

GENOME-WIDE SNP ASSOCIATION ANALYSIS REVEALS GENOMIC SIGNATURE OF LOCAL ADAPTATION IN EUROPEAN BEECH (FAGUS SYLVATICA L.)

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climate adaptation, Fagus sylvatica, candidate genes association analysis, Single Nucleotide Polymorphism (SNPs), abiotic stress

Local adaptation is one of the essential evolutionary mechanisms that allow species to thrive in heterogeneous environments. Understanding the dynamics and mechanisms of local adaptation in natural populations provides the basis for predicting responses to environmental changes, including those associated with global climate change. Local adaptation is expected to alter the allele frequencies of genes that influence fitness in particular environments. Local adaptation is best studied in long-lived sessile organisms with large effective populations covering large and variable environments such as forest trees. European beech (*Fagus sylvatica* L.) is one of the most economically and ecologically important deciduous trees in Europe, yet little is known about its genomic adaptive diversity and its adaptive potential. The adaptation potential of beech to climate change has been widely discussed. Although beech is considered a sensitive tree species in the context of projected environmental changes, some authors conclude that beech will not lose its importance and adaptive capacity in the future. However, changes in beech marginal populations have already

been observed, and several modelling studies predict range shifts of this species in the context of global warming. Therefore, a deeper understanding of its potential to adapt to changing environmental conditions is needed. In this study, using a candidate gene approach, we investigated the association between SNPs and environmental factor variation in 12 beech (*Fagus sylvatica* L.) populations located in 5 different biogeoclimatic regions and subjected to different silvicultural regimes. This work presents for the first time the results of the study of genetic differentiation among European beech populations in different management conditions, presumably associated with adaptation to different climatic conditions, based on a pooled analysis of many bioclimatic variables, together with a large number of genetic markers, single nucleotide polymorphisms (SNPs). In total, 5,143 SNPs were genotyped in 194 individuals. Among them, both climate region-specific and population-specific polymorphisms were observed. Association analyses are currently in progress. Four different methods (PCAdapt, LFMM, BayeScEnv and RDA) were used for the analyses to observe a correlation between SNPs and variation in some environmental factors and presumably associated with local adaptation.