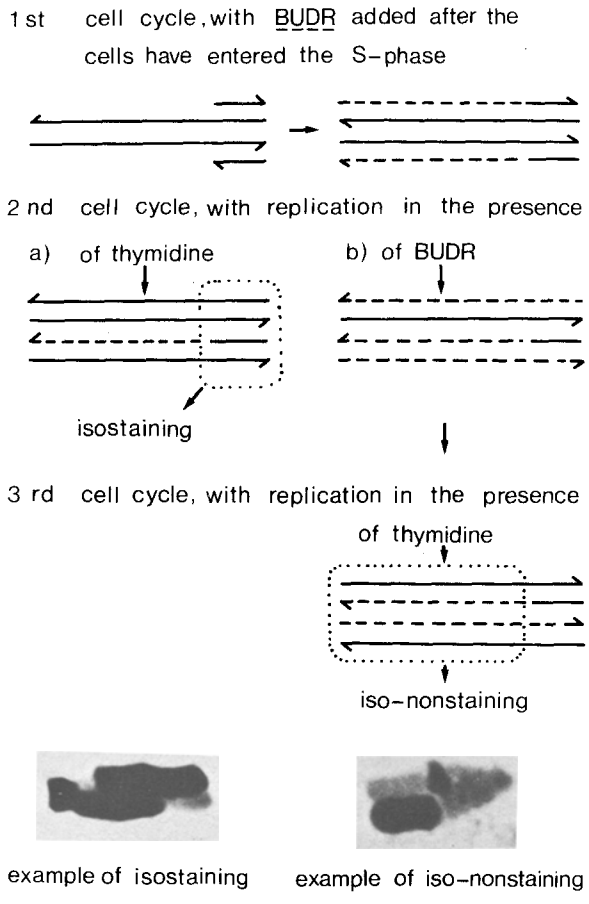


Origination of isostaining and iso-nonstaining, respectively. Full line: chromatid without BrdUrd, broken line: chromatid with one BrdUrd-substituted DNA strand. *a* Possible mechanism of origination of 'isostaining' after BrdUrd incorporation; *b* possible mechanism of origination of 'iso-nonstaining' after BrdUrd incorporation.

occurrence of isostaining in these cells can be explained according to the scheme shown in the figure a. On the other hand, the phenomenon of iso-nonstaining could result from a faster cycling (e.g. 16 h) of some cells, i.e., cells that have passed the period of DNA synthesis more than once during the 17 h of BrdUrd application (figure, b). With respect to isolabelling observed autoradiographically, Wolff et al.[10] arrived at a similar interpretation. Crossen et al.[2] also reported iso-nonstaining in cells exposed to BrdUrd for more than 2 cell cycles. Additionally, it may be possible that fast cycling cells pass, prior to the last DNA-replication period in thymidine, 2 DNA-replications which are only incompletely covered by the time period of BrdUrd application. Under these circumstances, the late replicating sections of the 1st cell cycle, and the early replicating sections of the 2nd, may incorporate BrdUrd. If chromosome regions which had incorporated BrdUrd during both cell cycles overlap, isostaining or iso-nonstaining may occur after an additional cell cycle in thymidine. The differences in the frequency of appearance of isostaining and iso-nonstaining between slides from different individual roots (ranging from 0 to 24%) support our interpretation, since significant deviations of cell cycle parameters have been found to occur also between individual roots[6].

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## Karyotypic variation in Chilean lizards of the genus *Liolaemus* (Iguanidae)

Madeleine Lamborot, A. Espinoza and E. Alvarez[1]

*Departamento de Biología, Facultad de Ciencias, Casilla 653, Universidad de Chile, Santiago (Chile), 17 November 1978*

*Summary.* Most of 12 taxa karyotypes retain 6 pairs of metacentric macrochromosomes (primitive), but show reduced numbers of microchromosomes (2n = 34, 32 and 30). Others show increased diploid numbers due to macrochromosomal fissions (up to 4 fissions, 2n = 40). One shows a fission polymorphism.

