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Activation of Soybean Plant Defense Signaling Pathways in Response to Soybean Aphid (Aphis Glycines Matsumura) and Soybean Mosaic Virus

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I. BACKGROUND

- Soybean Plant
  - Soybean (Glycine max) also called the “miracle crop”, is the primary source of vegetable protein and oil for millions of people all over the world [1] (Fig. 1).
  - Currently, U.S. is the leading producer of soybean in the world with 83.18 million metric tons [1].

- Soybean Aphid
  - The biggest threat to soybean production is an insect pest, the Soybean Aphid (SBA) (Fig. 2).
  - Aphid feeding causes leaf puckering, plant stunting, reduced pod and/or seed counts, contributing up to 45% yield loss [2].

- Soybean Mosaic Virus
  - In addition to direct damage through feeding, SBA cause indirect damage by transmitting plant viruses such as the Soybean mosaic virus (SMV) (Fig. 3) [3].
  - The major impact of SMV is the effect on seed quality.

II. LONG-TERM AND SHORT-TERM OBJECTIVES

- Long-term Objective
  - To identify plant genes that contribute host plant resistance to aphids and aphid-transmitted viruses and may be used to develop resistant soybean varieties.

- Short-term Objective
  - Determine the timing and nature of plant defense responses against SBA infestation and SMV infection.

III. METHODS

- Plant, insect and virus source
  - Soybean variety AG3432 was used for all experiments. Plants were grown at 24 ± 1°C and 16:8 hours (light:dark cycle).
  - Soybean aphids were obtained from Purdue University, West Lafayette.
  - SMV-infected plants were obtained from University of Illinois.

- Experimental Design
  - The experiment design consisted of three plant treatments - 1) infestation with twenty SMV-infected soybean aphids, 2) infestation with twenty uninfected aphids, and 3) no treatment or control plants. There were 2 replicates per treatment.
  - Plant tissues were collected at five sampling time points – 0h, 3h, 6h, 12h, and 24h post-release of aphids.

- Gene Expression Analysis
  - Plant RNA was extracted following Trizol® extraction method. The quality and quantity of the RNA was verified using a Nanodrop® Spectrophotometer.
  - The DNA-free RNA was used for complementary DNA (cDNA) synthesis and gene expression analysis using reverse-transcriptase-Polymerase Chain Reaction (RT-PCR).

IV. RESULTS

- Plant Defense Gene Expression
  - The two main plant defense pathways that were analyzed in the study were: Salicylic acid (SA) -pathway and Jasmonic acid (JA) -pathway.
  - The SA pathway is predominantly induced against pathogens and the JA pathway is activated in response to insect feeding [4].
  - In our study, GmPR1 – marker gene for SA pathway was activated in response to feeding by uninfected SBA and SMV-infected SBA (Fig. 4).
  - GmJAR1, a marker for JA pathway, was activated to a greater extent in response to feeding by SMV-infected aphids (Fig. 4).

To summarize, simultaneous attack by SBA and SMV results in the activation of both SA and JA defense pathways in soybean plants.

V. REFERENCES


VI. ACKNOWLEDGEMENTS

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