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

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

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

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

Rhizomucormycosis in caecilian amphibians

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

L. Russell & T.J.C. Beebee

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

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

H. Seligmann

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

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