Special Issue

Molecular Phylogenetics and Phylogeography of Seed Plants

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 phylogenic 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.

Guest Editor

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Deadline for manuscript submissions

closed (25 September 2023)

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Impact Factor 2.8
CiteScore 5.5
Indexed in PubMed

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