

**GENETIC DIFFERENTIATION OF ENDEMIC SPECIES OF THE GENERA
PODARCIS IN THE BALEARIC ARCHIPELAGO INFERRED FROM PARTIAL
CYTOCHROME *B* SEQUENCES**

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The lacertids are represented in the Balearic archipelago (Western of Mediterranean Sea), by two endemic species of the genera *Podarcis*: *Podarcis lilfordi* in Gymnesies Islands (Mallorca, Menorca, Cabrera and around minor islets) and *Podarcis pityusensis* in Pityuses Islands (Eivissa, Formentera and their around islets).

The different populations that are living now in the Balearic archipelago form a polytypic taxa, compounded by a large number of subspecies or local races. Morphological analyses pointed out to the hypothesis of one subspecies for each minor island or islet. Previous enzymatic polymorphisms showed a high level of intrapopulation diversity but a low disagreement between populations. Thus, the high number of subspecies described by means of morphological data, were not confirmed at the enzymatic level.

In order to know the genetic variability of these two species at the molecular level, we have sequenced a 306 bp fragment of the mitochondrial cytochrome b gene. The sampled localities are some islands and islets of the Pityuses (Eivissa, Formentera, s'Espardell, s'Espalmador) and the Gymnesies (Cabrera, Dragonera). DNA was extracted from tail tips from live individuals, and the animals were released again in the same place of capture. Amplification was done by PCR. Both strands of the amplified DNA were sequenced, of at least 3 individuals of each locality, on an automated ABI 310 sequencer (Perkin Elmer).

The sequences obtained were aligned and compared between themselves and with others from *P. hispanica* and *P. muralis* (data from Genbank). Sequence divergence between taxa was calculated by the Kimura's two parameters method. Phylogenies were constructed assuming constant and variable evolutionary rates.

The obtained results were compared with data from other authors as well as with enzymatic data from previous studies carried out on these two species.

These preliminary analyses showed a correlation between enzymatic and molecular results, the large morphological differentiation did not agree with the molecular variation found. Ergo, some of the subspecies described on neighbouring islands cannot be considered as such, at molecular level, and are within the limits of intrapopulation variation.

A 400 bp region of the 12S rRNA gene is actually being carried out in these samples for a better understanding of the genetic structure of these endemic species.