

## MORPHOLOGICAL VARIATIONS IN THE COMMON LIZARD, *Lacerta (Zootoca) vivipara*

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Knowledge on variations in the reproductive modes, karyotypes, and mtDNA sequences of *Lacerta (Zootoca) vivipara* made headway but the morphological differences between any forms or populations remain unclear. That is why we studied different patterns of morphological variability using nine biometrics and 10 meristic variables on 242 common lizards: 119 oviparous (French, Spanish, and Slovenian), 114 viviparous (French, Bulgarian, and Russian), and nine hybrids. Our analyses confirm, for each population, the existence of a clear sexual dimorphism. Observed differences between reproductive strains (oviparous vs. viviparous) could not be connected immediately with the reproductive mode. Results of comparison between regions correspond to the geographical origin of the samples. We observe three clusters: western (Pyrenees and France), Slovenian, and eastern (Bulgaria, Russia, and Siberia). Comparisons of samples defined by their karyotypes are very similar. *L. (Z.) v. carniolica* subspecies is different for a majority of the studied variables. Our results show the special interest of the Russian samples but do not support the validity of the sachalinensis subspecies. The absence of clear relation between morphological and genetic structure of the species reveals that samples of the “complex” of common lizards are very closely related and have likely relatively recently diverged.

**Keywords:** variability, common lizard, *Lacerta (Zootoca) vivipara*, viviparity, oviparity, morphometry.

### INTRODUCTION

The common lizard, *Lacerta (Zootoca) vivipara*, has the greatest distribution area known for lizards (Dely and Böhme, 1984). In spite of that, the species structure and variability remains poorly understood. Two last de-

acades contributed much to our knowledge on variations in the reproductive mode, karyotypes and mitochondrial DNA sequences of common lizards (for review see Odierna et al., 2001; Surget-Groba et al., 2001). Meanwhile the morphological differences between any forms or populations of the species are still unclear and the notice of Boulenger (1920:130) remains actual: “It is highly remarkable for a species with so wide a distribution, and living under such varied conditions of climate and soil, to show no definable geographical races; very variable in scaling and coloration, the differences which have been adduced in favor of the establishment of varieties are purely individual, as the large material on which the above description is based amply shows.”

To fulfill the gap in the knowledge of the common lizard morphological variability we have undertaken a large-scale morphometrical comparison of specimens from different area parts.

The main purpose of the study was to look for any morphological peculiarities connected with the repro-

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ductive mode of different populations. But we were also interested in any other patterns of morphological variability, e.g., connected with sex, geographic position, taxonomic status, and karyotype.

## MATERIAL AND METHODS

242 specimens of the common lizard were used for the study: 106 males and 136 females. They came from 40 localities: 4 in Spain, 19 in France, 4 in Slovenia and nearby Italy area, 6 in Bulgaria and two in Russia (one in Moscow region and one in the Central Siberia) (*Appendix 1* specifies these data and the used abbreviations whose last letter is O for “oviparous” or V for “viviparous”). The sample includes both identified oviparous population groups, from Cantabria and Pyrenees (SPO; FRO) (Heulin and Guillaume, 1989) and from Slovenia and Italy (Böhme et al., 1999; Heulin et al., 2000; Ghielmi et al., 2001) as well as different viviparous populations. Laboratory hybrids (HYB) (9 specimens) between Pyrenees oviparous and French viviparous lizards were also included in the analysis. We find here also populations of all main karyotypes (Odierna et al., 2001; Surget-Groba et al., 2001), and of both certain subspecies: nominal and *L. (Z.) vivipara carniolica* (Mayer et al., 2000) (SLO).

Only adult specimens (snout-vent length  $\geq 41$  mm for males and  $\geq 44$  mm for females) were used in morphometric analyses. All measured animals were fixed in alcohol at least three weeks before the procedure (Pérez-Mellado and Gosá, 1988). To minimize the influence of different collaborators involved in the measurements the standard illustrated instruction form was worked out by one of the authors (B. Heulin).

Twenty-one variables were used for comparisons including linear measurements, pholidosis characters, and one index (see *Appendix 2*). For “between sexes” and “between samples” comparisons (Tables 1 and 2, respectively), we also used two ratios of biometry (Ltrn/SVL; Ltpl/SVL) and two of pholidosis counts (Dor/Vent; Dor/SDos).

Discriminant and cluster analyses were employed to reveal similarity patterns among geographic samples, karyomorphs, reproductive mode groups, and sex groups. Males and females were considered separately. Both original and standardized (by dispersion) sets of data were used in analyses: size factor was removed due to standardization, which was crucial for the cluster analysis. Moreover, for several analyses, the entire set of

data was arbitrarily divided in the following geographical groups: Pyrenees, France, Slovenia, Bulgaria, European Russia, and Siberia, for which average values of standardized characters were calculated.

