

Screening of EST Clones Influencing Amylose Synthesis in Wheat Endosperm Using cDNA Microarray

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Genetic factors influencing amylose synthesis in wheat endosperm were investigated by microarray technology. The array was developed by duplicates of 3367 selected expressed sequence tags (ESTs) from two libraries of a wheat cultivar Chinese Spring (CS); one from developing grains at 10 days post anthesis (DPA) and another from 30 DPA. Differential expression of ESTs in three near-isogenic genotypes with different Wx gene composition, the wild type CS, a partial waxy type and the perfect waxy type, were analyzed using total RNA of immature grains at 10 DPA. Of the tested ESTs, about 1% (28 clones) showed differential expressions among genotypes and, according to the BLAST analysis, 18 of those displayed homologous counterparts. Expression of those clones was highest in CS, followed by the partial and the perfect waxy type. Most of the functionally known ESTs either belonged to chloroplast DNA or genes coding for ribosomal RNA. UDP-Glucose pyrophosphorylase, one of the identified clones involved in the starch synthesis pathway, was expressed highly in CS than in the other two waxy genotypes.

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