

Breeding for the Control of Peanut Smut Disease and Genetics of the Pathogen

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Peanut smut disease can cause up to 50 % loss in Argentina where the disease is endemic. Though peanut smut has not been reported in the United States, the USDA-ARS-National Peanut Research Laboratory has worked in collaboration with several research institutions in Argentina to develop molecular tools to understand both, plant resistance and the genetics of the pathogen. We sequenced the 123,773 bp mitochondrial genome and several nuclear genes of *Thecaphora frezii* (succinate dehydrogenase, ergosterol biosynthesis, cytochrome p450 and beta tubulin) that are target of fungicides applied to the peanut crop. This not only provided the basic molecular tools to study the population genetics of *T. frezii*, but also detected mutations that confer resistance to strobilurin fungicides. Introgression of resistance was studied in 94 recombinant inbred lines (RILs) from wild diploid peanuts, and 45 lines resulting from crosses with resistant landraces. In both cases, molecular markers linked to disease resistance were identified. The pathogen, *T. frezii* has shown resistance to most fungicides commonly used in the peanut crop. The study of the genetic diversity of *T. frezii* is still in progress, and a smut resistant variety has been released.