Forward stepwise discriminant analysis was applied to the original non standardized data (indices were not included) in each of the comparisons, with “F-to-remove” threshold value conventionally taken equal to 3.2. Due to this only those characters for which *F* estimate was highly significant ( $p < 0.001$ ) appeared to be included in the discriminant functions. Cluster analysis was applied to the group averages of standardized data, Euclidean distance was used as dissimilarity estimate, and UPGMA algorithm was used to produce phenograms.

The statistical package STATISTICA 5.5 (StatSoft, 1999) was used for all calculations.

## RESULTS AND DISCUSSION

### Sexual Differences

Our results agree with the earlier findings (Angel, 1927; Wermuth, 1955; Stugren and Vancea, 1961; Lanza, 1963; Castroviejo et al., 1970; Borcea, 1978; Dely, 1981; Cortès, 1988) on apparent sexual dimorphism in *L. (Z.) vivipara*. The comparison of all males with all females reveals significant differences in nearly all variables except SDos, Gul, La4M, SciM, and  $D_{10}$  (Table 1). Degree of sexual dimorphism appeared to vary insignificantly between largest samples but in no case sex differences are opposite in different samples: that is, there is no examples of a character having large value for males in one sample and for females in another (Table 1). The number of characters significantly related with sex varies between samples. The variation range from 6 (Siberian viviparous) to 16 (Pyrenean oviparous) may be explained not only by sample sizes but also by the interpopulation differences in the sexual dimorphism (Table 1). In the whole sample, the most input in sex differences is especially provided by Vent, but also by some size-related variables and their ratios (Ltrn/SVL and Ltpl/SVL) while the four variables of pholidosis SDos, La4M, SciM, and  $D_{10}$  obviously don't have any relation to sex. On the other hand we practically never could find a diagnostic difference between character values for male and females. So no one of analyzed characters could be used for certain sex identification in the *L. vivipara* in general.

