



genes



Special Issue Reprint

Repetitive DNA Sequences

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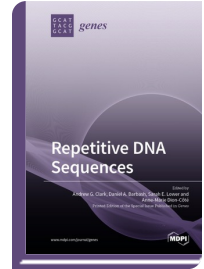
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Repetitive DNA is ubiquitous in eukaryotic genomes, and, in many species, comprises the bulk of the genome. Repeats include transposable elements that can self-mobilize and disperse around the genome, and tandemly-repeated satellite DNAs that increase in copy number due to replication slippage and unequal crossing over. Despite their abundance, repetitive DNA is often ignored in genomic studies due to technical challenges in their identification, assembly, and quantification. New technologies and methods are now providing the unprecedented power to analyze repetitive DNAs across diverse taxa. Repetitive DNA is of particular interest because it can represent distinct modes of genome evolution. Some repetitive DNA forms essential genome structures, such as telomeres and centromeres, which are required for proper chromosome maintenance and segregation, whereas others form piRNA clusters that regulate transposable elements; thus, these elements are expected to evolve under purifying selection. In contrast, other repeats evolve selfishly and produce genetic conflicts with their host species that drive adaptive evolution of host defense systems. However, the majority of repeats likely accumulate in eukaryotes in the absence of selection due to mechanisms of transposition and unequal crossing over. Even these neutral repeats may indirectly influence genome evolution as they reach high abundance. In this Special Issue, the contributing authors explore these questions from a range of perspectives.



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