

## MARKER-TRAIT ASSOCIATIONS OF AGRONOMIC TRAITS FROM THE CEREALMED DURUM WHEAT PANEL AS ASSESSED IN MULTI-ENVIRONMENT TRIALS UNDER CONSERVATIVE AGRICULTURE

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Developing a biodiversity-based agriculture is currently considered an innovation target to enhance cropping sustainability and food security in the frame of climate changes. The constant reduction of biodiversity, due to intensive agriculture, is affecting all components of the farming ecosystem (crop varieties, crop species, soil microbioma, etc) and is

increasingly considered a constraint for the development of sustainable cropping systems. Conservation agriculture (CA) is a promising option for solving soil degradation and fertility and sustainable management of water resource, however genotypes adapted to this specific agronomic practice need to be selected. In the frame of the CerealMed Project (PRIMA2019) dedicated to "Enhancing diversity in Mediterranean cereal farming systems", a wide and largely underutilized phenotypic diversity present in durum wheat germplasm has been characterised towards the identification of genotypes fitting with the modern sustainability /CA principles. A 300 lines germplasm panel made of elite, cultivars/ breeding lines originated from stress-prone durum growing area was selected for evaluation in a multi-environmental trial network across a range of Mediterranean environments (Morocco, Egypt, Turkey, Italy) for two years (augmented design field experiments). The panel is a subset of the Global Durum Panel previously established by the EWG of Wheat Initiative "Durum wheat genomics and breeding" and provided with Illumina 90k SNP data. Traits considered for phenotyping were agronomic traits relevant for adaptation and grain yield, like plant phenology, ground cover and biomass accumulation throughout the growing cycle (estimated through RGB pictures and estimation of vegetation index), growth habit, leaf posture habit (insertion angle and orientation), yield and components. Meteorological data and soil humidity are also being registered throughout the entire plant growth cycle. Data from the first-year trials indicated a large phenotypic variation for all the traits evaluated. A genome-wide association analysis (GWAS) is on going based on a large panel of SNP by fitting a Mixed Linear model, that includes a kinship matrix as random term to account for genetic relatedness due to population structure. Stability of GWAS results in respect to environment is being assessed through a second-year experimental fields, as well as the agronomic performance of the best genotypes.

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