An orthologous satellite DNA family between Muridae and Cricetidae (Rodentia)

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Satellite DNA (satDNA) sequences seem to be located at genomic regions prone to chromosome rearrangements, and it is believed that, somehow, their dynamic nature promotes chromosomal evolution. SatDNA sequences are a common feature of higher eukaryotes and in a given genome several unrelated satDNA families may coexist. Each of these families is usually confined to one or more groups of phylogenetically related species, but some of them can be found in phylogenetically distant species, suggesting evolutionary conservation. The highly repetitive DNA component—the satellite I (satI) family, from the laboratory rat (*Rattus norvegicus* (RNO; Rodentia, Muridae)), is composed of tandemly repeated 370 bp monomers. In the present study we succeeded in isolating this satDNA family (or variant) from a RNO phylogenetically distant species—*Cricetus cricetus* (CCR; Rodentia, Cricetidae). Physical mapping, with species-specific satI probe, showed a different genome distribution in the two species: while in RNO chromosomes this satDNA sequence is localized at the peri(centromeric) regions of some RNO chromosomes, in CCR genome this satDNA sequence variant displays an interstitial distribution. SatI sequence seems to change slowly with the course of evolution. We suggest a (peri)centromeric location of this satellite DNA family in the Muroidea ancestral karyotype and, in the course of CCR genomic evolution, the evolutionary rearrangements reshuffled its genomic location.