

## **HARNESSING GENETIC DIVERSITY TO ENHANCE COLD TOLERANCE IN DURUM WHEAT THROUGH GENOME-WIDE ASSOCIATION APPROACH: A PATHWAY FOR CLIMATE-ADAPTIVE CULTIVAR DEVELOPMENT**

ANGIONE G.\*, ESPOSITO S.\*\*, DE VITA P.\*\*, LOTTI C.\*, TARANTO F.\*\*\*, NATOLI V.\*\*\*\*

\*) Department of Agriculture, Food, Natural Science, Engineering, University of Foggia, Via Napoli 25, 71122 Foggia, Italy

\*\*) Research Centre for Cereal and Industrial Crops (CREA-CI) - Council for Agricultural Research and Economics, SS 673 Meters 25200, 71122 Foggia, Italy

\*\*\*) Institute of Biosciences and Bioresources (CNR-IBBR), Via Amendola 165/A, 70126, Bari, Italy

\*\*\*\*) Genetic Services SRL, Contrada Catenaccio, snc 71026, Deliceto (FG), Italy

*climate change, SNP, GWAS, KASP*

In the context of climate changes, extreme temperatures along with unpredictable rainfall patterns, and drastic drops in temperatures, affect crop cycles, diseases, and pests. These factors significantly influence the yield potential of the most important crops, including durum wheat. Therefore, the development of new cultivars with superior traits is one of the main goals for durum wheat breeders. In the present study a panel of 280 durum wheat (*Triticum turgidum* ssp. *durum*) varieties, including spring and winter types from Northern (i.e., Russia) and Southern Europe (i.e., Italy) were investigated to identify genomic regions conferring cold tolerance and introgress into susceptible genotypes with high grain quality standards. The panel was genotyped using a 25K Infinium iSelect single nucleotide polymorphisms (SNPs) array and phenotyped for traits related to freezing tolerance and grain quality. Principal Coordinates Analysis (PCoA) based on roughly 6,478 high-quality SNPs divided the panel into two main groups, based on their origin and breeding groups. The latter observation was confirmed by the analysis of molecular variance (AMOVA), which revealed a 28% variance between the two main groups (Italy vs. Russia) and 72%

within groups. Parametric (Admixture) and non-parametric (AW-clust) approaches confirmed the observed pattern, with the accessions from Italy clustered in more subgroups compared with those from Russia, suggesting a lower genetic divergence within Russian genotypes. Genome-Wide Association Study analysis (GWAS) for traits related to frost tolerance revealed three associated SNPs on chromosome 5A, in the same region where it has been mapped the cold tolerance locus (*Fr2*). Two of them were successfully converted into Kompetitive Allele Specific PCR (KASP) markers and used to screen three BC1F2 populations obtained from the crosses among Russian cold-tolerant genotypes and high-quality Italian genotypes. The newly developed KASP markers will be used to select superior genotypes harboring tolerance to low temperatures but with higher yield performance and grain quality, to better cope with future climate scenarios.