

GENETIC AND MORPHOLOGICAL VARIABILITY OF *EULEPTES EUROPAEA* (GENÉ, 1839) (REPTILIA SAURIA SPHAERODACTILIDAE)

BENEDETTO LANZA⁽¹⁾, SILVIA BRUSCHI⁽²⁾, FRANCESCO NISTICÒ⁽³⁾

(1) Museo di Storia Naturale (Sezione Zoologica «La Specola» & Dipartimento di Biologia Animale e Genetica, Università degli Studi di Firenze, via Romana 17, I-50125 Firenze (Italy). E-mail: benedetto.lanza@libero.it

(2) Via A. Tavanti, 13, 50134 Firenze (Italy). Collaboratrice esterna del Dipartimento di Biologia Animale e Genetica, Università degli Studi di Firenze, Via Romana 17, I-50125 Firenze (Italy). E-mail: sil.brus@gmail.com

(3) Via F. Cilea, 10, I-87028, Praia a Mare (Cosenza, Italy)

Abstract – According to our research on the mostly island- and islet-dwelling Mediterranean gecko *Euleptes europaea*, no genetic and morphological interpopulational difference appear to be of taxonomic value.

Keywords: *Euleptes europaea*, morphology, genetics, variability.

Riassunto – Secondo le nostre ricerche su *Euleptes europaea*, gecko mediterraneo soprattutto macro e microinsulare, nessuna delle differenze genetiche e morfologiche interpopolazionali ha mostrato di possedere valore tassonomico.

Parole chiave: *Euleptes europaea*, morfologia, genetica, variabilità.

1. - Introduction

We studied genetics, size and lepidosis of *Euleptes europaea* (GENÉ, 1839) coming from nearly its entire range, in order to establish the degree of its variability. The subject appears to be of considerable interest as this mostly insular gecko occurs on a myriad of small islands, islets, rocks and rocklets, which should imply a relatively high genetic and morphological variability.

2. - Materials and methods

Genetic analysis has been conducted, with the decisive collaboration of the Dipartimento di Genetica e Biologia Molecolare dell'Università di Roma «La Sapienza» (Profs Luciano Bullini and Giuseppe Nascetti), on 31 putative gene loci codifying 27 enzymes and 4 non-enzymatic proteins, which were scored by means of allozyme horizontal electrophoresis in the following 32 specimens from 12 localities:

- Tagliu Rossu, near Santa Lucia di Portovecchio, Corsica (n = 1);
- Toro Grande Islet, Corsica (n = 2);
- Barrettini Island, Sardinia (n = 2);
- Santa Maria Island, Sardinia (n = 1);

- Soffi Island, Sardinia (n = 2);
- Paduleddu Sud Islet, Sardinia (n = 6);
- Camere Est Islet, Sardinia (n = 2);
- Molarotto Islet, Sardinia (n = 3);
- Stramanaro di Mezzo Rock, Sardinia (n = 4);
- Camize Rock, Sardinia (n = 3)
- Giglio Island, Tuscan Archipelago (n = 2)
- Giannutri Island, Tuscan Archipelago (n = 4)

Morphology has been studied on 567 specimens mostly preserved in the Sezione Zoologica «La Specola» of the Natural History Museum of Florence University (MZUF); a few ones come from the Museo Regionale di Scienze Naturali, Turin (MRSN) and Museo Civico di Storia Naturale «Giacomo Doria», Genova (MSNG).

The material come from:

- continental Liguria (n = 3) and 2 satellite islands (n = 29);
- Corsica (main island) (n = 10) and 27 satellite islands (n = 148);
- continental Tuscany (n = 14) and 18 satellite islands (n = 158);
- Sardinia (main island) (n = 109) and 22 satellite islands (n = 96);
- Aguglia Islet (Galite Archipelago, Tunisia) (n = 6).

In the statistical analysis a total of 450 specimens from 41 localities were considered (Fig. 1): the others have been excluded because damaged, or because the population sample was too little (n < 5). The following 16 characters have been studied:

- snout-vent length (SVL);
- number of scales between the nostril and the anterior edge of the orbit (P01);
- number of transversal scales of the snout along the midline between the eye and the nostril (P02);
- number of interorbital scales between the middle points of the palpebral fissures (P03);
- number of supralabial scales, from the rostral scale (excluded) to the supralabial scale situated on the vertical extension of the eye diameter (P04);
- number of sublabial scales, from the mental scale (excluded) to the supralabial scale situated on the vertical extension of the eye diameter (P05);
- minimum number of scales on a transversal line between the supranasal scales (P06);
- number of posmental scales (underlabial excluded) (P07);
- number of scales posterior to the postmental, and in contact with them (P08);
- number of scales along a transversal line at the middle of the body between the axilla and the groin (P09);
- number of dorsal scales on a longitudinal line along the vertebral column, from the junctures of the anterior and posterior limbs (P10);
- number of ventral scales on the midline of the body, between the median procloacal scale (included) and the mental (excluded) (P11);
- number of scales along the midline under the I finger between the adhesive organ and the fold between the finger and the sole (P12);
- number of scales along the midline under the I toe between the adhesive

