

Identifying the Alternative Host(s) of Groundnut Rosette Disease Virus Complex and the Vector Role in Disease Spread and Carryover

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Groundnut crop losses due to Groundnut rosette disease (GRD) are endemic across Sub-Saharan Africa. The disease causes significant economic losses, jeopardizing food security and the livelihoods of groundnut farmers. To date, no alternative host plants have been identified that could act as a source of inoculum. subsequently, the epidemiology of the disease is poorly understood, creating gaps in disease management options. GRD is caused by an interaction of 3 agents; groundnut rosette assistor virus (GRAV), groundnut rosette virus (GRV), and the satellite RNA (satRNA) of GRV. The disease is transmitted persistently by the aphid, *Aphis craccivora* Koch.

In this study, we have surveyed 3 GRD hotspots and 1 major growing district in the different agro-ecological zones of Uganda for GRD. In each zone, plants showing GRD symptoms and/or having colonies of *Aphis craccivora* were identified and samples were collected.

Using RT-PCR, in addition to the groundnut ratoon/groundkeeper plants, we have identified 2 alternative hosts with all the 3 GRD agents and the other 6 with both GRAV and satRNA. We have also established the to and from vector transmission possibility of the 3 GRD agents between groundnuts and 4 of the alternative hosts inclusive of *Crotalaria incana* L, *Cassia hirsuta* L, *Physalis peruviana* and *Sesamum angustifolium*.

Our study also examined the distribution and diversity of the vector in relation to the different hosts and the GRD agents within the described study area and identified 4 aphid species majority (63/98) of which were *Aphis craccivora*, which were also diverse with 10 haplotypes that exhibited specificity to particular hosts. With RT-PCR, GRD agents were mainly detected among *Aphis craccivora*. *Aphis citricidus* and *Aphis gossypii* were also diagnosed with GRV and satRNA.