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IDENTIFICATION AND CHARACTERIZATION OF SATELLITE DNA CONTENT IN XENARTHRA SPECIES WITH SEQUENCED GENOMES

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RESUMO

The Xenarthra superorder has species with some of the largest genomes among mammals. Nevertheless, repetitive DNAs, which make a significant portion of eukaryotic genomes (>50%), are still poorly studied in Xenarthra. Satellite DNAs (satDNAs) represent one of the main classes within this genomic fraction, being characterized by abundant tandemly repeated sequences organized in large arrays that can extend up to hundreds of Mb. They are major components of centromeric and telomeric heterochromatin and tend to evolve very rapidly in comparison with other genomic sequences. Despite their importance in shaping eukaryotic genomes, only one satDNA sequence has been identified in a Xenarthra species (Dasypus novemcinctus). Here, we used in silico and cytogenetic analyses to identify and characterize the satDNAs from species within this superorder. First, we ran the RepeatExplorer pipeline in the sequenced genomes of Choloepus didactylus and C. hoffmanni available on GenBank. By running this pipeline, which identifies repetitive DNAs by clustering similar sequence reads, we identified two putative satDNA sequences in the C. didactylus and C. hoffmanni genomes (named SATCHO1 and SATCHO2). Searches using SATCHO1 and SATCHO2 as queries against the Repbase and GenBank databases did not reveal similarity with any previously described DNA sequence. SATCHO1, the most abundant putative satDNA in both species (comprises about 13% and 2.6% of C. didactylus and C. hoffmanni genomes), is composed of ~ 117 bp monomers, and SATCHO2, the second most abundant (comprises about 0.62% and 0.23% of C. didactylus and C. hoffmanni genomes), is composed of ~ 2,292 bp monomers, which is an unusual size for satDNAs. Fluorescence in situ hybridization experiments revealed that SATCHO1 and SATCHO2 overlap with CBG bands in the (peri)centromeric constitutive heterochromatin of all C. hoffmanni chromosomes, except the X. These results confirmed that both repetitive sequences have features of satDNAs. Moreover, we identified typical features of centromeric sequences in both satDNAs, such as dyad symmetries, which are thought to promote non-B DNA structures like stem-loops and cruciform. BLAST searches in the Whole Genome Shotgun (WGS) database and PCR experiments revealed the presence of SATCHO1 in Bradypus variegatus and Myrmecophaga tridactyla. However, SATCHO1 was shown to exist as large tandemly repeated arrays only in the Choloepus species. We are currently working on the identification and characterization of satDNAs in the sequenced genomes of the anteaters M. tridactyla and Tamandua

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tetradactyla in order investigate the evolution and distribution of these repetitive sequences in different Xenarthra species. Having all results in hand, we also expect to understand how satDNAs have contributed for shaping the genome of this basal eutherian group.

PALAVRAS-CHAVE: Chromosomes, F I S H , Heterochromatin, RepeatExplorer, Repetitive DNAs.

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