DEMOGRAPHIC AND ADAPTIVE CONSEQUENCES OF LONG-RANGE COLONIZATION IN ALEPPO PINE


*) CIFOR-INIA (Center of Forest Research), Carretera de La Coruña km 7.5, 28040 Madrid, Spain
**) Department of Agricultural Biotechnology, GenExpress, University of Florence, Via della 17 Lastruccia 14/16, 50019 Sesto Fiorentino (Firenze), Italy
***) Plant Genetics Institute, National Research Council, Via Madonna del Piano 10, 50019 Sesto Fiorentino (Firenze), Italy

demography, selection, genetic drift, colonization, local adaptation

The evolutionary outcomes of range expansion/contraction depend on the biological system considered and on the interactions among the evolutionary forces in place. In this study, we examine the consequences of long-range colonization on the demography and local adaptation of a widespread Mediterranean conifer (*Pinus halepensis* Mill.). To that aim, we used cpSSRs and coalescence modelling of nuclear genes to infer the demographic history of natural populations covering the species range. Ten drought-response candidate genes were then examined for their patterns of polymorphism and tested for selection considering plausible demographic scenarios. Our results revealed a marked loss of genetic diversity from the refugial core region, located in Greece, to its western range, as well as molecular signatures of intense and recent bottlenecks. Moreover, we found an excess of derived polymorphisms in several genes sampled in the recently colonized range but not in the refugial area, a potential result of the action of natural selection during long-range colonization. Wide-range expansions/contractions of forest trees are accompanied by strong selective pressures, resulting in distinct evolutionary units, a knowledge that is of crucial importance for the conservation and management of forests in the face of the current process of climate change.