Characterization and Epidemiology of Rice Yellow Mottle Virus Disease in Uganda

ABSTRACT

Rice (*Oryza sativa L*) is a critical global food crop, providing 20% of calorie intake for over 3.3 billion people. In Uganda, annual rice production is approximately 350,000 MT, contributing $104 million in import substitution. However, domestic production falls short of demand, largely due to low yields (2.5 tons/ha) caused by pests and diseases. Rice yellow mottle virus disease (RYMVD), caused by Rice yellow mottle virus (RYMV), is the most significant biotic constraint, with yield losses ranging from 10–100%. Despite introducing resistant varieties, RYMV infections have increased, particularly in new areas like northern and western lowlands. The surge in infections and reports of resistance-breaking isolates suggest the virus may have mutated, necessitating deeper investigation.

This study aimed to enhance knowledge of RYMV diversity and epidemiology for improved management in Uganda's lowland areas. The research objectives included: assessing the occurrence and distribution of resistance-breaking isolates, quantifying molecular diversity and relationships with African strains, and evaluating pesticide use and variety mixtures in managing RYMV dynamics. Using DAS-ELISA, RT-PCR, and differential cultivars, resistance-breaking isolates were confirmed, predominantly in eastern Uganda. The *rymv1-2* gene was found ineffective, while *rymv1-3* and *rymv1-5* were identified as reliable candidates for resistance breeding. Molecular analysis revealed limited RYMV diversity (3% nt, 1% aa) among Ugandan isolates, clustering closely with strains from Kenya, Tanzania, and Madagascar, but distant from West African isolates.

A novel RT-PCR diagnostic assay targeting the coat protein region was optimized, detecting RYMV with high accuracy. Field trials demonstrated that Neem oil application and variety mixtures significantly reduced RYMV spread and vector diversity. Applying insecticides during the juvenile plant stage minimized yield losses. These findings suggest prioritizing *rymv1-3* and *rymv1-5* for breeding programs, alongside gene pyramiding strategies. The developed assay offers a rapid detection tool for screening new cultivars, and further large-scale trials on pesticides and variety mixtures are recommended for validation.

Keywords: Reverse transcriptase, polymerase chain reaction (RT-PCR)