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POPULATION VULNERABILITY OF A KEYSTONE MEDITERRANEAN TREE UNDER FUTURE CLIMATE – AN ECOLOGICAL GENOMICS APPROACH

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Genetic variation is the raw material for population adaptation to climate change. Forest trees often exhibit extensive genetic variation within and among populations; however they may be particularly at risk under climate change due to their long generation times and slow migration rates. Combining phenotypic data from a clonal common garden network (CLONAPIN) of maritime pine (*Pinus pinaster* Ait.) with a new single nucleotide polymorphism (SNPs) dataset (4TREE assay), we explored different ways to use ecological genomics approaches to predict forest tree population responses to climate change. First, we applied quantitative genetics analyses and multilocus GWAS to estimate the degree of polygenicity of fitness-related traits (survival, height, phenology, functional, and biotic-stress response) and assess its variation across environments and years. Most of the analysed traits showed evidence of divergent selection in natural populations and we further observed a remarkably stable degree of polygenicity, averaging 6% (range of 0%–27%), across traits, environments and years. Second, we used a new generation of models combining ecological and genomic information to predict height growth variation, aiming at improving trait prediction at large geographical scales. Models combining climate of origin and gene pool of the provenances as well as height-associated positive-effect alleles (PEAs) captured most of the genetic component of height growth and better predicted new provenances compared with standard climate-based population response functions. Regionally selected PEAs were better predictors than globally selected PEAs, showing high predictive ability in some environments even when included alone in

the models, and highlighting the relevance of conditionally neutral modes of adaptation. Third, we predicted the extent to which the current gene-environment relationships (via GEA) will be disrupted under climate change for each population, using genomic data to estimate the genetic offset, which can also be understood as an important component of population vulnerability. As the genetic offset predictions were highly dependent on the modelling approach used to generate them, we evaluated which approach best explained phenotypic data from common gardens and mortality rates from natural populations, using National Forest Inventory Data from France and Spain. Overall, our work showed promising results for the integration of genomics in the prediction of future forest tree populations to climate change. However, approaches to predict potential maladaptation in natural populations are still under development, in particular for species with strong population structure such as maritime pine, and our results confirm that their predictions should not be used in conservation or management strategies without validation steps based on independent data.