

ANALYSIS OF POLYMORPHISMS BETWEEN *SBEIIA* HOMOELOGOUS GENES IN WILD AND CULTIVATED WHEATS

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Starch branching enzymes play a crucial role in amylopectin synthesis determining the grade of branching of the glucan chains. SBEs cleave α -1, 4-glucosidic linkages and reattach released chains through α -1, 6-glucosidic linkages to the same or another α -1, 4-linked glucan chain.

While it is not completely clear the contribute of SBEI to starch structure, SBEII have been shown to be essential to maintain a normal ratio between amylose and amylopectin chains in cereals.

Bread wheat is an allohexaploid species that was formed through successive chromosome doubling of hybrids involving three ancestral diploid species *T. urartu*, *T. tauschii* and a species of the Aegilops section Sitopsis (Levy and Feldman 2004). *Aegilops speltoides* is commonly identified as the ancestral species more closely related to the wheat B genome but it remains unclear if the origin of B genome was monophyletic or originated from the introgression of several species. A more recent hypothesis suggests that several lines of *Aegilops speltoides* have contributed to the B genome formation of polyploidy wheats.

In this work the comparison of intronic regions of the three *SBEIIa* homoeologous genes showed the presence of several insertions/deletions. Several TE insertions were detected in B and D *SBEIIa* homoeoalleles.

Two insertions of 116 and 90 bp, localized respectively in intron XIV and XV, were identified in *SBEIIa*-B. Both of them resulted to be MITE (Miniature inverted repeat transposable) elements.

Two insertions of 130 bp localized in intron XI and of 150 bp in intron XVI of *SBEIIa*-D were classified as transposable elements by CENSOR analysis. The first sequence resulted similar to a transposon identified in *Triticum aestivum* (DNA-9-ta). The insertion in intron XVI resulted to be Thalos TA, a stowaway-like MITE belonging to the Tc1/mariner superfamily.

In order to establish new insights on the role of transposable elements in the evolution of polyploid wheats a collection of wild and cultivated polyploidy and diploid wheats was investigated to check the presence of the TEs identified in the bread wheat genomes.