Among karyotypically well-studied lizard families, iguanids show a great range of chromosomal diversity, largely due to Robertsonian mutations[2,3]. Most iguanid genera are small and retain primitive 2n = 36 patterns (12 metacentric macrochromosomes, 24 microchromosomes)[2,3], while most of the variability is concentrated in the 3 especially large genera, *Anolis, Sceloporus,* and *Liolaemus*[3]. The first 2 genera are well-known cytologically, but *Liolaemus* is poorly documented. Karyotypes are published for only 3 species, all with 2n = 34: *L. pictus* and *L. cyanogaster* from Chile[4], and *L. lutzae* from Brazil[5]. Unpublished evidence[6] suggests that *Liolaemus* 2n's may range from 30 to 40. Since more than 60 species of *Liolaemus* are found in Chile[7], many of them endemic, a survey of their chromosomal variability should be of considerable interest. Here we summarize results for 12 species and subspecies. Details will be published elsewhere.

Table 1 lists the species[8] and localities sampled. Voucher specimens actually are deposited in the collection of the laboratory of Cytogenetics of Facultad de Ciencias, Universidad de Chile. Chromosomes were prepared from bone marrow, spleen and testis of colchicine-treated animals using the well-known air-dried cell suspension technique[9]. Slides were stained with Giemsa. For each specimen, selected metaphases were photographed with a Leitz Ortholux microscope and several karyotypes analyzed.

Table 2 summarizes our results. Interspecific, intersubspecific and intrapopulation variations in chromosome numbers are documented. 2n's in the sample range from 30 to 40, due to changes in both macrochromosomes and

microchromosomes. For example, the 2n = 34 *L. lemniscatus* has 22 microchromosomes. Other species with 2n = 32, and with 2n = 30, respectively, have 20 and 18 microchromosomes. Note that *L. chilensis* shows intraspecific variation in microchromosome number. Although the most conspicuous variation among the first 8 species (table 2) involves differences in microchromosome numbers, some variation also occurs in the shapes of the pairs of No. 7 and No. 8. This will be described elsewhere. Conspicuous macrochromosomal modifications are found in *L. nigromaculatus* and *L. monticola*. All individuals of 3 subspecies of *L. nigromaculatus* have 8 pairs of acrocentric macrochromosomes, but retain the metacentric condition for the first 2 pairs[2,3]. They also have 20 microchromosomes to produce a 2n of 40. *L. monticola* shows complex intraspecific variation. *L. monticola chillanensis* retains a relatively conservative 2n = 32, with the standard 12 macrochromosomes and 20 microchromosomes. *L. monticola monticola* differs strikingly and also shows intrapopulation variation. Both populations sampled are characterized by 24 (not 20) microchromosomes and appear to be polymorphic for macrochromosomal modifications: 2–4 metacentric macrochromosomes (pairs 3 and/or 4 in the standard macrochromosomal configuration) are replaced by 4–8 acrocentrics. 2 individuals show only 5 acrocentrics (variant 3, table 2), in all the cells analyzed. Thus 2n's in *L. monticola monticola* range from 38 to 40 in the different variants.

Based on this initial survey, *Liolaemus*, like other speciose iguanid genera[3], seems to demonstrate extensive karyotypic variation. The first 8 species from table 2, plus the 3 published earlier[4,5], appear to retain a relatively primitive karyotype. The 6 pairs of macrochromosomes in this pattern are similar in size and shape to those of the 2n = 36 pattern believed to be primitive in iguanids[2,3]. 2n = 34 species differ from this ancestral configuration by reducing the number of microchromosomes by one pair, probably by centric fusion. Further reductions in 2n probably also involve centric fusions, as supported by the fact that pairs 7 and/or 8 in 2n = 32 and 30 karyotypes are intermediate in length between the usual microchromosomes and the smaller macrochromosomes. Increased 2n's in *L. monticola monticola* and in *L. nigromaculatus* can be explained by centric fissions of 1–2 pairs of macrochromosomes in *L. monticola monticola* and of 4 pairs of macrochromosomes in *L. nigromaculatus*. It is possible, but not confirmed, that the odd karyotype of variant 3 resulted from meiotic malassortment in a parent which was heterozygous for one of the fissions (i.e., with a variant 2 karyotype). Meiotic assortment has not yet been examined.

