

SHORTER CONTRIBUTIONS: HERPETOLOGY

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KARYOTYPE OF THE CUBAN LIZARD *CRICOSAURA TYPICA* AND ITS IMPLICATIONS FOR XANTUSIID PHYLOGENY.—Although described nearly 130 years ago, the xantusiid lizard *Cricosaura typica* is very poorly known, due largely to its occurrence in a remote region of eastern Cuba. Previous studies of xantusiid relationships have been hampered by the absence of chromosome data for this monotypic genus, which is morphologically distinct and geographically isolated from other members of the family (Bezy, 1972; Crother et al., 1986). Through a cooperative agreement between Pennsylvania State University, the Cuban Museum of Natural History, and the University of Havana, one of us (SBH) was able to travel to the eastern region of Cuba and secure eight animals, two of which were returned alive to the laboratory for karyotyping.

These animals (USNM 305440 and 305441), both females, were collected 2.8 km north of Uvero in Santiago de Cuba province. They were injected intraperitoneally with a 0.1% solution of colchicine (0.2 ml/g body weight) and were sacrificed by cryotherapy after six hours. Intestine, spleen, and gonads were removed and minced in a hypotonic (0.8%) sodium citrate solution; the cells were recovered and fixed in methanol-acetic acid (3:1). Slides were prepared using the splash technique (Macgregor and Varley, 1988), stained with a 0.4% Giemsa stain in a potassium phosphate/sodium phosphate buffer, and mounted.

It has been noted previously that xantusiid lizards have a low level of mitotic activity (Bezy, 1972). We recovered only a few mitotic spreads that appeared to be complete (two for animal 305440; three for 305441), possibly due to the fact that bone marrow was not used. Although the chromosomes from animal 305440 are slightly more condensed, the karyotypes obtained from each animal are consistent in number and morphology (Fig. 1). There are 12 macrochromosomes and 12 microchromosomes in the diploid complement, with a total of 36 chromosome arms. The macrochromosomes are similar in size. Pair 1 is submetacentric, pairs 2 and 5 are subtelocentric, and pairs 3, 4, and 6 are metacentric (following the centromere clas-

sification of Bezy, 1972). The microchromosomes vary in size, with two larger pairs, an intermediate pair, and three smaller pairs.

All other species of xantusiid lizards that have been examined have a larger chromosome complement, in both chromosome and arm number. The four species of *Xantusia* studied have a diploid number of 40 (18 macrochromosomes), whereas the eight species of *Lepidophyma* studied have either 36 or 38 chromosomes (16 or 18 macrochromosomes), except for an individual with triploid cells in a unisexual population of *L. flavimaculatum* (Bezy, 1972, 1984). In addition, both genera have a pair of metacentric chromosomes that are much larger in size than any other in the complement; the remaining chromosomes are fairly similar in size and are predominately subtelocentric. The terminal satellite that appears on pair 3 in some species of *Lepidophyma* and *Xantusia* was not seen in any of the *Cricosaura* spreads. Because of the differences in karyotype morphology between *Cricosaura* and these genera, it was not possible to determine homology between the individual chromosomes. Therefore, *Cricosaura* could not be placed in the karyotype phylogeny proposed by Bezy (1972). However, by comparison with taxa outside the Xantusiidae, some phylogenetic information can be obtained from the *Cricosaura* karyotype.

Most workers agree that the Iguania (Agamidae, Chamaeleontidae, and Iguanidae) is the sister taxon to the remaining squamates (Estes et al., 1988; Presch, 1988; Schwenk, 1988). The karyotype formula of 12 macrochromosomes and 24 microchromosomes occurs in each of the families comprising the Iguania. This formula also is found in members of the Anguillidae, Teiidae, and Cordylidae (karyotype numbers of dibamids, snakes, and amphisbaenids are not considered here because of their uncertain relationships [Estes et al., 1988]). Because of this broad distribution among lizard families, including a number of basal lineages (as determined by morphology), the 12 + 24 formula has been considered to represent the primitive lizard karyotype (Gorman, 1973; Bickham, 1984; Olmo, 1986). This has been challenged by King (1981) who proposed that the primitive karyotype consisted of a large number of acrocentric chromosomes and that karyotypic evolution occurs mainly through fusion, with

