

## Genome-wide survey and expression analysis of F-box genes in wheat

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### Abstract

The ubiquitin-proteasome pathway is the major regulatory mechanism in a number of cellular processes for selective degradation of proteins and involves three steps: (1) ATP dependent activation of ubiquitin by E1 enzyme, (2) transfer of activated ubiquitin to E2 and (3) transfer of ubiquitin to the protein to be degraded by E3 complex. F-box proteins are subunit of SCF complex and involved in specificity for a target substrate to be degraded. F-box proteins regulate many important biological processes such as embryogenesis, floral development, plant growth and development, biotic and abiotic stress, hormonal responses and senescence. However, little is known about the F-box genes in wheat. The draft genome sequence of wheat (IWGSC Reference Sequence v1.0 assembly) used to analysis a genome-wide survey of the F-box gene family in wheat. The Hidden Markov Model (HMM) profiles of F-box (PF00646), F-box-like (PF12937), F-box-like 2 (PF13013), FBA (PF04300), FBA\_1 (PF07734), FBA\_2 (PF07735), FBA\_3 (PF08268) and FBD (PF08387) domains were downloaded from Pfam database were searched against IWGSC Reference Sequence v1.0 assembly. RNA-seq paired-end libraries from different stages of wheat, such as stages of seedling, tillering, booting, day after flowering (DAF) 1, DAF 10, DAF 20, and DAF 30 were conducted and sequenced by Illumina HiSeq2000 for expression analysis of F-box protein genes. Basic analysis including Hisat, HTseq, DEseq, gene ontology analysis and KEGG mapping were conducted for differentially expressed gene analysis and their annotation mappings of DEGs from various stages. About 950 F-box domain proteins identified by Pfam were mapped to wheat reference genome sequence by blastX (e-value < 0.05). Among them, more than 140 putative F-box protein genes were selected by fold changes cut-offs of > 2, significance p-value < 0.01, and FDR<0.01. Expression profiling of selected F-box protein genes were shown by heatmap analysis, and average linkage and squared Euclidean distance of putative 144 F-box protein genes by expression patterns were calculated for clustering analysis. This work may provide valuable and basic information for further investigation of protein degradation mechanism by ubiquitin proteasome system using F-box proteins during wheat development stages.

Keywords: F-box proteins, developmental stages, wheat, RNA-seq.

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