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Poster Abstract – B.07

MUTAGENESIS TO MODIFY STARCH AND GLUTEN COMPOSITION IN BREAD WHEAT cv CADENZA

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Gluten and starch represent the main factors influencing different end-use characteristics of wheat flour. Reserve starch is a biopolymer constituted predominantly by two polysaccharides, amylose and amylopectin. Amylopectin is highly branched and constitutes about 75 percent of starch; amylose is an unbranched polymer and constitutes the remaining part. Four starch synthases (SSs) are involved in amylopectin synthesis, along with branching and debranching enzymes; whereas the granule bound starch synthases (waxy proteins) are responsible for amylose synthesis in storage tissues. Glutenins are polymeric structures formed by high (HMW) and low (LMW) molecular weight subunits. HMW glutenin subunits are encoded by different genes located at three loci (*Glu-A1*, *Glu-B1*, *Glu-D1*) present on wheat chromosomes 1A, 1B and 1D and are particularly important as they determine dough strength and elasticity.

The use of chemical mutagenesis to produce novel allelic variation has represented a powerful tool to increase genetic diversity to be used in crop improvement.

In this work EMS treated seeds of the bread wheat cv Cadenza have been used and mutations generated by the mutagen treatment were identified by combining a protein analysis (SDS-PAGE) and a TILLING approach at the gene level. We focused on granule starch synthases and high molecular weight glutenin subunits. Several knockout mutations for starch granule proteins 1 (Sgp-A1, Sgp-B1, Sgp-D1), waxy (Wx-A1, Wx-B1, Wx-D1) and HMW glutenin subunits were identified by SDS-PAGE and characterized at DNA level in order to detect the mutation responsible for gene silencing. Sgp-1 proteins are implicated in amylopectin synthesis and their absence is responsible for an increase in apparent amylose content. Waxy isoforms, differently, are involved in the elongation of amylose chains: genotypes of null alleles at 'waxy' loci show a reduced amylose content. Silencing of different HMW glutenin subunits can provide useful information on their role on breadmaking quality of flours.

TILLING analysis for starch synthases II (SSIIs or Sgp-1 proteins), using genome specific primers, has revealed a larger number of alleles arising from different missense, truncation and splice junction mutations.