

GENOME WIDE ASSOCIATION STUDY OF FREE ASPARAGINE CONTENT IN DURUM WHEAT GRAIN

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Acrylamide, a molecule which is known to be toxic to the nervous system, reduce fertility and suspected to be carcinogenic, has been detected in many foods after high temperature processing. In wheat derivatives, the quantity of free asparagine (fAsn) has been identified as a key factor in acrylamide formation. Therefore, the control of fAsn content in wheat seeds is of current interest in contemporary crop and food sciences. Exploring natural variation for fAsn content in the seeds of different wheat genotypes could help breeders to identify novel beneficial traits and useful genes for breeding programs.

The aim of the project is to study the natural variation for fAsn levels in durum wheat (*Triticum turgidum* L. ssp. *durum* (Desf.)) grains to identify candidate genes controlling fAsn seed content.

To this purpose, 215 durum wheat genotypes (including 193 durum wheat

landraces), which originate from 35 different countries, were selected from the international Global Durum Panel (GDP), which was previously genotyped using Illumina iSelect 90K SNP array technology.

Population structure analysis indicated that the selected panel maintained a high level of genetic variability, comparable to that observed for the original GDP population. Clustering analysis identified four groups, matching the geographic region of origin of these genotypes. Linkage disequilibrium (LD) was measured using r^2 and calculated on the SNPs dataset using TASSEL5. This analysis showed that in our collection LD extends till 4.4 Mbp.

The selected panel of 215 genotypes was sown in one location for three years. The field experiments were established in a randomized complete block design with five check cultivars that were each replicated seven times. The quantification of fAsn levels in whole-grain samples from the first two years of field trials was obtained using an enzymatic/spectrophotometric method. The analysis showed the presence of a good variability for fAsn. A preliminary multi-locus genome-wide association study was performed, and SNPs associated with grain fAsn content were found. In addition, 100 genotypes were selected from first year field trial to be investigated by High Resolution $^1\text{H-NMR}$ (Proton Nuclear Magnetic Resonance) spectroscopy, for an in-depth analysis of metabolite composition.

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