AFLPs TO ASSESS THE CONTROVERSIAL STATUS OF *POPULUS ALBA L.* OF SARDINIA

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Summary
AFLP analysis on 105 *P. alba* trees, sampled from spontaneous populations of the North-West of Sardinia island, revealed a clear clonal structure, with the presence of only three genotypes geographically clustered.

Keywords
AFLP, *Populus alba*, Sardinia

Introduction
Populus alba L. is a common species of the present-day central-European and Mediterranean riparian forest. In the framework of the project *Biodiversity of Natural and Cultivated Poplar*, supported by the no profit Bussolera-Branca Foundation, a survey of AFLPs (Amplified Fragment Length Polymorphisms) and SSRs (Simple Sequence Repeats) was conducted to evaluate genetic diversity of 68 individuals of white poplar, 18 part of al larger Italian gene bank collection and 50 representative of a natural population of the river Ticino (Northern Italy). The molecular analysis demonstrated a high level of genetic variability in both cases and the presence of hybrid individuals (*P.* x *canescens*) within the population of the river Ticino [1]. On the basis of these results and on recent evidences available in literature of the indigenous status of white poplar in the western Mediterranean basin [2], we decided to extend the survey to the spontaneous populations of *P. alba* largely present in Sardinia, whose origin is still a subject for discussion.

Material and Methods
A total of 105 trees of *P. alba* were sampled in 2003 from spontaneous formations in natural and semi-natural habitat types, over a large area (ca. 2,500 km^2) located in the North-West of Sardinia, the second largest island of the Mediterranean sea. All sampled trees were labelled with a plastic tag, geo-referenced (GPS, 12 parallel channels) and coded. DNA was purified from 20 mg of dried apical shoots using the "DNeasy Plant Mini" kit (Qiagen Italia-Milano), and AFLP analysis was performed [3] using the following three primer pair combinations: E+AAC-M+ACC; E+AAG-M+ACC; E+ATC-M+AGC. Geographic coordinates of sampled trees, collection sites' features and AFLP profiles were stored on a GIS system (ESRI Arc-GIS) for further geographical visualisation and molecular analysis of the data.

Results and discussion

The AFLP analysis originated a wide array of reproducible and informative DNA bands (Fig 1), however only three different genotypes were observed among the 105 assayed *P. alba* trees and the distribution of the genotypes is somewhat clustered in the survey area (Fig. 2).
The genus *Populus* was described for the first time for Sardinia by Fara in 1580 and *P. alba* was confirmed later by Moris [4] as largely distributed on the island. The lack paleobotanical evidences of an ancient presence of *P. alba* in Sardinia, e.g. in the early Holocene, as demonstrated for southern France [2], together AFLP results raise the question about the origin status of this taxon. AFLP and geographical analyses would suggest that the present-day spontaneous population of white poplar of the North-West of Sardinia has been originated by vegetative propagation from only three ancestor genotypes. Several hypotheses on the anthropic origin of the Sardinian white poplar can be drawn. The island in fact was colonised at first by people living during the Bono Highinu and Ozieri period and later by Phoenicians and Romans, who are often considered the principal responsible for the anthropic and historical expansion of *P. alba* range in the Mediterranean basin. However many other introduction routes and periods are possible. Our molecular data, at present, cannot confirm or refuse any of the hypotheses, therefore a deeply survey at molecular level of *P. alba* populations present in the Mediterranean basin is necessary to track the origins of Sardinian white poplar. To this end, since 2004, we started a second collection campaign on south Sardinia and on other islands and sites of the Mediterranean basin.

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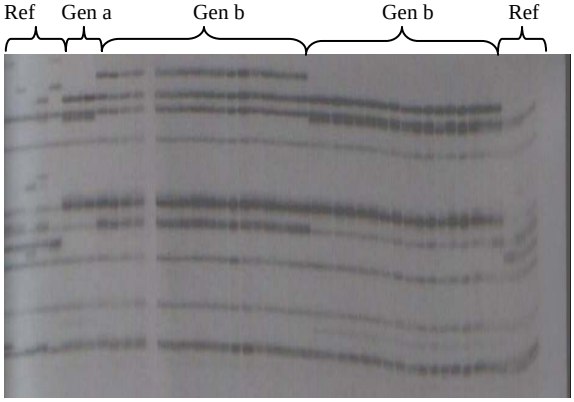

Fig. 1

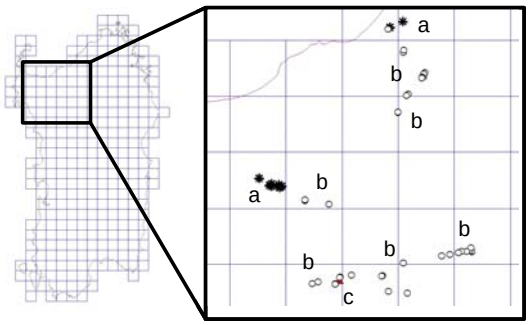

Fig. 2

Fig.1 X ray film showing AFLP genotypes a and b of *P. alba* from Sardinia

Fig 2 The distribution of the 105 *P. alba* sampled trees and of the three different genotypes (coded with the letters: a, b, c) is plotted on a UTM grid sized 10 x 10 km