

Are genomes doomed to repeat? Why?

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Repetitive DNAs are, most likely, the genetic factors responsible for promoting genomic plasticity and therefore higher rates of chromosome mutation (Slamovits and Rossi 2002; Adega et al. 2009). Different authors suggested a key role for satellite DNA (satDNA) in the origination of chromosome alterations thought to depend, among other factors, on the ability of the repetitive DNA to change its copy number and to mobilize through the genome (Chaves et al. 2003; Adega et al. 2008, 2009; Louzada et al. 2008). Chromosome rearrangements would have low effects on the euchromatic genome by keeping syntenic segments intact since the breakpoints occur in repetitive DNA blocks. Moreover, satellite DNAs and their transcripts seem to have an active regulatory role in eukaryotic organisms; chromatin modulation and control of gene expression are some of the traits in which satellite DNAs could be involved. Here, special emphasis will be given to the “hallmarks” that constitute true evidences of the involvement of heterochromatic regions and satellite DNA in the evolution of chromosomes and in genomes’ remodelling. The value of satellite DNA as model for chromosome rearrangements and implications in function will be highlighted with examples from various mammalian groups such as Cetartiodactyla, Rodentia and Carnivora.

References

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