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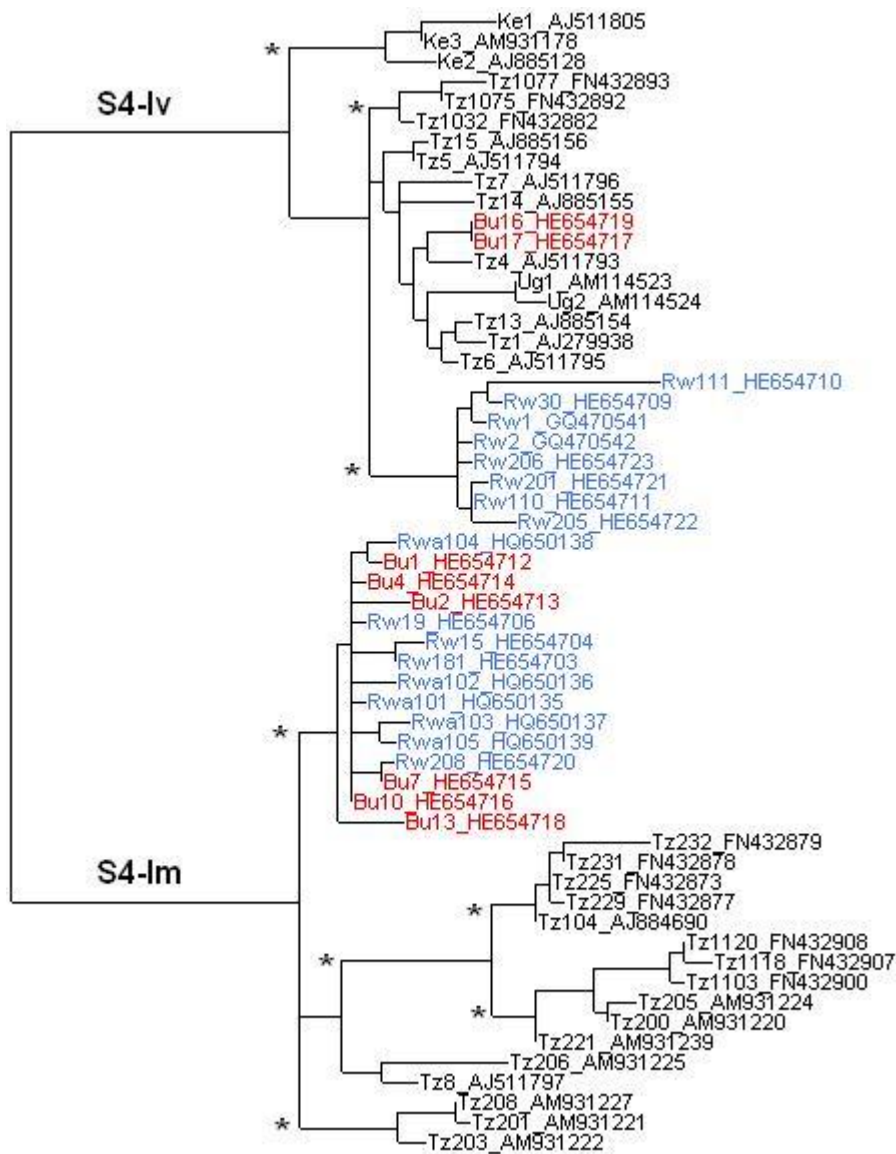
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## First Report of *Rice yellow mottle virus* on Rice in Burundi

**I. Ndikumana**, Crop Production Unit, Rwanda Agriculture Board, P.O. Box 5016, Kigali, Rwanda ; **A. Pinel-Galzi**, UMR RPB, Institut de recherche pour le developpement (IRD), BP 64501, 34394 Montpellier cedex 5, France; **Z. Negussie**, Africa Rice Center (AfricaRice), P. O. Box 33581, Dar es Salaam, Tanzania; **S. N'chimbi Msolla** and **P. Njau**, Sokoine University of Agriculture, P.O. Box 3000 Morogoro, Tanzania; **R. K. Singh**, International Rice Research Institute (IRRI), P. O. Box 33581, Dar es Salaam, Tanzania; **I. R. Choi**, IRRI, DAPO Box 7777, Metro Manila, Philippines; **J. Bigirimana**, University of Burundi, P.O. Box 5132 Bujumbura, Burundi; and **D. Fargette** and **E. Hébrard**, UMR RPB, IRD, BP 64501, 34394 Montpellier cedex 5, France.

Since the mid-1980's, rice cultivation has expanded rapidly in Burundi to reach in 2011 ca. 50,000 ha. In 2007, leaf mottling, reduced tillering and stunting symptoms were observed on rice at Gatumba near Bujumbura causing small patches in less than 10% of the fields. *Rice yellow mottle virus* (RYMV, genus *Sobemovirus*) - which has seriously threatened rice cultivation in Africa (1) and was recently described in the neighbouring Rwanda (3) was suspected to be involved because of similar symptoms. To identify the pathogen which caused the disease in Burundi, a survey was performed in the major rice-producing regions of Burundi and Rwanda. Six locations in Burundi and four in Rwanda were investigated in April and October 2011. Disease incidence in the fields was estimated to be 15%  $\pm$  5%. Symptomatic leaves of 24 cultivated rice plants were collected and tested by DAS-ELISA using polyclonal antibodies raised against the RYMV isolate Mg1 (2). All tested samples reacted positively. Four isolates were inoculated on susceptible *Oryza sativa* cultivar IR64 (2). The typical symptoms of RYMV were reproduced seven days after inoculation whereas the noninoculated controls remained healthy. Total RNA was extracted with RNeasy Plant Mini kit (QIAGEN, Hilden, Germany) from 12 samples. The RYMV coat protein gene was amplified by RT-PCR with primers 5'CGCTCAACATCCTTTTCAGGGTAG3' and 5'CAAAGATGGCCAGGAA3' (3). The sequences were deposited in GenBank (Accessions HE654712 to HE654723). To characterize the isolates, the sequences of the tested samples were compared in a phylogenic tree including a set of 45 sequences of isolates from Rwanda, Uganda, western Kenya and northern Tanzania (2,3). Six isolates from western Burundi namely Bu1, Bu2, Bu4, Bu7, Bu10 and Bu13 (Accessions HE654712 to HE654716 and HE654718) and the isolate Rw208 (HE654720) from south-western Rwanda belonged to strain S4-lm previously reported near the Lakes Malawi and Tanganyika. They fell within the group gathering isolates from the western Bugarama plain of Rwanda (3). The isolates Bu16 (HE654719) and Bu17 (HE654717) from Mishiha at eastern Burundi belonged to strain S4-lv previously reported around the Lake Victoria. However, they did not cluster with the isolates from eastern and southern provinces of Rwanda. They were genetically more closely related to isolates of strain S4-lv from northern Tanzania. Overall, the phylogeography of RYMV in Burundi and Rwanda region was similar. In the western plain of the two countries, the isolates belonged to the S4-lm lineage whereas at the east of the two countries at midland altitude, they belonged to the S4-lv lineage. The presence of RYMV in Burundi should be considered in the future integrative pest management strategies for rice cultivation in the country.

*References:* (1) D. Fargette et al. Annu. Rev. Phytopathol. 44:235, 2006. (2) Z. L. Kanyeka et al. Afr. Crop Sci. J. 15:201, 2007. (3) I. Ndikumana et al. New Dis. