

## IDENTIFICATION OF REGIONS OF PROVENANCE IN COMMON ASH

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### Summary

Neutral DNA markers (microsatellites) were used as a tool to study genetic variability distribution of common ash in northern Italy, and to group the 31 studied populations according to their genetic similarity. The ecological characteristics of the collection sites were analysed and homogeneous regions were defined. Patterns of genetic and ecological variations were compared, allowing us to identify six areas that are both ecologically and genetically homogeneous.

### Keywords

*Fraxinus excelsior*, Genetic differentiation, Genetic variability, Propagative material, Provenance Regions

### Contribution

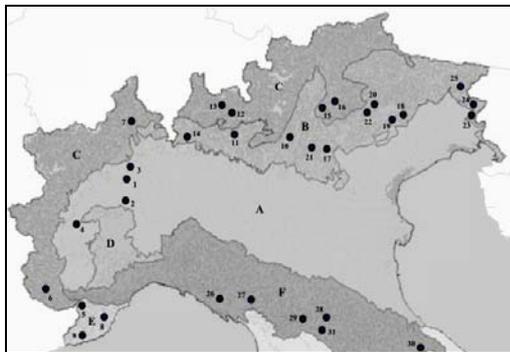
Common ash (*Fraxinus excelsior* L.) is a forest tree widespread in most of Europe. Forest management in Europe has shown increasing interest in the last 40 years, mainly due to the high demand for its quality timber. Furthermore, common ash has been recognized as a prominent element of forest ecosystems which provide substantial benefits for human society. In spite of its importance as forest tree species, the population genetics of common ash received relatively little attention and only a few European countries are managing gene conservation programmes [1]. Italian Government has recently issued the act no. 386/2003, that implements the European Council Directive 1999/105/CE, concerning the marketing of forest reproductive material. One of the most important feature of the act is the definition of Region of Provenance, that is “...*the area or group of areas subjected to sufficiently uniform ecological conditions in which stands or seed sources showing similar phenotypic or genetic characters are found...*”. The identification of Regions of Provenance is therefore a basic aspect for a rational management of activities linked with forest trees propagation, including afforestation and in situ genetic preservation [2]. Regions of Provenance should be defined according to adaptative features of the populations. However, the scoring of such characters is very difficult, due to the high demand in time and space of the needed cultivation trials. The purpose of this study was the evaluation of neutral DNA markers (microsatellites) as a tool to study genetic variability distribution of common ash in northern Italy, and to group populations according to their genetic similarity. 31 natural ash populations, representing the locations where the species grows in Italy (Tab. 1), were sampled and DNA was extracted from young leaves or winter buds. Six microsatellite primer pairs were used to detect genetic variability [3]. Levels of within and among populations variability were estimated and genetic differentiation was calculated. Additionally, the ecological characteristics of the collection sites were analysed and homogeneous regions were defined. Lastly, patterns of genetic and ecological variations were compared, in order to identify areas that are both ecologically and genetically homogeneous.

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N.	Province	Population	N.	Province	Population	N.	Province	Population
1	Vercelli	Lame del Sesia	11	Bergamo	Ponteranica	22	Treviso	Fagarè
2	Vercelli	Partecipanza	12	Bergamo	San Pellegrino	23	Udine	Chianei
3	Vercelli	Spazzacamini	13	Sondrio	Val Masino	24	Udine	Ponte Vittorio
4	Cuneo	Merlino	14	Como	Corni di Canzo	25	Udine	Preone
5	Cuneo	P. delle Gorre	15	Trento	Valle Sella	26	Parma	Alta Val Ceno
6	Cuneo	Oncino	16	Trento	V. Mocheni	27	Parma	Monte Valoria
7	Verbania	Valle Divedro	17	Vicenza	Contrada Sorto	28	Bologna	Alta Val Reno
8	Savona	V. Bormida	18	Belluno	Broz	29	Modena	S. Anna Pelago
9	Imperia	Valle Tanaro	19	Belluno	Sedico	30	Forlì	Campigna
10	Brescia	P. Spino	20	Belluno	Peaio-Vinigo	31	Pistoia	Abetone
			21	Verona	Schivazzi			

*Tab. 1: The common ash populations analysed in the study.*

Applied methodology proved to be useful to define Regions of Provenance, that are a basic aspect for an ecologically correct management of forest genetic resources. Common ash populations from Northern Italy proved to have a large genetic variability and all the examined populations showed a consistent excess of homozygotes: this can apply for an inbreeding rate much higher than the expected in one prevalently outcrossed species. Distribution of genetic variability is only partially related with geographical distances between populations; moreover genetic differentiation among populations is quite low, probably due to the lack of barrier to gene flow. The soil seems not to influence the distribution of genetic variability, while the climatic conditions appear to have a major effect. Despite the low genetic differentiation it has been possible to identify six Regions of Provenance (namely Alps with crystalline soil, Po Valley, Alps with calcareous soil, Hilly regions of Piedmont, Apennines and Ligurian mountains), sufficiently homogeneous both for ecological and genetic conditions (Fig. 1).



*Fig. 1: Provenance Regions for common ash in northern Italy. A, Po Valley; B, Alps with calcareous soil; C, Alps with crystalline soil; D, Hilly regions of Piedmont; E, Ligurian mountains; F, Apennines.*

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