The role of historical and evolutionary factors on the dynamics of forest tree populations

Silvia Fineschi[1], Francesca Bagnoli[1], G.G. Vendramin[21]

In order to understand the dynamics of forest populations we pursue two main objectives:

1. *Describing and monitoring genetic diversity*. Monitoring can be done at different geographic and spatial scales and addresses both neutral and adaptive traits;
2. *Identification of key factors shaping the genetic diversity*. We consider both **past factors** (by addressing post-glacial history) and **current and future factors** (by studying mating system, gene flow and colonisation dynamics).

1. Describing and monitoring genetic diversity

Molecular phylogeography is the study of geographic distribution of genealogical lineages, especially those at the intraspecific level. In its narrow definition molecular phylogeography involves the analysis of spatial distribution of alleles (haplotypes), taking into account their phylogeographic relationships.

In plants three different genomes can be studied: the nuclear DNA (2n), that is biparentllay inherited, and the organellar DNA (Fig. 1). The oranellar genomes have a uniparentally mode of inheritance: the mitochondrial DNA (n) is maternally inherited in all organisms, whereas the chloroplast DNA (n) is maternally inherited (via seeds) in most Angiosperms and paternally inherited (via pollen) in most Gymnosperms.

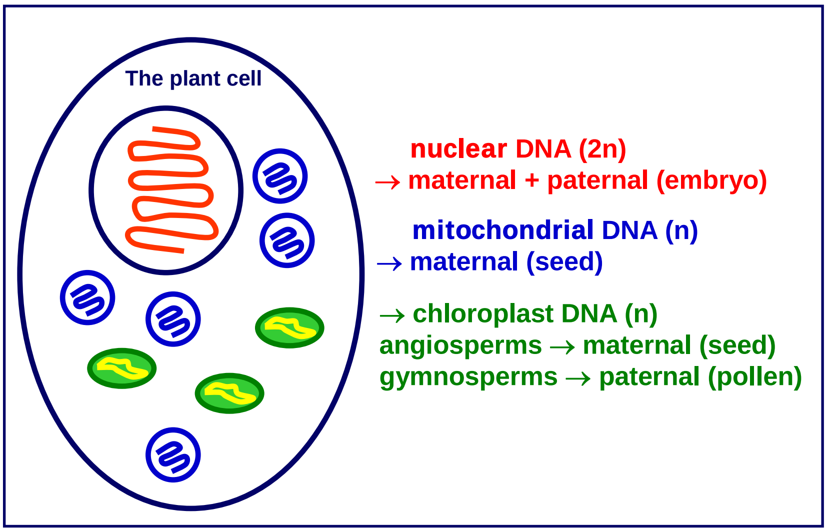
The main difference between organellar and nuclear genetic markers is that either maternal or paternal lineages can be observed. Moreover, the effective population size is smaller for organellar compared to nuclear markers, and a limited gene flow can be studied. In addition, population differentiation is more evident, what is of particular importance for phylogeographic studies.

Two different organellar molecular markers are mostly used in population genetics: cpDNA PCR-RFLP and microsatellites. Polymorphism can be detected if site mutations, and/or length polymorphisms (base insertion/deletion) are present.

---

[1] [1] CNR Istituto per la Protezione delle Piante, via Madonna del Piano 10, 50019 Sesto Fiorentino, Firenze, Italy
[2] CNR Istituto di Genetica Vegetale, via Madonna del Piano 10, 50019 Sesto Fiorentino, Firenze, Italy

Fig. 1: Inheritance of Plant Genomes



2. *Identification of key factors shaping the genetic diversity.*

Key factors in shaping the genetic diversity of plant populations can be grouped in three main categories: i) Historic factors, such as climatic changes, that occurred during the glacial and post-glacial periods; ii) Life history traits that are characteristic of each single species (pollination, seed dispersal mechanisms, mode of propagation); iii) Influence and consequences of the human intervention (agriculture and pasturage, deforestation, cultivation, urbanisation).

