

Genome Wide Association Studies Reveal Novel Loci for Resistance to Groundnut Rosette Disease in Cultivated Peanut (*Arachis hypogaea* L.)

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Groundnut Rosette Disease (GRD) is the most devastating biotic stress of peanut in Africa. The disease is widespread in Sub-Saharan Africa (SSA) and its off-shore islands resulting in 100% yield loss in severe cases. GRD is caused by a complex of three viral agents, transmitted by an aphid, *Aphis craccivora* Koch. Host plant resistance towards aphids or the virus is the most effective approach in the management of the disease for resource limited farmers across Africa. Efforts from breeding programs across Africa have resulted in the release of tolerant varieties however, the genetic basis of GRD resistance is not fully understood. Insights into the genetic control of GRD resistance will guide breeding approaches and facilitate marker assisted-breeding.

Two hundred genotypes representative of the diversity of peanut across breeding programs in Africa were phenotyped in two seasons; across two GRD hotspots (Serere and Nakabango) in Uganda. Data was collected on Percentage Disease Incidence and GRD severity at 4, 8 and 12 weeks after planting. Genotyping was performed using the Axiom Arachis Vs2 SNP array. BLUPs for percentage disease incidence in each location were generated in R version 4.0.3. GWAS analysis was done using MLM methods in TASSEL 5.2.20 with a Bonferroni cut off of $P < 6.15E-06$ as the significance threshold. Candidate genes within 6Kb of the associated SNPs were identified on Peanutbase. Consistent and significant SNP associations with GRD resistance were observed across locations and seasons with 90% of the significant SNPs located on either Chromosome A04 or B04. Several putative genes were identified including a disease resistance protein of the TIR-NBS-LRR whose role is to provide signal transduction and elicit defense response against pathogens in the plant and an Argonaute family protein which plays a central role in RNA silencing of the Virus. Results reported in this study provide insight into the genetic architecture of GRD resistance and thus the basis for development of molecular markers for Marker assisted selection for GRD resistance.