

# Genetic Variation in Insular Populations of the Balearic Lizard *Podarcis lilfordi*

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The herpetofauna of the Balearic Islands in spite of its poor representation of only sixteen species, shows some extremely interesting endemisms such as two species of lizards and the toad *Baleaphryne muletensis* /Alcover and Mayol, 1982/. The two lizards, *Podarcis lilfordi* /Gunther/ and *P. pityusensis* /Boscá/, are evolutionary offshoots of the Iberian *P. muralis* - *P. hispanica* source, which diverged since the breaking of the last geological connection between Balears and the Iberian Peninsula in Pliocene times about four million years ago.

*Podarcis pityusensis* is distributed in Eivissa, Formentera and the islets surrounding both of them, whereas *P. lilfordi* is found in the small islands and islets close to the major Balearic Islands /Gymnesies/ but has almost completely disappeared on the latter because of certain still poorly understood reasons. Since the two Balearic species of *Podarcis* are polytypic taxa compounded of a large number of subspecies or local races, these particular features provide a valuable source of material in the field of insular population genetics. A detailed analysis on the taxonomy, morphometrics and biogeography of *P. pityusensis* subspecies has been undertaken by Cirer /1981/ and Salvador /1984/, but parallel studies on *P. lilfordi* are still lacking. On the other hand, several authors have published reports dealing with the evolutionary genetics of *Podarcis* and *Lacerta* /Gorman, 1975; Mayer and Tiedemann, 1980, 1982; Nascetti et al., 1981; Guillaume and Lanza, 1982/, therefore, these lacertids have become relatively well known in these respects very recently.

The present work on the allozymes of *Podarcis lilfordi* insular populations extends genetic knowledge of the Mediterranean lacertids and should be considered along with that of Cirer and Guillaume /this issue/ on another Balearic lizard, *Podarcis pityusensis*. In addition, we have also analysed an introduced Majorcan population of the latter species to gain some insight on the allozymic similarity between the two Balearic species of *Podarcis*.

## MATERIALS AND METHODS

Seven subspecies of *P. lilfordi* coming from small islands and islets near Mallorca have been worked out in the present survey. These are the following: *P. l. gigliolii* Bedriaga from Sa Dragonera, *P. l. jordansi* L. Muller from Na Foradada, *P. l. pobrae* Salvador from Na Pobra, *P. l. conejerae* Muller from Sa Coniera /Illa des Conis/, *P. l. kuligae* Muller from Cabrera and Ses Rates, and *P. l. xapaticola* Salvador from

S'Esclatasang. The geographical locations of these islets and of the two sampling sites in Cabrera are depicted in Figs 1 and 2. In addition to these populations of *P. lilfordi* we have also subjected to electrophoretic analysis a sample of *P. pityusensis* from an introduced population of Sa Murada /Palma de Mallorca/.

The lizards caught in the wild were immediately carried to the laboratory where they were kept frozen at  $-40^{\circ}\text{C}$  until analysis. For electrophoresis, the heart, liver, kidneys and ovaries or testes were dissected and homogenized in a 0.2 M Tris buffer adjusted to pH 7.2 with 1N HCl. The techniques used were those by Selander et al. /1971/ with some minor modifications.

## RESULTS

The number of specimens analyzed for each population captured in 1982-84 was largely dependent on the number of individuals allowed since the *Podarcis* are protected species, and on the success of our collection expeditions to the diverse islands and islets. For these reasons some of the samples are large while others are very small, in agreement also with the insular area. We have used the following seventeen loci for the present study: EST-A, EST-B, EST-C, EST-D, EST-E, EST-F, PGI, PGM, MDH, XDH, LDH-1, LDH-2, LAP, IDH, GOT-1, GOT-2 and ALB. All the analyzed electromorphs out of those of PGI and GOT-2 showed anodic mobility. The frequencies of the detected alleles in the seventeen loci are given in Tab. 2. As can be seen, the locus GOT-2 is unique with an absolute lack of polymorphism though others such as ALB and LDH-1 are fixed in most populations and show a very low level of polymorphism. In contrast, some systems like EST-B, MDH, LAP and GOT-1 are highly polymorphic. It should also be noted that some alleles are unique for certain populations but none of them has acquired fixation; rather they tend to be at the lowest frequencies. This situation holds true both for the population of *P. pityusensis* as well as those of *P. lilfordi*. An interesting fact to be remarked is the clear differentiation between the two populations of Cabrera for some enzymes, XDH, PGI, LAP, MDH and IDH, the population of Cabrera-Far is much less polymorphic than that of Cabrera-Port. The indices of genetic similarity /I/ and distance /D/ proposed by Nei /1972/ were calculated between all pairs of population samples from each different island and islet, and the results imply that the two populations from Cabrera have been joined and considered together. The results of these intercomparisons are represented in a matrix /Tab. 1/, where it appears that I between populations of *P. lilfordi*

Table 1. Genetic similarities /I; above diagonal/ and distances /D; below diagonal/ as defined by Nei /1972/ between nine populations of *P. lilfordi* and a population of *P. pityusensis*.

