The Responses of Transgenic Soybean Plants Carrying FvPO1 to Pseudomonas syringae pv glycinae.

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Abstract
The United States of America is the world leader in soybean production. Soybean yields are subject to losses based on both biotic and abiotic stresses. Disease stress is a serious concern for soybean growers and an area of focus for soybean breeders and geneticists. Transgenic approaches can provide interesting and novel sources of resistance which can be used to protect soybean from a wide array of pathogens. In this study we investigated the ability of transgenic soybean lines expressing a fungal polyamine oxidase gene to provide resistance to the bacterial pathogen Pseudomonas syringae pv glycinae.

Background
The United States is the leading soybean producer and exporter with more than 80 percent of soybean acres found in the upper Midwest. Soybean suffers yield losses from both biotic and abiotic stresses. The biotic stresses include fungal pathogens like Fusarium virguliforme which is responsible for soybean sudden death syndrome (SDS), and bacterial pathogen Pseudomonas syringae pv glycinae. A fungal polyamine oxidase, FvPO1, is found to be upregulated when soybeans become infected with F. virguliforme. It is suggested that when plants defend themselves against a pathogen, plant polyamine oxidases play a role in the plant’s defense mechanism. Mutant F. virguliforme which lack FvPO1 have been found to be more virulent than the wild-type strain. Transgenic soybeans carrying the FvPO1 gene have shown some resistance to SDS. Pseudomonas syringae pv. glycinae causes one of the most common foliar diseases affecting soybean production. Young leaves infected by bacterial blight can be identified by dark spots encompassed by a yellowish halo. To examine whether the FvPO1 gene may provide resistance against other soybean pathogens the FvPO1 transgenic plants were used in resistance screening with Pseudomonas syringae pv glycinae.

Objectives
Investigation of the response of transgenic soybeans carrying the FvPO1 gene for their response to bacterial pathogen P. syringae pv glycinae.

Materials and Methods
Grow transgenic soybeans in growth chamber for 2 weeks.
Grow bacterial culture on 10 mM MgCl₂.
Dip inoculate plants and return plants to growth chamber.
Sample leaves after 1, 5, and 8 days with leaf borer and grind leaf sample and plate of trypsicoy agar plates.
Count colonies on plates after 48 hours.
Repeat experiment analyze data using ANOVA and t-test.

Observations and Conclusion
• On average there were no significant differences between Williams 82 cfu counts and that of the transgenic FvPO1 lines.
• We observed that there was large variations in cfus within the different transgenic line. We hypothesized that this might be dependent of FvPO1 expression.
• An interesting observation was that transgenic line 9A12 has increased bacterial cfu count during 1 dpi which could be also from sampling error.
• In replication 1 there was significantly increased bacterial cfu count in lines 9A12, 9B4 and 9B5 (p < 0.05) during 1dpi time point. This trend was only consistent with line 9A12 during the second replication.
• There was little expression of the EF1B gene during RT-PCR. If there was more time available repeat PCR experiments would be conducted to correct this problem.

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