Sclerotinia sclerotiorum IN NORTH AMERICA: RECENT DISEASE OUTBREAKS AND VARIABILITY OF POPULATIONS ACROSS THE UNITED STATES AND MEXICO

S.E. EVERHART[1]; Z.N. KAMVAR[1]; B.S. AMARADASA[1,2]; T.J.J. MIORINI[1]; R. JHALA[1]; A., PANNULLO[1]; R. HIGGINS[1]; J.R. STEADMAN[1].
University of Nebraska, Lincoln, NE, USA / University of Florida, Gainesville, FL, USA. E-mail: everhart@unl.edu

Disease outbreaks caused by *Sclerotinia sclerotiorum* are highly variable and typically driven by regionally favorable weather. Characterization of phenotypic and genotypic variability can yield important insight into pathogen biology and epidemiology. We will provide an update on recent disease outbreaks throughout North America, with a focus on dry bean. We have also completed a comprehensive genotypic and phenotypic characterization of more than 400 isolates of *S. sclerotiorum* from common dry bean in the United States, Mexico, France, and Australia, as well as soybean in the U.S. and Brazil. Genotypes were determined using SSR loci and phenotypic characterization included mycelial compatibility group, aggressiveness, and fungicide sensitivity. In an analysis of 366 *S. sclerotiorum* isolates from 19 dry and snap bean cultivars in 10 states in the U.S., Mexico, Australia, and France, collected from 2003 to 2012, we identified a total of 165 multilocus genotypes. Discriminate analysis of principal components using clone corrected data showed state/country of origin was the best separator. The Mexican population was highly divergent, showing closest association with the California population. There was no significant difference (p=0.057) between populations once the Mexican population was removed. Despite overall genetic linkage, no linkage was observed for some populations. Results suggest that despite large physical separation, divergence of populations is low, although currently available SSR loci may not be sufficiently variable for population resolution. This is not surprising given the low rate of recombination thought to occur.

Keywords: Population structure; Genotypic variation; Phenotypic variation.