- organ and the fold between the finger and the sole (P13);
- number of scales along the midline under the IV finger between the adhesive organ and the fold between the finger and the sole (P14);
- number of scales along the midline under the IV toe between the adhesive organ and the fold between the finger and the sole (P15).

Bilateral characters have been measured on both sides of the body; in statistical analysis only the right side has been considered, the left side only when the right one was damaged. Data have been studied with both univariate and multivariate methods. First of all ANOVA has been applied to all characters to analyze sexual dimorphism, and to snout-vent length to check if differences among localities could be detected; then all other characters have been analysed with (M)AN(C)OVA (with snout-vent length eventually used as a covariate). Further on discriminant analysis has been conducted to study the differences among the populations, and a matrix of Mahalanobis distances has been produced and used to construct an UPGMA tree and a MDS (Multidimensional Scaling) bidimensional plot.

3. - Results and conclusions

Genetic research allowed to establish the presence of a very low divergence and heterozygosity, although studied populations were completely isolated, with up to about 200 km between the extreme ones.

Morphological analysis on sexual dimorphism (AN(C)OVA) revealed that the differences between males and females are rarely significant (Tab. 1), so all adults and juveniles have been analysed together.

ANOVA conducted on adults showed that there is a very highly significant difference in SVL among localities, even if Scheffé test did not reveal any significant difference among pairs of localities ($p > 0.99$ in all cases). The same results were obtained when juveniles have been added to the analysis. Then pholidotic characters have then been tested, first with MAN(C)OVA and then with AN(C)OVA: results showed very highly significant differences in all characters except P07 (MANOVA: $F_{15,600} = 3.56$, $p < 0.001$; MANCOVA: $F_{15,600} = 3.56$, $p < 0.001$; ANOVA and ANCOVA: cfr. Tab. 2). Scheffé test conducted on the single characters between pairs of localities shows again little differences: it is very highly significant ($p < 0.001$) just in characters P09 (pairs SA4-SCI and SA4-SA2) and P11 (pairs SA4-SPO and SA4-GIA); highly significant ($p < 0.01$) in character P09 (pair SA4-GIA); significant ($p < 0.05$) in characters P09 (pair SA5-SA2) and P11 (pair SA4-SCI).

Finally, multivariate analysis could not detect any kind of geographic trend, since for instance the five sardinian localities in the analysis are scattered along the graphics (Figs. 2 and 3).

In conclusions, we detected neither genetic nor morphologic difference of taxonomic value.

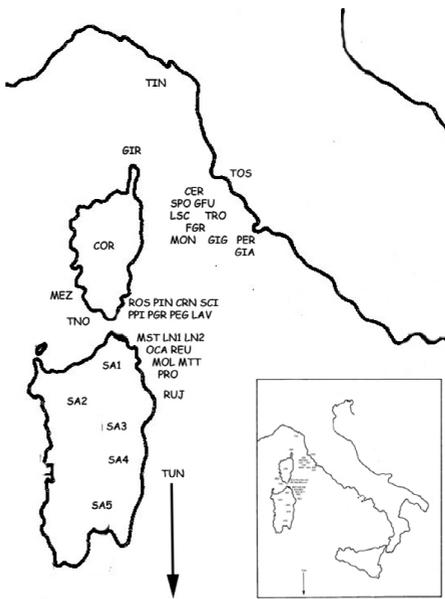


Fig. 1 - Map of the studied localities.

Var.	ANOVA			ANCOVA		
	df	F	p	df	F	p
SVL ¹	1, 397	27.85	<0.001	-	-	-
P01	1, 421	0.01	0.91	1, 396	0.66	0.42
P02	1, 421	1.70	0.20	1, 396	0.31	0.58
P03	1, 421	0.00	0.95	1, 396	0.01	0.93
P04	1, 421	0.91	0.34	1, 396	0.08	0.78
P05	1, 421	0.75	0.39	1, 396	0.49	0.49
P06	1, 421	0.42	0.52	1, 396	0.60	0.44
P07	1, 421	0.21	0.65	1, 396	0.91	0.34
P08	1, 421	0.24	0.62	1, 396	1.64	0.20
P09	1, 421	0.00	0.99	1, 396	0.08	0.78
P10	1, 421	4.60	0.03	1, 396	5.97	0.02
P11	1, 421	3.30	0.07	1, 396	4.59	0.03
P12	1, 421	1.05	0.31	1, 396	2.20	0.14
P13	1, 421	3.36	0.07	1, 396	6.50	0.01
P14	1, 421	0.89	0.35	1, 396	1.14	0.29
P15	1, 421	6.90	0.01	1, 396	6.92	0.01

Tab. 1 - AN(C)OVA conducted to detect sexual dimorphism.

