

GENETICS OF COLONIZATION IN A TREELINE ECOTONE IN THE ALPS

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Summary

In this study we analysed gene flow and spatial genetic structure in an alpine population of Norway spruce (*Picea abies* Karst.) using molecular markers. We investigated genetic consequences of migration and colonization of old pastures at the treeline, an ecotone shifting upward because of the combined effect of climatic changes and abandonment of traditional cattle rearing in our study area (Paneveggio forest, eastern Trentino, Italy) .

Keywords

Norway spruce, treeline, genetic structure, colonization, gene flow.

Contribution

In recent years we assisted to climatic change leading to an increase of mean temperature, and this climatic change involved also Alpine area (Theurillat and Guisan, 2001). Change in land use is also evident for these areas, with abandonment of traditional cattle rearing activity. These two factors are causing a progressive shift upward of alpine treeline, the zone between the continuous mountain forest and the last isolated forest tree individuals, with colonization of old pastures by mountain conifers species like Norway spruce, European larch and European stone pine.

The study of migration at the treeline is particularly interesting because of the high selective pressure due to extreme ecological factors (temperature, wind, soil, competition, predation) affecting survival in this area (Dullinger et al., 2004).

Colonization events define the genetic characteristics of the invading populations, affecting their evolutionary potential. Gene flow represents the driving force determining genetic patterns of colonizing populations (Rogers et al., 1999).

Indirect and direct methods are available to study gene flow. Indirect methods, like Wright's *F*-statistics and spatial autocorrelation, permit to evaluate the extent of past gene flow, while direct methods, like parentage analysis, are useful to study contemporary gene flow, giving a measure of pollen and seed dispersal.

The aim of this study is to quantify the extent of gene flow in a population of Norway spruce in the upper part of Paneveggio forest (Trentino - Italy) and to evaluate the genetic origin of individuals contributing to the colonization of abandoned pastures, using both direct and indirect methods.

The studied population is located in the upper part of the Paneveggio forest. We sampled four areas at different altitudes, three in the continuous forest (1695, 1815 and 1865 meters a.s.l.), and the last across the treeline, between 1927 and 2150 meters a.s.l.. In all 1000 individuals have been sampled (200 in each of the three lower areas and 400 in the upper one).

Genetic analysis has been performed using microsatellite markers and fragments have been characterized using CEQ 8000 sequencer.

We calculated F -statistics and Nei's pairwise genetic distance matrix among areas. At a finer spatial scale, we carried out spatial autocorrelation analysis in all plots and parentage analysis in the treeline area. This area has been exhaustively sampled (all the trees, saplings and potential parents, have been collected).

Preliminary results, using 5 microsatellites, showed a very low level of F_{ST} (0.005) between plot along the altitudinal transect. The mean number of alleles per population and the mean number of private alleles are slightly higher in treeline area (Tab.1), but this result depends on different sample size, in fact no statistical differences in allelic richness have been detected. Minimum Nei's genetic distance have been found between the central of the three areas in the forest and the treeline area (0.007), but no statistical differences was found between the pairwise values. No spatial genetic structure has been detected using spatial autocorrelation analysis in the three lower plots, instead genotype clustering has been found in the treeline plot, with a patch size of 80 m. (Fig.1). Finally, investigating genetic structure of treeline area, we obtained an exclusion parentage probability (0.9988) using the general formula proposed by Grundel and Reetz (1981).

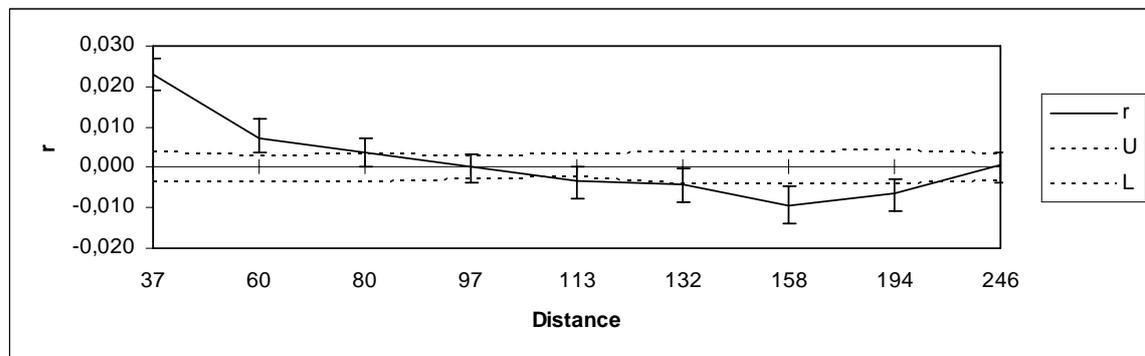


Fig.1 Treeline area correlogram calculated using Smouse and Peakall method (1999).

	VB1	VB2	VB3	VB4
Population	1695	1815	1865	Treeline
Na	12,20	13,00	12,20	14,60
Na Freq. \geq 5%	5,00	4,40	4,40	5,20
No. Private Alleles	0,60	1,00	0,60	1,40

Tab.1 Mean number of alleles, mean numbers of alleles with frequency over 5% and number of private alleles in the four subpopulations.

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