit high dietary specialization and population densities, and females reproduce biannually on average. In southern Iberian Peninsula, adult vipers forage on a wide prey spectrum, are in very low population densities, and females reproduce triennially on average. The Iberian Peninsula shows a north-south cline in many climatic parameters (i. e. dryer and hotter to the south). This clinal variation can affect some life-history traits of species with large Iberian range, as it has been suggested in many taxa. We speculate that geographic differences in availability of the primary prey for adult vipers (small mammals) can stress the energetic dynamics of *V. latastei*, reducing its ability to reproduce more frequently, hence conditioning population demography and finally local extinction risk.

Body condition index and sexual dimorphism in newborns of *Vipera aspis*

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The body condition index (BCI) has been used only for assessing reproductive status in snakes. Up to now nothing is known about BCI at birth. We considered two European populations of *Vipera aspis* (Bosco Fontana, N-Italy, and Chizé, NW-France,) to assess i) whether newborn's sex and SVL influence BCI at birth and ii) differences of birth BCI between the two areas. Italian newborns (49 males, 38 females from 12 females) had average SVL=188.3 mm for males and 189.8mm for females, average weight=5.6g for males and 5.9g for females and average BCI=0.93 for males and 1.12 for females. French newborns (27 males and 29 females from 10 females) had average SVL=174.6mm for males and 176.2mm for female, average weight=5.7g for males and 6.3g for females and average BCI=0.91 for males and 1.07 for females. Sex and SVL effects on BCI were not independent, but interacted significantly (GLM model, $F_{1,118} = 6.95$ $p < 0.01$); significant differences were also detected among PF ($LR^2 = 149.58$, d.f.=1, $p < .0001$), but not between areas ($LR^2 = 0.132$, d.f. =1, $p = 0.72$). The higher BCI in newborn females could indicate a different growth model between embryos of two sexes. Moreover in both sexes higher SVL correspond to lower BCI. Therefore, it is possible to suppose the existence of two alternative growing patterns: longer individuals with lower BCI and shorter individuals with higher BCI; the first ones could be more mobile and eat larger preys, while the second ones could store higher fat reserves and remain longer near the birth sites, thus reducing trophic and spatial competition.

Reproductive biology in an insular Golden Lancehead, *Bothrops insularis*

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Apparently reproduction is a conservative trait among snakes of the genus *Bothrops*. The golden lancehead inhabits a small island (43 ha), approximately 30 Km from the coast in south-eastern Brazil. This population is morphological and ecologically differentiated from its mainland sister-species, *B. jararaca*. In the present study we intend to check if any reproductive parameters of *B. insularis* are also distinct. Dissection of preserved specimens (n=156) combined with field data provide information on reproductive output, reproductive cycles and storage of sperm by females. Vitellogenesis occurs in spring and ovulation in later spring (November and December). Courtship in the field was observed in early autumn (March) and mid-winter (June). Thus, mating seems to be not coincident with follicular yolking (mid-spring). Uterine muscular twisting apparently allows *Bothrops insularis* to store sperm for only four (or more) months prior to ovulation. Parturition occurs from late summer to early autumn (January still April). Litter size ranged from 2 – 10 neonates (mean = 6.0). *Bothrops insularis* show a low degree of fecundity since its litter size is smaller than those of close relatives. Reproductive output in golden lancehead may be constrained by local resource availability. In males, the mean volume of the testis (e.g., reflects spermatogenic activity) were greater in spring than in summer. Our results indicate that reproductive cycles in both males and females seem to be seasonal, with vitellogenesis and spermatogenesis occurring exclusively in spring.

Reproductive traits of female *Crotalus polystictus* in central México

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Little information is available concerning the reproductive traits of *Crotalus polystictus*, a medium sized rattlesnake endemic to central México. As part of a long-term, mark-recapture study, we collected female rattlesnakes from an agricultural valley located within the cordillera neovolcanica uplift in the Estado de México during the summers of 2003-2007. All snakes encountered were marked and measured, and adult females were retained in captivity until parturition. We present resulting data on the size and age of reproductive females, litter number, neonate size, time of parturition, and reproductive frequency from female snakes. *Crotalus polystictus* is a fecund rattlesnake with a rapid reproductive cycle. Some females may reproduce as early as their second year, almost all recaptured females reproduced in each year captured, and almost all adult females encountered in early summer were gravid. Litter size was positively correlated with maternal size, while neonate size remained relatively constant between females. We recorded birth dates in May-August, roughly corresponding with the arrival of monsoon rains in central México.

