## PALAEOGEOGRAPHY AND DNA: *Podarcis* PHYLOGENETIC RELATIONSHIPS RECAPITULATE GREECE'S PALAEOGEOGRAPHIC HISTORY (P)

## P. Lymberakis<sup>1</sup>, N. Poulakakis<sup>1,2</sup>, E. Valakos<sup>3</sup>, M. Mylonas<sup>1,2</sup>

<sup>1</sup> Natural History Museum of Crete, University of Crete, Irakleio, Greece <sup>2</sup> Department of Biology, University of Crete, Irakleio, Greece <sup>3</sup> Section of Animal and Human Physiology, Department of Biology, University of Athens, Greece

We studied the phylogenetic relationships among Greek species of *Podarcis* (Sauria: Lacertidae) as inferred from partial mtDNA sequences. The results were applied on a molecular clock model as to calculate the time of separation among the populations studied. To tune the molecular clock we considered a geological event on which there is a consensus among geologists, namely the separation of Peloponnese from Crete. This event is considered to have occurred between 5 and 5.5 Mya.

Taking in account this date we conclude that *P. erhardii* and *P. muralis* shared a common ancestor from 9.5-10.5 Mya respectively. Primitive *P. erhardii*, originating from NW Greece, descended southwards splitting in two main clades: One on the landmass which today we recognize as the Cyclades island group, and a second going further to the south. The two species we recognize today as *P. peloponnesiaca* in Peloponnisos and *P. erhardii* in Crete actually originate from this second clade. In other words *P. erhardii* is paraphyletic with respect to *P. peloponnesiaca*. Genetic distances among, as well as extant distribution of *P. erhardii* on Crete and satellite island populations, indicate that at least one splitting, one re-colonization and one extinction events occurred on the island.

Key words: Podarcis, Greece, palaeogeography, molecular clock

## PHYLOGENETIC RELATIONSHIPS AMONG AMPHISBAENIAN REPTILES BASED ON COMPLETE MITOCHONDRIAL GENOMIC SEQUENCES (P)

J. R. Macey<sup>1,2</sup>, T. J. Papenfuss<sup>2</sup>, J. V. Kuehl<sup>1</sup>, H. M. Fourcade<sup>1</sup>, J. L. Boore<sup>1,3</sup>

<sup>1</sup> Joint Genome Institute and Lawrence Berkeley National Laboratory, Walnut Creek, USA <sup>2</sup> Museum of Vertebrate Zoology, University of California, Berkeley, USA <sup>3</sup> Integrative Biology, University of California, Berkeley, USA

Amphisbaenian reptile phylogenetics are determined at two levels using complete mitochondrial genomic sequences. Examination of members from the four Amphisbaenian families (Gans, 1978, Trans. Zool. Soc. London 34: 347-416) reveals that Rhinuridae is placed in a basal position, and Bipedidae is the sister taxon to a clade containing Amphisbaenidae and Trogonophidae. These results suggest that Amphisbaenian reptiles predate the breakup of Pangaea because successive basal taxa (Rhineuridae and Bipedidae) are situated in tectonic regions of Laurasia and nested taxa are found in Gondwanan regions (Amphisbaenidae and Trogonophidae). The family level work also indicates a parallel reduction in limbs from an ancestor having four legs. The two-limbed Bipedidae is nested within the remaining amphisbaenian limbless taxa. A detailed sampling in the Bipedidae indicates that populations of Bipes tridactylus are the sister taxon to a clade containing B. canaliculatus and B. biporus populations. Within the Bipedidae, independent evolution of toe reduction has occurred from an ancestor having five toes as observed in the derived *B. biporus*. We present a new phylogenetic hypothesis for the Bipedidae that in topology is more consistent than previous work with plate tectonic separation of peninsular Baja California from the west coast of Mexico. A synapomorphic trait defining the Bipedidae is a shift from the mitochondrial gene order that is typically observed among vertebrates to the derived state of trnE and nad6. In addition, a tandem duplication of trnT and trnP is observed in B. biporus populations. The pattern of pseudogene formation in this duplication is not identical among populations and provides insight into mechanisms driving mitochondrial genomic rearrangement.

Key words: Amphisbaenia, Rhineuridae, Bipedidae, Amphisbaenidae, Trogonophidae, plate tectonics