

(O4-04)

Expression analysis of several EST clones related to drought stress in sweetpotato (*Ipomoea batatas*L.)

Sun-Hyung Kim¹, Wan-Keun Song^{1,2}, Kee-Yeun Kim¹, Suk-Yun Kwon¹, Haeng-Soon Lee¹, In-Chul Lee², Sang-Soo Kwak^{1*}

¹Environmental Biotechnology Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), 305-806 Daejeon; ²Department of Biology, Daejeon University, 300-716 Daejeon

Drought stress impedes the growth and productivity of various crop species. Genome-wide expression analysis has identified a number of drought stress induced up- and/or down-regulated genes. Sweetpotato (*Ipomoea batatas* L.) is 7th important food crop in the world. To date, sweetpotato has not been exploited to understand the molecular basis of its drought stress tolerance, even though it is quite a tolerance to unfavorable growth conditions including drought condition. cDNA libraries were constructed from root tissues by subjecting to dehydration. The 983 clones was read in this experiment. The expressed sequence tags (ESTs) represent up to 773 independent genes, 124 clusters and 649 singletons. These 773 cDNAs could be classified into two groups based on the BLAST search results. The first group consists of 535 cDNAs which were assigned a function by aligning them with the translated sequences of the GenBank nucleotide sequence database using the BLASTX algorithm. The second group, comprising 238 cDNAs have no homologies with any genes in the database. The 538 cDNAs belong to different groups of genes involved in ion transport, cell division, metabolism, and protein synthesis, etc. Sequence comparison of these clones using BLASTX led to the identification of 14 putative abiotic stress-related genes. At different stages of development and stress conditions, the expression patterns of 14 genes were analyzed through RT-PCR in detail, and their direct and indirect relationship with drought tolerance mechanism is discussed. The putative ESTs will serve as useful resource to understand the molecular basis of abiotic stress tolerance in plants.

* corresponding author: Tel. 042-860-4432, e-mail: sskwak@kribb.re.kr

(O4-05)

Differential expression of *FLOWERING LOCUS C (FLC)* isolated from *B. rapa* L. ssp. *pekinensis* and effects on flowering time in Chinese cabbage.

Soo Yun Kim, Jungsun Kim, Soo-Jin Kwon, Beom-Seok Park, ¹Young-Doo Park, Ho-Il Kim, Seok-Chul Suh, Yeon-Hee Lee*

National Institute of Agricultural Biotechnology, RDA, Suwon, Korea, ¹Kyunghee University, Korea

Chinese cabbage plants remain in the vegetative growth phase until they have experienced prolonged exposure to cold temperature, known as vernalization. This inhibition to flowering is due to high level of *FLOWERING LOCUS C (FLC)* expression. In order to increase product