Tropentag, October 7-9, 2008, Hohenheim

"Competition for Resources in a Changing World:
New Drive for Rural Development"

Combination of Antifungal Genes (chitinase and glucanase) to Increase the Resistance Level of Transgenic Pea against Fungal Diseases

Awah Anna Selatsa[1], Jutta Papenbrock[2], Hassan Fathi[1], Hans-Jörg Jacobsen[1]

[1] *University of Hannover, Department of Plant Biotechnology, Germany*
[2] *Leibniz Universität Hannover, Institut für Botanik, Germany*

Abstract

Pea (*Pisum sativum*) is an important grain legume worldwide, used both as a source of dietary protein for human and animal nutrition. The protein concentration of peas ranges from 15.5 to 39.7 %. Its production, however, is affected by different pests and diseases among which fungal diseases are the most important ones. A major objective in breeding therefore is to improve the resistance of pea to fungal diseases which can cause considerable loss of more than 30 %. In addition, most phytopathogenic fungi leave mycotoxin residues in the crop. In order to control fungal infections, pea transgenic lines with enhanced resistance to fungal diseases through heterologous expression of chitinase and glucanase genes have been established.

One way of enhancing or broadening resistance is to combine these transgenes expressing several resistance genes into a single line via conventional crossing. The aim of this study was to enhance the resistance level of transgenic pea plants (expressing chitinase and glucanase individually) against fungal diseases. The transgenic lines expressing both chitinase and glucanase were characterised at the molecular level, segregation and stability expression were analysed. Finally, the transgenic hybrids will further be tested for their resistance against different phytopathogenic fungi following resistance assay procedures leading to the establishment of resistance assays.

To achieve the above objective, 24 out of 29 hybrid plants were grown in the F1 generation. Transgene detection was made by PCR using different primer combinations (Chit 555 and Gluc 823). The results clearly showed the integration of chitinase and glucanase genes in the crossed plants. Stability expression was confirmed in the F2 where 182 F1 seeds were grown. Ninety-three plants were homozygous for our genes. Mendelian segregation pattern (9:3:3:1) was observed. Activity assays were performed and some of the crossed transgenic plants are showing an increased effect in activity.

Keywords: Combined transgenes, expression stability, fungal resistance, pea

Contact Address: Awah Anna Selatsa, University of Hannover, Department of Plant Biotechnology, Dorotheenstr.7 527, 30419 Hannover, Germany, e-mail: annybrown2000@yahoo.com