

RNA sequence analysis of diseased groundnut (*Arachis hypogaea*) reveals the full genome of groundnut rosette assistor virus (GRAV).

## Abstract

The complete genome sequences for two variant isolates of groundnut rosette assistor virus (GRAV) have been determined from symptomatic groundnut plants in western Kenya. The sequences of the two GRAV isolates (sc7.1 and sc7.2) are 84.2% identical at the nucleotide level and 98.5% identical at the coat protein level. The variants sc7.1 and sc7.2 comprise 5850 and 5879 nucleotides respectively, and show similar genome organizations with 7 predicted ORFs (P0, P1, P2, P3a, P3 (coat protein, CP), P4 (movement protein, MP) and P5 (coat protein-readthrough protein, CP-RT). Currently, GRAV is an unassigned virus in the *Luteoviridae* family, due to the fact that only the sequence of the coat protein was previously obtained. The presence of both ORF0 and ORF 4 within the genome sequence determined in the current work suggest that GRAV should be classified as a member of the genus *Polerovirus*.

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