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Decoding the Genomic Evolution of Pathogenic Eukaryotes Through Integrated Multi-Omics Approaches

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Deadline for manuscript submissions:
closed (20 August 2024)

Message from the Guest Editors

Dear Colleagues,

Global initiatives, such as The Earth BioGenome Project (EBP), are working to expand and accelerate the development of genomic resources encompassing all extant eukaryotes. Advances in high-throughput sequencing technologies, coupled with robust computational and machine learning approaches, are revolutionizing our understanding of molecular mechanisms that drive the diversification of life.

In this Special Issue, we invite scholarly contributions, including review articles and original research, that focus on exploring the evolution of eukaryotic pathogens. Emphasis should be placed on harnessing the potential of multi-omic technologies and innovative tools capable of capturing changes in the genomic architecture, as well as precisely tracking fluctuations in transcriptomic, proteomic, epigenomic, and metabolomic perturbations. Undoubtedly, the insights derived from these technologies will significantly enrich our understanding of infectious diseases and open new avenues for solutions in public health and agriculture.

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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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