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

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Deadline for manuscript
submissions:

13 December 2024

Message from the Guest Editors

Dear Colleagues,

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 genome-wide 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.

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Guest Editors



mdpi.com/si/154987

Special Issue



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