TABLE 1. Differences Between Sexes in Samples of *Lacerta vivipara*

Char- acter	Entire sample			Louviv (FRO)			Paimpont (FRV)			Moscow (RUV)			Siberia (SIV)		
	$\sigma\sigma$ (106)	$\varphi\varphi$ (136)	<i>t</i>	$\sigma\sigma$ (10)	$\varphi\varphi$ (8)	<i>t</i>	$\sigma\sigma$ (16)	$\varphi\varphi$ (26)	<i>t</i>	$\sigma\sigma$ (13)	$\varphi\varphi$ (11)	<i>t</i>	$\sigma\sigma$ (8)	$\varphi\varphi$ (10)	<i>t</i>
SVL	50.09 39.1-61.0	54.27 44-70.25	-6.65	48.25 45-51	51.94 44-56	-2.62	49.78 41.05-56	58.11 49-65.5	-6.83	50.31 46-55	51.64 48-60	-1.17	46.63 42-51	52.40 48-61	-3.20
Ltm	33.37 25.3-4.3	38.67 29.28-52.1	-9.92	31.64 28.5-34	36.84 30.3-39.2	-4.33	33.15 27.28-38.6	42.00 34.6-48.15	-8.99	33.19 29.2-37.6	36.15 32.2-42.95	-2.76	31.10 27.7-34.2	36.77 32.9-44.8	-3.66
Hnl	16.72 12.7-20.4	15.61 7.6-19.35	6.64	16.62 14.5-18.55	15.09 13.7-16.8	2.87	16.63 12.75-18.2	16.11 14.4-17.75	1.61	17.12 16.5-17.8	15.49 14.2-17.05	5.35	15.53 14.3-16.8	15.64 14.8-16.6	-0.30
Hw	7.33 5.5-9.3	6.87 5.35-8.25	5.57	7.26 6.25-7.75	6.67 6.05-7.15	2.89	7.39 5.5-8.4	7.14 6.45-7.85	1.42	7.68 7.25-7.95	6.80 6.4-7.8	7.25	6.79 6.2-7.15	6.97 6.7-7.65	-1.18
Lpil	10.52 8.4-12.8	9.77 7.6-12.25	7.03	10.47 9.55-11.4	9.52 9-10.05	4.19	10.54 8.4-11.6	10.10 9.3-11.25	2.24	10.84 10.3-11.6	9.73 9.15-10.55	6.56	9.73 8.8-10.55	9.74 9.35-10.45	-0.06
Wpil	5.90 4.5-7.05	5.52 4.65-6.7	6.45	5.97 5.7-6.3	5.41 5.05-5.8	4.26	5.87 4.55-6.6	5.65 5.1-6.1	1.72	6.22 5.85-6.7	5.51 5.15-6.45	5.74	5.52 5.2-6.1	5.51 5.15-6	0.95
Hhd	5.62 4.25-6.95	5.29 4.02-9.65	4.57	5.88 5.1-6.4	5.53 5.1-5.95	1.80	5.42 4.45-6.4	5.28 4.65-6.1	1.03	5.88 5.1-6.45	5.21 4.9-5.65	4.75	5.40 4.85-5.9	5.51 5.1-6.2	-0.66
Ltal	14.86 10.95-19.5	14.26 10.8-17.75	3.37	14.88 12.8-16.4	13.49 12.1-15	2.72	15.18 12.15-17.3	15.36 13.3-17.05	-0.48	14.08 11.85-15.75	13.59 12.65-15	1.45	14.35 12.45-15.75	14.39 12.95-15.5	-0.08
Lpl	20.91 15.65-29.55	19.57 16-24.6	5.08	20.86 19.4-22.6	18.31 16-20	4.39	21.01 17.4-23.5	20.53 17.85-22.55	1.00	21.55 19-23.7	18.95 16.3-21.7	4.51	20.29 17.35-23.3	20.36 18.45-22.05	-0.09
Lpl	13.68 9.4-19.8	12.93 9.15-16.6	3.71	13.94 12.55-15.35	12.07 10-13.65	3.60	13.92 11.1-16.1	13.76 11.7-15.5	0.37	14.18 12.9-15.65	12.39 10.1-14.7	3.92	13.28 10.95-15.8	13.51 11.95-14.7	-0.38
L4F	7.23 5.3-9.75	6.64 5.4-8.55	6.32	6.93 5.35-8.1	6.24 6-6.5	2.29	7.09 6.25-8.2	6.77 6.05-7.8	2.08	7.37 6.1-8.15	6.57 5.8-7.2	3.94	7.01 6.4-7.55	6.85 5.75-7.85	0.68
Dor	73.28 62-83	77.49 67-94	-7.04	76.40 72-82	81.00 70-85	-2.39	75.50 69-83	80.38 71-94	-3.30	70.46 68-73	74.91 68-85	-3.23	68.25 62-72	71.20 67-78	-1.86
SDos	32.31 27-38	31.71 25-37	1.81	33.50 30-36	33.00 30-36	0.52	34.50 30-38	34.19 30-37	0.43	30.31 28-33	29.82 28-33	0.82	28.88 27-32	28.20 25-31	0.83
Vent	23.24 20-27	26.71 22-32	-17.69	22.40 21-24	26.13 25-29	-7.15	24.25 23-27	28.08 25-32	-8.27	23.23 21-25	26.82 25-29	-7.51	23.38 20-26	26.60 24-29	-4.29
Coll	7.88 3-10	7.55 3-12	2.04	7.80 7-9	6.50 3-8	2.36	8.25 3-10	7.73 6-10	1.33	6.92 6-9	6.55 6-8	1.09	6.63 5-8	6.80 5-8	-0.38
Gul	18.01 15-22	17.88 14-23	0.68	17.00 16-19	18.25 16-21	-1.82	18.56 17-21	17.65 15-22	2.13	19.38 18-22	18.45 17-20	1.95	19.00 17-22	18.80 16-23	0.21
FPM	11.17 8.5-14.5	10.75 7.5-14.5	2.74	10.90 10-13	11.38 10.5-12	-1.22	10.94 9.5-12	10.60 9-12	1.45	10.65 9.5-11.5	9.55 7.5-11	2.77	9.94 8.5-11	9.60 8.5-11	0.76
La4M	18.14 15-22	17.95 15.5-23.5	1.02	17.50 15-19.5	17.69 16-19	-0.31	18.03 15-20	18.44 16.5-20.5	-1.00	18.12 15.5-20	18.55 16.5-21.5	-0.74	17.13 15.5-19	16.90 15.5-18	0.53
SciM	4.39 2.5-6	4.39 3.5-6	0.08	4.60 4-5.5	4.13 3.5-4.5	2.06	4.63 4-6	4.69 3.5-5.5	-0.41	4.58 4-5	4.86 4-5.5	-1.47	4.31 4-5.5	4.25 4-5	0.30
LbM	3.85 3-7	3.64 2.5-7.5	2.70	3.55 3-4	3.44 3-4	-0.41	3.97 3-4.5	3.85 3-4	1.28	3.88 3.5-4.5	4.14 3.5-5	-1.78	3.94 3.5-4.5	3.75 3-4	1.03

TABLE 1 (continued)

