

## **Understanding the Genetics of Resistance to Groundnut Rosette Disease**

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Groundnut Rosette Virus (GRV) causing Rosette Disease (GRD) in groundnuts, is the most destructive disease in Sub-Saharan Africa. While the development of GRD resistant varieties is the most sustainable way of managing the disease, the genetics of resistance is not well understood. In Zambia, most of the farmer-preferred groundnut varieties are susceptible to GRD and there are no genetic and genomic resources developed to enhance the selection and improve the understanding of GRD resistance. The aim of the current study was to make use of existing resources to understand the genetic control of GRD resistance in Zambian groundnut. An existing bi-parental mapping population was phenotyped in two seasons under screen house conditions for their response to GRD. The top ten most susceptible and top most resistant genotypes were selected for QTL-sequencing using Illumina technology. Phenotypic and genotypic data were analysed using Genstat v18 and in-house scripts respectively. A joint phenotypic and genotypic data analysis was done to establish marker-trait associations using SVS software. Molecular markers with significant associations were selected for further development of KASP assays for future routine marker-assisted selection for GRD resistance. The new markers were validated across six bi-parental mapping populations developed between known sources of resistance and susceptible farmer-preferred genotypes in Zambia. We observed strong signals across the syntenic locations of chromosomes 4 and 14 suggesting the involvement of a major gene in the control of GRD resistance. Our results provide an immediate resource for more efficient selection for GRD resistance. We recommend the identification of more sources of resistance and pyramiding the desirable loci into farmer-preferred varieties to avoid future breakdown of the resistance observed.