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Virus Evolution and Mutagenesis

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Deadline for manuscript submissions:
closed (30 June 2020)

Message from the Guest Editors

Experimental evolution has immensely benefited from the study of viral evolution. Viruses have relatively rapid replication rates, which allows for the quantitative study of mutational processes and their impact on evolutionary rates, natural selection and population diversity. In particular, RNA viruses are known to exhibit high mutation rates and generate virus quasispecies, which harbor populations of closely-related genomes (i.e., mutant swarms or clouds) that lends to direct experimentation of fitness selection, adaptation, and virus evolution in connection with viral pathogenesis. The parallels between viral quasispecies and that of tumor cell heterogeneity and dynamics have also led to deeper insights into both areas of investigation.

This Special Issue on "Virus Evolution and Mutagenesis" seeks author contributions on topics that include replication fidelity, virus mutagenesis, mutation rates, population complexity, insights from deep sequencing, error thresholds, lethal mutagenesis, mutation-selection balance, recombination, fitness landscapes, mutational robustness, virus complementation/interference, and tumor cell heterogeneity and dynamics.

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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving 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. Why not consider *Genes* for your next genetics paper?

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