Strikingly, the overall pattern of chromosomal variability in *Liolaemus* closely resembles patterns of variability in *Anolis*

Table 1. Species and localities of our samples of *Liolaemus*

| Species, subspecies | Locality |
|---|---|
| 1. *L. lemniscatus* | Campus Facultad de Ciencias, prov. Santiago, 580 m |
| 2. *L. nigroviridis minor* | Lagunillas, prov. Santiago, 1850 m |
| 3. *L. altissimus altissimus* | Rio San Francisco, prov. Santiago 1400 m; Lagunillas, prov. Santiago, 1850 m |
| 4. *L. gravenhorsti* | El Monte, prov. Santiago, 450 m La Pintana, prov. Santiago, 790 m |
| 5. *L. tenuis tenuis* | Campus Facultad de Ciencias, prov. Santiago, 580 m; San Alfonso, prov. Santiago, 1500 m; La Ermita, prov. Santiago, 1400 m |
| 6. *L. chilensis* | El Monte, prov. Santiago, 450 m San Alfonso, prov. Santiago, 1500 m; Cerro La Virgen, prov. Valparaíso, 335 m |
| 7. *L. fuscus* | La Ermita, prov. Santiago, 1400 m |
| 8. *L. monticola chillanensis* | Termas de Chillán, prov. Ñuble, 1750 m |
| 9. *L. monticola monticola* | San Alfonso, prov. Santiago, 1500 m; La Ermita, prov. Santiago, 1400 m |
| 10. *L. nigromaculatus zapallarensis* | Quintero, prov. Valparaíso, 6 m |
| 11. *L. nigromaculatus kuhlmani* | Los Vilos, prov. Coquimbo, 10 m |
| 12. *L. nigromaculatus (sieversi* or *ater)* | La Pampilla, prov. Coquimbo, 20 m |

Table 2.

| Species, subspecies | No. of individuals karyotyped | No. of macrochromosomes | No. of microchromosomes | Karyotype description* |
|---|---|---|---|---|
| 1. *L. lemniscatus* | 15 | 12 | 22 | 2n = 34, 12V + 22 m |
| 2. *L. nigroviridis minor* | 6 | 12 | 22 | 2n = 34, 12V + 22 m |
| 3. *L. altissimus altissimus* | 10 | 12 | 20 | 2n = 32, 12V + 20 m |
| 4. *L. gravenhorsti* | 8 | 12 | 20 | 2n = 32, 12V + 20 m |
| 5. *L. tenuis tenuis* | 10 | 12 | 20 | 2n = 32, 12V + 20 m |
| 6. *L. chilensis* | 10 | 12 | 18 or 20 | 2n = 30 or 32, 12V + 18 or 20 m |
| 7. *L. fuscus* | 6 | 12 | 20 | 2n = 32, 12V + 20 m |
| 8. *L. monticola chillanensis* | 14 | 12 | 20 | 2n = 32, 12V + 20 m |
| 9. *L. nigromaculatus zapallarensis* | 9 | 20 | 20 | 2n = 40, 4V + 16I + 20 m |
| 10. *L. nigromaculatus kuhlmani* | 4 | 20 | 20 | 2n = 40, 4V + 16I + 20 m |
| 11. *L. nigromaculatus* ssp. | 4 | 20 | 20 | 2n = 40, 4V + 16I + 20 m |
| 12. *L. monticola monticola* | 24 (Loc. A = 16; loc. B = 8)** | | | |
| Variant 1 | | 14 | 24 | 2n = 38, 10V + 4I + 24 m |
| Variant 2 | | 15 | 24 | 2n = 39, 9V + 6I + 24 m |
| Variant 3 | | 14 | 24 | 2n = 38, 9V + 5I + 24 m |
| Variant 4 | | 16 | 24 | 2n = 40, 8V + 8I + 24 m |

* V: Metacentric or submetacentric macrochromosomes. Pair 2 is submetacentric with a satellite on the long arm in all individuals examined. I: Acrocentric or subacrocentric macrochromosomes. ** Loc. A: San Alfonso; loc. B: La Ermita.

and *Sceloporus*. Each genus includes several more or less independent sequences of Robertsonian derivation, some involving fusions and others involving fissions. Also, as seen here in *L. monticola monticola* fissioning sequences in these other genera frequently involve Robertsonian polymorphisms as well as differences fixed between species (e.g. *Sceloporus grammicus*[11,12], *Anolis monticola*[13,14] and *Anolis grahami*[15]). The great morphological differences between these 3 genera and the strong geographic barriers which separate the Chilean *Liolaemus* from all other genera with similarly derived karyotypes, argue against any attempt to claim that karyotypes other than the 2n=34 or 36 are primitive in the *Liolaemus* radiation. Rather, we think that the similar patterns of karyotypic variation among these genera suggest that they evolved in similar ways under the control of similar evolutionary circumstances[3].