To the first category belong climatic oscillations that characterised the Quaternary, and can be reordered by available climatic data (Fig. 2).

Fig. 2: Europe during last glacial maximum, 18'000 (^{14}C) years B.P.

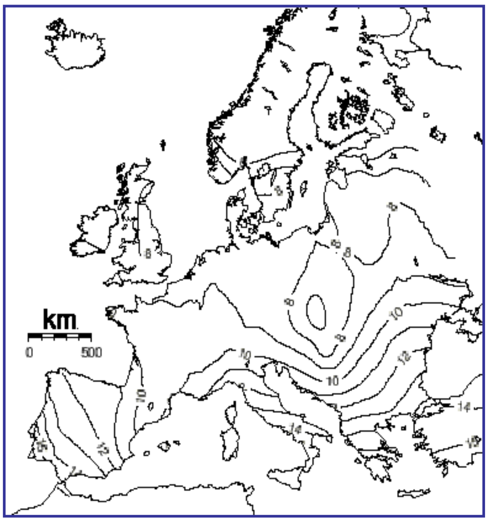
Huntley, B., Birks, H.J.B., 1983. An Atlas of Past and Present Pollen Maps for Europe: 0–13,000 Years Ago. Cambridge University Press, Cambridge, UK.

This very cold and dry phase was the extreme point of the last glacial period. Forest and woodlands were almost non-existent, except for isolated pockets in Southern Europe. Basically such conditions existed throughout the period between about 22'000 and 13'000 years B.P.

To understand the history and the dynamics of vegetation, a precious information is provided by fossil pollen data. The morphology of fossil pollen grains is a systematic trait: on the basis of taxonomic pollen identification in fossil deposits, we can track the distribution of different plant genera (rarely species) in space and time. The isochrone maps (Fig. 3) join to each other those locations where coeval pollen records are found, thus giving an indication where the most ancient populations were placed. In Europe, most ancient isochrones are generally located in the south or in the east; northern populations are usually more recent since the colonisation of new areas from ice age refugia followed a south to north or an east to west migration.

Fig. 3: Isochrone map of *Quercus*

Huntley, B., Birks, H.J.B., 1983. An Atlas of Past and Present Pollen Maps for Europe: 0–13,000 Years Ago. Cambridge University Press, Cambridge, UK.



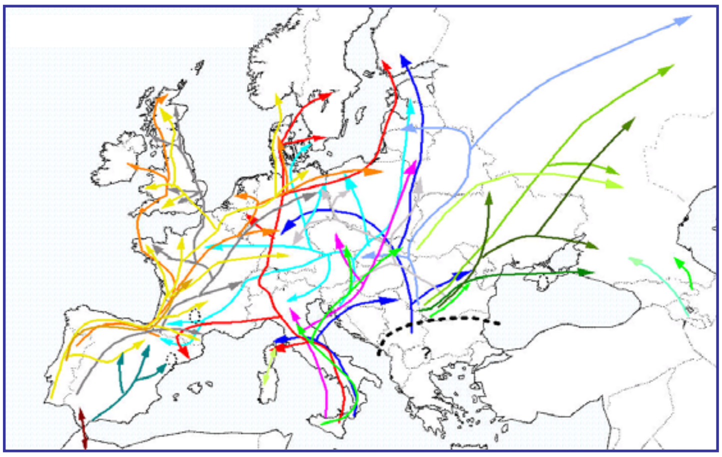
Phylogeography studies are useful not only for understanding the history of tree species and migration dynamics that characterised their post glacial colonisation, but also for tracing possible future scenarios. In fact, following climate changes we expect that the present distribution range of many plant species will be considerably modified in much shorter time as compared to the time span occurred since the last ice time. In this sense we have to consider that several areas, not presently occupied by a given species, may represent areas predicted to be climatically suitable in the future. Under this assumption, areas currently occupied by boreal and temperate species would become more suitable for Mediterranean species.

