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

T. Goldberg, E. Nevo & G. Degani

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

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

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

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

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

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

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

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