Reducing Root Rots in soybean through better understanding of host defense to *Fusarium graminearum*

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Fusarium root rot (FRR) is an important disease in many soybean production areas and is caused by various *Fusarium* species, the *Fusarium graminearum* (*Fg*) that is associated with Fusarium head blight (FHB) in cereals, is a potential threat for soybean as wheat-soybean rotation is widely practiced and *Fg* has been recently confirmed to cause soybean root rot. While defense mechanisms of wheat against the FHB agent *Fg* have been investigated in length in wheat, no such studies were reported in soybean. To better understand this soybean-*Fg* interaction, we evaluated the expression of ten defense-related genes associated with either the salicylic or jasmonic acid defense signaling pathways: PAL2, ICS1, ICS2, AOS2, OPR3, JAR1, NPR1, PR-2, PR-3, and PR-4. The expression of ICS1, ICS2, and PAL2 genes was more pronounced in moderately resistant soybean cultivar compared to susceptible ones. Additionally, AOS2 showed significant expression at 24 hpi, while JAR1 exhibited significant expression at 6 hpi in moderately resistant cultivar, along with OPR3. These results indicate that both salicylic and jasmonic acid pathways are involved in soybean defense against *Fg* at different timings and add to the data gathered to elucidate the signaling mechanisms in this host-pathogen interaction. Together, these data may contribute to reducing the effect of FRR on soybean yield.