

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

L. Russell & T.J.C. Beebee

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

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

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

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

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