TRANSCRIPTOMIC ANALYSES OF BOTH HOST AND PATHOGEN DURING Sclerotinia sclerotiorum INFECTION OF SOYBEAN

Wei Wei¹, Bernarda Calla¹, Xing Wu¹, Laureen Blahut-Beatty², Daina Simmonds², and Steven J. Clough*^{1,3}

¹University of Illinois, Department of Crop Science, Urbana, IL USA

²Agriculture and Agri-Food Canada, Ottawa, ON Canada

³US Department of Agriculture-Agricultural Research Services, Urbana, IL USA

*Presenter's email: steven.clough@ars.usda.gov

Breeding for resistance to Sclerotinia remains to be a real challenge in crops like soybean, where no single gene provides strong resistance, but instead, multiple genes work together to provide partial resistance. If breeders knew what genes were playing an active role in defense, they might be able to use that information to design effective molecular markers in marker assisted selection (MAS). We have been conducting transcriptomic analyses of soybean response to Sclerotinia to gain an insight into the gene activation/inactivation that occurs during infection, in hopes of identifying some key defense related genes that could be tagged and used in MAS. In addition, we have gene expression data from the pathogen, allowing for the development of hypotheses on how both the plant and the pathogen are behaving. We see soybean gene expression consistent with the activation of multiple defenses, as well as with induction of genes encoding negative regulators of a possible HR-like cell death. Using a transgenic (OxO) that degrades the pathogen-released oxalic acid (OA), we can see that OA enhances the down-regulation of defenses, and that OA might be chelating iron away from plant host proteins, which could play a role in this weakening of defenses. Looking at gene expression from the fungus, it was interesting to see that, when inoculated on the OxO host, an OA biosynthetic gene increased in expression, showing that the fungus might be increasing OA levels if necessary. The fungus also increased expression of several virulence factors when inoculated on the OxO plants. We conclude that anything that the host can do to reduce the effects of OA and increase defenses, will improve the odds of the host surviving the infection, and therefore, MAS will be an effective approach once defense-associated genes and loci are identified. Additionally, we conclude that the pathogen senses when OA levels might not be adequate and it responds with increased expression of its weapons.

Keywords: Oxalic acid. White mold. Transcriptomics. Soybean