

MAPPING OF MICROSATELLITE SEQUENCES IN TWO LIZARDS FROM
THE TUPINAMBINAE SUBFAMILY (SQUAMATA, TEIIDAE)

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Abstract:

The Teiidae family (Reptiles, Squamata) has two subfamilies and includes lizards with oviparous reproduction and wide distribution in Brazilian biomes. Karyotypic studies in this group are still scarce and show that the species of the subfamily Teiinae presents $2n$ ranging from 46 to 56 while the subfamily Tupinambinae with $2n$ between 34 to 38. Furthermore, a clear distinction between macro and microchromosomes is observed only in Tupinambinae. These data are mostly based on classical cytogenetic analyses. Thus, the present work aimed to analyze the karyotype of two species of the Tupinambinae subfamily (*Crocodylus amazonicus* and *Tupinambis teguixin*), applying both classical and molecular cytogenetic techniques, in order to better understand the genomic organization and karyotypic evolution of this group. For this, we performed conventional staining, C-banding, and Fluorescent in Situ Hybridization (FISH) experiments using probes corresponding to microsatellite sequences. The specimens were captured using pitfall traps installed in two municipalities in the state of Pará (Abaetetuba and Moju). The species *C. amazonicus* presented a $2n=34$ with 12 macrochromosomes and 22 microchromosomes while we observed $2n=36$ in *T. teguixin*, with 12 macrochromosomes and 24 microchromosomes. C-banding revealed constitutive heterochromatic blocks in the centromeric region of the chromosomes, showing a similar pattern in both species, corroborating previous data. FISH experiments using microsatellite probes (CAG, GAA, GAG and CGG), showed a distinct accumulation of these sequences between macro and microchromosomes in both species. For *C. amazonicus*, expressive signals were evidenced in the pericentromeric regions of the macrochromosomes with the probes CAG, GAA, CGG and telomeric signals in the macrochromosomes with GAG. On the other hand, all microchromosomes showed conspicuous signals for all probes used. In *T. teguixin*, the centromeric regions of the macrochromosomes showed intense signals for GAA, few visible signals for CAG, and also in the secondary constrictions of pair 2 and pericentromeric of pair 5. In addition, we observed telomeric signals for GAG, similarly to *C. amazonicus*. Parallel to what was exposed for *C. amazonicus*, all microchromosomes also showed signals for the all the probes used. These results show distinct distribution and frequencies for the different sequences mapped, evidencing an active participation of microsatellites in the karyotypic evolution of the family. New findings that complement these results will allow a better understanding of the dynamics of repetitive sequences in the genomic organization of these animals.

Palavras-chave: Teiidae; chromosomes; repetitive sequences; ;

Support / Acknowledgment

FAPESPA IFPA CAMPUS ABAETETUBA INSTITUTO EVANDRO CHAGAS