**Progress in understanding the *Sclerotinia sclerotiorum* pathosystem.**

**Abstract**

*Sclerotinia sclerotiorum*, a predominately necrotrophic fungal pathogen with a broad host range, causes a significant yield-limiting disease of soybean called Sclerotinia stem rot. Resistance mechanisms against this pathogen in soybean are poorly understood, thus hindering the commercial deployment of resistant varieties. I will discuss the use of a multiomic approach utilizing RNA sequencing, gas chromatography–mass spectrometry-based metabolomics and chemical genomics in yeast to decipher the molecular mechanisms governing resistance to *S. sclerotiorum* in soybean. The combined results show that resistance to *S. sclerotiorum* in soybean is associated in part with an early accumulation of JA-Ile ((+)-7-iso-jasmonoyl-L-isoleucine), a bioactive jasmonate, increased ability to scavenge reactive oxygen species, and importantly, a reprogramming of the phenylpropanoid pathway leading to increased antifungal activities. Using chemical genomics in yeast, we further show that this antifungal activity targets ergosterol biosynthesis in the fungus, by disrupting enzymes involved in lipid and sterol biosynthesis. Overall, our results are consistent with a model where resistance to *S. sclerotiorum* in soybean coincides with an early recognition of the pathogen, leading to the modulation of the redox capacity of the host and the production of antifungal metabolites.