

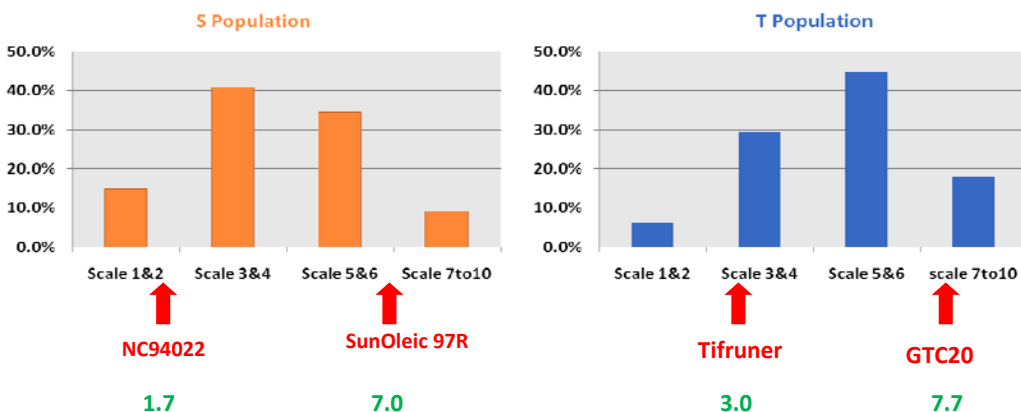
Characterization and Genetic Mapping of Disease Resistance Genes to TSWV and White Mold and Development of Molecular Markers for Breeding Selection

Baozhu Guo, Albert Culbreath, Tim Brenneman, Charles Chen and Corley Holbrook

USDA-ARS and University of Georgia Department of Plant Pathology, Tifton and Dawson

Peanut is vulnerable to a range of diseases, such as tomato spotted wilt virus (TSWV), early (*Cercospora arachidicola*) and late (*Cercosporidium personatum*) leaf spots, and southern stem rot/white mold (*Sclerotium rolfsii*). In peanut production areas in the southeastern U.S., tomato spotted wilt virus disease caused by tomato spotted wilt tospovirus (TSWV) has become more prevalent and more severe. White mold also is a common and often destructive disease of peanut. The most promising solution for managing peanut diseases is using resistant cultivars. Tifrunner has been released as a resistant cultivar to TSWV and leaf spots. New breeding line NC94022 (botanical variety *hirsuta*) has been identified with higher resistance to TSWV by Culbreath et al. (2005). A cultivar having disease resistance and high yield would present tremendous advantages for Georgia peanut growers to remain competitive.

Progress made in 2009: With the support of Georgia Peanut Commission in the past years with financial assistance to a graduate student, we have made progress in developing SSR polymorphic markers in cultivated peanuts, which have been used to assess genetic diversity in cultivated peanuts. Two years field evaluation for resistance to TSWV and leaf spots have confirmed the high resistance to TSWV in NC94022 and Tifrunner. Two genetic mapping populations have been developed, total 248 F6:7s for Tifrunner x GT-C20 and 352 F6:7s for SunOleic 97R x NC94022. 2009 field trails were conducted to evaluate the RILs (F6:7, recombinant inbred lines) for resistance to TSWV and leaf spots (see below chart), and screened about 5000 SSR markers between the parental lines of these two populations for polymorphisms. In 2010, we will complete genotyping the two populations, phenotype S population for TSWV, leaf spot and seed oleic oil content. We will have markers/QTLs for TSWV and high oleic lines. These two mapping populations are in Puerto Rico Winter Nursery for seed increase.



2009 TSWV severity ratings (1-10 scale, 1 = health, 10 = 100% infected and stunted) on July 4 and August 24. Distribution of TSWV disease ratings of two mapping populations based on 352 F5/6 RILs (5'-row) of S-population and 248 F5/6 RILs (5'-rows) of T-population with 2 replications