Patterns of cpDNA diversity within a beech refugial area

Haplotype distribution in Mt. Paggeo (NE Greece)

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Beech (Fagus sylvatica L.) is a broadleaved tree species with major importance for forestry in Europe. Its post-glacial migration history has gained importance in recent years, due to the considerations of the expected climate change. In Eurasia, the species is represented from two subspecies, the western beech (Fagus sylvatica ssp. sylvatica) and the eastern beech (F. sylvatica ssp. orientalis).

Several studies involving pollen profiles, fossil records and genetic markers have revealed the location of glacial refugia and the later expansion of the species to its current distribution. The aim of the study is to describe the genetic structure of cpDNA haplotypes within a putative refugial area and to discuss the possible parameters that resulted in this structure.

The present expansion of beech in Europe derives mainly from refugia located in Slovenia. The Italian refugia did not expand in major movements of beech lineages (Magri et al. 2006). At least, three refugia and four different lineages were indicated for beech in Greece. One lineage originates from the NW refugium of Piedra, while a second one originates from a refugium in W Rodopi. The European lineage arrived from the north and a lineage originating from the eastern populations of the subspecies orientalis indicates an introgression zone (Hatziskakis et al. 2009).

The beech population of Mt. Paggeo was studied. This population is isolated and covers a wide range of sites, as far as altitude, slope, exposure and soil is concerned. Preliminary results have indicated the existence of a refugium in the broader region, while an influence from eastern and central beech lineages was also assumed. Eight subpopulations were sampled, each represented by 20 trees (160 trees in total).

DNA was isolated from fresh leaves. PCR amplification used three cpDNA SSR primers (Weising & Gardner 1999) that have been reported as polymorphic in Greece. Amplification procedure followed Gailing & von Wuehlisch (2004). Only ccmp7 showed polymorphism and 6 haplotypes were identified.

Diversity within subpopulations and differentiation among subpopulations were both found very high. The distribution of the haplotypes in space indicates a clear pattern influenced possibly by the mountain relief. The NE side of the mountains contains mainly haplotype (2), which derives presumably from the local refugium. Haplotypes 1 and 3, probably representing the lineage from the W Rodopi refugium, appear mainly in the E side of Mt Paggeo. The W side of the mountain is dominated by haplotypes 4, 5 and 6 that represent the lineage coming from the East of Greece and having most probably influence from the subspecies orientalis.

The current profile of the mountain indicates a complex movement of lineages in space and time. The existence of “orientalis” haplotypes in higher altitudes is in contradiction with the results in other mountains, where the “orientalis” subspecies was found in lower altitudes (Papageorgiou et al. 2008).

References