

We are unable to supply this entire article because the publisher requires payment of a copyright fee. You may be able to obtain a copy from your local library, or from various commercial document delivery services.

From Forest Nursery Notes, Summer 2007

47. © Genetic variability and divergence among Italian populations of common ash (*Fraxinus excelsior* L.). Ferrazzini, D., Monteleone, I., and Belletti, P. Annals of Forest Science 64:159-168. 2007.

Genetic variability and divergence among Italian populations of common ash (*Fraxinus excelsior* L.)

Diana FERRAZZINI, Ignazio MONTELEONE, Piero BELLETTI*

University of Turin, DIVAPRA Plant Genetics and Breeding, via Leonardo da Vinci 44, 10095 Grugliasco, Italy

(Received 4 April 2006; accepted 6 July 2006)

Abstract – The level of genetic variation throughout the Italian range of common ash (*Fraxinus excelsior* L.) was estimated using six microsatellite markers. High levels of allelic diversity was detected. The levels of expected heterozygosity for each of the populations ranged from 0.726 to 0.871, with an average of 0.798, and indicated that populations have a high level of genetic variation. A general and significant homozygote excess was found at most loci in all populations, with an overall mean F_{IS} of 0.284. Possible explanations for such situations are discussed. Only 4.9% of the total diversity was attributable to differentiation among populations. Although divergence among pedo-climatic regions explained only a small part of the variance it was possible to observe some partial clustering of populations belonging to the same regions. The contribution of the results in relation to the definition of the most appropriate strategies to collect forest reproductive material is discussed.

genetic variation / microsatellite / population differentiation / seed zone designation / *Fraxinus excelsior*

Résumé – Variabilité génétique et différenciation entre populations italiennes de frêne commun (*Fraxinus excelsior* L.). Le niveau de variation génétique dans l'aire de distribution naturelle du frêne commun (*Fraxinus excelsior* L.) en Italie a été estimé à l'aide de six marqueurs microsatellite. Des niveaux élevés de diversité allélique ont été détectés. L'hétérozygotie théorique varie de 0,726 à 0,871, avec une moyenne de 0,798, ce qui indique que les populations ont un niveau élevé de variation génétique. Un excès général et significatif de l'homozygotie a été trouvé pour la plupart des loci dans toutes les populations, avec une moyenne globale F_{IS} de 0,284. Des explications possibles pour de telles situations sont proposées. Seulement 4,9 % de toute la diversité est attribuable à la différenciation entre populations. Bien que la divergence entre régions pédo-climatiques explique une petite partie de la variation, il est possible d'observer des regroupements partiels de populations appartenant aux mêmes régions. La contribution de ces résultats à la définition des stratégies les plus appropriées pour rassembler le matériel forestier de reproduction est discutée.

diversité génétique / microsatellite / différenciation entre populations / région de provenance / *Fraxinus excelsior*

1. INTRODUCTION

Forest trees are non-mobile and long-lived organisms which grow under environmental conditions that are heterogeneous in time and space. Moreover, they are exposed to many stress factors, most of which are due to human activities: pollution, climate change, habitat fragmentation. In order to survive these threats, and to persist over time, a high adaptive potential is needed: this is mainly determined by the within-species genetic diversity [4, 46]. Programmes aimed at the conservation of forest genetic resources should address the issue of maintenance of this diversity [21, 31, 35, 47]. To this end, knowledge of genetic variation, as well as information on mating system and pollen and seed dispersal, are of the utmost importance. Molecular markers are now available and can provide us with the relevant means to acquire information on the genetic structure of populations and to study the pattern of distribution of within-species variability. In particular, simple sequence repeats (SSRs, also known as microsatellites) are commonly used in genetic studies of plant populations. SSRs are tandem repeats of short DNA sequences (1 to 6 base pairs); they are highly polymorphic, widely distributed throughout

the genome and codominant. Allelic variation can be detected quickly by the DNA-polymerase chain reaction (PCR) technique.

Common ash, *Fraxinus excelsior* L., is a postpioneer heliophilous tree species which grows in mixed deciduous forests all over Europe, from the Atlantic Ocean to the Don river and the Caucasian mountains, and from the southern part of Scandinavia to the Mediterranean Sea. It is a colonizing species, often found with a spatially discontinuous distribution in mixtures with other trees. However, when ecological conditions become very favourable it can be encountered in pure stands. The species has a complex mating system, showing variation in sex expression from pure male to pure female individuals, and with all kinds of hermaphroditic intermediates [17, 29, 37]. Pollen and fruits (samaras) are wind-dispersed. According to fossil pollen data obtained by Huntley and Birks [26], the species expanded in the Early Holocene from the northern Apennine and from the northern and north-western Black Sea coasts. Heuertz et al. [24] also suggested the eastern Alps and Iberian Peninsula as further refuge areas.

A number of research groups have recently undertaken studies on this species all over Europe [1, 5, 6, 10, 22, 23, 25, 27, 29], and several European Union projects have

* Corresponding author: piero.belletti@unito.it