



## Rice yellow mottle virus in rice in Rwanda: first report and evidence of strain circulation

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Rice yellow mottle virus (RYMV), of the genus *Sobemovirus*, has a narrow host range restricted to wild and cultivated rice (*Oryza sativa* and *O. glaberrima*) and a few other poaceous species (Bakker, 1974). RYMV is transmitted by beetles (Bakker, 1974), by various mammals (Sarra & Peters, 2003) but not by seeds (Bakker, 1974). It is also transmitted by man during cultural practices (Traoré *et al.*, 2006). First reported in Kenya in 1966, RYMV was later found in many rice-producing countries in Africa, but not in most parts of Central Africa (Traoré *et al.*, 2009). Rwanda is a mountainous country at the eastern part of Central Africa bordered by the Democratic Republic of Congo in the west, Burundi in the south, Uganda in the North, and Tanzania in the east. Recently, a joint survey by the Africa Rice Center (AfricaRice) and the Institut des Sciences Agronomiques du Rwanda (ISAR) reported a high incidence of plants with yellowing and mottling symptoms ending in complete crop failure at Cyabayaga in northern Rwanda and at Cyili in the southeast (Fig. 1). In 2009, plants with these symptoms (Fig. 2) were collected from local (Gakire) and improved (WAT 543-45-2, WAT 1395-B-24-2) rice varieties in three major rice-producing regions of Rwanda (Bugarama, Cyili, Cyabyaga). Mechanical inoculation of leaf extracts on the susceptible rice varieties BG90-2, Bouaké 189 and IR64 reproduced the typical RYMV symptoms.

A 1008-nt product obtained from fourteen isolates from the three rice-producing regions of Rwanda (including the 720-nt long coat protein gene which was subsequently used for phylogenetic analysis) was amplified by reverse transcriptase-polymerase chain reaction and sequenced (Pinel *et al.*, 2000). The primer set consisted of 5'-CAAAGATGGCCAGGAA-3' (forward primer) and 5'-CTCCCCACCCATCCCGAGAATT-3' (reverse primer). Sequencing thus permits the presence of RYMV in Rwanda to be confirmed for the first time, although symptoms of RYMV have been observed for several years (Fig. 1). The sequences were compared to a set of 39 isolates from Tanzania, Uganda and Kenya (Pinel-Galzi *et al.*, 2009). Isolates from Rwanda belonged to two different strains (Fig. 3). One strain consisted of isolates from southern Uganda, western Kenya and northern Tanzania collected around Lake Victoria and accordingly referred to as "Lake Victoria" strain (S4-lv) (Pinel-Galzi *et al.*, 2009). The other strain consisted of isolates mostly found in southwest Tanzania along Lake Malawi and, accordingly, referred to as "Lake Malawi" strain (S4-lm) (Pinel-Galzi *et al.*, 2009). The two strains differed by approximately 7% in nucleotide sequence. Within each strain, the isolates of Rwanda formed a monophyletic clade with a high branch support (>0.9) and shared over 97% nucleotide identity. Year-round growth of wild and cultivated rice

around Lake Victoria ensures host continuity in time and space that facilitates spread and accounts for the presence of S4-lv strain in Rwanda. Presence of the S4-lm strain in rice-growing regions, mostly near the Congo and Burundi borders, suggests the spread of RYMV over long distances, possibly along the rice growing regions of eastern Tanzania bordering Lake Tanganyika. Rwanda is the only country with a geographical overlap of the S4-lv and S4-lm strains, suggesting the current spread of these strains despite intervening hills and mountains.

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Figure 1



Figure 2

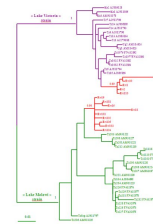


Figure 3

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