

Analyses of expressed sequence tags (ESTs) from panicles of the indica rice cultivar MR84 during grain filling stages and molecular characterisation of ADP-glucose pyrophosphorylase small subunit

ABSTRACT

Rice grain filling is a critical factor that affects yield. In this study, we analyzed the transcripts from rice panicles of the indica rice cultivar MR84 during reproductive and grain filling stages by using expressed sequence tag (EST) approach. Subtractive hybridizations were conducted using three pools of mRNA encompassing panicle initiation, booting, heading, flowering, pollination, fertilization, early/mid and late grain developmental phases. A total of 2366 clones were obtained from these subtractive hybridizations and 718 of them were sequenced. Approximately 36% of the sequenced cDNAs from rice panicles during panicle initiation to heading encoded for pollen allergens, whereas, the remaining ESTs encoded proteins involved in metabolism, transportation, gene expression and other functions. Most of the ESTs from heading to milk stage were storage proteins or involve in metabolisms, whereas, majority of the gene sequences from milk stage to maturation encoded putative storage proteins (61 %) e.g. glutelins and prolamins. Starch is the main component of rice seed dry weight and its biosynthesis largely drives rice yield. Herein, a partial cDNA sequence (I-AGPS1) for the plastidial form of ADP-glucose pyrophosphorylase small subunit, which is involved in the rate-limiting step of starch biosynthesis in higher plants, was isolated from MR84. This gene was preferentially expressed in the grains of milk and dough stage, but unlike its homolog from japonica cultivar, was undetected in rice leaves.

Keyword: ADP-glucose pyrophosphorylase small subunit; cDNA subtraction; Expressed sequence tags (ESTs); Rice grain development