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Poster Abstract – F.05

BREEDING FOR THE *WAXY* CHARACTER IN COMMON WHEAT ITALIAN GERMPLASM

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Waxy mutations in bread wheat derive from the loss of functionality of the granule-bound starch synthase I (GBSSI), the key enzyme in amylose synthesis, whose coding loci, *Wx-A1*, *Wx-D1* and *Wx-B1* occurr on the short arms of chromosome 7A and 7D and on the long arm of chromosome 4A, respectively.

Waxy wheats may find useful application in the production of modified food starch and for the improvement of the shelf-life of baked products; moreover, they strongly influence Asian noodle quality.

A breeding program was set up to develop *waxy* wheat lines adapted to Italian environments from partial-*waxy* cultivars previously identified from a screening of Italian germplasm.

The study was performed by electrophoretic fractionation of the GBSS isoforms and PCR analysis.

F3 generations were grown in the field and selected for agronomic traits. Single F3 plants were collected and single grains analysed by means of SDS-PAGE in order to pinpoint *waxy* mutations. Double-null mutants were identified.

A set of specific primers was used to analyse sample plants in order to define their efficiency in the detection of each mutation. Some discrepancies were highlighted, suggesting the presence of new *waxy* alleles in the Italian germplasm: to confirm the hypothesis some PCR products were sequenced.