

Quaternary history of the pine processionary moth : role of topography and host tree in shaping the population genetic structure

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The pine processionary moth, *Thaumetopoea pityocampa*, belongs to a circum-Mediterranean species complex associated to pine and cedar species. In recent years, it has expanded to upper latitudes or elevations in several European countries due to increased winter temperatures. This rapid response to current climatic changes due to its cold sensitivity suggests that its past distribution is likely to have been strongly affected by Pleistocene climate changes.

In general, thermophilic species have expanded during warm periods and responded to cold phases by local extinctions in northern and mountainous regions, while arctic and alpine species exhibit opposite responses. However, there is increasing evidence of more complex patterns of response, because many species have intermediate ecological requirements or habitat-generalist traits.

A fragment of the mitochondrial cytochrome c oxidase subunit I gene was used to investigate the Quaternary history of the pine processionary moth, whose range is constrained by both cold winter and high summer temperatures.

In western Europe, we identified four genetic lineages that are strongly geographically structured, but surprisingly they are not isolated by the unsuitable high elevation areas of the main mountain ranges. The mountainous areas from the Betic Chain to the eastern Pyrenees (and maybe up to the Massif Central and the Alps) appear to have offered suitable environmental conditions along the slopes during the ice ages, and the current distribution reflects expansion from these bottlenecked refugial populations.

P. sylvestris and particularly *Pinus nigra* are the preferred host plants and they probably persisted in all the glacial refugia of this insect. However, the different contributions of the identified refugia to post-glacial expansion might be explained by differences in host plant species richness. For example, a lineage restricted to the Pyrenean range did not contribute to the northward post-glacial colonization contrary to an Iberian lineage with a more southern origin. *P. nigra* and *P. sylvestris* were probably the main continuously available hosts in the eastern Pyrenees, while *P. pinaster* was also probably present and abundant in the eastern Iberian Chain. Consequently, the Pyrenean lineage of the pine processionary moth could have been trapped elevationally by tracking mountain pines, while the eastern Iberian lineage could have expanded latitudinally by tracking thermophilic lowland pine species. Interestingly, the expansion pathway from eastern Spain to southwestern France corresponds to one of the migration routes suggested for *P. pinaster*, which would be consistent with the moth following the migration route of one of its hosts.

Rather than showing that mountains acted as physical barriers to dispersal, our results suggest that topography played a major role in shaping the distribution of maternal lineages through the demographic history of its main host plants.

Keywords : Pine processionary moth, Black pine, Scots pine, Maritime pine, mitochondrial DNA, glacial refugia, range expansion, vertical migration, mountainous area, western Europe.