

Naturalis - J. W. Arntzen (see <http://science.naturalis.nl/research/people/cv/Arntzen>)

Student projects per December 31, 2007

Island lizards in the Ria de Arosa, Galicia, Spain.

The two lizard species Podarcis bocagei and P. hispanica are thought to have different biogeographical histories, with shallow and relatively deep (ca. 10,000 years) periods of isolation on islands of the Ria de Arosa in Galicia, Spain, respectively. This hypothesis (see publication 1) predicts: i) low versus high levels of 'fluctuating asymmetry' and ii) high versus low levels of genetic variability. Hypotheses will be tested using: i) geometrical morphometrics and ii) microsatellite genetic markers (*), with mainland populations as a reference. This project builds upon the MSc.-studies of Erik Rotteveel, Iris van Gelder and Juke Loman.

GIS-analysis of atlas data.

The production and maintenance of databases that record the distribution of organisms, such as amphibians and reptiles, is in full swing. Atlases are currently appearing for species-rich southern European countries such as Portugal, Spain, Italy and Greece. The near-complete coverage of themapping the European herpetofauna opens up the possibility to analyze with GIS (geographical information systems) factors that are responsible for the absence of records. The particular question is: are these absences 'true absences' reflecting habitat poverty, or 'false absences' reflecting a lack of prospecting ? This work builds upon publication 2.

Does pond-loss imply species-loss ?

Changes in agricultural land use, in particular the pasture to arable conversion, is leading to a dramatic loss of ponds in the western European landscape. Because ponds are the preferred breeding sites of many amphibian species, landscape change translates into amphibian decline. MSc.-student Nuno Curado has documented pond-loss as a function of landscape change in the French department Pas-de-Calais, by comparing data from 1975 and 2007. A follow-up study would analyze how landscape change would work out: i) on 13 different species individually, and ii) to affect connectivity between the remaining ponds and populations.

Nuclear genes in phylogeny building

Molecular phylogenetics has been largely relying on the DNA-sequencing of mitochondrial DNA, but since the molecule is relatively small (and has some other disadvantages as well) the end is in sight (see publications 3 and 4). We are moving over to the sequencing of nuclear genes. PhD-student Goncalo Themudo has developed primers for to the DNA-sequencing of five nuclear genes in Triturus salamanders. The challenge is to build a reliable tree of life even if the phylogenetic signal may be confounded by recombination, incomplete lineage sorting and introgression. (*)

Phylogeny and historical biogeography of ... satellite DNA's

This project aims to analyze the phylogeny and historical biogeography not of species but of short sequences of DNA's that are known as 'satellites'. Just like species have their distributions over regions and continents, satellites are located on chromosomes. Species move and diversify as do DNA-satellites and global processes like species dispersal, continental drift, speciation and diversification have their parallels in the nucleus. This project aims to construct the 'phylogeny'

and 'historical biogeography' of a selected family of DNA-satellites by using global methods. See publication 5. This work will be carried out under co-supervision of Prof. John Brookfield at the University of Nottingham, UK.

References (see <http://science.naturalis.nl/research/people/cv/Arntzen>)

- 1 Morphological and genetical differentiation of lizards (*Podarcis bocagei* and *P. hispanica*) in the Ria de Arosa archipelago (Galicia, Spain) resulting from vicariance and occasional dispersal. Pp. 365-401 in: Biogeography, Time and Place. Distributions, Barriers and Islands. Editor W. Renema. Springer, Dordrecht, The Netherlands (2007).
- 2 From descriptive to predictive distribution models: a working example with Iberian amphibians and reptiles. *Frontiers in Zoology* 8: 3 (2006).
- 3 A Bayesian approach on molecules, morphology and behavior: reconsidering phylogenetic and evolutionary patterns of the Salamandridae with emphasis on *Triturus* newts. *Journal Experimental Zoology (Mol. Devol. Evol.)*. 308B: 139-162 (2007).
- 4 The phylogeny of crested newts (*Triturus cristatus* superspecies): nuclear and mitochondrial genetic characters suggest a hard polytomy, in line with the paleogeography of the centre of origin. *Contributions to Zoology* 76: 261-278 (2007).
- 5 Classification and molecular organization of satellites elucidated by phylogenetic network analysis - examples from *Triturus* salamanders and *Palorus* beetles. *Chromosoma* 111: 284-288 (2001).

(*) experience with molecular lab work required, e.g. through the IBL-course 'Moleculaire Technieken'