Identification of Novel STARCH synthase Genes using *de novo* Assembly and Heat-induced Expression and Activity Assay in Developing Wheat (Triticum aestivum)

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Abstract—Terminal heat stress (HS) is one of the major problems in wheat cultivation; reduces quantity and quality of the grains. Enzymes associated with starch biosynthesis is severely affected by heat stress especially starch synthases (SSs). Different isoforms of SS has been reported from rice, maize etc.; limited information is available in wheat. Here, we report cloning of three putative SS genes (transcript_7326, transcript_24546 and transcript_38472) from HD985 cultivar of wheat by data-mining generated from whole transcriptome analysis of wheat under HS. The sequences were in silico characterized and submitted in NCBI GenBank. Glucosyltransferase domain was observed in all the three sequences. Based on clustalW alignment, SS has been classified into four distinct families. Expression analysis and activity assay of SS showed very high transcript level and activity during mealy-ripe stage compared to milky-ripe in HS-treated HD2985 compared to HD2329 cultivars of wheat. We observed decrease in the starch content under HS in both the cultivars; though overall content was high in HD2985 compared to HD2329. Similarly, guaiacol peroxidase, catalase, free amino acid and total antioxidant capacity was observed high during mealy-ripe in HD2985. HS during milky-ripe has more severe impact on the overall physiochemical properties of wheat grain and need to be targeted using different approaches in order to enhances the quality and yield of wheat under the heat stress.

Keywords: Transcript; Heat stress; Starch Synthase; qRT-PCR; Starch; Wheat; Catalase; Peroxidase; Total antioxidant capacity.