Char-acter	Entire sample		Louvie (FRO)			Paimpont (FRV)			Moscow (RUV)			Siberia (SIV)			
	$\sigma\sigma$ (106)	$\varphi\varphi$ (136)	$t$	$\sigma\sigma$ (10)	$\varphi\varphi$ (8)	$t$	$\sigma\sigma$ (16)	$\varphi\varphi$ (26)	$t$	$\sigma\sigma$ (13)	$\varphi\varphi$ (11)	$t$	$\sigma\sigma$ (8)	$\varphi\varphi$ (10)	$t$
$D_{10}$	0.93 0.49–1.42	0.90 0.3–1.49	1.12	0.85 0.58–1.34	0.79 0.63–0.99	0.73	0.97 0.72–1.38	0.95 0.58–1.32	0.52	1.03 0.73–1.42	1.07 0.79–1.4	–0.57	1.02 0.85–1.28	1.13 0.87–1.5	–1.37
FDM	9.80 5.00–16.06	8.80 2.76–15.27	<b>3.37</b>	8.88 6.43–15.29	7.49 6.00–9.01	1.51	10.23 8.01–15.05	9.56 5.88–13.02	1.20	11.10 8.48–16.06	10.44 7.61–14.75	0.81	9.86 8.94–12.69	11.08 8.71–15.27	–1.31
Ltm/SVL	66.54 61.33–72.62	71.12 62.06–76.88	<b>–16.11</b>	65.52 62.77–70.10	70.91 68.86–72.84	<b>–5.47</b>	66.54 62.31–68.94	72.23 70.42–74.11	<b>–13.06</b>	65.92 63.48–68.36	69.94 65.71–73.7	<b>–5.31</b>	66.68 65.95–68.06	70.05 68.0–73.44	<b>–5.21</b>
Ltp/SVL	41.78 32.73–50.08	36.22 28.99–49.60	<b>12.96</b>	43.26 39.90–45.96	35.32 30.36–37.64	<b>8.12</b>	42.22 39.11–45.63	35.39 31.34–39.80	<b>10.75</b>	42.86 38.78–46.2	36.73 33.96–41.73	<b>6.27</b>	43.49 40.89–47.23	38.98 34.24–43.7	<b>3.47</b>
Dor/Ven	3.17 2.62–4.05	2.91 2.29–3.42	<b>8.37</b>	3.41 3.22–3.73	3.10 2.80–3.36	<b>3.72</b>	3.12 2.67–3.46	2.87 2.29–3.38	<b>3.41</b>	3.04 2.8–3.32	2.80 2.43–3.04	<b>3.50</b>	2.93 2.77–3.14	2.68 2.52–2.89	<b>4.10</b>
Dor/SDos	2.28 1.94–2.73	2.45 2.00–2.93	<b>–7.97</b>	2.29 2.11–2.73	2.46 2.12–2.77	–1.95	2.20 1.94–2.59	2.36 2.03–2.73	<b>–2.37</b>	2.33 2.15–2.48	2.52 2.19–2.75	<b>–3.33</b>	2.37 2.07–2.56	2.53 2.23–2.72	–2.03

**Note.** Above, mean for a character; below, its limits; in bold are the  $t$ -values for the significant differences by  $p \leq 0.05$ .

Taking into consideration the high level of the differences between sexes in most cases we have made analyses separately for males and females.

### Comparison of the Viviparous and Oviparous Forms

The comparison of all oviparous samples with all viviparous ones shows that in the spite of very diverse geographic structure of both assemblages they are obviously different (Fig. 1). These assemblages are discriminated basically by the 1<sup>st</sup> canonical variable with which Vent, FPM, and Gul are highly correlated in males and Vent,  $D_{10}$ , and LTL in females. Thus, the Vent appears to be most significant in discriminating the groups defined by reproductive mode in both sexes. Certainly these differences could not be connected immediately with the reproductive mode while the Pyrenees and the Slovenian population groups much differ mutually not only geographically but also genetically (Surget-Groba et al., 2001). Nevertheless the separate pair wise comparison of each of the Pyrenees and the Slovenian forms with the integral viviparous sample reveals some coinciding differences (Table 2). They both have significantly less numbers of ventral scale rows and of supraciliar granules and significantly larger number of femoral pores than those of the viviparous assemblage. Besides, specimens of the both oviparous forms have significantly lower masseteric index  $D_{10}$ .

Surely those findings could only reflect the extremely high mosaic variability of the common lizard. But they could also be connected with the reproductive mode and/or with the closer lineage of both oviparous forms in comparison with the viviparous assemblage. In any case there is no single character allowing unambiguous discrimination of the specimens with specific reproductive mode in the common lizard.

Both oviparous forms differ from each other mostly by size with Slovenia specimens being much large (Table 2). There are only few significant differences in meristic characters between them.

As expected the laboratory hybrids of viviparous and oviparous forms have intermediate morphological characteristics (Fig. 1).