Ecological traits of two Mediterranean vipers (*V. aspis* and *V. latastei*) in a sympatry area: growth, reproduction and diet

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In the high course of Ebro River (North of Iberian Peninsula) there is sympatry between *Vipera aspis* and *V. latastei*, where mixed populations of “true” and intermediate forms are found in syntopy. Between 2004-2006, 180 *V. aspis*, 167 *V. latastei* and 84 intermediate forms were captured in the sympatry area. Age and SVL at sexual maturation was lower in *V. aspis* (males: $x=4\text{yr}/300\text{mm}$; females: $x=4\text{ yr}/340\text{mm}$) than in *V. latastei* (males: $x=5\text{yr}/370\text{mm}$; females: $x=5\text{yr}/400\text{mm}$). Percentage of reproductive females was higher in *V. aspis* and intermediate forms (42% and 56%, respectively) than in *V. latastei* (33%), suggesting biennial reproduction for the former and triennial for the later. Number of enlarged follicles was identical in *V. latastei* and *V. aspis* ($x=8.4$) but lower in the intermediate forms ($x=5.9$). Feeding frequency was identical between all forms and sexes (between 17.3 and 29.7%). Diet composition was identical between all forms and sexes with high overlap (Pianka's O_{jk} between 0.810 and 0.997). Apparently, *V. aspis* presents selective advantages over *V. latastei*, with low age and size at sexual maturation, high reproductive frequency and identical potential fecundity. Reproductive dynamics suggests a more successful performance for *V. aspis* than for *V. latastei* and that *V. aspis* has the potential to spatially displace *V. latastei* when in contact. However, competition on the trophic niche should regulate the spatial dynamics of the contact zone. Intermediate forms appear to have lower fitness than “true” forms due to lesser potential fecundity. Additional ecological and genetical data are being collected. Funded by FCT (POCTI/BIA-BDE/55596/2004)

Wednesday, 26 September
11:00 – 12:00

Session 7: Distribution and Ecology

Niche conservatism in vipers: habitat use by sympatric species in a savanna area in south-eastern Brazil

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Recent studies indicate that many of the general patterns found in natural communities result from niche conservatism. Sympatric, closely related species are good subjects to test this hypothesis. We present information on abundance and habitat use in an assemblage of vipers inhabiting a Cerrado area in south-eastern Brazil. Snakes were sampled by combining six standard methods during a long-term study. Five vipers occurred in the area. *Crotalus durissus* and *Bothrops alternatus* were the most abundant snakes in the region within the 35 snake species which comprise the local assemblage. *Bothrops itapetiningae* and *B. moojeni* occurred in intermediate abundances, and *B. pauloensis* was locally rare. *Crotalus durissus* was the most eurytopic viper, common in different habitats of both well preserved and disturbed areas. *Bothrops alternatus* was found both in wet (gallery forests or swamp areas) and dry habitats (grasslands), and also in human-disturbed areas. *Bothrops itapetiningae* (another member of the *B. alternatus* species group) was restricted to dry habitats (grasslands and open savannas) and was not found in human-disturbed areas. *Bothrops moojeni* (in the *B. atrox* species group) was virtually restricted to gallery forests and wet habitats and relatively common in human-disturbed areas. *Bothrops pauloensis* (in the *B. neuwiedi* group) was almost restricted to human-disturbed areas. Considering the clades to which each species belongs, as well as the ecology of the same species in other areas, we conclude that these patterns of habitat use are mostly a consequence of niche conservatism.



Vipers of the Krasnodarsky Territory, Russia

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Six species of shield-head vipers occur in the Krasnodarsky Territory, including four of the “kaznakovi”-complex (*Pelias magnifica*, *P. orlovi*, *P. kaznakovi*, *P. dinniki*) and two of the “ursinii”-complex (*P. renardi*, *P. lotievi*). *Pelias magnifica* is an endemic relict species (Near Threatened, NT) occurring along Skalisty Ridge and Adygey Republic. Population density is extremely low (3 specimens/day sampling, DS). *Pelias orlovi* is an endemic species (Endangered, ENA2ad), covering the lowest north-western part of Large Caucasus from the Papay mountain on the west to the top of Large Pseushkho on the east. Population density is also extremely low (3 specimens/DS). *Pelias kaznakovi* is a relict endemic species (Endangered, ENA2abc) threatened by continuous decline in habitat suitability. It ranges from the foothills of the Black Sea coast to the border with Abkhazia, and also the northern slopes of Western Caucasus. It has disappeared from many localities where it was frequent in the beginning of XX century. High population density (10 specimens/DS) can be found in the Sochi National Park. Limiting factors include deliberate killing, habitat reduction, intensive catching, and recreation in the Black Sea coast. *Pelias dinniki* is relatively numerous (Near Threatened, NT), but long-term persistence of populations will depend on human activities. The range covers the middle-mountains and alpine belts of Large Caucasus. With the exception of Caucasian State Nature Biosphere Reserve, suitable habitats are decreasing in most of the range, and catching and direct elimination threatens populations. *Pelias renardi* is considered Vulnerable (VUA1c) at the regional level. Decreasing of population size and suitable habitats is also related with human activities. Average population density is reasonable (11 specimens/ha) and high population density occurs in the Krasnodarsky Territory (30 specimens/ha). *Pelias lotievi* is a naturally rare endemic species (Near Threatened, NT), being on the north-western limit of its range. Isolated populations can be found on the Peredovoy Ridge between Small and Large Laba Rivers. It can be locally abundant (40 specimens/ha), but usually densities are low (3 specimens/km in sub-alpine habitats).



