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VARIABLE PATTERNS OF CONTEMPORARY GENE FLOW IN BEECH (*FAGUS SYLVATICA* L.) ACROSS EUROPE

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Common beech (*Fagus sylvatica* L.) is one of a few keystone tree species found across much of Europe. Forests dominated by beech are found over a remarkably wide range of environments and are often rich repositories of species diversity for plants, animals and microorganisms. The structuring role of beech in forest ecosystems is well recognized, even though the mechanisms underlying the ecosystems' stability and their adaptation potential are only starting to be understood. Using spatially explicit parentage models and microsatellite markers, we investigated patterns of contemporary gene flow as revealed by naturally established seedlings. The studies were conducted across a wide range of environments including natural old-growth forests in Poland, managed stands in Germany, populations in mountains in France and a low-density scattered stand in the Netherlands. Patterns of contemporary gene flow appeared to vary across populations. Pollen dispersal was similar for most of the stands (moderate pollen immigration rate, m_p=0.6, and fat-tailed dispersal kernels). However, pollen dispersal was lowest in the old-growth natural forest (low immigration rate, m_p=0.5, and an exponential dispersal kernel), while the scattered population in the Netherlands exhibited the most extensive pollen dispersal (high pollen immigration rate, m_p>0.7, and an extremely fat-tailed dispersal kernel). On the other hand, while seed dispersal was fairly restricted in natural and managed stands (low seed immigration rates and exponential dispersal kernels), it appeared to be high in one mountainous forest and the scattered population (seed immigration rate m_s>0.3 and fat-tailed dispersal kernel). Variable patterns of contemporary gene flow in beech indicate its ability to persist under climate change through migration and adaptation facilitated by gene exchange among populations. However, this potential may depend on the stand structure, as well as its age and location.

Keywords: adaptation, *Fagus sylvatica*, gene flow, parentage analysis, pollen dispersal, seed dispersal