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PrhA is a Bacterium-plant Cell Contact Sensor in *Pseudomonas syringae*

Jun Seung Lee, Ji Young Cha and Hyung Suk Baik

Department of Microbiology, College of Natural Sciences, Pusan National University, Busan 609-735, Korea

Pseudomonas syringae is a plant pathogenic bacterium and its *hrp* gene cluster is key pathogenicity determinant. *hrp* gene cluster is most strongly expressed in various minimal media that mimic plant apoplastic fluids. However, recent studies provide evidence that specific plant factor induce *R. solanacearum hrp* gene cluster expression. Upon co-culture with host cell suspensions, the expression of the regulatory *hrpB* gene is induced up to 20-fold more than in minimal medium. This specific plant cell induction of *hrp* gene cluster is controlled by PrhA. In this study, we amplified *prhA* gene of *P. syringae* pv. *tabaci* by PCR and constructed *ΔprhA* mutant by allelic exchange. Mutant strain exhibited reduced virulence in host plant. We postulated that PrhA of *P. syringae* is putative bacterium-plant cell contact sensor and used *hrpA*::*gfp* promoter fusion. This work provides evidence that the recently characterized plant-responsive regulatory cascade induces *hrp* gene expression in *P. syringae* in the presence of plant cells.

Key words: *Pseudomonas syringae*, plant pathogenesis, *hrp* gene cluster

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Assessment of Genetic Purity of Hybrid Seeds in Watermelon (*Citrullus lanatus*) Using Microsatellite Markers

Yong-Sham Kwon, You-Hwan Oh, Seung-In Yi, Seon-Phil Choi,
Yoon-Seob Shin[1] and Seung-Gyun Yang[1]

Variety Testing Division, National Seed Management Office, MAF, Suwon 443-400, Korea;
[1]Breeding Institute, Nong Woo Bio Co. Yeoju 468-885, Gyeonggi, Korea

Microsatellite markers were used for assessing variation within parental lines and testing the genetic purity of hybrid seeds in watermelon. Twenty polymorphic microsatellite markers were employed for fingerprinting 5 watermelon hybrid and their parental lines. These markers were discriminated across 5 hybrid varieties and parents lines. To test genetic purity of 2 F1 varieties, Two sets of markers (WM139, WM392) were screened for P1, P2, F1 and F2 plants derived from 'Geumcheon(P1)/Geumcheon(P2)' and 'Speed(P1)/Speed(P2)'. These markers, WM139 and WM392, were found to be heterozygous in F1 plants of two crosses, respectively. In addition, we are analyzed to segregation mode and chi-square goodness-of-fit tests for microsatellite markers in the F2 population derived from two F1 hybrids, 'Geumcheon' and 'Speed'. The segregation ratio of the DNA markers was fitted to theoretical segregation mode of 1:2:1. Interestingly, a segregation distortion was detected by WM392 in F2 plants derived from 'Geumcheon'. These markers could be an efficient implement in the process of quality testing of hybrid seeds in watermelon varieties.

Key words: Microsatellite, purity test, watermelon