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Physical location of satellite DNA I family in *Peromyscus eremicus* (Rodentia, Cricetidae)

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In eukaryotic genomes, there are sequences whose functions are not yet been well established, namely the satellite DNA sequences (satDNA). Due to the abundance of these sequences in the majority of mammalian genomes and the importance of the roles assigned to them (e.g., involvement in centromere evolution and function, heterochromatin formation and organization, and probably in chromosomal evolution), satDNA are important targets for genomic studies. This work aimed to analyze a family of satellite DNA—satellite DNA I (satDNA I)—from *Rattus norvegicus* (RNO; Rodentia, Muridae) genome in a phylogenetically distant species, *Peromyscus eremicus* (PER; Rodentia, Cricetidae), through its isolation and physical mapping. We succeeded in isolating this satDNA I family (or variant) from PER genome by PCR amplification with specific primers. The isolated sequence was physically mapped on PER chromosomes by fluorescence in situ hybridization (FISH), followed by sequential C-banding to confirm the eventual distribution of this sequence in constitutive heterochromatin. All these procedures were also carried out in RNO genome, used as control. Physical mapping, with species-specific satDNA I family in PER, showed that it seems to be localized at the peri(centromeric) regions and/or at the heterochromatic p-arms of PER chromosomes. In RNO chromosomes, satDNA I family is localized at the peri(centromeric) regions of the majority of autosomic RNO chromosomes, being absent from the sex chromosomes. The presence of this satDNA family in two different Rodentia families suggests that it was already present in their common ancestor, having at least 23.3–24.7 Mya (divergence time between Cricetidae and Muridae). SatDNA I

family seems to change slowly with the course of evolution, reflecting, probably, the involvement in a specific and important genomic function.
Keywords: Satellite DNA I family, Rattus norvegicus, Peromyscus eremicus, FISH