### Comparison Between Regions

The samples analyzed can be divided objectively into several regional groups listed above: they are the Pyrenees (including SPO and FRO populations — cf. Appendix 1), France (FV), Slovenia (SLO), Bulgaria

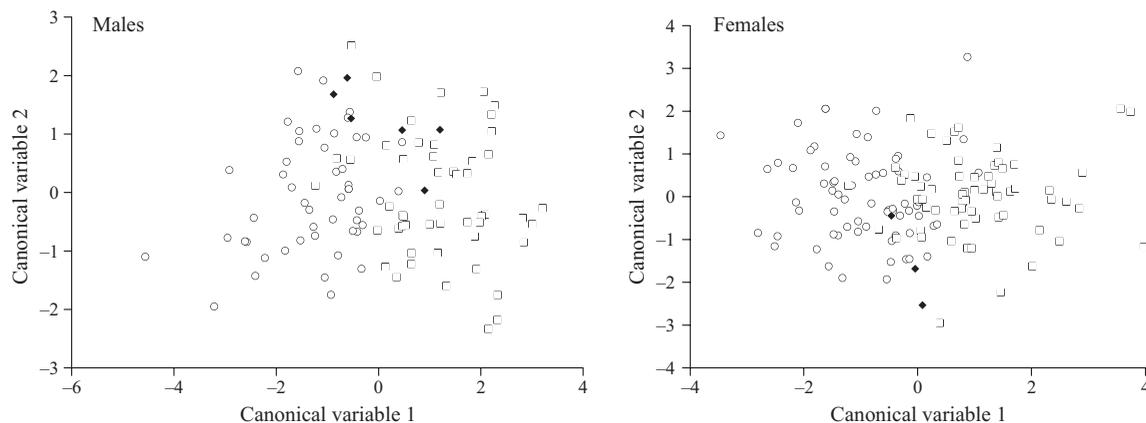


Fig. 1. Results of the discriminant analysis of differences among oviparous and viviparous samples: ○, oviparous; □, viviparous; ◆, hybrids.

(BV), European Russia (RV), and Siberia groups. The cluster analysis gives a quite expected picture of their similarity relationships (Fig. 2). In both sexes the regional samples form three quite pronounced clusters: Western (Pyrenees and France), Slovenian, and Eastern (Bulgaria and Russia). The Slovenia sample is positioned somewhat closer to the western samples. In general the results of cluster analysis correspond to the geographical position of the samples.

Discriminant analysis of the differences among regional groups reveals the following details of similarity relations. When all regions are analyzed simultaneously (i.e., Slovenian group is included), the most input in the differences is provided by LPIL in both sexes which discriminates basically Slovenia from other regions. However, if the just above group is excluded from the analysis, HW alone appeared to be most discriminating char-

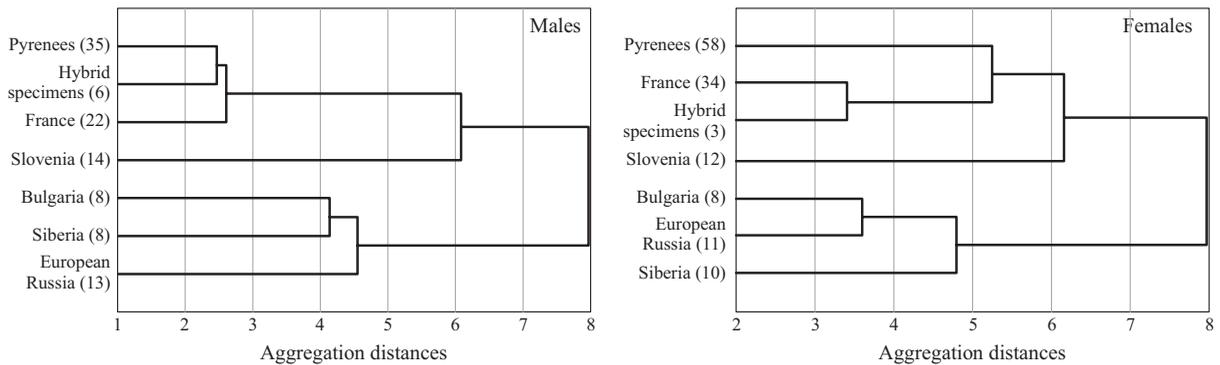
acter in males while it is added with SDos and LBM in females.