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## Intersubspecific sex chromosome difference in *Citellus citellus* L. (Rodentia, Sciuridae)

R.G. Belcheva and D.Ts. Peshev[1]

*Department of Genetics, Faculty of Biology, University of Sofia (Bulgaria), 23 June 1978*

*Summary.* The autosomal karyotypes of all subspecies studied of *Citellus citellus* from Bulgaria do not differ. The X chromosome, by contrast, is different in 1 of the subspecies where it seems to have undergone a pericentric inversion.

The species *Citellus citellus* L. is represented in Bulgaria by 4 subspecies[2,3]: *C.c. balcanicus* Markov, *C.c. martinoi* Peshev, *C.c. lascarevi* Martino, *C.c.* ssp. *nova* Markov. Zivkovic et al.[4,5], and Savic et al.[6] have described the karyotypes of *C.c. citellus*, *C.c. balcanicus* and *C.c. lascarevi*. These authors do not mention any chromosomal differences between these subspecies. Specimens from the most Eastern population of *C. citellus* (Moldavia - USSR), whose subspecific position is not established, had a karyotype identical to that of the subspecies from the Balkans[7]. From the published data, it appears that there are no differences in the various subspecies of *C. citellus* concerning the number and the morphology of autosomes as well as the morphology of the sex chromosomes (2n=40, $NF^a$=66).
We have studied the karyotype of different populations of *C. citellus* from Bulgaria by means of the bone marrow

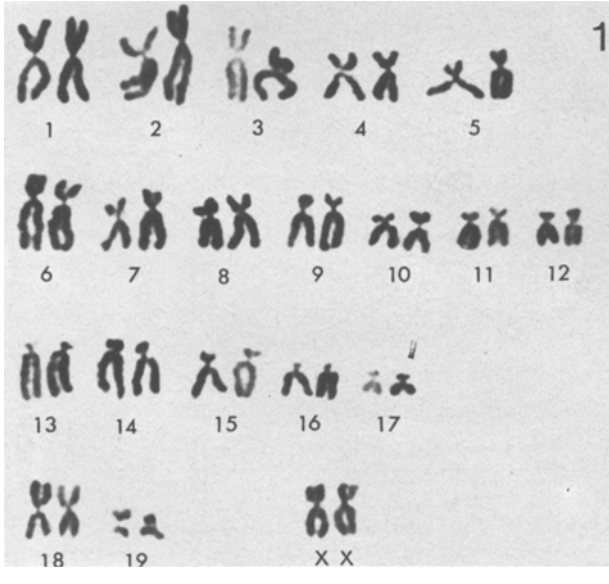


Fig. 1. Representative karyotype of *C.c. balcanicus* female.

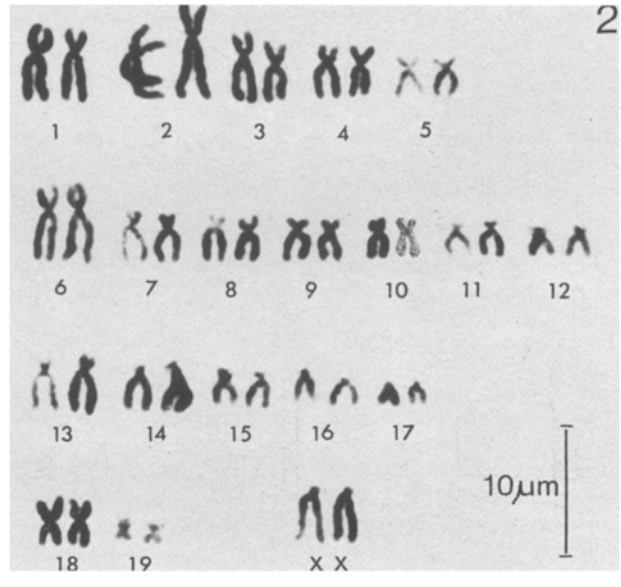


Fig. 2. Representative karyotype of *C.c. lascarevi* female.