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DISSECTING THE ROLE OF DEMOGRAPHY AND NATURAL SELECTION IN SHAPING POPULATION GENETIC STRUCTURE OF TWO MEDITERRANEAN CONIFERS: *PINUS PINASTER* AND *PINUS HALEPENSIS*

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Deciphering the molecular basis of adaptation in non-model tree species still represents a daunting task, not only because of limited access to all areas of the genome, but also because factors other than natural selection – such as demography – can shape the genetic structure of populations, therefore mimicking natural selection. In this study, the main objective was to dissect the respective role of demography and natural selection in shaping population genetic structure of two Mediterranean conifers, *Pinus pinaster* Ait. and *Pinus halepensis* Mill., which differ in levels and distribution of genetic variation and width of ecological niche. We examined natural populations at the species distribution scale, with two main objectives: 1) Characterize the evolutionary and demographic history of the populations. First, insights on demography and population structure were gained by screening supposedly neutral markers (chloroplast and nuclear microsatellites) on the same populations. Second, coalescence simulations were built considering neutral marker information and using only DNA sequence silent polymorphisms. 2) Identify candidate genes associated to important traits that are under natural selection. For this objective some functional genes putatively associated with drought stress tolerance and phenology were used, in a comparative (among-species) framework. The nucleotide variation detected within these genes allowed us to detect loci subject to selection (for instance, some dehydrins) by combining various neutrality tests, in particular compound tests, and to infer likely demographic scenarios in both species. Furthermore, our data allowed us to perform some comparative analyses between two Mediterranean conifer species with contrasting genetic diversity levels and demographic histories.