

Characterize Leaf Spot Resistant Loci Through Image Analysis of Advanced Breeding Lines in the NCSU Peanut Breeding Program

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Phenotypic data for leaf spot has historically been collected visually. The subjective nature of evaluating leaf spot resistance on a whole-plot basis may introduce rater, trial and/or environmental biases leading to inaccurate selection. Data collected using a scaled convention limits the evaluation to overall leaf spot symptoms on a whole-plot basis. In addition, efforts to manually count individual lesions, especially while differentiating early versus late leaf spot, have been limited and error-prone. In order to address this issues, a total of 220 genotypes were grown at the Peanut Belt Research Station (Lewiston-Woodville, NC) for the characterization of leaf spot pressure and differentiation in resistance using a low-throughput image-based method. During the evaluation process (August – October), plots were routinely rated visually using the Florida scale (1-9); leaf tissue from each plot was evaluated for percent leaf spot lesions using customized Fiji (ImageJ) scripts; and aerial images were captured using a Mavic 2 Pro drone in order to evaluate percent defoliation. The overall objective of this project was to correlate the visual ratings to the weighted evaluation of percent leaf spot lesions and defoliation and to identify and target introgression blocks associated to resistance. Results after the first year of analysis indicate a distribution of leaf spot ratings, especially among lines that were whole-genome sequenced. The alignment of the whole-genome sequences should reveal resistance blocks that have been selected within the NCSU peanut breeding program stemming from introgressions from plant introductions (PI) and from wild diploid sources, *A. cardenasii* and *A. diogeni*.