

THE GLOBAL DURUM GENOMIC RESOURCE IN USE: A COLLABORATIVE GENOMICS INITIATIVE TO LEVERAGE GENETIC RESOURCES FOR INCREASING AND CHARACTERIZING THE BREEDING VALUE OF DURUM VARIETIES

DE SARIO F.*, LIU C.*, BOZZOLI M.*, FORESTAN C.*, RATTI C.*, BRUSCHI M.*, NOVI J. B.*, CAMPANA M.*, SCIARA G.*, ORMANBEKOVA D.*, CORNETI S.*, CONFORTINI A.*, VIVIANI A.*, STEFANELLI S.*, GIULINI A.***, BARDELLI T.**, NOVARINA E.**, GADALETA A.***, MAZZUCOTELLI E.***, DESIDERIO F.****, VIOLA P.*****, INVERNIZZI C.*****, OLIVERI F.*****, MASTRANGELO A. M.*****, MARONE D.*****, RONCALLO P.*****, BASSI F.*****, PEROVIC D.*****, CATTIVELLI L.****, TUBEROSA R.*, MACCAFERRI M.*

*) Alma Mater Studiorum Bologna, University of Bologna

**) Research Centre for Plant Protection and Certification

***) Department of Agricultural and Environmental Science

****) CREA Research Centre for Genomics and Bioinformatics

*****) APSOV Sementi S.P.

*****) Council for Agricultural Research and Economics, Research Centre for Cereal and Industrial Crops

*****) Centro de Recursos Naturales Renovables de la Zona

Semiárida(CERZOS), Departamento de Agronomía, Universidad Nacional del Sur (UNS)-CONICET

*****) International Center for Agricultural Research in the Dry Areas (ICARDA)

*****) Julius Kühn-Institut JKI, Federal Research Institute for Cultivated Plants

genetic resources, GWAS, Distinctness-Uniformity-Stability (DUS), INNOVAR

Breeding of cereal crops can be boosted by leveraging genomics tools. In the last five years wheat benefited of tremendous advances in genomics. Through an international collaborative initiative, partners including University of Bologna, CREA and many Institutions worldwide coordinated by the Wheat Initiative, Durum Wheat Expert Working Group and the International Durum Wheat Genome Sequencing Consortium assembled a golden-standard Svevo Durum wheat genome and developed a comprehensive Global

Durum Genomic Resources including: (i) the Tetraploid Global Collection (TGC, 1,856 tetraploids), (ii) the Global Durum Panel (GDP; 1,033 varieties worldwide), the INNOVAR panel (250 European varieties) and (iii) the Tetraploid Core Collection (TCC; 350 accessions). In the framework of INNOVAR and CEREALMED projects we aimed at identifying pivotal genetic determinants (loci/QTLs) of relevant traits like phenology, response to diseases, grain yield potential. The outcome is of interest to breeders and aims to provide a framework to augment the wheat CPVO Distinctness-Uniformity-Stability (DUS) variety registration protocols by genomics and detailed phenotyping. The panels, previously genotyped with Illumina 90K SNP Chip array, were phenotyped for spike fertility traits, Soil-Borne-Cereal-Mosaic-Virus (SBCMV) and yellow rust response across Mediterranean environments, and DUS traits. GWAS detected a strong QTL peak on chr. 2A responsible for grain number increase per central spikelet, confirmed as GNI-2A, a paralogue of GNI1 (Sakuma et al., 2019). A strong candidate gene was detected within a 4 kb deletion, first identified in durum wheat cv. Altar-84 and identical-by-descent to some successful varieties in Italy, Spain and North Africa. As for the genetically controlled disease resistances, three major QTL clusters were detected for YR resistance (chr1B, chr4A and 7B) with other additional QTLs deriving from multi-environmental trials from GDP collections, and a major QTL was detected on chr2B for resistance to SBCMV in modern varieties panel (GDP and INNOVAR), confirmed as Sbm2 (Maccaferri et al., 2011). These results will represent an important source to improve varietal registration European protocols (DUS) and breeding selection processes. Genome editing is going to be conducted on candidate genes for the main traits, including GNI-2A and Sbm2 QTLs.

This research has been supported by the project "CerealMed"- Enhancing diversity in Mediterranean cereal farming systems, funded by PRIMA2019-Section 2. and by the H2020 FP7 "INNOVAR" - Next generation variety testing for improved cropping on European farmland.