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SSH(suppression subtractive hybridization) 방법을 이용한 야생벼(*Oryza grandiglumis*) 유래 유용 유전자 탐색

신상현, 김혜정, 정영주, 정영수¹⁾, 강경호, 최해춘²⁾, 조성기, 신정섭³⁾

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Isolation of wild rice(*Oryza grandiglumis*) specific gene using PCR-base suppression subtractive hybridization

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실험목적

CCDD genome의 야생 벼 *Oryza grandiglumis*에서 wounding 및 병충해 침입에 대한 반응기작으로 차별 발현되는 유전자들을 탐색하여 유전자원화하고 기능을 확인함

재료 및 방법

○ 공시재료: 야생 벼 (*Oryza grandiglumis*)

○ 실험방법

- 1) 야생 벼(*Oryza grandiglumis*) wounding 및 fungal elicitor 처리
- 2) Suppression Subtractive Hybridization (SSH)
- 3) 유전자들의 염기서열 분석 및 발현 검정

실험결과

○ wounding 및 fungal elicitor 처리와 비처리 재료간의 SSH를 통해 776개의 clone 확보

- Primary screen(dot blot) 결과 115개의 유발 유전자 확인
- 염기서열 분석 및 유용한 유전자 확인(Table 1)
- 현재 유용 유전자들에 대한 individual northern 및 Race를 통한 전체 유전자 확보 실험 진행중

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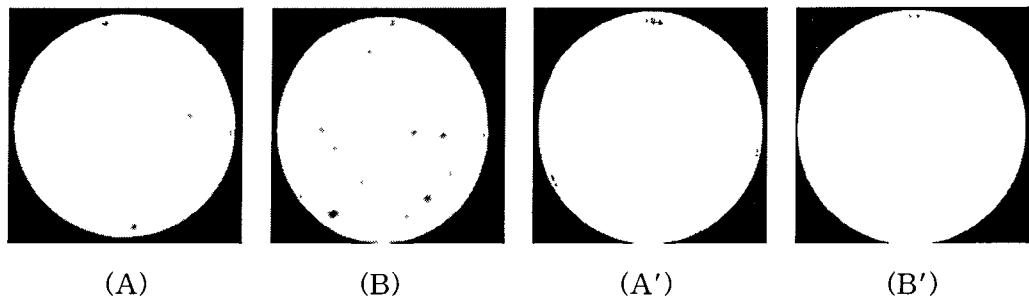


Fig. 1. RNA dot blot screen of arrayed subtractive clones with forward-subtracted cDNA probes (A & B) and reverse-subtracted cDNA probes(A' & B'). Membrane A and A' arrayed same clones from # 406 to # 540 , and membrane B and B' arrayed # 541 to # 675.

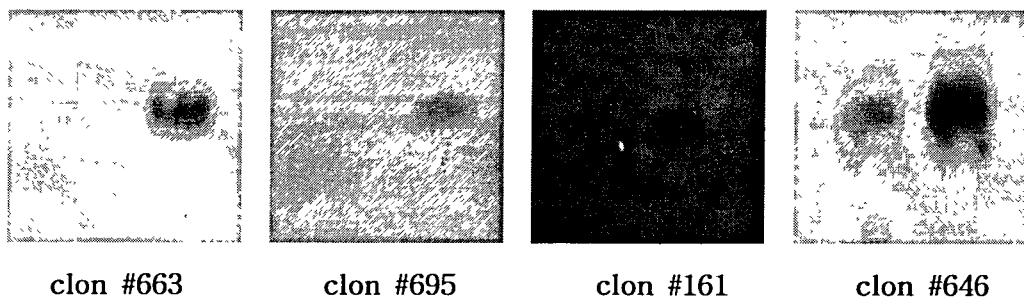


Fig 2. Confirmation of primary screened subtractive clones by individual northern blot.

Clon #663: putative integral membrane protein

Clon #695: putative endo-1,4,-beta-glucanase

Clon #161: putative Na⁺-D-glucose cotransport regulator gene

Clon #646: putative pseudo-response regulator 5

Table 1. Differentially expressed wild rice(*O. grandiglumis*) cDNA clones induced upon wounding and fungal elicitor

clon #	best homology to	clon #	best homology to
8	ARE1-like protein (<i>A. thaliana</i>)	78	carbonate dehydratase (<i>A. thaliana</i>)
23	Pol polyprotein (<i>A. thaliana</i>)	86	unknown
31	<i>A. thaliana</i> BAC T12C245	92	Bowman-Birk proteinase inhibitors (<i>O. sativa</i>)
37	rubisco activase	94	metallothionein-like protein (<i>O. sativa</i>)
39	Actin (<i>Nicotiana tabacum</i>)	95	ribose 5-phosphate isomerase (<i>A. thaliana</i>)
44	ABA and salt stress-responsive rice cDNA	99	photosystem I protein
48	transcription factor E2F (<i>Xenopus laevis</i>)	605	phosphoesterase (<i>Pyrococcus horikoshii</i>)
49	ABC transporter (<i>A. thaliana</i>)	611	gal-pol polyprotein (<i>O. sativa</i>)
55	transposase (<i>O. sativa</i>)	646	pseudo-response regulation 5 (<i>A. thaliana</i>)
71	integral membrane protein (<i>A. thaliana</i>)	660	3-phosphoshikimate 1-vinyltransferase
74	unknown	663	integral membrane protein (<i>A. thaliana</i>)
76	hypothetical transmembrane protein	686	forkhead homolog 4 (<i>Drosophila</i>)
77	phosphonbulokinase (<i>Triticum aestivum</i>)	695	endo-1,4-beta-glucanse (<i>P. horikoshii</i>)