

### **Genetic Diversity and Gene Flow of *Quercus crispula* in a Semi-Fragmented Forest Together With Neighboring Forests**

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#### **Abstract**

The genetic diversity and differentiation in *Quercus crispula* populations in the Chichibu Mountains, central Japan, were evaluated using six microsatellite markers. Gene flow into a 2500-m<sup>2</sup> semi-fragment of a natural forest from the neighboring natural forest at a distance of more than 50m was also evaluated using parentage analysis. All five populations in the mountains had similar levels of genetic diversity ( $H_e = 0.752\text{--}0.792$ ), and the level of population differentiation was low ( $F_{ST} = 0.016$ ). The semi-fragmented stand showed similar genetic diversity with the neighboring unfragmented forests, and Hardy-Weinberg disequilibrium was not found ( $F_{IS} = 0.083$  in adults, 0.025 in seedlings). In the semifragment, 70 seedlings were examined; according to the parentage analysis, eight of the 70 seedlings (ca. 11%) had neither of the parent trees in this fragment. These seeds must have been transported from a distance of more than 50 m; therefore, there could be a possibility that the seeds were dispersed by birds. A similar trend of seed flow into the fragment was also confirmed by genotyping endocarps of hypogeal cotyledons, while more frequent seed flow was found in the neighboring unfragmented forest. Of the remaining 62 seedlings, the maternal trees (but not the paternal trees) of 29 seedlings and both parent trees of 33 seedlings were detected in the semi-fragment. These results indicate that the gene flow among the populations occurs frequently via pollen dispersal and occasionally via seed dispersal and that, at least the current levels of genetic diversity have been maintained in such fragmented forests.

**Key words:** forest fragmentation, microsatellites, parentage analysis, *Quercus crispula*.