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GENETIC SIGNATURE OF A 150-YEAR-OLD POPULATION BOTTLENECK IN *FAGUS SYLVATICA* DESPITE RAPID POPULATION EXPANSION

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A major expected consequence of climate change is altitudinal and latitudinal shifts in the geographic ranges of plant species. These shifts and the associated demographic fluctuations have been shown to have pervasive consequences for genetic diversity. For instance, imprints of postglacial recolonization events on genetic structure can still be observed after millennia and at the continental scale. However, explicit empirical tests of how specific contraction/expansion processes may shape patterns of genetic diversity remain scarce. In particular, there are few studies addressing these processes at the scale at which dispersal and expansion actually take place and at which management guidelines are required, i.e. at the local scale and over several generations. This study takes advantage of a unique opportunity to investigate recolonization dynamics and their consequence for population genetic diversity in European beech (*Fagus sylvatica* L.) on Mont Ventoux, France, at an intermediate spatial and temporal scale employing a combination of historical records and genetic data. From the 12th century to the mid-18th century human activities reduced the beech forest on Mont Ventoux to a few remnant stands, whereupon forest management policy and practices changed to favour expansion of beech forest. Analyses of historical forest maps and management documents showed that beech refugia were not as scarce as has been reported. Since 1876 beech forests have expanded by as much as 65%, moving at an average rate of 35 to 42 m/year. Current patterns of genetic diversity and differentiation were investigated using 1825 individuals in 51 plots from three regions on Mont Ventoux genotyped at 13 microsatellite markers. The strongest differentiation was between plots ($F_{\text{plots}}^{\text{total}} = 3.5\%$), with a surprisingly low level of differentiation between zones ($F_{\text{zone}}^{\text{total}} = 0.9\%$). Isolation by distance was detected up to 750 m. The approximate Bayesian computation (ABC) method for estimating the probabilities of demographic scenarios based on microsatellite data supported the hypotheses of a bottleneck between 160 and 300 years ago, consistent with historical data. Hypotheses to explain the absence of differentiation between the northern and southern slope despite the bottleneck are discussed.

Keywords: bottleneck, colonisation, DIY-ABC, genetic structure, microsatellite