

Marker-trait association identified candidate starch biosynthesis pathway genes for starch and amylose-lipid complex gelatinization in wheat (*Triticum aestivum* L.)

Scientists at DBT's National Agri-Food Biotechnology Institute (NABI), Mohali measured the gelatinization properties in a set of 226 wheat varieties using Differential Scanning Calorimetry (DSC) and their thermograms identified two endothermic peaks: first peak of starch gelatinization and second peak of amylose-lipid complex. The four parameters (onset temp, peak temp, conclusion temp, and enthalpy) of both gelatinization peaks showed wide variation among the varieties. Marker-trait association studies using the genotyping data of 258 SSRs and gelatinization data on the wheat varieties identified 24 and 6 markers associated for starch and amylose-lipid complex gelatinization properties, respectively.



Using wheat reference genome sequence and LD decay information, 12 starch biosynthesis pathway genes (SBP) were identified, which were co-located within 50Mb of the associated markers. Four out of 12 genes (*SSIV*, *SBEIIb*, *PHO*, and *PUL*) were located within 5.2Mb. Out of 24, 17 markers were involved in epistatic interactions. These markers are novel for wheat starch gelatinization properties, and would be useful for gene discovery and marker assisted selection for the improvement of starch quality in wheat.

During processing of wheat flour, its starch component undergoes gelatinization, an important physicochemical property, affecting cooking and nutrition quality of its food products. Genetic loci controlling gelatinization properties of starch and amylose-lipid complex is unknown in wheat.

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