Preliminary study of population ecology of an insular population of the Nose-horned viper (*Vipera ammodytes*) from Former Yugoslav Republic of Macedonia

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The Nose-horned viper (*Vipera ammodytes*) was studied at the Golem grad island at the Prespa Lake in FYR of Macedonia. This island is included in the "Galicica" National Park and has status of strictly protected area. The island has an area of approximately 18ha, and is situated at 850 m a. s. l. Vegetation consists of association *Pruno webbii* – *Juniperetum excelsae*. The preliminary study was conducted during 5 consecutive days in both spring and summer. Each individual was captured by hand, sexed and marked for future research. Also, the cloacal temperature and several morphological traits were measured. Corresponding geographic coordinates, microhabitat and climatic data for each specimen were recorded at the capture site, as well as behaviour. Average number of recorded specimens was around ten per day, in an area of approximately 10 ha. On the basis of collected data, we made preliminary estimation of population density and sex ratio, as well as of reproductive status of the females. Also, we discuss here variation in microhabitat preferences and daily activity in regard to sex and season.

Session 8: Conservation

Population viability analysis of a local population of *Vipera ursinii* in north-eastern Montenegro

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A local population of *Vipera ursinii* from the Bjelasica Mountain in North-eastern Montenegro has been studied over five consecutive years (2002-2006) for population parameters, including abundance, age structure, age at first reproduction, sex ratio, sex ratio at birth, clutch size, mortality rate etc. Population trends were estimated by Population Viability Analysis (PVA) using Vortex 9.5 computer model (Miller and Lacy, 2005). As input data we used both the results from our field study and literature data from long-term population study made by Beron (1992, 1997) in French Alps. Only one possible scenario was used to predict the likely outcome of population change of this particular population. Model includes probability of one type of environmental catastrophe with negative impact on reproduction. The results should be considered with caution having in mind short period of research and constraints in calculation of probability of environmental catastrophe. The outcomes of this simulation could help in predicting long term viability of the analysed population as well as to contribute to establishment of active conservation management of this species in Montenegro.



Present state of *Vipera renardi* in Ukraine (distribution, habitats, abundance, biology, problems of conservation)

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In Ukraine *Vipera renardi* is distributed in the southern part of the Forest-Steppe zone, in the Steppe zone, on foothills and the northern slopes of the Crimean Mountains. In lowlands, it inhabits true and semi-desert pristine steppes (including pastures), salt meadows, slopes of hills and gullies, sandy river terraces and estuaries with psammophytous and halophytous vegetation, idle fields and vineyards, dams, banks, abandoned fields and road sides with steppe and weed vegetation, forest shelter-belts, glades and edges of natural forests. In the Crimean Mountains, it inhabits edges of deciduous forests, dry meadows with shrubs, mountain meadow steppes, stony slopes with sub-Mediterranean vegetation. Usual abundance is 1–5, in optimal conditions 20–50, in the Sivash region on some small (0.1–1.5 ha) plots it can reach 75–187 ind./ha. In different regions of Ukraine, *V. renardi* is active from the end of February – March until late October – early December, the mating period occurs within the second half of March – end of May. Pregnancy lasts from 84 to 130 days. Females produce 1–31 young (usually 4–20) in the second half of July – first half of September. Sexual maturation occurs after the II or III winter at 29–38 cm body length (Kotenko & Kukushkin 2005). Regional and seasonal differences in growth rates, moulting and diet will be address. Problems related with conservation will also be considered. In some areas of the country *V. renardi* has completely vanished, and it is included to the Red Data Book of Ukraine as a Vulnerable species.



Current condition and conservation status of vipers in Volga-Kama Region

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Volga-Kama Region (VKR) is situated between 52 – 59° N. and 45 – 56° E. The area is about 525 thousand km², and includes 15 republics and regions of Russia in full or parts. VKR covers the southern sites of the forest zone, the northern part of the steppe and the forest-steppe lands. The viper fauna of VKR includes 2 species: *Vipera berus* and *V. renardi*. Adder is represented by *V. b. berus* and *V. b. nikolskii*, and mixed morphology populations. Adder habitations are closely associated to forest biotopes. But forest areas are situated in northern and north-western parts of VKR and the allotment does not exceed 30.6%. In our estimation the adder area has been halved for the last 50 years due to fragmentation and native habitat degradation. Steppe vipers *V. r. renardi* are sporadically distributed in the southern part of VKR and *V. r. bashkirovi* are known from Tatarstan Republic, Samara and Ulyanovsk Oblasts. Some populations might disappear in the near future. Despite vipers are under conservation status in VKR, the species are under protection only in 23 Nature Reserves: 10 zapovedniks, 8 national parks and 5 zakazniks. These represent 5.7 thousand km², which is 1.1% of total VKR. Adder is common in 12 Nature Reserves, rare in 6 and singled in 1. Steppe viper inhabits 4 Nature Reserves only. The extreme north population, which was described as *V. r. bashkirovi*, is protected in Zakaznik “Spasskiy”.