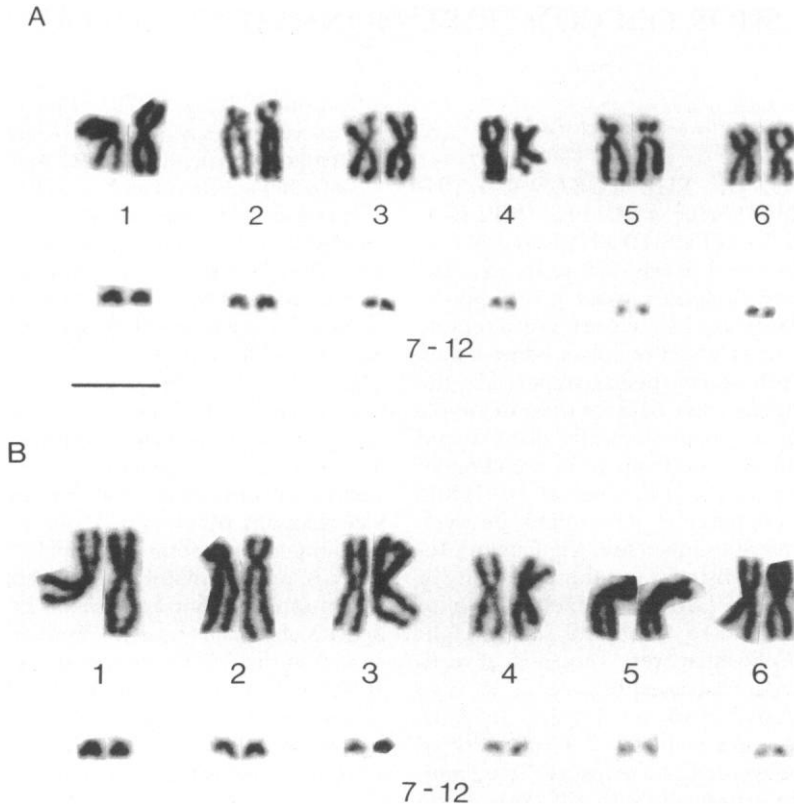


Fig. 1. Karyotypes of two female *Cricosaura typica*: (A) USNM 305440; (B) USNM 305441. The scale bar represents 10 μm .

fission playing a minimal role. The number of macrochromosomes in *Cricosaura* (12), is not inconsistent with the first hypothesis, although its karyotype has fewer microchromosomes (12) than does the proposed primitive karyotype.

Based upon morphological data, the family Xantusiidae most recently has been placed in the Scincomorpha, either as a member of the Lacertoidea, the sister group to the Teiidae/Gymnophthalmidae/Lacertidae clade (Estes et al., 1988), or as the sister group of the Scincidae (Presch, 1988). A sister-group relationship to the Gekkota has also been suggested (Schwenk, 1988). Although the members of the Gekkota appear to have a unique and highly derived karyotype (most chromosomes are acrocentric and there is no clear differentiation between macro- and microchromosomes), all the scincomorph (Lacertoidea + Scincoidea) families except the Lacertidae (Gorman, 1970) have taxa with a chromosome complement consisting of 12 or 10 bi-armed macrochromosomes. The taxa

with that karyotype are often considered to be basal within their respective groups (Deweese and Wright, 1970; Olmo and Odierna, 1980; Capriglione, 1987), lending support to the hypothesis that the primitive number of macrochromosomes is 12, as seen in *Cricosaura*.

A recent analysis of the relationships within the Xantusiidae using DNA sequence data from two mitochondrial genes (Hedges et al., 1991) found that *Cricosaura* is the basal clade within the family and the sister group to *Xantusia* + *Lepidophyma*, rather than the sister group of *Lepidophyma* (exclusive of *Xantusia*) as suggested by an analysis of morphological data (Crother et al., 1986). The karyotype data are consistent with the phylogeny derived from DNA sequence data. The karyotype of *Cricosaura typica* could have been transformed into that of the other genera through a series of fissions that reduced the macrochromosomes and gave rise to additional macrochromosomes and microchromosomes. Other information indicating

chromosome homology, such as banding, is needed to further illuminate chromosome evolution within the Xantusiidae.

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FREEZE TOLERANCE AS AN OVERWINTERING ADAPTATION IN COPE'S GREY TREEFROG (*HYLA CHRYSOSCELIS*).—Many temperate zone ectotherms are confronted with severe environmental challenges during winter. Aquatic forms usually are protected from freezing temperatures owing to the high thermal buffering capacity of water. Terrestrial vertebrate ectotherms generally avoid extreme winter temperatures by hibernating within insulated refuges below the frostline; however, some may be exposed to potentially lethal environmental temperatures. Those overwintering above the frostline must survive either by extensive supercooling or by tolerating the formation of ice within body tissues.

Deep and prolonged supercooling is a major overwintering adaptation of many terrestrial invertebrates (Lee, 1989). However, the biophysical constraints of large body mass (i.e., water volume) preclude this strategy for most verte-