

Abstract

Forest genetic monitoring in a biodiversity hotspot

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Abstract: Genetic monitoring of forest trees are of the utmost importance for securing the maintenance of species adaptive potential. Genetic monitoring, the quantification of temporal changes in population genetic variation and structure, introduces prognosis and assists in defining tools for the management of genetic resources. Forest genetic monitoring (FGM) becomes imperative in biodiversity hotspots, such as Greece, one of the most species-rich European countries, where >7000 native plant taxa (~20% endemics) exist, and 28% of its land base is included in the Natura 2000 Special Areas of Conservation network. Moreover, (meta-)analyses of genetic data have shown that Greek forest tree populations present significantly higher values of polymorphism and differentiation when compared to average values reported in the international literature [2]. FGM studies in Greece involve *Abies borissi regis*, *Castanea sativa*, *Fagus sylvatica*, *Quercus petraea*, *Quercus robur*, *Pinus nigra* and *Prunus avium*. FGM uses the genecological approach and employs 11-26 SSR loci in different cohorts (mature and juvenile trees), while the average time interval between assessments is 12.9 years. Results so far for *A. borissi regis* and *Fagus sylvatica* indicate maintenance of genetic diversity over time, but a slight drop of N_e in the juvenile cohort of hybrid fir compared to the mature trees.

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