Special Issue

Molecular Evolutionary Genetics Analysis in Forest Trees

Message from the Guest Editors

The forest tree genome has a complex structure, including a large number of repetitive sequences. It also exhibits high levels of heterozygosity and polymorphism, which collectively influence genetic variation and evolution. With the development of biotechnology, more and more new technologies and methods are being applied. These technologies and methods provide strong support for a deeper understanding of the genetic variation and evolution of forestry. The application of molecular evolutionary genetics in forestry is very extensive, including, but not limited to, forest tree breeding, biodiversity conservation, ecosystem restoration, etc., which not only has important values for understanding the adaptive evolution, population dynamics, and phylogenetic relationships of forestry, but also plays a guiding role in forest breeding and improvement. Potential topics include, but are not limited to:

- Gene mutations and variations in forestry;
- Genetics and evolution of forestry populations;
- Evolutionary genetics analysis of forestry genomes;
- Molecular markers and genetic linkage maps in forestry;
- Evolution analysis of key gene families in forestry.

Guest Editors

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Forests (ISSN 1999-4907) is an international and cross-disciplinary, scholarly forestry journal. The distinguished editorial board and refereeing process ensures the highest degree of scientific rigor and review of all published articles. Original research articles and timely reviews are released online, with unlimited free access. Our goal is to have *Forests* be recognized as one of the foremost publication outlets for high quality, leading edge research in this broad and diverse field. We therefore invite you to be one of our authors, and in doing so share your important research findings with the global forestry community.

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