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Does human-induced selection influence the spatial genetic structure diversity and dynamics in beech forests?

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Background

Forest ecosystems have an "internal capacity" to adapt to environmental disturbances thanks to their genetic variability. The Italian forests are the result of a millenary coevolution between ecological and socio-economic reality. Over the time, the cultivation of the forest has led sensitive modifications to biodiversity of the stands, resulting in a reduction of their complexity.

Therefore, it is interesting to examine the relationship between the silvicultural system and the genetic variability of the forest.

Methods

This study examined the effects of silvicultural systems on the genetic diversity in two beech high forest stands in the Apennines (central Italy). To this end, we did a comparison between a even-aged stand managed by the uniform shelterwood system (named Nature Reserve of "Pian degli Ontani") and a uneven-aged stand managed with a type of single tree selection felling carried out according to traditional knowledge (named Baldo's Forest).

All trees were genotyped using four primer pairs of nSSR loci (FS1-15, FS4-46, FS1-25 and FCM5).

General estimates of genetic diversity in the stands from nSSR data were calculated using SPAGeDi 1.3a. The spatial genetic structure of the stands was analyzed by STRUCTURE program and Geneland software.

Results and Conclusions

The comparison between the two stands showed no significant differences in genetic diversity measures, while significant differences were observed on the number of rare alleles.

However, the most significant differences between the two beech forests have been detected in the spatial structure of genetic diversity.

The even-aged stand of Nature Reserve of "Pian degli Ontani" presents a structure of random type, devoid of family groups, characterized by gene flows limited in space and with low recombination rates. In contrast, uneven-aged stand of Baldo's Forest presents a spatial structure of genetic diversity grouped into families, with wide dispersion gene rates, high rates of recombination and a greater number of rare alleles.

The spatial structure of the genetic diversity found in the uneven-aged beech forest was similar to that observed in previous studies carried out in old-growth beech forests in the Apennines (see Paffetti et al., 2012 [1]).

The single tree selection felling, which is repeated at short intervals of time (every 5-6 years), seems to lead to a faster fragmentation of family groups, thus speeding up the evolutionary dynamics of the managed stand compared to the old-growth forest.

Competing interests
The author declares that they have no competing interests.

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References

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