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과제 일련번호: 3

Functional analysis of a plant galactinol synthase gene involved in rice disease resistance

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Integration of a galactinol synthase (*CsGo/S1*) gene, that produces galactinol by catalyzing the first step in the biosynthesis of raffinose family oligosaccharides from UDP-galactose and myo-inositol, under the control of a CaMV 35S promoter into tobacco genome showed increased accumulation of galactinol content, and conferred resistance of high degree in leaves of the T₁ lines against infection with a fungal (*Botrytis cinerea*4709) or a bacterial (*Erwinia carotovora*SCC1) pathogen. Phylogenetic and expression kinetic analyses indicate that the *CsGo/S1* gene is an ortholog of the Arabidopsis *AtGo/S1* gene. Arabidopsis *AtGo/S1::TDNA* mutant lines showed more susceptible phenotype while *AtGo/S1*-overexpressed T₁ lines showed highly resistant phenotype against the fungal or bacterial infection compared with wild-type. Relative expression levels of the *AtVSP* and *AtPDF1.2* genes are much higher in Arabidopsis treated with galactinol compared with other sugars, suggesting that the functional role of galactinol in disease resistance may be associated with jasmonic acid-dependent signaling pathway in plants. Addition of galactinol into cultural medium or infiltration of galactinol into plant leaves conferred resistance against challenging pathogen. These results suggest that accumulation of galactinol in leaves may have a functional role in plant disease resistance against pathogen infection. The T₁ and T₂ lines of the *CsGo/S1* transgenic rice plants are under cultivation for the mass propagation in collaboration with Honam Agricultural Research Institute, NICS, Rural Development Administration. Our preliminary results showed that some of the T₁ lines are more resistant to the infection with *Xanthomonas oryzae* than non-transgenic plants.

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