Special Issue

Genomic Epidemiology of SARS-CoV-2

Message from the Guest Editor

Tracking viral diversity has been useful in understanding viral evolution, transmission dynamics, clinical manifestations and reinfections; and in subsidizing public health policy. The SARS-CoV-2 pandemic has led to an unprecedented viral genomic surveillance effort and increased global sequencing capacity. Although more than 1000 lineages have already been described, SARS-CoV-2 diversity gained major focus after the World Health Organization designated the variants of interest (VOIs) and variants of concern (VOCs). A Special Issue of *Genes* entitled “Genomic Epidemiology of SARS-CoV-2” is receiving manuscripts exploring the epidemiological aspects of SARS-CoV-2 diversity and its impacts throughout the pandemic.

Guest Editor

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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?

Editor-in-Chief

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