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2013 SPRI/NPB research project Final Report (March 31, 2015)

Project End Date: 06/30/2014

Report Due Date: 3/31/2014

Funding Agency: SPRI/NPB

Project Title: Develop molecular markers and saturated genetic maps that can be used to identify quantitative trait loci (QTLs) associated with important agronomic traits such as resistance to TSWV, leaf spots and oil quality traits

Identification of peanut resistance genes and markers for TSWV and leaf spot diseases. Peanut is vulnerable to a range of diseases, such as leaf spots and Tomato spotted wilt, which cause yield loss and increase chemical control cost every year. The most promising solution for managing peanut diseases is using resistant cultivars. In collaboration with researchers at the University of Georgia and the University of Florida, we have developed two genetic maps from crosses of Tifrunner × GT-C20 and SunOleic 97R × NC94022. These two maps have been used for identification of molecular markers linked to resistance to the diseases of Tomato spotted wilt, early leaf spot and late leaf spot, and also used for identification of markers associated with oil quality such as high oleic acid and total oil content. Molecular markers will short breeding cycle from over 10 years to less than five years. Peanut growers have been supporting research to develop molecular markers for resistance and molecular breeding for resistant cultivars with high oleic content. The developed resistant cultivars will give farmers a better and more effective management tools for diseases and produce high quality peanuts. This is the first study for identification of molecular markers for TSWV and leaf spots, and future studies will be needed to refine the locations of these markers on the map.

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One mapping population derived from Tifrunner  $\times$  GT-C20 has shown great potential in developing high dense genetic map and identification of QTLs for important diseases, Tomato spotted wilt virus (TSWV) and leaf spot (LS). Both F<sub>2</sub> and F<sub>5</sub> generation-based maps were constructed previously with 318 and 239 marker loci, respectively. Higher map density could be achieved with the F<sub>2</sub> population (5.3 cM/locus) as compared to the F<sub>5</sub> (5.7 cM/locus). QTL analysis using multi-environment phenotyping data from F<sub>8</sub> and higher generation for disease resistance identified 54 QTLs in the F<sub>2</sub> population including two QTLs for thrips (12.14 – 19.43% PVE), 15 for TSWV (4.40–34.92% PVE) and 37 for LS (6.61–27.35% PVE). Twenty-three QTLs could be identified in F<sub>5</sub> map including one QTL for thrips (5.86% PVE), nine for TSWV (5.20 – 14.14% PVE) and 13 for LS (5.95–21.45% PVE). Consistent QTLs identified in each map have shown higher phenotypic variance than non-consistent QTLs. As expected, the number of QTLs and their estimates of phenotypic variance were lower in the F<sub>5</sub> population. This is the first QTL study reporting novel QTLs for thrips, TSWV and LS in peanut, and thus, future studies will be conducted to refine these QTLs.

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