Ten years of adder (*Vipera b. berus*) research – results and conservation recommendations

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Although the European Adder (*Vipera b. berus*) inhabits a huge distributional range, it is listed as threatened in most countries. The main reasons are destruction or alteration of habitats. Therefore suboptimal habitats are gaining increasing importance as refuge sites for this snake. As the landscape in Central Europe is generally fragmented and local snake populations are isolated, larger local populations become increasingly important for the long-term survival of this species. However, populations of more than 100 adult individuals are rare. In the central German state of Hessen only two such populations are known. Our work has been conducted in one of them. During the last 10 years about 700 individuals have been identified, belonging to 11 sub-populations in one larger forest area. We herein discuss general demographic and other general features of this population. For example we cannot support the existence of sexual differences in the colouration of the Rostralia as proposed by Burghardt (2005; Zeitschrift für Feldherpetologie 12: 254-259). Overall a shift in the abundances between the sub-populations could be observed, probably due to habitat changes in some areas. Currently we are working on a management plan based on a simple monitoring concept that allows laymen without prior experience to conduct basic but effective habitat amelioration. For a long term survival of this fragile population it is especially important that the local foresters conduct management actions, based on their own initiative and guidance.

How conservative is vulnerability to extinction in Brazilian pitvipers?

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If vulnerability to extinction is conservative in a given clade, it would be safe to infer the vulnerability of a given species based on the vulnerability of its closest relatives. That could help in conservation planning, since there will be no need to have detailed biological data for all species in a clade to assess the conservation status of every species in that clade. Here we explore how conservative vulnerability to extinction is among Brazilian pitvipers. Using ecological data obtained during several years of field and laboratory work, we produced scores for seven intrinsic factors that supposedly affect the vulnerability to extinction in pitvipers: body size, fecundity, food breadth, habitat breadth, distribution area, latitudinal range and ability to dwell in disturbed habitats. A presence/absence matrix was produced for each state of each factor (0-3), and this matrix was used in a cluster analysis (Jaccard, UPGMA); the resulting clusters were checked for phylogenetic consistency (i. e., if close relatives appeared close to each other). Except for the *B. neuwiedi* complex, for which six of eight species appeared together in one of the main clusters obtained, species from the other clades appeared throughout the tree diagram. Although some features supposedly related to vulnerability to extinction are known to be conservative in Neotropical pitvipers (food breadth, habitat breadth), most are not (body size, fecundity, distribution area, latitudinal range), and this may explain our results. Therefore, caution is necessary when extrapolating vulnerability to extinction in Neotropical pitvipers. Funded by FAPESP.

Session 9: Workshop “GIS and Vipers”**Deciphering evolutionary patterns and conservation units in *Vipera latastei-monticola* with Geostatistics and Geographical Information Systems (GIS)**

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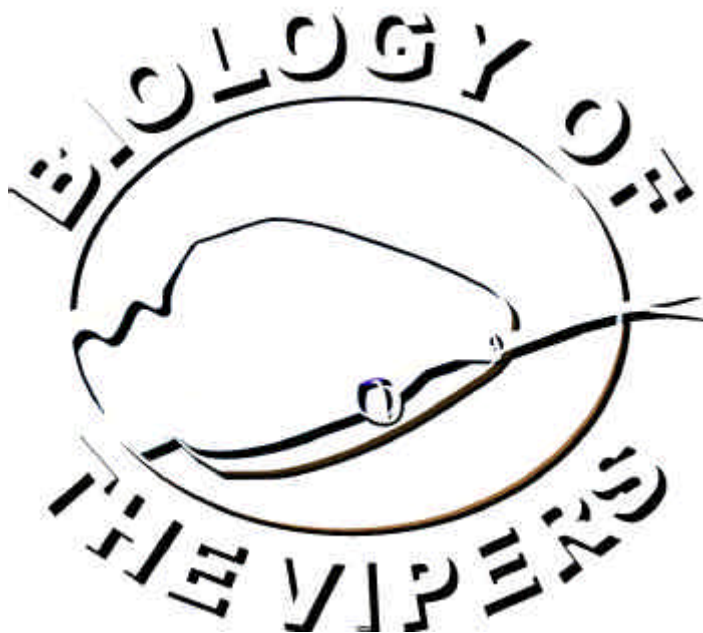
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Vipera latastei occurs in the Iberian Peninsula and North Africa. Former morphological studies reported two subspecies, *V.l. gaditana* and *V.l. latastei*, and a species, *V. monticola*, corresponding to High Atlas populations previously described for *V. latastei*. This study combines geostatistics and phylogenetic methodologies in order to map patterns of morphological and genetic variation, determine if there is genetic substructuring, and identify morphological and genetical correspondences in differentiated groups of *V. latastei-monticola*. A total of 10 morphological traits collected from 630 vipers and mitochondrial DNA (partial cytb and ND4 genes) sequences from 81 vipers were analysed with Geostatistics in a GIS. Spatial interpolation by Kriging revealed clinal variation patterns and areas of sharp transition between morphological character states and phylogenetic lineages along a north-south oriented axis in Iberia. Phylogenetic analysis identified two major lineages; one including the Iberian samples, separated in two distinct groups (*gaditana* and *latastei*) with a genetic divergence of 4.9% and divided also by a north-south axis. The other clade includes the Moroccan and Algerian samples. Divergence between African and Iberian groups of *V. latastei* was 5.9%, a substantial intraspecific variation, comparing with other reptiles. Probably these groups separated around 4.75 to 7.71 Myr ago, a temporal range including the formation of the Strait of Gibraltar. Other geographic variation patterns identified by Spatial PCA are probably explained through a combination of vicariant separation of Iberian and African populations, followed by evolution under similar environmental conditions; and population refugia during the Quaternary glaciations with differentiation followed by secondary contact along ecological barriers. Taxonomic status of African populations should be further investigated. Funded by FCT (POCTI/BIA-BDE/55596/2004)



