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## Overexpression of pineapple *BAA1* gene encoding cysteine protease in transgenic cabbage (*Brassica rapa*) plants results in enhanced bacterial disease resistance

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### Objectives

To obtain the generation and characterization of transgenic cabbage plants overexpressing pineapple *BAA 1*, the transgenic lines were exhibited significant enhancement of resistance to important bacterial diseases.

### Materials and Methods

1. Materials : T3 generation transgenic cabbage plants(Osome).

2. Methods :

- Molecular characterization (Southern blot, RT-PCR analysis, RealTime PCR, Northern blot)
- Disease screens of transgenic plants (*Pectobacterium carotovorum*ssp. *Carotovorum* *Xanthomonas campestris* pv. *Campestris*)

### Results and Discussion

Genomic PCR were further used to analyze the transgenic segregation rate in the T1 generation, and to determine the homozygosity in the T2 generation. The overall horticultural traits and development of these transgenic lines were similar to wild-type plants for over four generations (from T0 to T3) under regular greenhouse conditions. Transgene expression in transgenic lines was analyzed in T1 and T2 plants by northern blot analysis. Transgenic transcripts were detected in all R1 transgenic lines at varied levels by northern blot or RT-PCR analysis, but transgenic transcripts were not detected in wild-type plants. Based on the transgenic transcript levels, the transgenic lines could be classified into three groups: high transgene expressers, Lines 61 and 63, medium transgene expressers, Lines 62 and low transgene expressers, Lines 64 and 65.

Disease screens against five important tropical diseases revealed that the tested transgenic lines conferred significant level of enhanced resistance to bacterial soft rot (BS) and bacterial black rot (BB). Transgenic lines that accumulated higher levels of BAA1 proteins exhibited higher levels and a broader spectrum of enhanced resistance to the diseases, and enhanced disease-resistance was stably inherited.

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