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 $\alpha$-1, 4-glucosidic linkages and reattach released chains through $\alpha$-1, 6-glucosidic linkages to the same or another $\alpha$-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 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 polyploid and diploid wheats was investigated to check the presence of the TEs identified in the bread wheat genomes.