Special Issue

Genome-Wide Identification and Expression Analysis for the Genetic Improvement of Forest Plants

Message from the Guest Editors

With the rapid development of molecular biology and genomics, genetic breeding has become an efficient way to improve the quality and productivity of forest plants. Genome-wide identification and analysis of genes related to various important traits is essential for the genetic improvement programs of forest plants. Recent advances in high-throughput sequencing technologies have enabled us to gain insights into the genetic mechanisms that underlie growth traits in forest plant species. Multiple sequencing technologies with increased accuracy have also allowed us to perform more accurate identification of functional genes. We would like to announce this Special Issue, which will concentrate on articles focused on accurate genomewide identification and expression analysis of genes related to growth traits in various types of forest plants with ecological or economic importance. Studies concerned with the improvement of identification methods, population-level functional diversity analysis, or functional verification of candidate genes are most welcome.

Guest Editors

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Message from the Editor-in-Chief

Forests (ISSN 1999-4907) is an international and crossdisciplinary, 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.

Editor-in-Chief

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