



Setting the stage for improving oat for adaptation to Mediterranean conditions

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Oat (*Avena sativa* L.) is an important cereal crop, cultivated in most parts of the world as both food and fodder. This cereal is better adapted to temperate and humid climates than to drier (e.g., Mediterranean) climates. However, over the last number of decades, there has been a steady increase in the area of oat cultivation around the Mediterranean rim, due to its relatively good agronomic performance (better than that of wheat or barley) under harsh environmental conditions. Thus, Spain has become the country with the largest cultivated area of oats in the European Union. This increase in cultivated area has been higher and faster than the corresponding breeding effort to improve the adaptation of this crop to southern agro-climatic conditions, and there is a significant gap when comparing yields in northern and southern areas. Therefore, there is an urgent need for improving oat adaptation to Mediterranean conditions.

To this end, the “Breeding for Resistance to Biotic and Abiotic Stresses” group of the Institute for Sustainable Agriculture, part of the Spanish Council for Scientific Research (IAS-CSIC), is establishing theoretical and empirical baselines that will advance our knowledge of factors that will benefit oat yield. We are generating this knowledge using different approaches, from genetic, genomic, and bioinformatics studies to agronomic determinations and the identification of resistance mechanisms to drought and disease. These studies are also being carried out at different levels, from field studies to physiological, cellular, and molecular studies on both leaves and roots.

In FJ Canales’ recent PhD thesis work, done under the supervision of Dr. E Prats and Dr. N Rispaïl, an oat collection consisting of 709 accessions from 24 different countries, including mainly Mediterranean red and white oat landraces, was exhaustively characterized. An interactive map was created to provide easy access to the main morphological and passport information. It provides an essential resource for future oat breeding for Mediterranean areas, in that oat breeders may select accessions with the added context of agronomic and geospatial data. The map was conceived to be a dynamic tool, to which further information developed on these accessions will be added, including disease and abiotic stress resistance data. This will also facilitate oat breeding to address climate change. The map will be made available once it is published.

We dissected the oat accessions’ genetic relationships by performing a detailed genetic diversity study using genotyping-by-sequencing. We also carried out an association analysis for heading date, a trait of fundamental importance for the local adaptation of oats to Mediterranean environments. The results confirmed the suitability of this collection and the usefulness of the genetic information collected (1). In addition, we assessed the contribution of environmental



and genetic variation and their interaction to phenotypic variation and agronomic performance in the oat collection. The main aim was to provide a theoretical basis, such that oat performance in Mediterranean environments and the local adaptation of the best performing landraces could be explained in the context of different climate and edaphic variables (2).

Looking deeper into the identification of resistance mechanisms to drought, we dissected different phenotypes associated with tolerance responses to drought in both above-ground and below-ground organs. We shed light on the role of lipids in drought tolerance in oats by profiling more than 90 fatty acids for each of the main lipid classes and free fatty acids in two well-characterized oat genotypes differing in their response to drought. Results suggest a role for jasmonates and specific fatty acids in different lipid classes in coping with drought stress in oat (3).

In previous work, we observed that salicylic acid (SA) levels significantly increased in drought resistant oat plants as compared to a susceptible cultivar, and exogenous SA treatment alleviated drought symptoms. The next step was to investigate the salicylic-polyamine interaction during drought response in oats through exogenous SA application and direct polyamine quantification and gene expression analysis. Based on the results, we propose that salicylic acid modulates drought responses in oat by regulating polyamine content and biosynthesis (4).

In addition, we dissected the main root system architecture components that contribute to drought tolerance in oats. We set up a fast and reliable screening method through the comparison of similar root traits in seedlings grown in pots or in rhizotrons, as well as in adult plants grown in large containers under climatic field conditions. We observed that the drought tolerant genotype showed increases in root length, branching rate, root surface area, and length of fine roots, while the coarse-to-fine ratio decreased when compared with the susceptible genotype. We also observed a high and significant correlation between various morphological root traits within and between experiments, identifying several of them as appropriate markers to identify drought tolerant oat genotypes. Stimulation of fine root growth was one of the most prominent coping responses associated with gradual soil water depletion in both seedling and adult plants. Measuring this trait might contribute to easier and faster phenotyping of large numbers of plants (5).

At the molecular, physiological, and morphological levels, we studied the role of roots during drought stress further and explored in detail two different strategies observed in resistant and susceptible oat genotypes: a more conservative “water saving” strategy and a “water spending” strategy. These were evaluated over an imposed water deficit time course under controlled conditions. The resistance genotype strategy, comprising different molecular, physiological, and morphological changes, allowed for the maintenance of higher water potential, reducing drought symptoms and promoting growth under water deficit conditions. This allowed us to determine specific phenotypes contributing to the resistance response that could be used to improve the performance of the oat crop under drought conditions (6).



At the molecular level, we looked deeper into the jasmonate (JA) signaling pathway and investigated the dynamic changes in the JA profile in roots and leaves of the two oat genotypes well-characterized for drought resistance. Results suggest that OPDA (12-oxo phytodienoic acid) specifically decreases under water deficit conditions in oat, promoting the growth of new roots and favouring the proportion of smaller diameter roots, which are crucial for maintaining water status in the plant (7).

The information generated in this thesis will assist in the improvement of the oat crop for adaptation to Mediterranean agroclimatic conditions in the current scenario of climate change.

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