

Special Issue on
**Cytogenomic and Bioinformatic Approaches to
Understand Repeat Profiles in Eukaryotic Genomes**

CALL FOR PAPERS

Difficulties in sequencing and assembly of long arrays composed of highly similar tandem repeats have resulted in the fact that those sequences are seriously underrepresented in genome sequencing outputs, either due to the challenges posed by their assembly, or due to their masking by genome annotation pipelines. With the advent of new sequencing technologies, several bioinformatic tools have emerged that aid our understanding of the dark side of genomes (repetitive regions). This has enabled the field of chromosome research (cytogenetics) of model and mainly nonmodel organisms to enter the era of cytogenomics, which combines bioinformatic analyses of genomes and cytogenetics. Additionally, phylogenomic repeat-based approaches have made it possible to trace the evolutionary history of many organisms, as these sequences can exhibit extraordinary preservation throughout long evolutionary periods.

We invite researchers to contribute original articles as well as reviews exploiting advances in the emerging field of cytogenomics (and related approaches) to study evolutionary, functional, and structural aspects of repetitive DNA in eukaryotic genomes. Special interest is in works showing the use of high-throughput technologies to gain further knowledge, for example, regarding tandem repeats and transposable element evolution, in order to shed light on the different repeat profile patterns found in eukaryotes, both from the molecular to the chromosomal level.

Potential topics include but are not limited to the following:

- ▶ Application of high-throughput sequencing (HTS) to investigate genome repeat profiles
- ▶ Repeat-based phylogenomic inference approaches
- ▶ Cytogenomic approaches to understand repeat evolution in eukaryotic genomes
- ▶ Tandem repeat structure and evolution (include tandemly repeated genes)
- ▶ Transposable elements from molecular to chromosomal level
- ▶ Presence of the same nucleotide sequence in the form of tandem and interspersed repeats (interconnectedness of satellite DNAs and mobile elements)
- ▶ Repeat profiles helping differentiating genomes (i.e., genome-specific repeats, B chromosomes, sexual chromosomes, and hybrids)
- ▶ Impact of repetitive families (i.e., LTR retrotransposons) on genome size variation
- ▶ Genome plasticity of repetitive fraction in correlation with environmental variability/ecological traits
- ▶ New bioinformatic tools aiding in identifying and characterising genomic repeat profiles
- ▶ Comparison of available bioinformatic tools for repeat identification and characterisation
- ▶ Combining different *in situ* and *in silico* methods in the process of repeat identification and characterisation

Authors can submit their manuscripts through the Manuscript Tracking System at <https://mts.hindawi.com/submit/journals/ijg/cbau/>.

Papers are published upon acceptance, regardless of the Special Issue publication date.

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Submission Deadline

Friday, 28 September 2018

Publication Date

February 2019