

## **Genome-wide Approach to Investigate Peanut (*Arachis hypogaea*) Resistance to Early Leaf Spot and Late Leaf Spot Using a Peanut MAGIC Population**

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As DNA sequencing costs decrease and bioinformatics advances, it is increasingly feasible for genetic and genomic mapping studies to be based on whole genome sequencing data, even for large populations. The resolution of genetic mapping is often insufficient to pinpoint causal genes in bi-parental and smaller-sized populations. Recently, we developed a multiparent advanced generation intercross (MAGIC) population with eight parental founders to conduct high-resolution mapping of quantitative traits, including peanut early leaf spot (ELS) and late leaf spot (LLS). This population comprises 2775 F<sub>7</sub> recombinant inbred lines (RILs). A subset of 310 RILs were randomly selected to evaluate the suitability of the population for genetic and genomic studies and to map the causal QTLs or genes precisely. The genotyping was conducted by whole genome re-sequencing at low coverage, and SNPs were called using a new sequence analysis pipeline KHUFU. The phenotypic data collected in the first year include disease rating for leaf spots, total seed oil chemistry, pod constriction and reticulation, 100 pod-weight, 100 seed-weight, and shelling percentage. These phenotypic data showed significant variation within this MAGIC population and demonstrated normal distribution for all traits, indicating the potential utility of this MAGIC as a new genetic resource for dissection of complex traits and for breeding selection. The controlled inoculation in the greenhouse and laboratory will be carried out for parental lines to confirm the resistance/susceptibility to ELS and LLS pathogens. Analysis of sequencing data and multi-year phenotypic data are in progress. This peanut MAGIC could serve as an important resource used for fine map of disease resistance, yield, and quality.