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Whole-Genome Sequencing and Population Genomics of Parasitic Infections

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Deadline for manuscript
submissions:

closed (25 November 2020)

Message from the Guest Editor

Parasitic diseases contribute substantially to the global burden of disease. In the absence of vaccines, the prevention of these parasitic diseases relies solely on chemotherapy. Thus, there is an urgent need to broaden therapeutic horizons against these parasitic infections, and to do so, we need to have comprehensive knowledge of their life cycles, their genomes, and their population genetic structures. This understanding is critical to evaluating the impact of transmission methods in fixing and spreading important genes related to virulence and drug resistance through populations. With the advent of next-generation sequencing (NGS), comparative genomics has revolutionized our understanding of the architecture of parasitic genomes and how they are evolving and establishing within the population, including the role of asexual versus sexual recombination in this process. Hence, the overarching theme of this Special Issue is the recent advances in NGS, comparative genomics, and evolution analysis that have accelerated the field's progress in understanding population genomics and in developing new therapeutics against these parasitic diseases.



mdpi.com/si/44917

Special Issue



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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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