

Electrophoretic Analysis of the Pityusic Islands Lizard

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Electrophoretic methods were often successfully used for the resolution of taxonomical problems in the genus *Lacerta* or *Podarcis* /see for instance Gorman et al., 1975; Uzzell & Darevsky, 1975; Guillaume et al., 1976/. For this reason, we have applied it to study the "Rassenkreiss" formed by the 36 subspecies of *Podarcis pityusensis*, among which some are not clearly defined because of the great intraspecific variability of this group.

Awaiting the results of a global revision of this species, undertaken by A. M. Cirer, we consider that there is one population per island, except for Formentera which has two: *P. p. formenterae* and *P. p. grueni*.

ANIMALS AND METHODS

This study is the continuation of a previous work /Guillaume and Cirer, in press/, in which we presented our results on 71 animals of 10 subspecies. The methodology remains the same as before: horizontal electrophoresis on starch gel /12 %/. We present now the results on 193 animals of 20 subspecies /Tab. 1, above/. We studied three additional loci on liver samples, with Tris-citrate-borate buffer pH 8,2 /"Poulik"/: - the locus MPI - Mannose-Phosphate-Isomerase, and - two loci of SOD - Sorbitol-dehydrogenase, SOD-1 and SOD-2 coding for proteins of low and fast migration respectively.

The denominations AAT-1 and AAT-2 correspond to those of GOT-1 and GOT-2 of the precedent works. The list of the 19 loci and 54 alleles studied appear in Tab. 1, left hand side column.

RESULTS

a/ Analysis of allelic frequencies

Tab. 1 summarizes all our results on the 20 populations of *Podarcis pityusensis*. The four *P. muralis* which were used as a control have been selected as being homomorphous for each locus at the more typical allele of this species. Because of sampling difficulties or a voluntary collection limitation - as in the case of some endangered subspecies - /Martinez-Rica and Cirer, 1982/, eight of our samples /code numbers: 7, 9, 10, 11, 17, 19, 20, and 21/ count less than five animals. We did not consider them for

our analysis, but noted the results as small samples may sometimes be representative /see further/.

Firstly, Tab. 1 shows that three loci are monomorphic: LDH-B, PGM-1, and G-6-PD-1, and three others are diagnostic between *P. pityusensis* and the control sample of *P. muralis*: AAT-1, IDH, and the EST-"X". On the whole, for the *P. pityusensis* subspecies we studied, the more frequent allele for each locus seems to be generally the same. This confirms the common phyletic origin of these animals in spite of their great morphological diversity. Apart from exceptions, probably due to sample size /see above/, the following remain different: - the frequency 100 % of the allele N of the locus PGM-2 in *P. p. caldesiana*. Unfortunately, our data is incomplete for this locus; - the frequency 100 % of the allele 100 of the locus G-6-PD-2 in *P. p. grueni*; - the frequency 79 % of the phenotype "C" of the locus EST-"X" in *P. p. maluquerorum*.

Among the other alleles, some are interesting as they only appear in one or two subspecies, generally at very low frequencies /between 2 and 9 %/. The same phenomenon was observed in *P. lifordi* by Ramon et al. /this volume/. Two alleles, however, by rather high frequency might reflect a differentiation of the carrier populations: - the allele coding for the enzyme AAT-2 of mobility "115", present at 39 % in *P. p. formenterae*. /This confirms the results of our precedent work in which we found a frequency of 40 % base upon a sample of only 5 animals/; - the allele coding for the G-6-PD-2 "fast", 120, present at a 22 % frequency in *P. p. vedrae* and at 9 % in *P. p. formenterae*.

The average heterozygosity of most populations studied is very high in comparison to other insular lizards /e.g. Gorman et al., 1975 on *P. mellisellensis* and *P. sicula*/, but agrees perfectly with the results obtained by Ramon et al. /this volume/ on *P. lifordi*.

b/ Analysis of the matrix

The data in Tab. 1 was used to calculate the NEI's genetic identity and the distance coefficients between each pair of populations, which constitute Tab. 2.

One can immediately note that the average values of \bar{I} / $.609$ / and \bar{D} / $.496$ / between *P. muralis* and *P. pityusensis* are in the usual range of different species / $.750 \geq \bar{I} \geq .600$; $.300 \leq \bar{D} \leq .500$; Guillaume and Cirer, in press/.

According to the same estimate, $\bar{I} \geq .830$ / $\bar{D} \leq .180$ / would be an indicative value of intra-specificity and we note that almost all the figures within *P. pityusensis* are much higher than .950.

Thus, because of this high degree of genetic identity and in accordance to our genetic results only, we would be inclined to speak better in terms of populations rather than in terms of subspecies. Even here the concordance with the results of Ramon et al. /this volume/ on *Podarcis lifordi* is amazing!

The only I lower than .900 are those between *P. p. vedrae* /14/ and *P. p. caldesiana* /3/, and those of *P. p. grueni* /12/ related to *P. p. caldesiana* /3/, *P. p. negrae* /8/, *P. p. formenterae* /13/, *P. p. maluquerorum* /15/, *P. p. frailensis* /16/, and *P. p. kammeriana* /18/.

