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과제 일련번호: 23

Identification of an extra-early maturity barley *VDAC* by yeast two-hybridization screening.

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In the previous study, we isolated a noble gene, *HvSAMS*, which was differentially expressed during grain development of early mature barley. In order to identify proteins that interacted with HvSAMS, a yeast two hybridization library [Transformants : 4.48 X 10^6 cell/ml (SD/Leu-/Trp-)] was constructed. The initial screening identified 21 potential HvSAMS-interacting clones and finally 4 interacting clones were selected. One clone that showed homology to wheat VDAC1, was selected and was designated as *HvVDAC* (*Hordeum vulgare Voltage Dependent Anion Channels*). The cDNA encoding *HvVDAC* contained a 828 bp open reading frame (ORF) that encoded 275 amino acids. The sequence comparison indicated that *HvVDAC* was similar to wheat *VDAC1* as 93% homology. Southern blotting analysis of barley DNA using a DIG labled full-length cDNA probe of *HvVDAC* and *EcoR* I, *Xba* I, *Hind* III digestion showed one hybridized. Two bands could be detected if the DNA was restricted with *Xho* I. Transcript levels of *HvVDAC* mRNA were detected at 3, 7, and 10 DAF (Days After Fertilization) and in grain tissues. In order to examine the responses of *HvVDAC* by elicitors, 4 week-old leaves were treated with NaCl, wounding, ABA, GA3, ABA+GA3, and spermidine. The *HvVDAC* gene showed little change for 12 h and then became to increase from 24 h in ABA, GA3, ABA+GA3, and NaCl treatment. After ethephon treatment, *HvVDAC* gene expression reached a peak at 6 and 24 h. Ethephon is broken down into ethylene, hydrochloric acid (HCl) and phosphoric acid (H_3PO_3). However, HCl and H_3PO_3 did not affect the expression of *HvVDAC* gene. Transcripts of the *HvVDAC* was rapidly increased from 30 min to 3 h and then slightly decreased in wounding treatment.

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