	CA	RA	ES	CO	PO	FO	MO	GU	DR	<u>P.pit.</u>
CA		.894	.841	.878	.864	.912	.886	.936	.870	.814
RA	.112		.970	.872	.944	.864	.908	.863	.874	.862
ES	.173	.030		.833	.952	.818	.841	.951	.817	.807
CO	.130	.136	.182		.912	.906	.901	.947	.868	.854
PO	.146	.058	.049	.092		.840	.896	.893	.863	.855
FO	.092	.146	.200	.098	.174		.958	.950	.903	.849
MO	.121	.097	.173	.104	.109	.043		.941	.868	.792
GU	.073	.147	.050	.054	.113	.051	.061		.903	.769
DR	.140	.135	.102	.141	.147	.102	.142	.102		.840
<u>P.pit.</u>	.205	.149	.214	.158	.157	.164	.233	.262	.175	

ranges from 0,958 to 0,817 and  $\bar{D}$  from 0,200 to 0,040. The intercomparisons of the *P. lilfordi* populations with that of *P. pityusensis* shows lesser genetic homology than between the former themselves, but with a clear overlapping of some values.

#### DISCUSSION AND CONCLUSIONS

The allozyme variability detected in most of the distinct insular Majorcan populations of *P. lilfordi* and in the introduced population of *P. pityusensis* is clearly higher than the average for reptiles. The mean heterozygosities of all but two populations of *P. lilfordi* and that of the *P. pityusensis* were broadly higher than the average in seventeen species of reptiles  $\bar{H}=0,047$  /Nevo, 1978/. The genetic similarities and distances between island populations of *P. lilfordi* are consistent roughly with their geographic separation. For example, the population of Sa Dragonera has relatively low similarity  $I=0,865$  and high distance  $D=0,145$  with respect to the averaged populations of the Cabrera archipelago, in correspondance with their separation which is about 65 km. Again the islets of Na Moltona and Na Guardia, which are about four times closer to the Cabrera archipelago than to Sa Dragonera, display higher genetic similarity and lower distance with the former  $I=0,910$  and  $D=0,094$  than with the latter  $I=0,865$  and  $D=0,122$ . However, the same kind of intercomparisons between each pair of populations from the Cabrera archipelago are not always in good agreement with their geographic distance since certain higher genetic similarities, such as between Na Pobra and S'Esclatasang  $I=0,952$ , Na Pobra and Ses Rates  $I=0,944$  and Na Foradada and Cabrera  $I=0,912$ , cannot be explained by geographic distance. Furthermore the two checked populations of Cabrera are quite different for some loci as we have mentioned above. Maybe by enlarging the number or surveyed loci and by increasing the size of smaller samples it would be possible to get a clearer picture of the evolutionary facts involved in the colonization of this archipelago, but in the present state of knowledge the situation seems rather complex. This remains the same whether we deal with the subspecies of the current taxonomy within *P. lilfordi* or with the individual populations as we have done, so we chose the latter alternative of using the term populations on these allozyme grounds more in accordance with genetic views than that of subspecies.

The population of *P. pityusensis* from Palma de Mallorca is on-average more differentiated in relation to those of *P. lilfordi* than these latter between themselves,  $\bar{I} = 0,827$  and  $\bar{D} = 0,191$  against  $\bar{I} = 0,893$  and  $\bar{D} = 0,112$ . This low degree of genetic distance supports their allied evolutionary interrelationships, similar to those reported by Nascetti et al. /1981/ among Italian populations of *P. muralis*, *P. sicula* and *P. lilfordensis*, and by Cirer and Guillaume /this volume/ between Spanish populations of *P. pityusensis* and *P. muralis*, possibly explaining their relatively recent phylogenetic origin.

This research has been sponsored as the project no 1361/82 of the CAICYT.

