Proceedings of the LXVI SIGA Annual Congress
Bari, 5/8 September, 2023
ISBN: **978-88-944843-4-2**

Poster Communication Abstract – 2.10

EXPLOITING A LOW-LINKAGE DISEQUILIBRIUM, HIGHLY DIVERSE COLLECTION OF WILD EMMER (T. DICOCCOIDES) FOR GWAS TARGETED TO TRAITS OF ADAPTIVE AND AGRICULTURAL VALUE

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genetic diversity, breeding for resilience, wild emmer wheat, GWAS, enviroment adaptation

Triticum dicoccoides is the tetraploid progenitor of the BBAA subgenomes of durum and bread wheat and is an important source of genetic variation for wheat breeding. As a consequence of strong domestication bottleneck, it is known that the genomes of domesticated emmer (*T. dicoccum*) and *Triticum turgidum* ssps. are strongly depleted in polymorphisms (Maccaferri et al. 2019).

Our objective was to assess the phenotypic diversity for traits of adaptive and agricultural interest, including root traits in 200 accessions of a comprehensive collection of sequenced T. dicoccoides, all provided with whole-genome resequencing and suitable to highly precise GWAS, aiming at identifying novel QTLs governing root traits.

The collection includes Turkey-to-Israel populations and subpopulations. The two lineages spread in the North-Eastern Turkey, Iran and Iraq and in the Southern Levant, including Lebanon, Giordania, Syria and Israel are strongly differentiated and structured into sub-populations, representing wide genetic variability.

The panel has been grown in the field in Cadriano, 2023, and traits as Heading date, tiller elevation angle, number of tillers and spikes /plant, number of spikelets per spike and grain size and shape are being recorded from the field trial.

As for roots system architecture traits, pre-germinated seedlings were grown on filter paper sheets placed on black polycarbonate screening plates soaked in a modified Hoagland nutrient solution. After ten days in growth chamber, images of seminal roots were collected for measuring the following traits: root growth angle, primary root and total root length, root diameter, root network area, lateral root density and length.

All phenotipic data will be analyzed with a linear mixed model.

Based on the availability of the Illumina re-sequenced genomes, A k-mer based GWAS analysis similar to what was already performed in collaboration with John Innes Center (Dr. Brande Wulff lab) using the pipeline published in Gaurav et al., Nat Biotechnol 40, 422–431 (2022), will be carried out.

Population structure, GWAS QTL results and candidate genes will be reported and discussed

Acknowledgements

Research supported by the project “CerealMed”- Enhancing diversity in Mediterranean cereal farming systems, funded by PRIMA2019-Section 2 and by the “Wheatsecurity” SusCrop – FACCE – JPI project.