

Progress report on Expansion of resistance sources to leaf spots and TSWV for peanut breeding

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Our year 2020 proposal had two main objectives 1) phenotypic selection for LS resistance among BC₁F₂ individuals from top yielding BC₁F₁s derived from backcrosses of [IpaDur]^{4x}, [Valsten]^{4x}, [IpaCor]^{4x} and [IpaSten]^{4x}. 2) Due to the field TSWV resistance identified in [MagSten]^{4x}, backcrosses using F₁ hybrids from 5-646-10 x [MagSten]^{4x} and 13-1014 x [MagSten]^{4x} would be made this year.

To achieve the first research objective, 1200 BC₁F₂ seeds from 40 best yielding BC₁F₁ plants (harvested from 10 plants of each of the four allotetraploid combinations) were planted in the Rigdon farm on June 1st, 2020. Planting density was kept at two seeds per foot. Most of the BC₁F₂ seeds germinated and leaf disks were taken from seedlings and stored in -80 C for DNA extraction. Due to the presence of 25% wild genome in these backcross materials, most of the BC₁F₂ plants demonstrated wild canopy architecture. The highly branching canopy with long



Figure 1. Dense planting and lack of weed control prevented effective disease rating of BC₁F₂ individuals.

spreading vines resulted in intertwining of branches among neighboring plants. In addition, weed control of Rigdon farm was not managed properly which exacerbated the challenge of performing proper disease ratings of single plants (Figure 1). Since we could not collect reliable phenotypic data on LS resistance, we decided not to pool the tissues for further QTL-seq analysis. The wild architecture of these materials demands more space in between plants for single plant disease evaluation. Paradoxically, if the plants are spaced out, the canopy density and architecture of some lines may not be sufficient to encourage LS development. Therefore, evaluating leaf spot resistance for single plants with high dosage of wild introgression was determined to be unrealistic. To make up for this the experiment, we will redo phenotyping on 200 lines of BC₁S₃ populations of the four combinations that will be harvested from Puerto Rico in March 2021. Although complete formation of back cross inbred lines (BILs) will need a couple more rounds of selfing,

BC₁S₃ will be advanced enough for an initial screen of disease resistance. The BC₁S₃ lines with sufficient seed number will be planted as replicated small plots at a seeding rate of 3 seed per foot in 2021. Based on our experience, this planting density will encourage the emergence of leaf spot disease. We will improve weed management this year as well. Data collected from the 2021 test will be reported to Peanut Commission in 2022.

As for objective 2, further backcrosses of 13-1125 x [5-646-10 x [MagSten410]^{4x}] were made yielding 78 BC₁F₁ hybrid seeds. Additional genotyping data analysis indicated that our [MagSten410]^{4x} should be [IpaCor]^{4x}. The misidentification could stem from the initial diploid cuttings from NC. Regardless, we will keep these BC₁F₁ lines separate for advancement and perform TSWV field tests in later generations.