Landscape-level Population Structure: Disentangling complex factors shaping populations of *Sclerotinia sclerotiorum*

Recent work in my lab has examined the landscape genetics of *Sclerotinia sclerotiorum* from dry bean across the U.S. (Kamvar et al. 2017 PeerJ). Since multi-site screening nurseries are used to identify dry bean lines with increased resistance to white mold, our work sought to determine whether pathogen populations within nurseries were genotypically and phenotypically representative of producer fields across the dry bean producing region of the U.S. We genotyped 366 isolates from states that collectively produce more than 85% of dry beans and were collected across 10 years from multi-site screening nurseries and nearby producer fields. Phenotypic traits, such as pathogen aggressiveness and mycelial compatibility group, were also determined. Since none of the typical multivariate methods used in population genetic analyses were capable of identifying factors underlying patterns of genetic variation, we adapted a method from community ecology, called distance-based redundancy analysis (dbRDA). This method simultaneously evaluated environmental, phenotypic, host, and temporal variation to identify variables most likely to be connecting and driving pathogen spread. An unexpected pattern in our data was that Mexican populations were more differentiated than those on different continents (France and Australia).

One hypothesis is that increased diversity arises in subtropical environments, which allow for more cycles of sexual reproduction and outcrossing. To test this, current projects are underway in my lab to characterize populations of *S. sclerotiorum* from Mexico and compare them to populations from soybean across the North Central U.S., (conducted by Ph.D. student, Edgar Nieto Lopez). We are also characterizing populations in subtropical regions of Brazil to capture continental-level structure (Pannullo et al. 2018 PeerJ Preprints).

Another hypothesis for increased diversity is that non-lethal fungicide exposure causes oxidative stress that increases mutation rates and genetic diversity within pathogen populations (Chen et al. 2015 Fungal Genet & Biol, Dowling et al. 2016 Phytopathology). To test this hypothesis in *S. sclerotiorum*, we performed a lab study that showed in vitro fungicide exposure increased mutation rates at SSR loci (Amaradasa and Everhart 2016 PLoS ONE), following which we are using whole-genome sequencing to characterize genomes of the fungicide-exposed isolates (conducted by Ph.D. student, Nikita Gambhir). Collectively, these studies are important for understanding the landscape genetics of *S. sclerotiorum* across the United States and elucidate mechanisms that may drive diversification and spread of this economically important plant pathogen.