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## Exploring the diverse world of cassava virus diseases: Advances and innovations

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### Abstract

Cassava is a staple crop for millions of people, yet its production is severely threatened by a wide range of viral diseases. Our work focuses on understanding cassava viruses, identifying sources of resistance, and developing practical strategies to protect this important crop. In our work, we use an extensive virus collection from South America, Africa, Brazil, and Asia to study both established and emerging pathogens affecting cassava.

Our research covers several interconnected areas. We identify and characterise causal agents of major cassava diseases, including cassava root rot, cassava witches' broom, cassava frog skin disease, cassava mosaic disease, and cassava brown streak disease. We also investigate host-virus interactions, with particular focus on cassava brown streak viruses and cassava mosaic viruses, using molecular tools, confocal microscopy, infectious clones, and modified viral genomes. These approaches allow us to follow infection processes in cassava and *Nicotiana benthamiana* and to better understand viral replication, movement, symptom development, and resistance responses. A major achievement of our work has been the identification and characterisation of cassava lines resistant to Cassava Brown Streak Disease, one of the most serious threats to food security in sub-Saharan Africa. By exploring cassava diversity from its center of origin in South America, we identified valuable resistant germplasm, defined resistance patterns, and supported the deployment of these resources to disease-affected regions in Eastern and Central Africa. We continue to expand this work by integrating additional resistance traits and evaluating the durability of resistance under field conditions. To uncover the mechanisms behind resistance, we combine high-throughput screening, omics technologies, high-resolution imaging, Genome-Wide Association Studies, mapping by sequencing, and small RNA analysis. These studies have highlighted viral and host factors involved in resistance, including the role of the Ham-1 gene in virus replication, movement, symptom expression, and resistance. Additional signals on chromosomes 11 and 3 suggest possible host genomic regions associated with CBSV and UCBSV resistance, while small RNA sequencing has revealed novel miRNAs and lipid-transfer-related genes that may contribute to plant immunity.

Overall, our research links fundamental virus biology with translational plant health solutions, aiming to support virus exclusion, resistance deployment, and sustainable cassava production for farming communities worldwide.

**Keywords:** Cassava, cassava brown streak disease, cassava mosaic disease, cassava viruses, food security, germplasm screening, host-virus interactions, plant health, plant immunity, virus resistance