### On the Subspecies Structure of the *Lacerta vivipara*

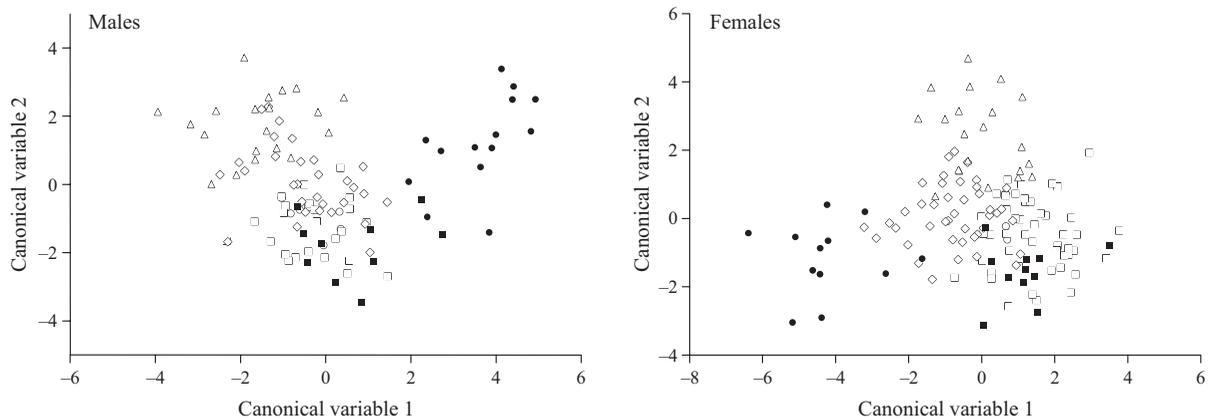
In all our comparisons the Slovenian samples take much isolated position (Figs. 1 and 2) what fits very well with the genetic, karyotypical and taxonomic distinction of the form (Mayer et al., 2000; Surget-Groba et al., 2001). There is no doubt about the validity of the subspecies *L. (Z.) v. carniolica*. Nevertheless it seems that the genetic and cytogenetic differences of the form seem to be expressed more clearly than morphological ones (Mayer et al., 2000). The comparison of the Slovenia samples with the other groups of our samples shows a number of significant differences (Table 2). In general our sample of *L. (Z.) v. carniolica* is distin-

TABLE 2. Pair Wise Comparison Between Samples: Characters for which Significant Differences Between Compared Samples Were Found

	Males	Females
All the viviparous/all the oviparous	SVL, Ltrn, Ltal, L4F, Dor, SDos, Vent, Gul, FPM, La4M, SciM, D <sub>10</sub> , FDM, Dor/Vent	SVL, Ltrn, Hnl, Hw, Lpil, Ltpl, Ltal, Lpl, Dor, Vent, FPM, SciM, LbM, D <sub>10</sub> , FDM, Dor/Vent
Slovenia and Italy samples/all the viviparous	SVL, Ltrn, Hnl, Hw, Lpil, Wpil, Hhd, Ltal, Ltpl, Lpl, L4F, Dor, Vent, FPM, La4M, SciM, LbM, D <sub>10</sub> , Dor/Vent, Ltpl/SVL, Ltrn/SVL	Hnl, Hw, Lpil, Wpil, Hhd, Ltal, Ltpl, Lpl, L4F, Vent, Coll, FPM, La4M, SciM, LbM, D <sub>10</sub> , FDM, Dor/Vent, Ltpl/SVL
Pyrenees samples/all the viviparous	Hw, Dor, Vent, Gul, FPM, SciM, LbM, D <sub>10</sub> , FDM, Dor/Vent, Ltpl/SVL	SVL, Ltrn, Hnl, Hw, Lpil, Wpil, Hhd, Ltal, Ltpl, Lpl, L4F, Dor, Vent, FPM, La4M, SciM, LbM, D <sub>10</sub> , FDM Dor/Vent, Ltpl/SVL
Slovenia and Italy samples/Pyrenees samples	SVL, Ltrn, Hnl, Hw, Lpil, Wpil, Hhd, Ltal, Ltpl, Lpl, L4F, FPM, LbM, FDM, Ltpl/SVL, Ltrn/SVL	SVL, Ltrn, Hnl, Hw, Lpil, Wpil, Hhd, Ltal, Ltpl, Lpl, L4F, Coll, FPM, La4M, LbM, Ltpl/SVL, Ltrn/SVL
Slovenia and Italy samples/Bulgaria samples	SVL, Ltrn, Hnl, Hw, Lpil, Wpil, Ltal, Ltpl, Lpl, L4F, Dor, SDos, Coll, D <sub>10</sub> , Dor/Vent	Hnl, Hw, Lpil, Wpil, Ltal, Ltpl, Lpl, L4F, Vent, FPM, La4M, D <sub>10</sub> , FDM, Dor/Vent
Moscow region/Siberia	SVL, Ltrn, Hnl, Hw, Lpil, Wpil, Hhd, Dor, SDos	Hhd, Ltal, Ltpl, Lpl, SDos, La4M, SciM, LbM



**Fig. 2.** Results of cluster analysis of differences between regional groups [Euclidian distances, Unweighted Pair Group Method with Arithmetic Mean (UPGMA)].



**Fig. 3.** Results of the discriminant analysis of differences among karyotype forms: ○, hybrid specimens (HYB); □, form of the French Pyrenees (FRO); ◇, western form (FRV, BU); △, eastern form (RUV, SIV); ●, Slovenian/Italian form (SLO); ■, Spanish form (SPO).

guished from any other samples of the species in having larger body size, less number of ventral scales rows, more numerous femoral pores, lower value of  $D_{10}$  index. At the same time there is no single character which could help to distinguish the forms with confidence and which could serve for diagnostic purposes.

Recently it was proposed that the populations from Eastern Europe and Asia should be considered as a separate subspecies named *Zootoca vivipara sachalinensis* (Mayer, Böhme, 2000). Our findings do not give certain support for validity of the taxon.

