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

Nadia Garma, Rhodesia Celoy, Mohammad Sayari, Mohamed El-Shetehy, Pawanpuneet Rehal, and Fouad Daayf, Department of Plant Science, University of Manitoba

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.