



Repetitive DNA Sequences in Eukaryotic Genomes

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Message from the Guest Editors

A large fraction of every eukaryotic genome is composed of noncoding DNA sequences existing in many copies. They are associated with many important biological functions, in defining the entire genome landscape, building centromeres and telomeres, participating in genome rearrangements, modulating gene expression, and being essential in genome resilience and evolution. Rapidly developing sequencing technologies, accessibility to datasets and novel bioinformatics strategies enabled studying the repeatomes and the satellitomes, while single-molecule sequencing technologies can elucidate long-range sequential order of tandem repeats. Cytogenetic experiments are valuable in studying repetitive DNA sequences on a chromosomal level, and phylogenetic approaches make possible tracing their evolutionary history across many taxa. Novel approaches combined with the classical studies, lead to better understanding of a genome/chromosome structure and evolution, and open possibilities for functional studies of these mysterious sequences.





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Message from the Editor-in-Chief

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