We will describe some case studies of angiosperm tree species characterised by different life history *traits* such as: distribution range, pollination and seed dispersal mechanisms; and by different *human impact* that the studied species experienced in their history.

We performed the analysis of PCR-RFLP and / or SSR, estimated the coefficient of genetic differentiation (G_{ST}), and described the most likely colonisation pathways and dynamics. Our case studies refer to these tree species:

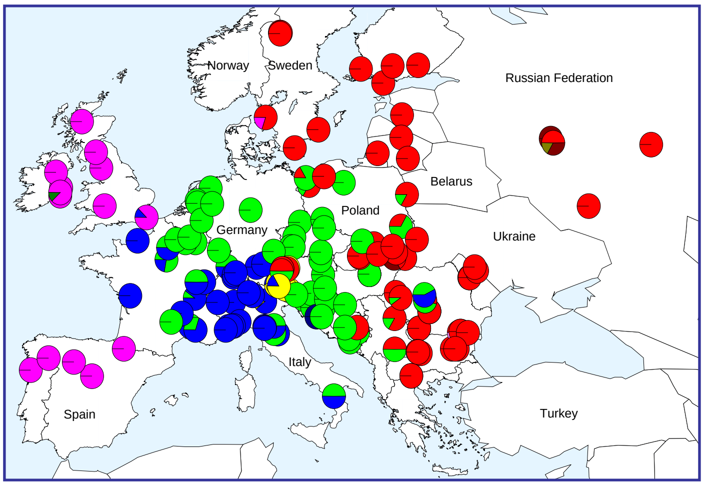
Quercus section Robur

Fig. 4: Quercus (section Robur) colonisation routes
R. J. Petit _et al_. 2002 _Forest Ecology and Management_, 156 (1-3): 5-26



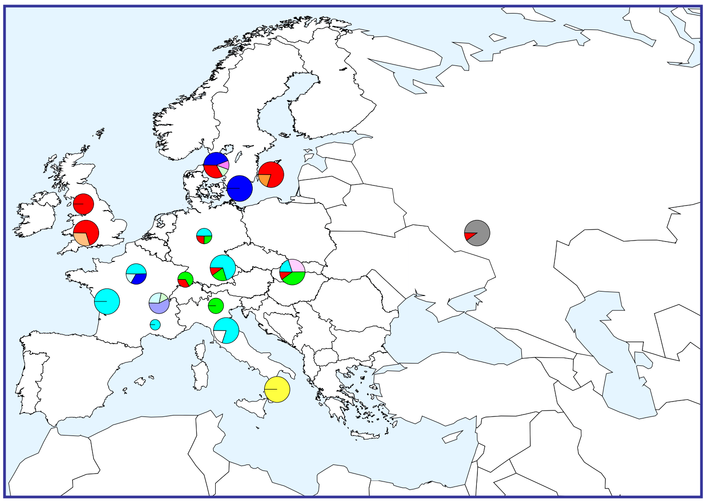
Fraxinus excelsior L.

Fig. 5: _Fraxinus excelsior:_ cpDNA haplotypes
and identification of migration routs
Heuertz _et al._ 2004 _Molecular Ecology_ 13: 3437-3452



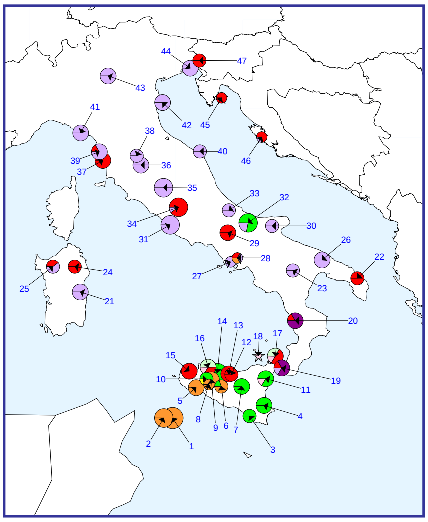
Tilia cordata Mill.

