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## Genome-wide Analysis of the F-box Protein Genes in Winter Crops

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### [Introduction]

Genes of the F-box family play specific roles in protein degradation by post-translational modification in several biological processes, including flowering, the regulation of circadian rhythms, photomorphogenesis, seed development, leaf senescence, and hormone signaling.

### [Materials and Methods]

HMM profiling of the F-box proteins was conducted with the HMM files of F-box (PF00646), F-box-like (PF12937), F-box-like2 (PF13013), FBA1 (PF07734), FBA2 (PF07735), FBA3 (PF08268), and FBD (PF08387) domains, against a protein database of the wheat, barley, and rye genome using the HMMER3 tool with default parameters. Genome wide transcriptome analysis of wheat, barley, and rye were performed under cold stress condition in seedling, and gene ontology and enrichment analysis of KEGG analysis were conducted by gene set enrichment analysis and KOBAS, respectively.

### [Results and Discussion]

We have identified a total of 1796, 511, 1127 F-box genes in wheat, barely, and rye genome, respectively, and these F-box genes were further divided into various subgroups based on specific domains. Gene ontology, KEGG, and KOG analysis of F-box genes of winter crops were investigated. Transcriptome and digital expression analysis revealed differential expression patterns of F-box genes from winter crops. Though F-box genes from different species showed high sequence homology, the expressed pattern of them did not corresponded to cold stress condition. The genome-wide analysis of F-box genes provides new opportunities for characterization of candidate F-box genes and elucidation of biological roles in winter crop under cold stress responses.

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