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Variability of *Sclerotinia minor*
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Genotypic Variation of Fungal Isolates. Each of 232 isolates of *S. minor* recovered from 12 fields in four peanut-producing counties (Gaines, Erath, Comanche, and Atascosa) in Texas were characterized for their genetic variability. Genotypic differences among the isolates were assessed by microsatellites. Five polymorphic loci were selected for genotyping of the collection of isolates (four isolates from Brazil were included as the out-group population). The number of alleles observed as each locus ranged from four to seven. Each unique genotype was designated with a name, resulting n the identification of 50 genotypes from Texas and one genotype from Brazil. The predominate genotype, TX1, consisting of 108 isolates, was designated a clone, defined in this study as five or more isolates with the same genotype. TX1 was found in every population from 10 of the 12 fields sampled. Genotypic differentiation indicated significant differences in genotypes based on location. Data sets of each multilocus genotype observed were analyzed to determine the role of sexual recombination in shaping the genotypic structure of the isolates sampled. The observed index of association for *S. minor* populations was significantly higher than the calculated index from 1000 artificially recombined data sets; therefore, the population is clonal.

We constructed a maximum parsimony tree from clonally corrected genotypes with the data scored as 0 or 1 for presence or absence of an allele. This parsimony tree demonstrated that there were 13 distinct clades and many unique individuals. Clade 1 included only TX1. The tree further demonstrated that the clades that contain more than one genotype were not isolated by county while clades with only one genotype were isolated by county. Also, many of the genotypes were isolated by field; TX1, TX2, and TX3 were the only genotypes that occurred in more than four fields. While each genotype had a unique distribution of aggressiveness, no significant differences in aggressiveness were found among the genotypes. The lack of significant differences among genotypes can be attributed to the wide array of aggressiveness within each genotype. In addition to using microsatellites, we have attempted to genotypically characterize the isolates by comparing stretches of sequences from selected genes. Thus far we compared sequences of the internal transcribed spacer region of rDNA (ITS), β-tublin gene, gene for the α-elongation factor, and intergenic spacer region of the rDNA gene repeat unit (IGS). Based on our preliminary data with five isolates from distinct clades, we found that the IGS sequence to be the most informative sequence as some differences have been found. The other regions of sequence were essentially identical. Thus, we will continue with this work using 23 to 30 selected isolates.

As mentioned in previous reports, we used a leaflet assay to differentiate among the isolates for aggressiveness. The National Peanut Board funded a continuation of this work as a mechanism to screen approximately 300 runner and Spanish lines of

peanuts. The research has just started and will attempt to correlate the assay with field ratings.

During the sampling of peanut debris for *S. minor*, we collected several sclerotia that upon culturing yielded isolates of *Botrytis cinerea.* As this can be a pathogen on peanuts, we collaborated with Dr. Jim Star to examine peanut cultivar susceptibility to and fungicide sensitivity of these isolates. Of the 53 isolates obtained from field samples, 34 were characterized as pathogenic, 3 as weakly pathogenic and 16 were non-pathogenic based on lesion diameter six days after inoculation on detached leaflets of the cultivars Florunner, NemaTAM, and Tamrun 96. The susceptibility of eight other cultivars and two breeding lines to an aggressive (Gi1E-6) and a less aggressive (DM1-R) isolate was also determined. The cultivars Flavorunner 458 and Valencia C had smaller lesions six days after inoculation with either pathogen than did the other genotypes tested. The breeding line TX 607 had smaller lesions than other genotypes when inoculated with Gi1E-6, but not when inoculated with DM1-R. Several of the pathogenic isolates were assayed for their sensitivity to the fungicides dicloran, fluazinam, and iprodione. Hyphal growth on potato dextrose agar amended with the different fungicides was used to characterize the response of the isolates. Significant variation in growth was observed among the isolates, but all isolates were considered sensitive to these fungicides.

The funds we have received for 2006 made the following publications possible:

Wheeler, T.A., Henry, M.A., and Kenerley, C.M. 2006. Spatial patterns of disease incidence with *Sclerotinia minor* in the initial year of infestation. American Peanut Research & Education Society. Annual Meeting, Savannah, GA (Abstract).

Starr, J.L., Raghvan, T., Henry, M.A., and Kenerley, C.M. 2006. *Botrytis* blight of peanut—pathogen fungicide tolerances and peanut cultivar susceptibility. American Peanut Research & Education Society. Annual Meeting, Savannah, GA (Abstract).

Henry, Merribeth A. 2006. Characterization of *Sclerotinia Minor* Populations in Texas. MS Thesis. Texas A&M University. 80 pages.

Starr, J.L., Raghvan, T., Henry, M.A., Kenerley, C.M., and Wheeler, T.A. 2006. *Bortytis* blight of peanut—cultivar susceptibility and pathogen fungicide sensitivity. Peanut Science (In Press).

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