Preface

Eukaryote genome complexity exceeds far beyond the sheer number of genes and genome size. Several ways to generate biological complexity include expansion of tandem and dispersed repetitive DNAs, segment duplications, gene family expansions, and whole-genome duplications. As a result, a large fraction of many eukaryotic genomes is represented by redundant DNA sequences. Ranging from simple repetitive sequences and amplified genes to whole chromosomes and extra-copies of genomes, redundant genomic parts contribute to overall genome complexity, setting up a challenge for their analysis and assemblies. The evolution of the redundant genomic fraction is highly dynamic and varies across different taxa. However, the organisms have elaborated many strategies to protect themselves from nonessential DNAs or to control them that include strict and programmed systems to eliminate repetitive elements, chromosomes, and chromatin in different species as well as epigenetic silencing. Effects of redundant DNA dynamics include many well-known genetic disorders, but in a long-term perspective, there are many evolutionary advantages, including genomic innovations.

For their article, Araújo et al. [2021] isolated the SINE-B1 mobile element from the South American spiny rat *Proechimys gr. goeldii* and analyzed its chromosomal distribution in three different karyomorphs. The authors detected enrichment of the repeat density at the pericentromeric regions of most chromosomes, including the elements involved in chromosome rearrangements (chromosome 1, sex chromosomes). The authors suggest that SINE-B1 may play an important role in the karyotypic variation by increasing the genome plasticity. Torgunakov et al. [2021] studied enigmatic homogeneously staining regions (HSR) of mouse chromosome 1, resulted from amplification of long-ranged repeated DNAs (~100-kb-long repeat units). They showed that HSRs despite their heterochromatic nature are involved in meiotic recombination, which contributes to considerable heterochromatic block variation ob-

served in natural populations of *Mus musculus*. Felicetti et al. [2021] demonstrate the enrichment of telomeric repeats and relatively low number of (GATA)_n sites in heterochromatic B chromosomes of the driftwood catfish *Trachelyopterus*. Ivanova et al. [2021] provide new evidence on how the tandemly arranged DNA repeats are organized and packed in the nuclei of pig and hamster. Bishani et al. [2021] employed NGS technology to characterize the most abundant tandemly arranged repetitive elements in several cyprinoid species, demonstrate their presence in B chromosomes of *Carassius gibelio*, and elucidate on the association between repeated DNA accumulation and polyploidization in fishes. A special focus was given to sex-chromosome evolution in Tago's brown frog complex by Kuwana et al. [2021] and to the karyotype evolution in murine cancer cell lines by Piaszinski et al. [2021] as well as in human uterine leiomyoma [Koltsova et al., 2021]. Dynamics of U2 small nuclear RNA clusters have been described in several frog species of the *Leptodactylus* genus [Gazoni et al., 2021].

Overall, in this Special Issue, we present original research manuscripts with a special focus on genome redundancy and karyotype evolution of fishes, amphibians, and mammals, manifested on several levels (abundance of various repetitive elements, appearance of extra-chromosomes and extrachromosomal DNA, and polyploidization). It seems that although new developing methods and technologies revolutionize genomics, so many trends in redundant DNA dynamics are yet to be discovered.

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