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

Oral Communication Abstract - 3.05

INNOVAR PROJECT: DEVELOPING HIGH-THROUGHPUT PHENOTYPING AND GENETIC METHODS AND TECHNOLOGIES TO IMPROVE ACCURACY IN AGRICULTURE AND IN WHEAT VARIETAL REGISTRATION PROTOCOLS

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genomics, phenomics, genotyping arrays, haplotypes, GWAS

INNOVAR is a H2020 European project where the principal aim is to update and augment valuable information in bread and durum wheat Distinctness, Uniformity and Stability (DUS) and Value for Cultivation and Use (VCU) variety registration procedure. In particular, the project focuses on building tools and models that augment current practices based on advances development three under strong as genomics, in area precision agriculture/remote sensing and machine learning. Towards this goal, two panels of ca. 270 each bread and durum European varieties were assembled for field trials across 13 environmental locations for 3 years (2020-2023). being collected using DUS actual VCU and CPV0 varietal Data are registration protocols (23 and 30 traits for VCU and DUS, respectively) as well as additional phenotypes related to wheat disease response, resilience to abiotic stresses (drought), vegetation indexes through UAV and handhelded instruments and grain yield components. The two panels were genotyped with a common Illumina iSelect SNP 90K Chip array, broadly used for wheat genotyping, and UAV high throughput phenotyping technology. UAV technologies used in 9 key wheat developmental stages played an important role by acquiring more then 20 vegetation indexes, which were used as

biomass development, photosynthetic activity, proxies of senescence, disease presence and yield expectation. In particular, vegetation indexes were used to estimate dynamic parameters associated to: a) ground coverage, b) biomass accumulation, c) nitrogen uptake and chlorophyll content, d) senescence rate. All these phenotypes provide a major improvement for variety registration methodologies, especially VCU as it represents a more accurate method less involving the use of subjective measurements. As regards to molecular technologies, the panels were surveyed based on haplotype SNP analysis for improved genetic relationships and GWAS. Approximately, 2288 and 4770 haplotype-blocks were identified for durum and bread wheat, respectively. Haplotypes provided more robust data to better estimate local and global Identity-by-descent, understanding genetic relationships and setting genetic similarity thresholds across varieties. Haplotypes were also surveyed to identify more robust putative GWAS-QTLs in comparison to single SNP markers. GWAS carried out on DUS identified several QTLs for all traditional and innovative traits (proxies from vegetation indexes) considered. As regards VCU, nine strong QTL for yield were identified and they physiological determinants in terms of causative traits and candidate genes are being enquired. Finally, these results will provide a framework for CPVO and breeders to set new and improved methods and practices for updating and improve in efficiency the plant varietal registration procedure, including the assessment of candidate variety against panels of already registered varieties.