

CANDIDATE-GENE RESEARCH TO UNDERSTANDING THE ROLE OF GENETIC DIVERSITY IN THE ADAPTIVE RESPONSE OF MEDITERRANEAN PINES

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Combining coalescence modelling, neutrality tests and environmental correlations, demographic history and non-neutral patterns of evolution in candidate genes related to drought stress and secondary compounds were investigated in two closely-related Mediterranean conifers, *Pinus pinaster* Ait. and *Pinus halepensis* Mill. Amplicons covering candidate genes were sequenced in a sample from the full range of these two species. Higher levels of nucleotide diversity in candidate genes for drought response were present in *P. pinaster* than in *P. halepensis*, despite its narrower range in the Mediterranean. Differences across species were also reflected in the haplotype distribution for each tree species, with *P. pinaster* showing many different haplotypes at similar frequencies and *P. halepensis* showing fewer haplotypes with only one that is common or even fixed. The low levels of nucleotide diversity in Aleppo pine are more noticeable in its western distribution where most genes were fixed or almost fixed for particular haplotypes, a probable consequence of long-range colonization of the Western Mediterranean from ancient Aleppo pine populations in the easternmost edge of its current distribution and a more acute impact of the Ice Ages in this range of the species. Molecular analyses also revealed intense and relatively recent bottlenecks in Aleppo pine as well as a time of split between North-African and Iberian populations of the species well predating the Last Glacial Maximum albeit not as old as the one estimated for maritime pine. In contrast, maritime pine seems to harbor large amounts of diversity for these genes due to a more stable demography; in addition, because of its more mesic distribution, higher environmental heterogeneity would have resulted in contrasted selective pressures that may have increased general levels of diversity at candidate genes. Using a wide range of neutrality tests, we found some of the candidate genes studied to evolve in non-neutral patterns. Interestingly, two of them showed statistical correlation with temperature variables, in particular with extremely high or low temperatures, and may constitute valuable tools for monitoring adaptive genetic diversity in these two Mediterranean pines. Our study shows that the use of complementary approaches can help capturing different aspects of the evolutionary processes that govern molecular variation at both intra- and inter-specific levels.