Var.	ANOVA			ANCOVA		
	df	F	p	df	F	p
SVL ²	40, 409	2.74	<0.001	-	-	-
P01	40, 409	2.16	<0.001	40, 408	2.16	<0.001
P02	40, 409	3.80	<0.001	40, 408	3.84	<0.001
P03	40, 409	5.50	<0.001	40, 408	5.50	<0.001
P04	40, 409	2.28	<0.001	40, 408	2.27	<0.001
P05	40, 409	2.76	<0.001	40, 408	2.73	<0.001
P06	40, 409	5.30	<0.001	40, 408	5.22	<0.001
P07	40, 409	1.17	0.23	40, 408	1.15	0.25
P08	40, 409	2.35	<0.001	40, 408	2.34	<0.001
P09	40, 409	7.50	<0.001	40, 408	7.22	<0.001
P10	40, 409	5.80	<0.001	40, 408	5.18	<0.001
P11	40, 409	7.40	<0.001	40, 408	6.90	<0.001
P12	40, 409	5.05	<0.001	40, 408	5.03	<0.001
P13	40, 409	5.39	<0.001	40, 408	5.36	<0.001
P14	40, 409	4.40	<0.001	40, 408	4.24	<0.001
P15	40, 409	3.30	<0.001	40, 408	3.34	<0.001

Tab. 1 - AN(C)OVA conducted among populations (¹: without juveniles; ²: with juveniles).

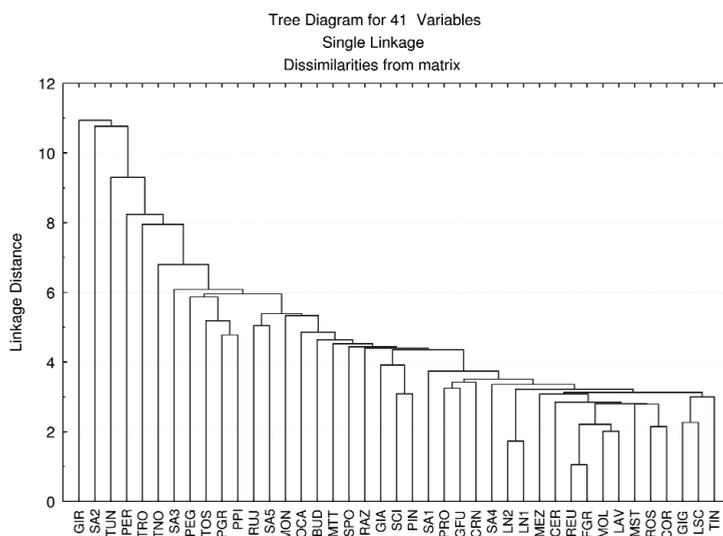


Fig. 2 - Results of the multivariate analysis: UPGMA tree.

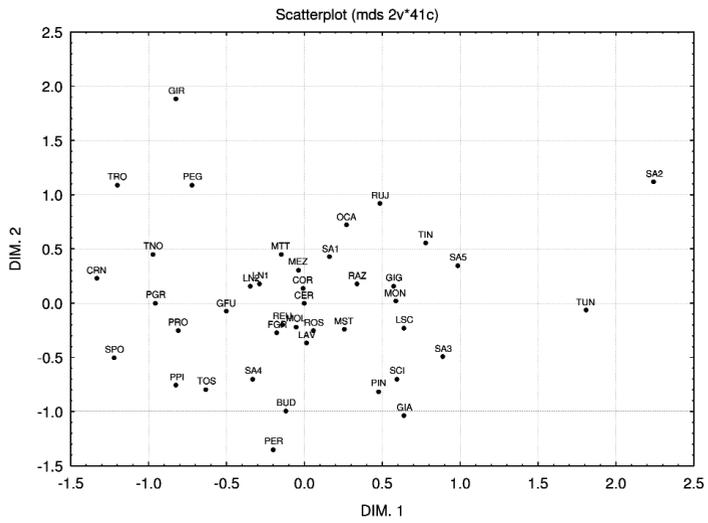


Fig. 3 - Results of the multivariate analysis: MDS scatterplot.

Lavoro consegnato il 17.03.2014