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## Novel identification of CBF genes in rye and phylogenetic relationship in the *Triticeae*

Yong Weon Seo and Woo Joo Jung  
University of Korea, Korea

C<sub>BF</sub>/DREB1 (C-repeat binding factor/Dehydration responsive element binding1) is one of the most important transcription factors to regulate other frost tolerance genes. Rye (*Secale cereale* L.) is the most cold-tolerant species in the *Triticeae* and its main QTL (Quantitative trait locus) is known as *Fr-2* (frost resistance), on which a cluster of CBF genes are present. Compared to a great number of the genes in other species such as wheat and barley, only a few CBF genes are known in rye. In this study, we identified novel CBF genes in rye from recently published rye genome sequences. We analyzed characteristics and structures of the proteins, and promoter regions of each gene. The newly identified CBF genes were named after its nearest homolog in the phylogenetic tree, and CBF families in the *Triticeae* were subdivided into more details than previously reported. The conserved domain search and the putative subcellular localization indicated their role as a transcription factor. PCR analysis using wheat-rye addition lines showed that most of the genes are on 5RL whereas some are located on 6RL or 2RL. Finally, the gene expressions under cold or PEG treatment depending on the photoperiod were analyzed. Their expressions were affected by the photoperiodic cycle, which might be the presence of light responsive elements in their promoter regions. Also, the gene's responsiveness was various to either cold or PEG treatment, which implies that the gene's roles are divided according to the kind of abiotic stresses. The obtained results could be utilized to develop cold tolerant cultivars in the *Triticeae*.

### Biography

Yong Weon Seo has his expertise in wheat molecular breeding for enhancing yield and improvement of stress tolerance. He uses wheat-rye translocations to introduce alien genetic resources into common wheat. Numerous marker systems tagging rye specific regions were developed by his group (NZJC 45:150, 43:241, Genomics Data 5:151, Genes Genet Syst 89:159, Genes and Genomics 35:795). His research focuses on functional analysis of genes responsible for early maturity that is a prerequisite trait for double cropping in Korea is one of his major projects (Mol Bio I Rep 43:1435, 40:969, Genes Genet Syst 90:293, Biologia Plantarum 58:218). He uses *Brachypodium distachyon* as a model system for molecular analysis of interest genes. Mutation breeding and mutagenesis in wheat are another his expertise (Cellulose 22:2419, Int J Radiat Biol 91:407, Radiat Environ Biophys 53:677).

seoag@korea.ac.kr

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