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Sommario/riassunto

Forest tree genetics and genomics are advancing at an accelerated rate, thanks to recent developments in high-throughput, next-generation sequencing capabilities, and novel biostatistical tools. Population and landscape genetics and genomics have seen the rise of new approaches implemented in large-scale studies that employ the use of genome-wide sampling. Such studies have started to discern the dynamics of neutral and adaptive variation in nature and the processes that underlie spatially explicit patterns of genetic and genomic variation in nature. The continuous development of genetic maps in forest trees and the expansion of QTL and association mapping approaches contribute to the unravelling of the genotype-phenotype relationship and lead to marker-assisted and genome-wide selection. However, major challenges lie ahead. Recent literature suggests that species demography and genetic diversity have been affected both by climatic oscillations and anthropogenically induced stresses in a way calls into question the possibility of future adaptation. Moreover, the pace of contemporary environmental change presents a great challenge to forest tree populations and their ability to adapt, taking into consideration their life history characteristics. Several questions emerge that include, but are not limited to, the interpretation of forest tree genome surveillance and their structural/functional properties, the adaptive and neutral processes that have shaped forest tree genomes, the analysis of phenotypic traits relevant to adaptation (especially adaptation under contemporary climate change), the link between epigenetics/epigenomics and phenotype/genotype, and the use of genetics/genomics as well as genetic monitoring to advance conservation priorities.
