karyotype evolution in particular lineages, most notable rearrangements of karyotypes occurred in several species-rich genera, particularly within the genus *Anolis*, *Liolaemus* and *Sceloporus*. Nevertheless, the number of chromosomes exhibits a strong phylogenetic signal even within these genera further supporting relatively high conservatism in karyotypes in this group. Although the squamate reptiles are remarkably variable in sex determination systems, only genotypic sex determination is known in iguanids. Wherever identified, sex chromosomes are only of the type XX/XY or of derived multiple sex chromosome system $X_1X_1X_2X_2/X_1X_2Y$. Many species possess yet unidentified, probably poorly differentiated sex chromosomes. The phylogenetic analysis strongly suggests several independent evolutionary origins of the multiple sex chromosomes within iguanids.

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Sex chromosome evolution in the lizard *Iberolacerta monticola* (Boulenger, 1905): karyological characterization of endemic Spanish populations.

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Lizards, with their astonishing diversity of sex determining modes and sex chromosome systems, constitute one of the most intriguing groups to study the origin and evolution of vertebrate sex determination.
Iberian Rock lizard species of genus *Iberolacerta* provide an opportunity to assess some of these questions, as these closely related taxa exhibit sex chromosomes at various stages of differentiation, ranging from cryptic to highly heteromorphic ZW chromosomes and even multiple chromosome systems ($Z_1Z_1Z_2Z_2$ / Z_1Z_2W).
Iberolacerta monticola populations from the North of the Iberian Peninsula were first reported to lack heteromorphic sex chromosomes. However, a preliminary study in an isolated population of this species identified a highly heterochromatinized female-specific chromosome. To further investigate this apparent intraspecific variability, we conducted a comparative cytogenetic analysis of these populations based on conventional (Ag-NOR, C-banding and fluorochrome staining) and molecular (FISH of major ribosomal genes and telomeric sequences) techniques. The results obtained certainly revealed the presence of a cytologically distinguishable ZW pair in both populations, that apparently show differences in W chromosome morphology. These findings shed light on the evolutionary mechanisms underlying karyotype and sex chromosome differentiation in lacertid lizards.

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Phylogenetic analysis of the karyotype evolution in geckos (Squamata: Gekkota)

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Gekkota is the species-rich and diverse group of squamate reptiles with almost global distribution. Recently, a new hypothesis about phylogenetic relationships within the group was proposed based on molecular data. We utilized it for the reconstruction of trends in karyotype evolution in geckos. We conducted phylogenetic analysis of published data about the gecko karyotypes (altogether available to us in 162 species) by Maximum likelihood and Maximum parsimony method. We corroborated that the ancestral karyotype number was $2n=38$. In the basal lineages (families Diplodactylidae, Carphodactylidae and Pygopodidae), there is a relatively high conservatism in chromosome numbers, although chromosomal rearrangement connected with shifts in centromere positions were rather frequent. In contrast, more phylogenetically derived lineages (families Eublepharidae, Sphaerodactylidae, Phyllodactylidae and Gekkonidae) possess large variability in chromosome numbers, which documents much higher frequency of interchromosomal rearrangements. A notable trend in karyotype evolution in Gekkota is the shift from the ancestral acrocentric to metacentric chromosomes. Another interesting feature of the group is the incredible variability in sex