

OB-01

Genome Wide Analysis of U-Box E3 Ubiquitin Ligases in Wheat (*Triticum aestivum* L.)

Min Jeong Hong¹, Dae Yeon Kim^{2*}

¹Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup, 56212, Korea

²Department of Plant Resources, College of Industrial Sciences, Kongju National University, 54, Daehak-ro, Yesan-eup, Yesan-gun, Chungnam 32439, Republic of Korea

[Introduction]

The ubiquitin-proteasome system (UPS), which regulates selective protein degradation via the 26S proteasome, is one of the major mechanisms for post-translational regulation of gene expression and protein quality control in eukaryotes. Recently, the reference sequence of a bread wheat cultivar, Chinese Spring, was released publicly and is available with gene annotations. In this study, U-box E3 genes were identified and classified based on a hidden Markov model (HMM) search using the wheat reference genome.

[Materials and Methods]

HMM profiling of U-box E3 proteins was conducted with the HMM files of U-box (PF04564) domains. BLASTP was conducted with an E-value threshold of 1×10^{-10} and sequence identity > 80% for synteny analysis. To analyze the expression of U-box E3 genes in different tissues and developmental stages, 310 RNA-sequencing samples were used to analyze the expression pattern of U-box E3 genes in response to stress.

[Results and Discussion]

The total of 213 U-box E3 genes were identified in wheat based on U-box and other functional domains in their genome sequences. Genome distribution with high sequence homology of U-Box E3 genes and synteny analysis of wheat U-box E3 genes was conducted with other plant species such as *Brachypodium distachyon*, barley, rice, *Triticum uratu*, and *Aegilops tauschii*. Expression analysis of U-box E3 genes during different developmental stages and tissues, and under abiotic stress were conducted to provide information on U-box E3 gene expression. This analysis of U-box E3 genes could provide valuable information to elucidate biological functions for a better understanding of U-box E3 genes in wheat.

[Acknowledgement]

This research was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (2022R111A1A01065420) and the Korea Atomic Energy Research Institute program (Project No. 523310-23)

*Corresponding author: E-mail, dykim@kongju.ac.kr Tel. +82-41-330-1205