### Karyotypes Comparison

Karyological structure of the common lizard includes several distinctive forms (Surget-Groba et al.,

2001). Their distribution limits coincide very much with the regional blocks (Surget-Groba et al., 2001). Our samples defined by geographical position or by karyotype are grouped in similar manner but with slight differences. Thus the Pyrenees populations are divided in two close but different cytogenetic morphs (Surget-Groba et al., 2001). On the contrary, the very remote Russian populations belong to the same unified karyotype (Surget-Groba et al., 2001).

Comparisons of karyotypical assemblages by discriminant and cluster analyses (Figs. 3 and 4, respectively) show pictures similar for both males and females and analogous with that of the regional comparison (Fig. 2). The eastern form is the most isolated one. In the another clade the Slovenian form takes a rather separated position. The Pyrenees karyotypical forms are very closes each other. Position of the western karyotypical is most

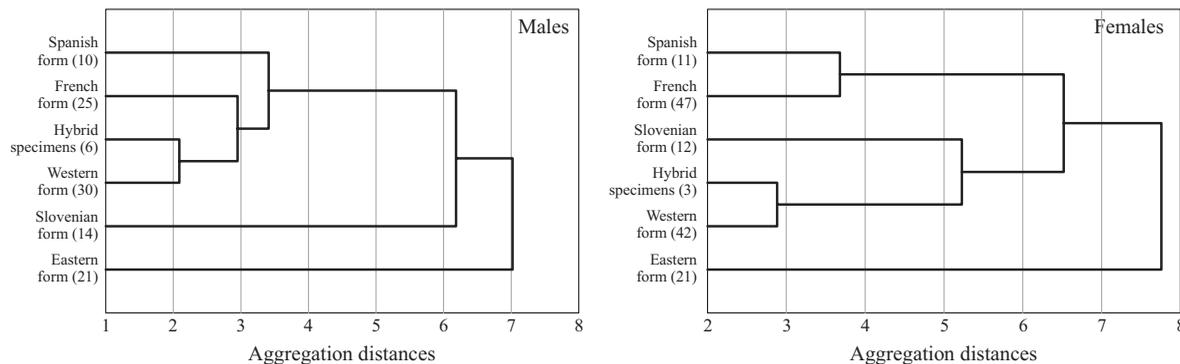


Fig. 4. Results of cluster analysis of differences among karyotype forms (Euclidian distances, UPGMA).

uncertain and some intermediate between different oviparous forms. Most contribution to differentiation of karyotypical forms belongs to FPM and L4F in both sexes; to these, Gul is added as discriminating factor in males while HW is added in females. This observation is of special interest as these characters seem to play only minor role in other aspects of intraspecies differentiation studied by us.

### Russian Populations

The Russian part of the species area is of special interest because of the contrast between its enormous extent and astonishing homogeneity of the inhabiting populations. The situation became especially obvious after recent findings showing diverse genetic structure of the out-Russian populations (for review see Surget-Groba et al., 2001).

Special studies of the common lizard population variations in the eastern part of the species area (Terentjev, 1948; Orlova, 1973; Orlova and Terbish, 1997) failed to reveal any certain structural differences. The information of a distinctive subspecies on the Sakhalin Island (Bannikov et al., 1977) is based on the inaccurate reference to the work of Pereleshin and Terentjev (1963). The authors have not found clear differences between the continental and Sakhalin samples, and the name *L. (Z.) vivipara sachalinensis* was not proposed by them as a valid one.

Our analysis shows that in spite of the far remote localities of the compared Russian populations they take the closest positions in the dendrogram both for males and females (Fig. 2). Nevertheless, there are some significant differences between samples from Moscow region and from Siberia (Tables 1 and 2). Especially pro-

nounced is difference in the number of the dorsal scale rows at the middle of the body which is significantly large in both males and females of the Moscow population. It should also be noted once more the remarkable difference between the populations in sexual dimorphism (Tables 1 and 2). But these differences could be more likely explained by the general interpopulation variations of the species than by the consistent between regions differences. The later should exist but further special studies with involving much more material from diverse localities are needed to reveal them.

### CONCLUSIONS

Versatile morphometric analysis of the common lizard over considerable part of its enormous distribution area shows that morphological variability of the species in general does not correspond to the diverse and clear genetic (molecular, karyotypic) structure of the species. We failed to reveal any reliable external characters which would distinguish populations with different karyotype, haplotype (region) or reproductive mode. It could be explained by relatively recent genetic differentiation of the species.

On the other hand some consistent differences could be marked between some of the common lizard forms. Thus, both oviparous forms of the common lizard differ well from all viviparous samples by several pholidosis characters. They have significantly less ventral scale rows and less supraciliar granules but they have significantly more femoral pores.  $D_{10}$  index also significantly discriminates forms of different reproductive mode. These differences may be connected with the evolutionary history of these forms.