POSTER COMMUNICATIONS



***Montivipera raddei* venom biochemistry and action on model membrane's properties**

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In spite of the high level of purification techniques and detailed analysis of different components of zootoxins, the mechanism of the interaction between venom and intact tissues in the living organism is still not clear. BLMs formed from natural lipids isolated from tissues of intoxicated animals represent an adequate model of the lipid moiety of biomembranes, which makes it possible to reconstruct the changes of some features characteristic of natural bilayer membranes under snake venom inflation. We isolated lipid fractions from the brain, heart, liver and muscle of nonpurebred white rats bitten by *Montivipera raddei* by the method of Keits. Model membranes were formed from the total lipid fraction on a teflon aperture by the method of Muller. The electrical parameters of the BLMs were determined on an electrometric device equipped with a Keithley 301 amplifier (USA) in a voltage-fixation mode; 0.1 M KCl, NaCl, LiCl, CaCl₂ and MgCl₂ served as ionic media. The presence of viper venom in organism lead to increasing of the electrical resistance of BLMs from liver and muscle lipids approximately on a sequence, while the BLMs from brain lipids has not shown noticeable differences of plastic properties compare the control. The low concentration of venom leads to appearance of channel activity. Especially it is noticeable in liver lipids in media of bivalent ions. Very likely; marked influence is due by the recently found disintegrins: a group of cysteine-rich peptides occurring in Crotalidae and Viperidae snake venoms (Calvete et al., 2003; McLane et al., 1998).

Body form and habitat use of Neotropical pitvipers of the *Bothrops atrox* species complex

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The pitvipers of the *Bothrops atrox* species complex occurs throughout most of South America. The morphology and habitat use of different Brazilian species of the *B. atrox* complex were analyzed in order to describe differences among them, and how these characters evolved in this lineage. We explored the relationships of body size and form (tail-body proportions and stoutness) with macrohabitat use in four morphologically distinct populations: *Bothrops atrox* from central Amazonia, *Bothrops marajoensis* from eastern Amazonia, *B. leucurus* from the Atlantic forest of eastern Brazil, and *B. moojeni* from gallery forests in savanna areas of central Brazil. The phylogenetic reconstruction of the morphological characters and habitat use indicated that, during the evolutionary history of the group, the tendency towards arboreality decreased slightly in *B. leucurus*; remained practically unaffected in *B. marajoensis* and in *B. moojeni*; and increased considerably in *B. atrox* from central Amazonia.

Phylogenetic relationships among vipers of the *Vipera ursinii* – *renardi* complex

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We sequenced 2250bp of mitochondrial DNA (cytochrome b, tRNA-Thr, control region, tRNA-Phe) for different meadow/steppe vipers. The taxa included *Vipera ursinii macrops*, *V. ursinii moldavica*, *V. ursinii rakosiensis* from Romania, *V. r. renardi*, *V. renardi tienshanica*, *V. lotievi* and *V. eriwanensis*. We compared our new data with published control region sequences of *V. ursinii rakosiensis* from Hungary and of *V. r. renardi* (Ujvari et al., 2005, Amphibia Reptilia 26, 287-292), and with cytochrome b sequences of *V. u. ursinii (wettsteini)* (Garrigues et al., 2005, Mol. Phylogenet. Evol. 35, 35-47). Our specimens originated from captive or natural populations and were sampled non-destructively by buccal swabbing. Phylogenetic analyses revealed two deeply divergent clades, one of which comprised all subspecies of *V. ursinii*, and the second including all the other taxa. The *ursinii* clade was further deeply subdivided into two clades (4.2% divergent at cyt b): one comprising closely related lowland forms *V. ursinii rakosiensis* and *V. ursinii moldavica*, and the second formed by mountain forms *V. ursinii macrops* and French *V. ursinii*, which were substantially divergent from each other (2.4 % divergence). For *V. r. renardi* we detected the same two haplotypes described by Ujvari et al., which were closely related to *V. lotievi*. These taxa therefore may be conspecific with each other and possibly also with *V. renardi tienshanica*. *Vipera eriwanensis* formed the most basal lineage within the *renardi* clade (2.0 % divergence from other taxa within the clade), and possessed a unique insertion within the control region. The research was supported by the grants GA CR 206/05/2334, DE06P04OMG008, MK00002327201, Biodiversity Research Centre LC06073, Academy of Sciences of the Czech Republic Grant IRP IAPG AV0Z 50450515 and GA SR VEGA 1/4332/07.

