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Dissection of preharvest sprouting tolerance in wheat using proteomic and genomic approaches

Naincy Girdharwal, Renu Deswal*, H S Dhaliwal, G S Randhawa and R Prasad

Indian Institute of Technology - Roorkee, India *Delhi University, India

Pre-harvest sprouting (PHS) is the germination of grains in spikes before harvest during rains resulting in deterioration of end-product quality. The major QTL for pre harvest sprouting tolerance (PHST) have been reported on chromosome 3AL and 4AL. The markers linked to QTL were used for validation of QTL in PHS tolerant wheat landraces along with two near isogenic lines (NILs) of *T. aestivum* PBW343. A total of 15 SSR primers were used of which two SSR primers gwm269 and XCQ118 of 4AL identified two PHST landraces. Two NILs of PBW343 (PHST0 and PHST9) derived from a cross between PHST line, SPR8198 and PBW 343 graded as 0 and 9 on a 10 point scale were used for proteomic studies. PHST0 has a QTL on 3AL that is tightly linked to red seed colour. Two dimensional electrophoresis

(2DE) was done for whole seed, mature embryos and immature embryos (fixed at different stages) followed by sequencing of differential spots. LC-MS-MS was done for three protein spots from the whole seed 2DE which were identified by MASCOT search as LMW glutenin and protein disulfide isomerase (PDI). PDI is responsible for protein folding and $\rm H_2O_2$ production during ABA response. From 2DE of immature embryo LC-MS-MS was done for one spot which was identified as serine carboxy peptidase-I which is involved in BRI1 (Brassinosteroid insensitive 1) signalling pathway in Arabidopsis. These two enzymes might be involved in PHST as they were present only in tolerant NIL PHST0. The Q-PCR for their expression profiles in the parent and NILs is in progress.