

Molecular characterization of *HvSAMS* gene in early maturity barley

Kim, JY^{*}, JH. Park, YM Jang, DY Kim, JH Jung, SH Jung and YW Seo[†]

Division of Biotechnology and Genetic Engineering, Korea University

극조숙 보리 종실에서 *HvSAMS* 유전자 검정

김재윤^{*}, 박재한, 장용민, 김대연, 정제형, 정승호, 서용원[†]

고려대학교 생명유전공학부

Objective

Previous study, we isolated a noble gene, which was differentially expressed gene in seed development of early maturity barley. The purpose of this study was to characterize and expression.

Materials and methods

Plant material : The grain of early maturity barley, K800, (GSHO 1732 GS96, *eam10*)

Northern Blot : Southern StarTM detection kit

Protein expression : pET32 a vector

Yeast II Hybridization : Matchmaker library (Cotransformation methods)

Results and Discussion

Previous study, we constructed a cDNA library (Final titer : 6.94×10^9 pfu/ml) from kernel of early maturity barley (possessing *eam10*). As screening cDNA library, we identified a noble gene, *HvSAMS* (*Hordeum vulgare* S-AdenosylMethionine Syntase). The whole coding regions of *HvSAMS* was cloned in the bacterial expression vector pET 32 and transformed into the host cells BL21. After induction with IPTG, a prominent band of 52 kDa could be detected in SDS-PAGE analysis (Fig. 1). Immunoblot analysis with a anti-HIS antibody revealed one band at a similar kDa range (data not shown).

HvSAMS transcripts were detected in plant growth hormones and elicitor treated leaves (Fig. 2). Most abundant was detected 24h or 48h after treatment.

We used *HvSAMS* as bait and constructed a yeast II hybridization (SD/-Leu : 1.27×10^7 cells) for potential *HvSAMS*-interacting proteins. With X-gal assay, 21 clones were selected. Further study is underway.

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[†]Corresponding author : Tel : 02-3290-3005 E-mail : seoag@koera.ac.kr

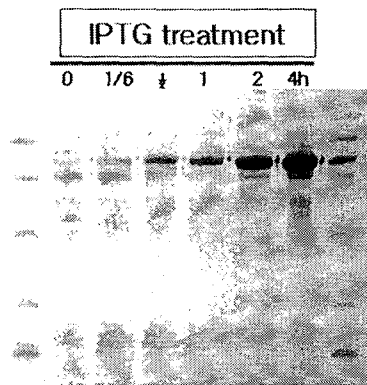


Fig. 1 Protein expression of *HvSAMS* in pET32a vector with 10mM IPTG

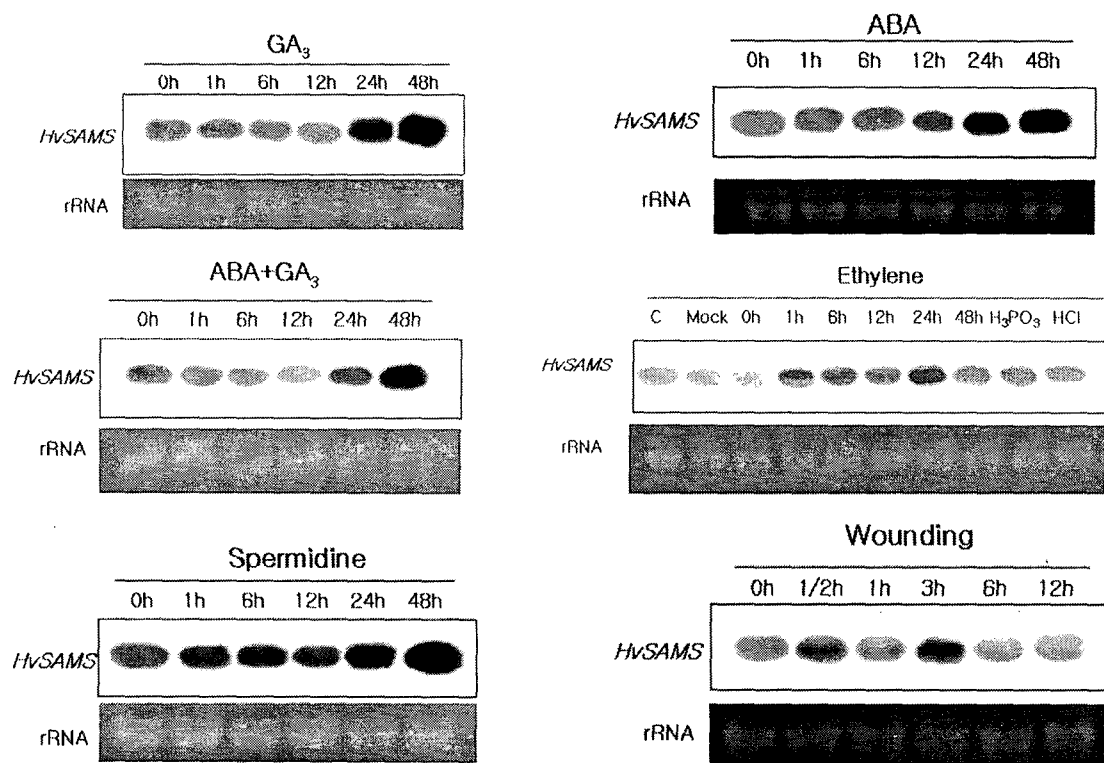


Fig. 2 Northern blot analysis of *HvSAMS* gene with plant growth hormones and elicitor treatments.