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THE CONTRIBUTION OF GENETICS AND GENOMICS TO THE CONSERVATION OF TREE GENETIC RESOURCES

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The recent development of new high-throughput sequencing and genotyping techniques has revolutionized the way we now do population and evolutionary genetics, with application to the conservation and sustainable management of forest genetic resources. Nowadays, even for non-model species, hundreds if not thousands of genes are easily sequenced, providing new tools to evaluate adaptive variation at the molecular level and to study demographical processes with a resolution that was unattainable just a few years ago. However, identification of the relevant genes is still a daunting challenge, as many forest tree species have large, complex genomes (for instance, those of conifers), and robust inferences rely on large sample sizes and association genetic studies based on multisite common garden tests, which are difficult to establish and maintain. In this talk, we review recent progress in this topic and identify active fields of research for the coming years. We also describe the main uses of these new genetic and genomic resources for the conservation and management of forest tree genetic resources, including the identification and definition of conservation genetic units, the monitoring of changes in genetic diversity due to environmental or human-induced pressure and the development of tools for tree origin certification and ‘assisted migration’. Finally, we present a cautionary tale about the use and misuse of genomic tools in sustainable forest management. Although our case studies focus on Mediterranean species, the conclusions drawn are far reaching and can be directly applied to other forest trees.

Keywords: conservation, forest trees, genomics, genetic resources, high-throughput genotyping, management