

Genetic and Genomic Characterization of MAGIC Peanut for Fine Mapping and Breeding Application

Ethan Thompson^{1,2}, Hui Wang^{1,2}, Walid Korani³, Albert K. Culbreath¹, C. C. Holbrook², Josh Clevenger³, Baozhu Guo²

¹University of Georgia, Department of Plant Pathology, Tifton, GA

²USDA-ARS, Crop Genetics and Breeding Research Unit, Tifton, GA

³HudsonAlpha Institute for Biotechnology, Huntsville, AL

Peanut (*Arachis hypogea* L.) is an important global crop and has low genetic diversity with an allotetraploid genome. Biparental populations have been dominating peanut genetic and genomic studies in recent decades. With the advances in genome sequencing and computational bioinformatics, multiparent population is needed for both dissecting genomic structure and breeding improvement. We have produced a multiparent advanced generation inter-cross (MAGIC) population with 2,775 recombinant inbred lines (RILs) derived from eight diverse founders, called MAGIC Peanut. The characterization of a subset of 310 RILs randomly selected from MAGIC Peanut shows that the MAGIC Peanut is a balanced and evenly differentiated mosaic of chromosomal segments from the eight founder parents. There are 138,151 SNPs identified using whole genome resequencing and reference-based SNPs called by the Khufu informatics pipeline. We demonstrated that this subset of MAGIC Peanut might achieve high-definition QTL mapping of quantitative traits such as seed/pod characterization and shelling percentage, and qualitative traits like oil quality and disease resistance of TSWV, leaf spots and nematodes. Therefore, the MAGIC Peanut is a powerful new resource in peanut to increase our understanding of the genetic and genomic basis of important quantitative traits and its application in breeding programs. MAGIC Peanut will be available for peanut research community to use.