

Mutmap and Whole Genome Re-Sequencing to Identify Gene(s) Controlling Peanut Resistance to Early Leaf Spot and/or Late Leaf Spot Diseases

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Early leaf spot (ELS) (*Passalora arachidicola*) and late leaf spot (LLS) (*Nothopassalora personata*) are two devastating foliar diseases in peanut (*Arachis hypogaea*) wherever peanuts are planted. Quantitative trait loci (QTLs) associated with peanut resistance to ELS and/or LLS have been reported but often were inconsistent. We developed a MutMap population derived from a crossing of a susceptible mutant 71-2 to the parental line Tifrunner, used for TILLING (Targeting Induced Local Lesions IN Genomes) mutagenesis. The objectives are to identify the associated gene(s) controlling the resistance/susceptibility to ELS or LLS or both by whole genome sequencing of the segregating population and phenotypic evaluation of the parent and mutant lines in the greenhouse by controlled inoculation and field study. This MutMap population consists of 97 segregating F_{2:3} lines (TL) which were sequenced at low coverage along with the parent, two mutants, the susceptible mutant 71-2 and the retained resistance mutant 90-1, including 12 lines derived from the cross of 71-2 x 90-1 (TM). We used a highly accurate sequence analysis pipeline called KHUFU, allowing for low coverage sequencing that can be used to genotype these two “TL” and “TM” populations with increased power and precision. Single nucleotide polymorphisms (SNPs) were called using the KHUFU pipeline, and SNPs specific for each line ranged from 5 to 8118. These sequencing data and SNPs have been analyzed to visualize genetic variation across the populations and initially to identify mutations in corresponding genome regions of resistance or susceptibility from published QTLs. We have found that there is increased SNP density in Chromosomes A02 to A06 and the “TL” and “TM” populations are similar enough to cluster together in phylogenetic trees, but diverse enough from each other to create a 4th group in structure analysis, meaning these populations can be used to aid in identifying the resistance gene(s) or genome regions harboring the genes or mutations causing the susceptibility. Phenotyping in the field and greenhouse are currently in progress. The associated genes, SNPs, and markers will be used for molecular breeding for ELS and LLS resistant peanut cultivars.