Fig. 6: *Tilia cordata:* cpDNA haplotypes
S. Fineschi *et al.* 2003 *Can. J. For. Res.* 33 (12): 2503-2508



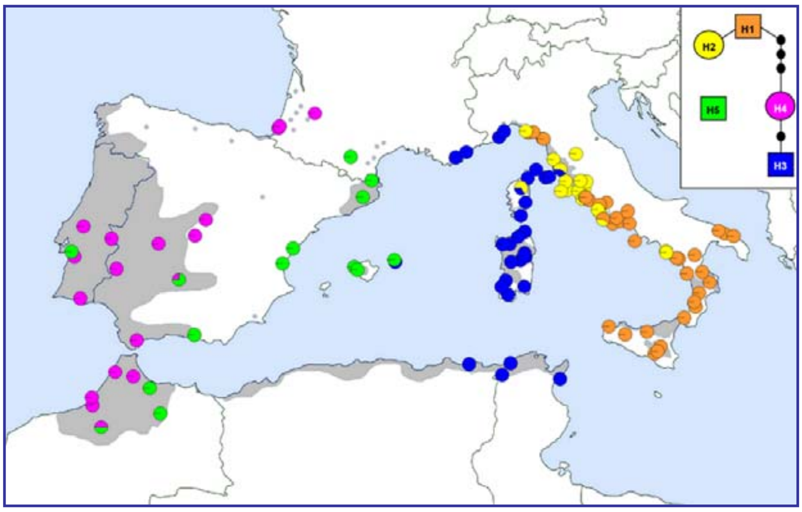
Quercus ilex L.

***Quercus ilex:* cpDNA haplotypes**
Fineschi *et al.* 2005 *Ann. For. Sci.* 62: 79-84



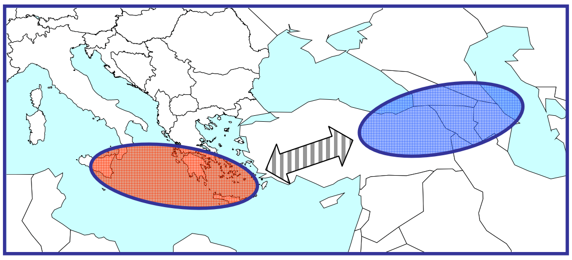
Quercus suber L.

Quercus suber: **cpDNA haplotypes**
Magri *et al.* 2007 *Molecualr Ecology* 16: 5259–5266

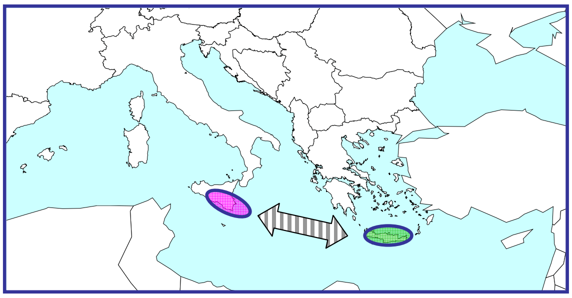


Zelkova sicula Di Pasquale, Garfì & Quézel

Fig. 9: Origin and separation of Mediterranean Zelkovas
Fineschi *et al.* (2002) *Conservation Genetics* 3:145-153



a <u>first event</u> separated the two Mediterranean species from Euro-Asian *Z. carpinifolia*;



a <u>second</u>, more recent event, caused the separation of the Mediterranean Zelkovas. Strong reduction of their distribution was followed by geographic and reproductive isolation

Our studies demonstrate that:

- Historic factors, human influence, and life history traits play a relevant role in shaping the present distribution of genetic diversity;
- Molecular approaches could be of value for conservation efforts by providing tools for measuring genetic diversity;
- Phylogeographic analysis allows to identify evolutionary relationships between populations;
- Molecular information is useful for certification of reproductive material;
- This information can be utilised for managing conservation of biodiversity.

However, caution is required when using molecular evidence based on the analysis of neutral markers for conservation actions, which also requires knowledge on the pattern of adaptive variation.