Special Issue

Genomics and High-Throughput Phenotyping to Characterize Forest Genetic Resources for Conservation and Breeding

Message from the Guest Editors

The advancements of technology in genomic and high-throughput phenotyping tools is creating new opportunities and challenges for the characterization of forest genetic resources (FGR). The information obtained by the use of these tools separately, but most preferably in an integrated manner, will constitute a basis for assessing the genetic and adaptive variation levels of FGR, the representativeness of their conservation efforts so far, their in situ and ex situ conservation needs, their resilience to biotic and abiotic factors, as well as their potential for use in forest tree breeding programs.

The aim of the Special Issue is to compile and present cutting-edge studies which focus on the use of genetic/genomic and high-throughput phenotyping methods in order to monitor and characterize FGR in terms of distinctiveness and genetic/adaptive variation. The development of such techniques will allow the detection of conservation gaps, as well as the identification of genetic resources that could be of significance for conservation and/or breeding programs.

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Deadline for manuscript submissions

closed (31 December 2023)



Forests

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Impact Factor 2.5 CiteScore 4.6



mdpi.com/si/171153

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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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