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ABSTRACTS FOR TALKS AND POSTERS

two clones, including three genes with high similarity to genes in *Arabidopsis* implicated in ABA signaling and drought tolerance.

To further test the function of these three differentially expressed poplar genes, we initially overexpressed them in transgenic *Arabidopsis*. We measured seed germination, root growth, fresh weight accumulation and water loss in wild type and transgenic *Arabidopsis* plants. Based on these parameters, transgenic *Arabidopsis* plants overexpressing a poplar ortholog exhibited drought hypersensitive and ABA-insensitive phenotype. In addition, we also observed a molecular phenotype in the form of reduced expression of genes with known function in drought tolerance providing evidence that the tested poplar gene is a negative regulator of drought tolerance also on the molecular level. Similarly, transgenic *Arabidopsis* overexpressing a second poplar gene showed a reduced water loss during drought stress indicating that this gene is a positive regulator of drought tolerance.

In light of these promising results, we have introduced the same DNA constructs into poplar plants. We intend to present our first analysis of drought responses of these plants as well as a perspective on how our results can be used for drought tolerance breeding in poplar based on both transgenic technology and marker-assisted selection based on natural variation.

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Geographic variation in phenology behaviour and response to drought of cork oak populations is crucial to cope with climate change

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Cork oak is widely distributed in the Western Mediterranean region, spanning a range of different environmental conditions, and frequently dominating open woodlands of high conservation and socio-economic value. Cork oak woodlands spread-out for over 715000 ha in Portugal, covering 21% of the national forested area and 30% of the world's cork producing area. Cork oak is well adapted to the seasonal drought of Mediterranean climate, following several decades of warming-up and frequent drought years. However, since the 70's, maximum and minimum temperatures have risen in Portugal about 0.5 °C each decade, corresponding to twice the average world temperature increment. In addition, since longer, more frequent, and more intense drought periods are expected, stress caused by the expansion of arid and semi-arid climate throughout the country will affect the species distribution. Consequently, not only established stands may be prone to tree mortality, but also the current reforestation effort may be jeopardized by low survival rates attributed to the use of unsuitable genetic material.

It is expected that, through genetic adaptation and/or phenotypic plasticity, cork oak populations may have developed significant differences in fitness and the traits related to it. In this context, provenance trials are the best resource of material to assess the variability between and within populations from seed sources sampled in a wide range of locations (stands) covering the geographical distribution of the species. This will enable to assess the levels and patterns of genetic variation for growth and traits determining adaptation to a specific environment, hence providing crucial information to select appropriate seed sources for planting, as well as to develop sustainable breeding and

gene conservation programs. In 1998, multi-site provenance trials were established at three locations in Portugal, as a part of the “European Network for the Evaluation of Genetic Resources of Cork Oak for Appropriate Use in Breeding and Gene Conservation Strategies”. Results from these field trials at 7 years from planting pointed out that seed origin must be considered in reforestation programs, since survival, growth and adaptive traits (phenology, water use efficiency - wue) showed significant differences among populations. Responses to drought (a major limitation to cork oak regeneration) of four contrasting populations, selected according to their field performance for growth, phenology and wue, were further studied under controlled-environment conditions where drought stress was induced. In addition, morphological (total height, root/shoot biomass), physiological (wue, water potential, relative water content and gas exchange) and biochemical (maximum quantum yield of PSII) traits were assessed in 6-month seedlings produced from acorns collected in the stands representing the four contrasting provenances. Results from the controlled experiment provided an indication that drought adaptation was mainly related to early stomatal closure and root investment, with these traits showing significant differences between the studied populations. We have also observed significant differences in growth rhythm, as well as dissimilar temporal drought responses, in the populations under study. In conclusion, both field trials and controlled environment showed consistent results and indicated an important influence of geographic origin on growth performance and wue.

Species specific versus parallel evolution of local adaptation in two white pine species: *Pinus monticola* and *Pinus strobus*

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Under rapid global warming, it is critical for us to better understand the capacity of forest trees to adapt to a changing climate, especially for species that are more at risk such as five-needle pines. Western white pine (*Pinus monticola*) and eastern white pine (*Pinus strobus*) have fragmented ranges and have suffered declines due to harvesting, fire suppression and the white pine blister rust. We identified and compared patterns of genetic diversity and adaptation to climate in these two species by using a set of 267 orthologous genes, including candidate genes for growth, bud phenology and resistance to biotic and abiotic stresses. From those genes, assays for ~200 single nucleotide polymorphism (SNP) markers for each species were developed. Each set of SNPs was genotyped on range-wide samples of 362 *P. monticola* individuals (61 populations) and 840 *P. strobus* individuals (133 populations). Genotyping resulted in 158 and 153 successful SNPs for *P. monticola* and *P. strobus* respectively. Depending on the species lineage and statistical models chosen, F_{st} outliers analyses revealed that from 4% to 25% of SNPs were candidates for natural selection, with the number of outliers being higher in *P. strobus* than in *P. monticola*. Similarly, ~25% of *P. monticola* SNPs and ~30% of *P. strobus* SNPs were significantly associated with one or more climate variables. Furthermore, out of the 79 genes containing SNPs in both species, ~25% showed signature of selection simultaneously in both species. These results indicated that a considerable amount of SNPs, genes and gene families are under strong selection in both *P. monticola* and *P. strobus*. However, a larger number of SNPs and genes that have contributed to local adaptation are specific to each species. This indicates that parallel and species specific evolution can have occurred to shape adaptation to