Morphological differences between individual populations, between regional groups of populations, or between karyotypical forms are minor. Nevertheless these differences are not random in general. In all cases they strongly correlate with the geographical dispositions of the compared samples.

The subspecies *L. (Z.) v. carniolica* is clearly separated from all other samples by external morphology. There are several characters by which this form differs significantly from all others. At the same time no one of the character used could diagnose this taxon. The validity of subspecies *L. (Z.) v. sachalinensis* was not confirmed.

The studied Russian populations are morphologically the close in spite of their remoteness from each other. It corresponds very well to genetic unity of the common lizards inhabiting the vast eastern part of the species area.

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## APPENDIX 1.

### Characteristics of the used sample

Oviparous			Viviparous			Hybrids (lab. Rennes)		Total by sex
Origin (number of localities)	Abbreviation	N	Origin (number of localities)	Abbreviation	N	Strain of parents	N	
<b>Males</b>								
France (15)	FRO	25	Bulgaria (5)	BUV	8	♂ oviparous × ♀ viviparous	6	
Spain (3)	SPO	10	France (3)	FRV	22			
Slovenia* (4)	SLO	14	Russia, Moscow (1)	RUV	13			
			Russia, Siberia (1)	SIV	8			
<b>Total males:</b>		<b>49</b>			<b>51</b>		<b>6</b>	<b>106</b>
<b>Females</b>								
France (19)	FRO	47	Bulgaria (6)	BUV	8	♂ oviparous × ♀ viviparous	1	
Spain (4)	SPO	11	France (4)	FRV	34	♂ viviparous × ♀ oviparous	2	
Slovenia* (4)	SLO	12	Russia, Moscow (1)	RUV	11			
			Russia, Siberia (1)	SIV	10			
<b>Total females:</b>		<b>70</b>			<b>63</b>		<b>3</b>	<b>136</b>
<b>Total by strain (♂ + ♀):</b>		<b>119</b>			<b>114</b>		<b>9</b>	<b>242</b>

\* Slovenia and NE Italy (on the surroundings of the Slovenian border).

## APPENDIX 2.

### Abbreviation, Description, and Methods of Measure or Calculation of the 21 Variables Used

Abbreviation	Description of the variable	Information about the used method of measure or calculation
<b>Measurements</b>		
1 SVL	Snout to vent length	From the tip of the snout to cloacal opening with strongly stretched lizard.
2 Ltrn	Length of the trunk	=SVL – Hnl
3 Hnl	Head + neck length	From the tip of the snout to collar (included)
4 Hw	Maximum head width	
5 Lpil	Length of the pileus (assimilated to head length)	From the tip of the snout to the posterior part of the occipital plate
6 Wpil	Pileus width	Measure in the middle of the parietal plates
7 Hhd	Maximum head height	
8 Ltal	Length of the complete anterior limb	>From the junction with the body to the tip of the longer finger (4 <sup>th</sup> ), the claw being excluded. The limb stretch and perpendicular to body
9 Ltpl	Length of the complete posterior limb	Length of the complete posterior limb measured as for Ltal
10 Lpl	Length of the posterior limb	=Ltpl – L4F
11 L4F	Length of the fourth finger of the posterior limb	The claw is excluded

Abbreviation	Description of the variable	Information about the used method of measure or calculation
<b>Pholidosis characters</b>		
1 <b>Dor</b>	Number of dorsal scales along a longitudinal line from the beginning of the tail to head plates	The starting point for counting (beginning of the tail) correspond to two rows before the posterior limb
2 <b>SDos</b>	Series of dorsal scales counted along a transversal line at mid-body	The frequently observed “dorsoventral” scales are not counted
3 <b>Vent</b>	Number of ventral scales along a longitudinal line, up to the collar	The starting point for counting correspond to the first row that clearly shows four sub-rectangular ventral scales
4 <b>Coll</b>	Number of collar scales	
5 <b>Gula</b>	Number of gular scales along a longitudinal line, between the collar and the chin plates	
6 <b>FPM</b>	Mean number of femoral pores	=Arithmetic mean of the numbers from the left and the right limb
7 <b>La4M</b>	Mean number of lamellae under the 4 <sup>th</sup> finger of the posterior limbs	=Arithmetic mean (left/right). If one finger was destroyed, we used the remaining unilateral value
8 <b>SciM</b>	Mean number of supraciliar plates	=Arithmetic mean of the left and right counts
9 <b>LbM</b>	Mean number of labial scales between the subocular scale and the rostral scale	=Arithmetic mean of the left and right counts
<b>Index</b>		
<b>D<sub>10</sub></b>	Masseteric index ≈ Mean diameter of the masseteric shield of an animal for which Lpil = 10 mm	See references of the measure in Guillaume (1988)

**Note.** Bold, abbreviations of the 19 independent variables used in cluster and discriminant analyses.