



Tropentag, September 10-12, 2025, hybrid conference

“Reconcile land system changes
with planetary health”

Mapping the path to resistance: Genetic and molecular strategies against cassava brown streak disease

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Abstract

The scope of our research focuses on cassava diseases worldwide, aiming to understand disease agents, develop control strategies, and mitigate their impact. We base our work on our expanding collection of viruses and virus-like agents originating from South America, Africa, and Asia and the worldwide collaboration among cassava researchers from international and local research institutions.

A key element of our virus work focuses on combating the severe Cassava Brown Streak Disease (CBSD) which is a critical threat to food security in Sub-Saharan Africa. We identified and characterised resistant cassava lines from South America, the center of origin of cassava, defined lines with differential virus resistance, organ specific resistance and immunity and deployed these valuable genetic resources to epicenters of the disease in Eastern and Central Africa and, to regions at risk for pre-emptive breeding.

To understand virus resistance responses of cassava, cDNA clones of cassava brown streak viruses and modified virus genomes were used to infect cassava and *Nicotiana benthamiana* to unravel viral and host genes associated with resistance. Notably, the Ham^{-1} gene was identified as a pivotal player for cassava infections implicated in virus replication, movement, symptom expression, and resistance in cassava.

To further understand plant resistance, we conducted Genome-Wide Association Studies (GWAS), mapping by sequencing, and small RNA analysis on resistant and susceptible plants. Weak signals from GWAS and GBS on chromosome 11 implicated NLR genes as potential contributors to CBSV resistance. Additional signals on chromosome 3 were associated with UCBSV resistance, warranting further verification. Small RNA sequencing further identified novel miRNAs implicating lipid transfer genes as potential players in plant immunity. Preliminary proteomic data provided evidence for a lipid-binding protein as candidate for resistance, while transcriptomic data highlighted heat shock proteins as important candidates in early stages of cassava infection.

To investigate the genetic relationships between South American cassava lines and those from other regions, we constructed a phylogenetic tree, which revealed distinct clusters. Additionally, weighted gene co-expression network analysis (WGCNA) using public RNA-seq data indicated co-expression of gene modules that warrant further investigation. These findings contribute to our understanding of viral and host factors regulating resistance to viruses infecting cassava.

Keywords: Cassava, South America

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