TESTING THE PHYLOGEOGRAPHIC STRUCTURE OF *PODARCIS* SSPP. POPULATIONS ISOLATED ON BALEARIC ISLETS, BASED ON MITOCHONDRIAL AND NUCLEAR GENE SEQUENCES

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Podarcis lilfordi and *Podarcis pityusensis* consist of an homogeneous clade of lacertids endemic of the Balearic archipelago, Western Mediterranean. Whereas the second species is made of populations spread both on the main islands of Ibiza and Formentera and on their surrounding islets, the former consists of isolated small populations living only on the satellite islets around Majorca and Minorca. Their main source populations became extinct historically, presumably following the human introduction of competitors and predators of higher performance. Here we show the first results of a study program devoted to testing the phylogeographic structure of both species along their range, aiming to contrast the reliability and importance of two alternative colonization mechanisms (Pérez-Mellado & Salvador, 1988). A first and classical view would follow an isolation-by-bathymetric-depth model, and involves a historical splitting of populations along the Holocene, following the rising sea level after the last glaciation. An alternative though compatible model would search for active gene flow along that period, involving a genetic pattern laying on isolation-by-distance, tuning the former hypothesis. This latter model would imply an attenuated metapopulation structure, with rescue effects and extinction proneness occurring at much lower frequencies than habitually referred. Further, it can be tested under the two Levins original metapopulation models: the island/mainland, in the case of *P.pityusensis*, and the internal model, in the case of *P.lilfordi*. Indeed, a metapopulation structure supporting some background colonization rate could be more feasible and active only locally, on those clusters of islets placed within bays with calm waters protected from wave stress, as it happens at least in some natural harbours and a coastal lagoon of NE Minorca. To that purpose and in order to assess the reliability of several molecular tools recently tested for the phylogeny of higher taxa including *Podarcis* species (Harris & Arnold, 1999), a two step geographical downscaling is made for different genetic markers. At a higher scale we compare selected single populations of *Podarcis* from Majorca, Minorca, Ibiza and Formentera, representing clusters supposed to have been differentiated during the Pliopleistocene. Successful markers are then tested at a lower scale, by comparing all known populations of *P. lilfordi* from Minorca. A total genomic DNA extraction on each of 7-10 tail tips from each islet is sequenced for mt-DNA cyt-b. Alignments of 330 bp sequences of cyt-b hardly allow for separate identification of the main islands clades, being less resolutive at lower levels. Both a longer cyt-b fragment containing over 1000 bp, and nuclear c-mos and Enol genes are currently being compared as pursuing a close-up of either

the subspecific nature or the attenuated metapopulation structure of such, otherwise, clearly and hierarchically fragmented distribution pattern of the Balearic *Podarcis*.