Date Submitted November 2008 NCARS / NCCES CODE: **NC-14**

IMPACT STATEMENT

Currently, spotted wilt of peanuts is one of the major diseases in the Virginia-Carolina growing area and can dramatically reduce seed weight and yield. Although TSWV is vectored by thrips, chemical control of the thrips usually does not result in reduction of spotted wilt incidence. Cultivar selection is the most important component for reducing the risk of spotted wilt. Therefore, breeding for resistant cultivars appears to have the most potential for minimizing the risk of losses to spotted wilt. Several cultivars with field resistance to TSWV have been released; however, none possesses true resistance to the virus *per se*. Accession GKP 10602 (PI 276235) of *Arachis diogoi* Hoehne, a weedy diploid South American relative of the cultivated peanut, has been shown to possess high levels of resistance to different isolates of TSWV and represents a possible donor of TSWV resistance for cultivar improvement. Marker assisted selection (MAS) is a technique used to improve the efficiency of selection by using DNA technology to determine the presence of desirable genes rather than waiting for gene expression. Markers showing strong association with TSWV resistance can be used to aid in transferring the resistance present in *A. diogoi* GKP 10602 into elite peanut breeding materials. Additionally, finding sources of TSWV resistance among cultivated materials, which would considerably increase the speed of recovery of desirable materials, is extremely important in breeding for spotted wilt resistance.

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__ EXTENSION _X_ RESEARCH
REPORT PERIOD **02/08-11/08**
_X_ INTERIM __ FINAL
Annual Summary

PROGRESS REPORT TO

National Peanut Board

and

North Carolina Peanut Growers Association

TITLE: **Marker Assisted Breeding for Tomato Spotted Wilt Virus (TSWV) resistance in Virginia-type peanuts.**

LEADERS: **S.R. Milla-Lewis, T.G. Isleib, and S.P. Tallury**

DEPARTMENT: **Crop Science**

REPORT:

Given that TSWV carries its own enzymes for replication within the host, and because of the waxy nature of the peanut leaf surface, the procedure for artificial inoculations is extremely sensitive and all conditions must be in place in order to have successful infection. For these reasons, in addition to working with F_2 populations our strategy has been to develop populations that allow replicated testing. Therefore, recombinant inbred lines (RILs) are currently in development and a set $F_{2:3}$ families have been developed. A total of 85 F_4 plants and 75 F_3 plants from the cross *A. kuhlmannii* 7639 x *A. diogoi* 10602 are growing in the greenhouse and being advanced by single seed descent for RIL development. Additionally, seeds from ten individual F_2 plants from the same cross were harvested spring. These $F_{2:3}$ families will be used to validate candidate markers previously identified as associated with TSWV resistance in wild species *A. diogoi*.

Regarding our work with F_2 populations, a total of 185 F_2 plants derived from the cross of Florunner x HTS 02-01 were grown in the greenhouse. Leaf samples were taken from these plants for DNA extractions. Subsequently, plants were inoculated twice with TSWV. Phenotypic data was collected three weeks after the second inoculation. Initially, a total of 170 plants showed symptoms of systemic infection, while fifteen plants presented only local symptoms. However, a month after inoculation all 185 plants showed symptoms of systemic infection. Moreover, all ten plants of HTS 02-01 were also systemically infected. It can be inferred from these results that either initial classification of HTS 02-01 as TSWV resistant was erroneous and while the genotype has some field resistant it is not resistant to the virus per se, or resistance has broken down over time. Marker evaluation of the F_2 population with two of the candidate markers indicated the first is the most likely explanation given that the markers where absent in all individuals.

Work is being conducted to search for new sources of resistance to TSWV among cultivated materials by performing artificial inoculations in the NCSU phytotron. Performing artificial inoculations in a controlled environment allows us to control the temperature accurately, which is extremely important in working with TSWV given that the virus is extremely sensitive to high temperatures. A total of 158 accessions are being evaluated for TSWV resistance: (1) The core of the core of the peanut germplasm collection, which consists of 108 accessions, and (2) a set of 50 breeding lines that show high levels of field resistance to spotted wilt. The experimental design is a split-split plot with three replications. The main-plot factor is virus inoculation treatment (isolates Lew2 collected from Lewiston, NC, and Suf23 collected from Suffolk, VA), and the subplot factor is plant genotype (158 accessions and breeding lines + two susceptible checks, NC 7 and NC 9, + one resistant check, *A. diogoi* 10602). Seventy percent of the genotypes have been evaluated on a first trial. A set of six accessions of the core of the core collection and five breeding lines showed no symptoms of systemic infection and appear to be virus resistant. These genotypes will be reevaluated on subsequent runs of the experiment to confirm their initial disease response.

SUMMARY OF EXPENDITURES: Expenditures for 2008 on this project total $4,271.24 including $2,108.94 for expendable greenhouse, laboratory supplies necessary to conduct the TSWV artificial inoculations, and use of the DNA marker facility, and $1,690.80 in salary used to support a student worker who was needed to aid with maintenance of plants, and provide assistance with artificial inoculations, DNA extractions and marker work, and $471.50 for travel to attend the APRES meetings in Oklahoma City, OK.