Distribution of *Vipera ursinii macrops* and related taxa in Croatia

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Only three species of Vipers occur in Croatia, and they are all protected by the Croatian Nature Protection Act. Unfortunately, very little is known about their precise distribution and new data is needed for further protection.

Balkan meadow viper (*Vipera ursinii macrops*): In Croatia, it is found only on southern parts of Velebit mountain, and on mountains Dinara, Troglav and Kamešnica belonging to Dinaric Alps massif. During our research (2007) all four of these localities have been confirmed and one new locality has been found. The new locality is kept in secrecy because of a very strong possibility of devastation by terrarists.

Adder (*Vipera berus* s.l.): The Bosnian adder (*Vipera berus bosniensis*) is reported from lowland parts of Croatia and high mountains peaks of Dinara (1851m) and Troglav (1955m) mountains. The lowland Bosnian adder is found between 0-200 m elevation in flood plains and wetlands of Sava and Drava river basins. The mountain Bosnian adder is only found in high mountain forests and meadows of the Dinaric alps. The mountain population from Gorski kotar is more likely to be a part of Alpine population of Common adder (*Vipera berus berus*) because of its connection to the Slovenian Alps.

Horned viper (*Vipera ammodytes ammodytes*): it is very common in Croatia and it is not found only in eastern lowland parts of the country (Slavonia and Podravina). It can be found from sea level to the highest mountain tips.



Spatial variability of morphological traits of common viper, *Vipera berus* in the Asian part of its area

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We have investigated 85 sexually mature individuals (37 females and 48 males) and 3 populations of *Vipera berus* from the south-eastern part of Western Siberia: I – from Tomsk region (latitude 56°21' to 57°54', southern taiga); II – from Novosibirsk region (latitude 55°33', northern forest-steppe); III – from Kemerovo region (latitude 55°31', 550-600 m a. s. l.; submontane birch-aspen taiga). Morphological differentiation of *V. berus* populations was estimated by 18 meristic and 21 plastic parameters and indexes. Sexual dimorphism was revealed in Tomsk population (I) by 5 characteristics and 10 indexes (5/10), in Novosibirsk population (II) – 2/3, and in Kemerovo one (III) – 4/4, ($p=0.05$). Maximum values of plastic traits and their indexes are characteristic for females from Tomsk population and males from Novosibirsk one, minimum – for females and males from Kemerovo population. Maximum values for most meristic traits were revealed in males of the lowland Tomsk population (I), and minimum – for the sub-montane Kemerovo population (II). Discriminant analysis of differences between females and males of these geographical populations displayed three isolated groups, which do not overlap with each other (100% of dispersion). Males and females from the flat Tomsk (I) and Novosibirsk populations (II) form the common cluster, and the sub-montane Kemerovo population (III) stands apart. Thus, there is evidence for local environmental factors determining intraspecific and geographical variation of *V. berus* morphological peculiarities. Growth conditions are the most optimal in the flat southern taiga, the less favourable – in sub-montane birch-aspen taiga of Kuznetskii Alatau.

Hematology and plasma chemistry of Nose-horned viper (*Vipera ammodytes*)

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Reptilian haematology is studied much less than haematology of warm blooded animals. Haematological values in different species of reptiles show greater variability than those in mammals and birds. Also there are differences in haematological values in single species depending of age, sex, food intake, disease and physiological state of an animal. The aim of the whole study was to determine some haematological values contributing to the biology of the Nose-horned Viper (*Vipera ammodytes*). This study was made on the population of the Nose-horned viper from Hrvatsko zagorje, as part of the future haematology research of reptiles in Croatia. Results shown here consider both haematological (thrombocytes, red and white blood cells count, differential blood count, haemoglobin concentration, hematokrit and sedimentation) and some plasma biochemical values (concentration of total protein, glucose, cholesterol, uric acid and triglycerides). The "Zoological record" database only cites five references concerning biological traits of Nose-horned viper. Therefore, results from this study can be used as a standard profile for future ecophysiological studies.

Peculiarity of *Vipera berus* in the oil region of Tatarstan Republic (Russian Federation)

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The Tartarstan Republic is located in the central area of *Vipera berus* range of Eastern Europe to Russia. In this region, a large number of observations of *V. berus* come from woodlands (75.1 %) and river flood plains (20%). Currently, there is an enormous development of oil fields which dominate the landscape, especially in the southeast of the Tatarstan Republic. This human activity has strong negative effects causing fragmentation and destruction of suitable habitats. Since *V. berus* has limited abilities to adapt to habitat change, there is risk of extinction for some populations. Population size for some localities has declined. This work analyzes threats to the populations and habitats of *V. berus* and discusses possible management actions to preserve populations in Tartarstan Republic.