DISCUSSION AND CONCLUSION

The dendrogram /Fig. 1/, built with the data of Tab. 2, following the classical "unweighted pair groups method of clustering" /Sokal and Sneath, 1963/ permits the visualization of the previous analysis, but should not be confused with a phyletic tree.

The best individualized subspecies is *P. p. grueni*, extremely adapted to its rigorous and peculiar habitat on Trocados island /north of Formentera/: flat sandy zones with almost no vegetation. In fact, this island, according to the lay-out of the sediments by littoral drift, has been at some time a peninsula; hybridization with *P. p. formenterae* has been observed, causing Rodriguez-Ruiz /1976/ not to consider it as a subspecies, but only as an ecotype of *P. p. formenterae*. As mixing does exist, we have to consider that the 100 % frequency of the allele 100 of G-6-PD-2 is probably overestimated as a result of the small sampling, and that allele 110 should be present in *P. p. grueni*. However, it is interesting to note that the identity coefficient $I = .895$ between *P. p. grueni* "ecotype" and *P. p. formenterae* is lower than those between *P. p. formenterae* and the other more isolated populations.

At a lower level, *P. p. maluquerorum* is distinguished /Fig. 1/. This subspecies is morphologically well differentiated by gigantism, melanism, and high rate of pholidosis. It is found on a group of islets and rocks /Bleda Islands/, probably the first islets to have been separated from the main island /Colom, 1978/. Although the extremely advanced morphological differentiation seems more clear than the genetical one, this discrimination seems to be normal.

For all the other subspecies, which have \bar{D} values close to or lower than .070, the electrophoretic technique does not allow for taxonomic conclusions, even though most of them differ from one another by coloration patterns and biometric characters.

Only complete revision, making a synthesis from the results of the different studies, will permit one to understand the complex evolution of the Balearic lizards: *P. pityusensis* and *P. lilfordi*. Indeed, we should not forget that Ramon et al. /this volume/ have shown that "intercomparisons of *P. lilfordi* populations with that of *P. pityusensis* show lesser genetic homology than between the former themselves...".

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NEI's genetic Identity (above) and Distance (below) Coefficients :

	<i>Podarcis muralis muralis</i>	<i>P. pityusensis pityusensis</i>	<i>P. p. caldesiana</i>	<i>P. p. espartellensis</i>	<i>P. p. shorcadosi</i>	<i>P. p. puercosensis</i>	<i>P. p. negrae</i>	<i>P. p. grueni</i>	<i>P. p. formenterae</i>	<i>P. p. vedrae</i>	<i>P. p. maluquerorum</i>	<i>P. p. frailensis</i>	<i>P. p. kameriana</i>
1		.620	.614	.644	.618	.609	.574	.649	.607	.634	.555	.609	.572
2	.478		.924	.981	.986	.995	.973	.924	.981	.983	.943	.958	.988
3	.487	.079		.956	.938	.978	.942	.854	.901	.893	.925	.911	.971
4	.441	.019	.045		.988	.991	.981	.906	.968	.964	.923	.962	.988
5	.482	.014	.064	.012		.988	.985	.914	.967	.968	.932	.964	.984
6	.496	.004	.022	.009	.011		.971	.906	.974	.970	.938	.950	.982
8	.556	.027	.060	.019	.016	.030		.869	.970	.962	.904	.957	.973
12	.433	.079	.158	.099	.090	.099	.140		.895	.910	.880	.868	.894
13	.489	.020	.105	.033	.033	.027	.030	.111		.979	.909	.952	.978
14	.456	.017	.113	.036	.032	.030	.039	.095	.021		.923	.978	.987
15	.588	.058	.078	.080	.071	.064	.100	.128	.096	.075		.909	.932
16	.495	.043	.094	.039	.036	.051	.044	.141	.049	.023	.096		.970
18	.557	.012	.029	.012	.016	.018	.028	.112	.022	.013	.070	.030	
	1	2	3	4	5	6	8	12	13	14	15	16	18

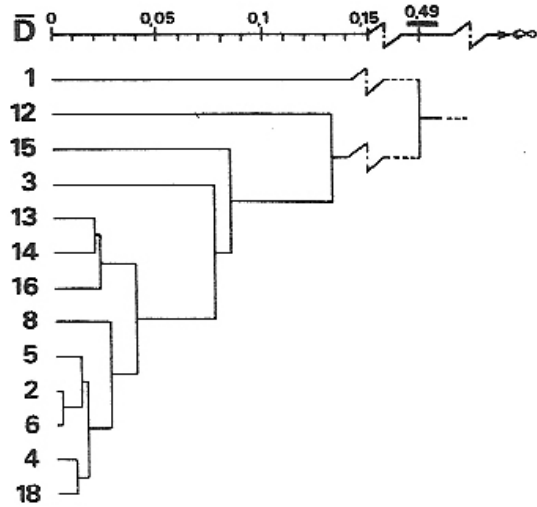


Fig. 1: Dendrogram based on NEI's genetic distance coefficients from 12 populations of *Podarcis pityusensis*.