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POLYMORPHISM OF STARCH GRANULE PROTEIN 1 (SGP-1) IN POLYPLOID AND DIPLOID WHEAT SPECIES

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Starch, sgp-1, wheat, polymorphism

Wheat reserve starch is produced by the concerted action of 4 different starch synthases, branching and debranching enzymes. Starch synthase IIa is a granule bound enzyme (known as Starch Granule Protein 1, Sgp-1) that plays an important role in amylopectin biosynthesis. In fact the knockout of Sgp-1 proteins is correlated with a high amylose content in cereals, such as wheat, rice and barley.

In this paper SDS-PAGE analysis permitted to identify novel polymorphisms for Sgp-1 proteins in diploid and polyploidy accessions. In particular we focused on A-, B-, and D-genome diploid ancestors (*T. urartu*, *Ae. speltoides* and *T. tauschii*) and on tetraploid and hexaploid cultivated species (AABB *T. turgidum*, AAGG *T. timopheevii* and AABBDD *T. aestivum*). A different electrophoretic mobility has been found between Sgp-1 of wild (*T. urartu* and *T. monococcum ssp boeoticum*) and cultivated (*T. monococcum ssp monococcum*) diploid wheats with A genome. Sgp-A1 proteins of *T. urartu* accessions have a SDS-PAGE mobility similar to those of tetraploid and hexaploid species, but they have an higher molecular weight than that of cultivated diploid accessions (*T. monococcum ssp monococcum*). In order to clarify this different mobility, the entire codon region of the two genes has been isolated and sequenced. Differences between deduced amino acidic sequences have been found. Moreover two accessions of *Ae. speltoides* resulted to have Sgp-S1 proteins with different molecular weight on SDS-PAGE gel, similar to Sgp-B1 of polyploid wheats and Sgp-G1 of *T. timopheevii*, respectively.

No polymorphism has been identified in D-genome ancestor accessions (*T. tauschii*) in comparison to Sgp-D1 of *T. aestivum*.