Population size and distribution of common northern viper *Vipera berus* in forest, forest-steppe and steppe zones of Ob-river valley (West Siberia)

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The count of reptiles was conducted in May – July 1967, 1976, 1977, 1992, 1999 – 2001, 2003 – 2005 in West Siberia. In the northern taiga zone, the highest density of *V. berus* was found on full-grown pine sites of degenerative marshes (0.5 individuals per one hectare). It was very rare in bird cherry trees and osiers brushwood of small rivers' flooded lands (0.06 and 0.04) and in the pine forests (0.02). In the middle taiga, the highest density of *V. berus* was found on upland swamps (0.6). It is rare in small-leaved forests (0.3). In the southern taiga, the highest density of *V. berus* was found in willow-birch forests in small rivers flooded lands and in upland swamps (3 - 4). Rarely (in 1.5 – 2 times), it can be met in lowland stocked swamps and in firry-cedar damp taiga (2). It is rare in small-leaved forests, field woodlands, coniferous-leaved swamped forests (0.3 - 0.5). In sub-boreal zone of taiga forests, the highest density of *V. berus* was found in forested upland and lowland swamps, in coppice forests with fields (1 - 2). It is rare in birch-pine, pine and small-leaved forests (0.7 – 0.1). In the northern forest-steppe zone, *V. berus* is numerous in birch-aspen forests (1) and very rare in fields with coppice forests (0.02). In the southern forest-steppe zone, it inhabits small-leaved forests, flood lands, forested lowland swamps (0.5) and non-flooded-land damp meadows (0.1) as well. Therefore, *V. berus* is more abundant in the southern taiga. Its abundance reduces to the south and north.

Evolutionary history of a threatened species: the meadow viper (*Vipera ursinii ursinii*) in France

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The meadow viper (*Vipera ursinii*) is an emblematic species of Provence mountains in southern France. However, it is currently considered at risk of extinction by IUCN. This study is conducted within the scope of a Life-Nature European program which aims at the conservation of viper populations in France. We had two main objectives: (i) to unravel the evolutionary history of French populations; (ii) to make some practical management recommendations. The reconstruction of a mtDNA phylogeny showed that French and Italian populations form a monophyletic assemblage that is highly divergent from other taxa included in the present study. Coalescent-based population genetics analyses suggested that most French populations diverged simultaneously during the penultimate interglacial period, when their grasslands habitats became isolated on top of mountains following altitudinal upwards shift of forested landscapes. In addition, current gene flow between populations seems to be driven by landscape topography. Last, preliminary analyses suggested that French populations exhibit ecomorphological local adaptation. These results are used to identify seven ESUS and we further discuss the way operational management units could be identified.



Rediscovery of *Vipera ursinii rakosiensis* in Transylvania

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The majority of publications refer the subspecies *Vipera ursinii rakosiensis* to be extinct in Transylvania from at least 40 years. Recently, it was rediscovered a small population and morphological analysis of adults and juveniles vipers confirmed the presence of the subspecies *V. ursinii rakosiensis* in Transylvania. Results of a survey of the region are presented. The current threats to the population are explained as well as the conservation measures needed.

Foraging cues used by Florida Cottonmouths at insular bird rookeries

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Previous studies have shown that snakes can localize prey utilizing ground-borne vibrations, and it has been proposed that such vibrations provide important cues for cottonmouth snakes (*Agkistrodon piscivorus conanti*) while foraging on fish that fall from island bird rookeries. We tested this hypothesis in a population of cottonmouth snakes inhabiting the Florida Gulf coast island of Seahorse Key, which supports a large colonial rookery of wading birds. During a six-month nesting period, birds of several species drop or regurgitate fish that are consumed by large numbers of terrestrial cottonmouth snakes residing at ground level beneath the rookery. We used both fish and fish models to investigate the behavioural responses of snakes to ground-borne vibrations and to olfactory cues. We report that presentation of ground-borne vibrations, without associated chemosensory or visual stimuli, failed to induce overt foraging behaviour from these snakes. However, presentation of a fish-based olfactory stimulus, without associated ground-borne vibration or motion, triggered a foraging response in the snakes. Observations suggest that snakes are attracted to fish carrion from sometimes considerable distances, and they will relocate home ranges when locations of bird nesting changes.



Occurrence of *Hepatozoon* sp. (Apicomplexa, Hepatozoidae) in different species of Brazilian snakes recently caught and donated to the Butantan Institute, São Paulo, Brazil.

