

The genetic diversity and pathogenicity of rice yellow mottle virus in Tanzania

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Tanzania is severely affected by Rice yellow mottle virus (RYMV). But, little information is known on the distribution, genetic diversity and pathogenicity of local strains of RYMV. Fifty three isolates collected from selected regions in Tanzania were characterized both serologically and molecularly then the pathogenicity of selected isolates was compared. Three RYMV strains S4, S5 and S6 were confirmed. An overall strain diversity was high with nucleotide divergence of 14.8%. The genetic diversity was exceptionally high in the eastern Tanzania ($7t$) = 6.1% and decreased westward to (n) = 1.8%. Isolates of strain S4 were recorded for the first time in the Eastern Arc Mountain region (EAM) and they were closely related to L. Malawi strain S4 isolates. Pathogenicity of RYMV isolates was largely cultivar dependent. There was a positive correlation ($r = 0.78$) between symptom intensity and yield loss. Eight virulent isolates broke the resistance found in Gigante and Tog5681. These isolates had a single substitution mutation at position 48 of the VPg sequence (changes from arg to glu). The findings have reinforced the proposition that EAM region is the centre of origin of RYMV and brings forth a clear view of dispersion of the strains from its centre of origin. The results also underlines the potential risk associated with the effectiveness of genetic control of rice yellow mottle virus based solely on the use of high resistance to RYMV. Farmers should be well informed of the different means of virus transmission because most of the massive infections occur following crop transplantation, weeding and irrigations.