

S2T5**Plant defense gene response by Russian wheat aphid honeydew and honeydew-associated bacteria**

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Abstract

Plant health outcomes are largely based on the dynamic interactions of multiple organisms in the phytobiome. Our previous work demonstrated that variation in Russian wheat aphid (RWA, *Diuraphis noxia*)-induced chlorosis on wheat is determined, in part, by aphid-associated bacteria. Aphids with high titers of bacteria induced gene expression and accumulation of salicylic acid (SA), a hormone that inhibits insect resistance, in susceptible wheat. High, sustained expression of SA biosynthetic genes was followed by downregulation of jasmonic acid (JA) biosynthetic genes; JA is associated with insect resistance. These trends in plant defense gene modulation were also evident in barley, an alternate host for RWA with considerable genetic resources. We hypothesize that aphid-associated bacteria contribute to aphid virulence by modulating the plants' insect defense mechanisms. Although saliva from aphids contains culturable bacteria, scanning electron microscopy (SEM) studies did not detect bacteria in high numbers in the aphid salivary glands or foreguts. However, the same genera of bacteria were detected in aphid honeydew as in saliva; thus, we are focusing on the role of honeydew in induction of plant defenses. In this presentation, we will report on the impact of honeydew and honeydew-associated bacteria on plant defense response pathways in barley.