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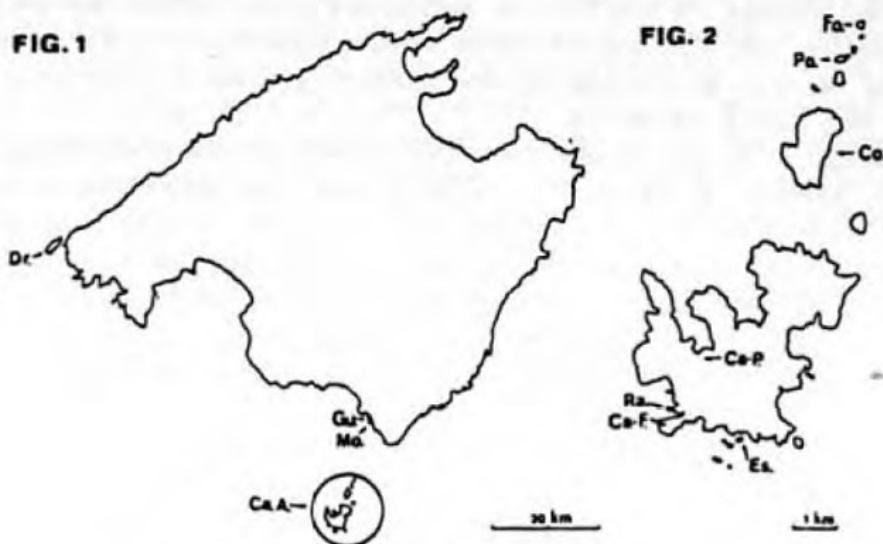


Fig. 1: Geographical locations of the insular populations of *Podarcis lilfordi* neighboring Mallorca. Dr. = Sa Dragonera, Gu = Na Guardia, Mo = Na Moltona, Ca.A = Cabrera Archipelago. Fig. 2: The same in the Cabrera Archipelago. Fo. = Foradada, Po = Na Pobra, Co. = Sa Coniera, Ca.P = Cabrera Port, Ca.Far. = Cabrera Far, Ra. = Ses Rates, Es. = S'Esclatasang.

Locus	a1.	Ca.F Ca.F RA ES CO FO MD GU DR P.pit										
		(28)	(12)	(6)	(11)	(54)	(10)	(26)	(20)	(40)	(71)	
COI.1	0.6 1.0 1.4	0 .625 .375	0 .409 .561	- - -	- - -	0 .568 .412	0 .350 .650	0 .731 .269	- - -	0 1 0	0 .962 .833	0 0 0
EST.A	A A -	.034 0 .966	.083 0 .917	0 0 1	.090 0 .910	.120 0 .815	.100 0 .900	.231 0 .769	0 0 1	.025 0 .950	0 0 1	.013 0 .987
EST.B	B B B	.638 .018 .340	.542 .042 .416	0 0 0	.727 .273	.454 .200 .482	.300 .269 .500	.577 0 .134	.600 0 .400	.600 0 .400	.527 0 .763	.237 0 0
EST.C	C C -	.948 .052 0	.834 0 .083	1 0 0	.759 .111 .130	1 0 0	.942 .058 0	1 0 0	1 0 0	1 0 .083	.908 0 .092	.908 0 0
EST.D	D D D	.966 .034 0	.833 .167 0	1 0 0	.861 .139 0	.800 0 .200	.768 0 .039	1 0 0	1 0 0	1 0 0	1 0 0	1 0 0
EST.E	E E E -	.966 .034 0 0	.750 .250 0 0	1 0 0 0	.727 .074 .019 .273	.800 0 0 .200	.885 0 0 0	1 0 0 0	1 0 0 0	.987 0 0 0	1 0 0 0	1 0 0 0
EST.F	F F F -	.907 .056 0 .037	1 0 0 0	.333 0 0 0	.917 .065 .018	.300 0 0 .700	.833 0 0 .039	1 0 0 0	1 0 0 0	.872 0 0 .028	.941 0 0 .013	.941 0 0 0
PGM	0.7 1.0 1.4 1.5	.035 .965 0 0	.042 .875 0 .083	0 1 0 0	.099 .991 0 0	.150 .850 0 0	0 .865 0 .115	- - - -	- - - -	- -.150 0 0	.402 .441 0 0	- - - -
XDH	0.8 1.0 1.6 1.7	.034 .500 .466 0	0 .750 .250 0	- - - -	0 1 0 0	0 .350 .500 0	0 .456 .500 .022	- - - -	- - - -	- -.181 0 0	.012 .976 .012 0	- - - -

Table 2. Allelic frequencies for seventeen loci in ten insular populations of *P. ilifordii* and one introduced population of *P. pityusensis*. Ca.F = Cabrera Port, Ca.F = Cabrera Far, RA = Ses Rates, ES = S'Esclatasang, CO = Sa Conlora, FO = Na Foradada, PO = Na Pobra, MO = Na Moltona, GU = Na Guardia, DR = Sa Dragonera, P.pit = *P. pityusensis*.