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Molecular Phylogenetics and Phylogeography of Seed Plants

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Message from the Guest Editor

With the rapid development of sequencing technology, the cost of acquiring genomic sequences has decreased dramatically. Consequently, large amounts of genomic data for seed plants have been generated in recent decades. Thus, we have encountered an excellent opportunity to conduct research at the genomic level on the phylogenetics and phylogeography of seed plants. Genome-scale phylogenetic analyses, or phylogenomics, can yield greater confidence of inferred phylogenetic relationships with little systematic bias, which is usually difficult in analyses using one or several gene sequences. Unlike phylogenomics, it is still a challenge for phylogeographic researchers to use population NGS data due to the difficulty of inferring haplotypic data from short reads sequences. Fortunately, programs with specific algorithms, such as BEAGLE and SHAPEIT, have been developed and can be used to impute and accurately phase population genomic data. This Special Issue will provide an overview of recent developments in this field of research, including critical perspectives on current and upcoming challenges.



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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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