

## **THE GRAIN NUMBER INCREASE 2 (GNI-2) ALLELE IN ALTAR\_C84 DURUM WHEAT AND ITS DERIVATIVES AS AN ADDITIONAL OPTION TO GENETICALLY INCREASE GRAIN YIELD POTENTIAL IN WHEAT**

LIU C.\*, DE SARIO F.\*, BOZZOLI M.\*, FORESTAN C.\*, MILNER SARA G.\*, FRASCAROLI E.\*, SAKUMA S.\*\*, GABAY G.\*\*\*, SNOWDON R.\*\*\*\*, SALVI S.\*, TUBEROSA R.\*, SCHNURBURSCH T.\*\*\*\*\*, MACCAFERRI M.\*

\*) Department of Agricultural Sciences, University of Bologna, 40127 Bologna, Italy

\*\*) Faculty of Agriculture, Tottori University, 680-8553 Tottori, Japan

\*\*\*) Department of Plant Sciences, University of California, Davis, CA 95616, USA

\*\*\*\*) Justus Liebig University, Giessen, German

\*\*\*\*\*) Leibniz Institute of Plant Genetics and Crop Plant Research, 06466 Gatersleben, Germany

*Grain yield potential, Grain number increase, wheat improvement, Marker-Assisted Selection*

Investigating and exploring the genetic bases of economically relevant traits is of utmost importance in enhancing grain yield potential for cereal crop breeding, and cereal agricultural genetics and genomics. Additionally, a better understanding of the effects of different source–sink ratios and stay-green or photosynthetic capacity measurements during the grain filling period on grain growth may be relevant in order to further increase cereal grain yield.

As a result of an initial explorative mapping study conducted on 338 RILs, deriving from a four-way cross among diverse elite durum wheat cultivars, namely, Neodur (French cv), Claudio (Italian cv), Colosseo (Italian cv), and Rascon/2\*Tarro (CIMMYT cv) (NCCR Population), a highly significant genomic region with a phenotypic variance explained (PVE) around 39% underlying the number of kernels per central spikelet (KNSL) and the number of kernels per spike (KNS) was mapped on chromosome 2A, named GNI-2A. The favorable allele, referred to as GNI-2A+/+ and contributing to a + 0.56

grain number increase per central spikelet, was first detected in the CIMMYT cv Rascon/2\*Tarro, a derivative of Altar\_C84 and, as a whole, it has been reported to be strongly conserved in the CIMMYT germplasm and carried by some of the current most cultivated Altar-c84-related-pedigree durum wheat varieties, such as Iride, Arcobaleno, Anco Marzio, Saragolla, Gallareta, Yupare.

Subsequently, a population of 1,500 F4 lines deriving from Relief (GNI-2A -/-) X Iride (GNI-2A +/+), was used for fine mapping and developing three pairs of heterogeneous inbred family-derived near-isogenic lines (HIF-NILs) that were selected by MAS, seed increased and validated for the GNI-2A effect. An ad-hoc designed experimental trial including all three selected congenic line pairs, both parental genotypes (Iride and Relief), and cv Altar-c84 (GNI-2A+/+) and cv Svevo (GNI-2A -/-) has been conducted for RNA-seq assays to obtain a transcriptome profiling of the gene network controlled by the investigated genomic region at target developmental stages: green anther, GA, yellow anther, (YA), tipping stage (TP), heading stage (HD) and anthesis (Fwt). Additionally, Physiological traits such as chlorophyll content (SPAD), water-soluble carbohydrates (WSC) content and gas exchange indexes (LICOR LI-6400 XT) have been measured to gain insight into the effects of the increased sink demand driven by the plus allele. Transcriptomic-based gene network associated to GNI-2A will be presented.

In conclusion, the GNI-2A + is a locus relevant for wheat improvement, found in the elite durum wheat germplasm. The tools for deploying the alleles at the breeding level have been developed and the locus characterization is underway.