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EFFECT OF THE INTERACTION BETWEEN GENE FLOW AND SELECTION ON LOCAL ADAPTATION: A CASE STUDY IN COMMON BEECH (*FAGUS SYLVATICA* L.)

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Plant species can respond to climate change by 1) migrating through seed dispersal to follow the shift in their present bioclimatic range, 2) adapting genetically to the new environment or 3) adjusting their phenotype through plasticity. Because trees are long lived and have high pollen/seed dispersal abilities, they are expected to use a combination of all of these strategies. For instance, when selection pressures are spatially heterogeneous we expect local adaptation of populations, with high level of gene flow counteracting these process by continually bringing maladapted genes. However, in the context of climate change, gene flow may bring pre-adapted genes. Populations distributed along altitudinal gradients represent a good opportunity to study the interaction between gene flow and selection in the development of local adaptation. In this study we examined the evolutionary potential of a common beech population (*Fagus sylvatica* L.) along an altitudinal gradient on Ventoux, France. The aim is to highlight genetic variations in quantitative traits potentially adaptive in the context of global warming, such as bud burst phenology, wood density and leaf morphological/physiological traits involved in carbon fixation. We present some initial *in-situ* heritability estimates based on the correlation between phenotypic traits and relatedness relationships estimated with molecular markers. We then quantified the level of contemporary gene flow within populations using parent–offspring genetic and spatial data analysis, in the frame of parentage analyses and spatially explicit mating model. This approach allowed us to estimate 1) the shape and the range of the dispersal curve for pollen and seed in common beech (mean dispersal of pollen = 42 m, mean dispersal distance of seeds = 15 m) and 2) the effect of various phenotypic traits potentially affecting male/female fecundity on relative reproductive success. Ultimately, the selection and dispersal processes experimentally characterized will be integrated in an individual-based simulation model to jointly analyse the respective roles of selection and gene flow in the evolution of quantitative traits.

Keywords: *Fagus sylvatica*, gene flow, local adaptation