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The goal of the current study was to observe the occurrence of *Hepatozoon* sp infection in recently caught venomous Brazilian snakes donated to the Butantan Institute, São Paulo, Brazil, from September 2000 to June 2004. Blood was collected from all snakes by ventral coccigeal venipuncture and blood smears were performed, air dried, fixed with methanol, stained with modified May-Grünwald-Giemsa (Rosenfeld, 1947) and microscopically examined. A total of 668 blood smears were examined from snakes belonging to four genera and 13 species: *Crotalus* – *C. durissus* (n=167), *Lachesis* – *L. muta* (n=3), *Micrurus* – *M. corallinus* (n=14) and *Bothrops* – *B. jararaca* (n=61), *B. jararacussu* (n=65), *B. alternatus* (n=81), *B. moojeni* (n=168), *B. neuwiedi* (n=63), *B. insularis* (n=2), *B. cotiara* (n=2), *B. fonsecai* (n=5), *B. erythromelas* (n=7) and *B. leucurus* (n=30). *Hepatozoon* sp infection was detected in 191 animals (28.6%). The occurrence in snakes was 18.6% for *Crotalus*, 100% for *Lachesis*, 7.1% for *Micrurus* and 32.2% for *Bothrops*. The highest occurrences were observed in *L. muta* (100%), *B. leucurus* (60.0%), *B. moojeni* (48.2%) and in *B. jararacussu* (44.6%). Due to the fact that this parasite is frequently seen in the peripheral blood of Brazilian venomous snakes, more studies are necessary to elucidate its life cycle, as well as the effects caused in its possible hosts. Financial support: FAPESP (grant # 05/54163-1); CNPq (grant # 301517/2006-1).

Haematological profile for selected species of *Bothrops* and *Crotalus* kept in captivity at the Butantan Institute, São Paulo, Brazil

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The aim of the present study was to determine the haematological profile for a group of *Bothrops* and *Crotalus* kept in captivity at the Butantan Institute, São Paulo, Brazil. From March to May of 2001, blood was collected from 173 clinically healthy snakes, including 15 *B. alternatus* (10 females; 5 males); 28 *B. jararaca* (16 f; 12 m); 15 *B. jararacussu* (10 f; 5 m); 10 *B. moojeni* (7 f; 3 m); 9 *B. neuwiedi* (5 f; 4 m); 21 *C. durissus collilineatus* (10 f; 11 m) and 49 *C. d. terrificus* (29 f; 20 m). Immediately after collection, blood smears were prepared and stained with modified May-Grünwald-Giemsa stain. Red blood cells (RB), white blood cells (WB) thrombocytes and differential leukocytes counts, packed cell volume (PCV), haemoglobin concentration and haematimetric indexes (MCV, MCH and MCHC) were determined according to routine protocols and formulae. Blood values were statistically ($p < 0.05$) evaluated according to Kolmogorov-Smirnov, Kruskal-Wallis, Dunn's and Mann Whitney tests, using a computer program (GraphPad Prism, version 4.3, Graph Pad Software, USA). The most relevant results obtained for genus *Bothrops* showed a significantly higher number of basophils in *B. jararaca* when compared to other species studied, and a significantly lower number of RB and haemoglobin concentration for *B. moojeni*. Among genus *Crotalus*, *C. d. terrificus* revealed a significantly higher number of RB when compared to *C. d. collilineatus*. The present data offer an important haematological normal value baseline for *Crotalus* and *Bothrops* snakes kept in captivity in Brazil. Financial support: FAPESP (grant # 05/54163-1); CNPq (grant # 301517/2006-1).



Serum biochemical profile for selected species of *Bothrops* and *Crotalus*, kept in captivity at the Butantan Institute, São Paulo, Brazil

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The purpose of this study was to determine biochemical data for *Crotalus* and *Bothrops* kept in captivity at the Butantan Institute, São Paulo, Brazil. From March to May of 2001, blood was collected from 173 clinically healthy snakes, including 15 *B. alternatus* (10 females; 5 males); 28 *B. jararaca* (16 f; 12 m); 15 *B. jararacussu* (10 f; 5 m); 10 *B. moojeni* (7 f; 3 m); 9 *B. neuwiedi* (5 f; 4 m); 21 *C. durissus collilineatus* (10 f; 11 m) and 49 *C. d. terrificus* (29 f; 20 m). Immediately after collection, 1.0ml of blood was placed in a tube without anticoagulant to obtain serum for biochemical analysis. The biochemical tests for calcium, total protein, albumin, alkaline phosphatase, phosphorous and urea were performed by specific colorimetric tests. To determine alanine aminotransferase, aspartate aminotransferase and creatine-kinase enzymes, glucose, creatinine, cholesterol and uric acid, heparinized total blood were used and measured by Reflotron (Roche). Data were statistically ($p < 0.05$) evaluated according to Kolmogorov-Smirnov, Kruskal-Wallis, Dunn's and Mann Whitney tests, using a computer program (GraphPad Prism, version 4.3, Graph Pad Software, USA). Data were marked variable among species and gender; however, the most relevant biochemical data revealed significantly higher levels of alanine aminotransferase for males of *B. alternatus*, *C.d. terrificus* and *C.d. collilineatus*, and higher levels of calcium and cholesterol for females when compared to males. The data presented in the present study corroborate the concept that snakes may present a marked variation on serum biochemical profile without pathological significance. Financial support: FAPESP (grant # 05/54163-1); CNPq (grant # 301517/2006-1)





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