

BOOK OF ABSTRACTS

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Genomic variation of European beech across its distribution range reveals patterns of local adaptation and future maladaptation

T3.8 Forest genomics as a vantage point to biodiversity and adaptation under global change

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Abstract: Local adaptation is key for ecotypic differentiation and species evolution. Understanding the underlying genomic patterns allows the prediction of future maladaptation and ecosystem stability. We used whole-genome resequencing to analyze more than 1000 individuals from 100 range-wide populations of European beech (*Fagus sylvatica*), one of the most important forest tree species in Europe. We show that genetic variation closely mirrors geography. Putatively adaptive variation identified by genotype-environment and genotype-phenotype associations exhibits highly polygenic architectures, involving thousands of associated sequence variants across the genome. By modelling the ‘genomic offset’ of these sequence variants under projected future climate conditions, we identify broad- and fine-scale variation highlighting geographic regions as well as populations at potential elevated risk of mortality or local extinction. Our results emphasize the importance of considering natural genetic variation within species for forest conservation under climate change.