Development of peanut varieties with stem rot resistance and potentially more synchronous maturity using marker assisted selection

Akshaya K Biswal[1], Peggy Ozias-Akins[1], Corley Holbrook[2], Tim Brenneman[1]
[1]University of Georgia Tifton Campus, Tifton, GA 31793, [2]USDA-ARS Coastal Plain Experiment Station, Tifton, GA USA 31793

In 2023, peanut stem rot (SR) (also known as white mold) caused an estimated $81.6 million in economic losses to Georgia peanut growers, including the disease management cost. Stem rot is caused by a fungus *Agroathelia rolfsii* that survives in the soil and crop debris. It germinates under favorable conditions leading to rapid mycelial growth and infection of plant tissues in contact with the soil. Cost of fungicide applications is steadily increasing every year. Therefore, developing disease resistant cultivars would bring economic and environmental benefits across the value chain. Buyer preference and economic factors such as yield, and market value are the deciding factors for selecting peanut cultivars by growers. Thus, our breeding program has crossed multiple cultivars and accessions to generate varieties with new combinations of alleles for SR resistance, yield, and quality. One such cross with potential for SR resistance was made between two high-yielding runner type cultivars MarcI and Georgia 12Y (GA-12Y). MarcI is early maturing, SR susceptible variety while GA-12Y is late maturing and resistant to both stem rot and tomato spotted wilt virus (TSWV). A second cross was made between a recombinant inbred line RIL703 and C2578-1, one of the advanced breeding lines of Dr. Corly Holbrook. RIL703 inherits high level of SR resistance from NC 3033.

Total 192 F3 lines from MarcI × GA-12Y cross (GA-12Y-population) and 96 F3 lines from C2578-1 × RIL703 cross (RIL703 population) were screened for SR resistance in 2024. A sophisticated phenotyping protocol, developed at UGA, Tifton, was used for SR screening. Briefly, five seedlings per row per 15 ft plot were transplanted evenly among the direct-seeded GA-12Y seedlings, one month after germination. A highly aggressive strain of *A. rolfsii* isolate (SR-18) was used for field inoculation. The disease symptoms were visible after about 2 weeks. The stem rot damage was rated after two, three, five weeks post-inoculation and during harvesting (eight weeks). Each hybrid plant was individually rated on a 0 – 5 scale for stem rot susceptibility. Seventy GA-12Y-derived lines and 33 RIL703-derived lines showed disease score 1 – 2 at the time of harvesting while susceptible controls and some hybrids died completely (Fig. 1). The hybrids matured 1 – 2 weeks later than MarcI. Our preliminary analysis indicated that some of the hybrid lines produced higher seed weight than both parents.

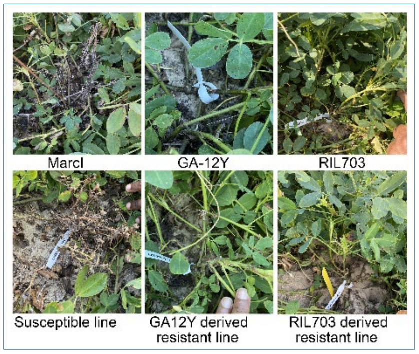

Figure 1: Selection of WM resistance

All lines were genotyped by sequencing at Hudson Alpha. Analysis of the genotypic and phenotypic data identified a genomic region on chromosome 9 of GA-12Y with strong correlation to the stem rot resistance from (Fig. 2). The analysis of RIL703 derived lines is in progress.

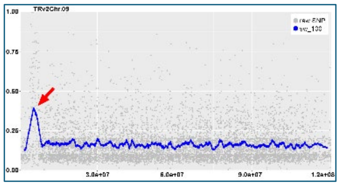

Figure 2:The Stem rot resistance genomic region from GA-12Y indicated by the red arrow.

F4 seeds, collected from each of 23 RIL703-derived and 52 GA-12Y-derived highly resistant lines, were multiplied in our greenhouse in Spring 2024. All F5 lines were evaluated for white mold resistance during Summer 2025 using small (5-ft) plots, in randomized block design with 1 – 3 replications depending on seed availability. Two plants per plot were manually inoculated with SR fungus. Though some plants from most of the lines showed high SR resistance, our analysis indicated that these lines are still segregating the SR resistance. Seeds were collected from the most resistant line from each plot and are being multiplied at the winter nursery in Puerto Rico. F7 lines will be assessed for SR resistance in summer 2026. Lines with high resistance and synchronous seed maturity will be selected for developing SR resistant variety. Molecular markers will be developed for fast and precise transfer of resistance to other farmer-preferred varieties.

In summary, we have identified 75 highly SR resistant peanut lines by field screening. Additionally, we have identified a genomic region responsible for GA-12Y derived stem rot resistance.