

EFFECTS OF HABITAT FRAGMENTATION ON GENETIC STRUCTURE OF BEECH POPULATIONS IN CENTRAL ITALY

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Summary

Twenty-five beech population (*Fagus sylvatica* L.) from Central Italy, representing three increasing level of fragmentation, were studied using 5 SSR markers to estimate the effect of fragmentation on genetic diversity and to investigate spatial distribution of genetic variability.

Keywords

Fagus sylvatica L, habitat fragmentation, F-statistic, spatial autocorrelation, gene flow

Contribution

An objective of an ecologically sustainable forest management is the conservation of genetic variability, a precondition for the future evolution and adaptability of local populations and species. To understand the impacts of forest management on genetic diversity is necessary to define the spatial distribution of genetic variability, the amount of gene flow and the effects of habitat fragmentation on genetic diversity.

Fragmentation has two major impact on forest: it subdivides populations in small units and imposes barriers to migration, determining profound effects on demographic and genetic structure of natural forest populations [1]. The two main consequences on genetic structure are the loss of genetic variability within each population and the higher degree of differentiation among fragmented populations [2].

During the last few decades, several authors have pointed out that a correct diagnosis of the status, threats and viability of a population needs the knowledge not only of the amount of genetic diversity but also of its spatial distribution. Genetic diversity may appear spatially structured at different scales such as population, subpopulation or among neighbouring individuals. This spatial patterns of variation is necessarily a product of the accumulated effects of migration and selection averaged over space and long periods of time [3]. Thus knowledge of spatial genetic structures provide a valuable tool for inferring these causal factor and the underlying genetic process (such as differential selective pressure, gene flow and drift).

Our goals in this research are to investigate the spatial distribution of genetic variability in fragmented populations and to estimate the effects on genetic bio-diversity of habitat fragmentation. For this purpose we studied 25 beech populations (*Fagus sylvatica* L.) from Central Italy chosen to represent three increasing level of fragmentation: near-marginal populations, remote-summit populations, remote-abyssal populations. Thirty plants per population were sampled and local coordinates were recorded for each plant. Individuals were characterized with 5 SSR markers. Analysis of polymorphism have been performed on a capillary sequencer CEQ2000 (Beckman).

By F-statistic analysis performed on genetic data, we found a significant higher F_{ST} value among near-abyssal populations (fig.1).

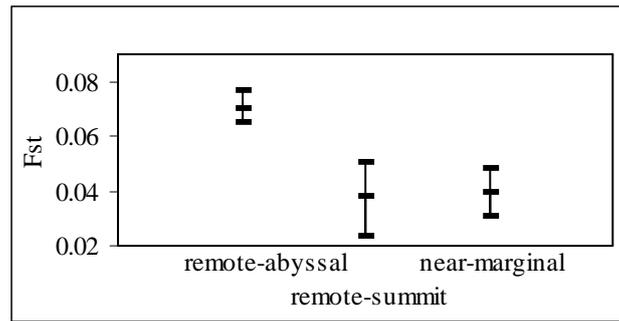


Fig1: Fst value with group of population.

The coordinates analysis performed on the pair-wise genetic matrix confirm previous results: remote-abyssal populations do not appear in a unique clear cluster, and are wide spread. Remote-summit population and near-marginal populations are less spread and are mostly found around the center of the plot. Analysis of variance on the number of alleles, on the F_{IS} and the expected heterozygosity values shows that the three groups populations (Near-Marginal, Remote-Summit and Remote-Abyssal) do not differ.

As reported from previous studies, spatial autocorrelation analysis shows a not homogeneous distribution of genetic variability. We found a tendency for a family structure in the distance classes up to 30-40 m, depending on population considered (fig.2).

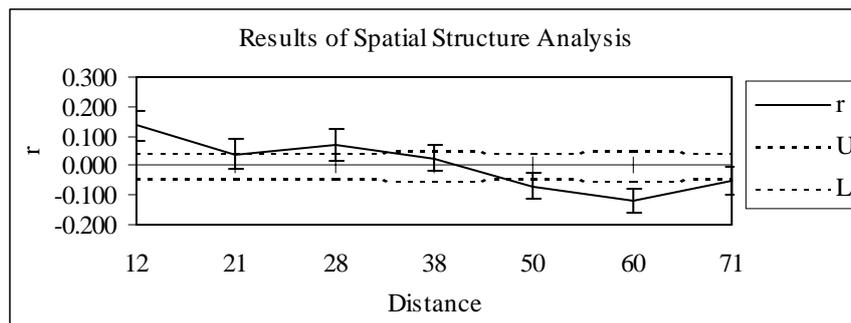


Fig2.: spatial structure averaged on all populations and all markers.

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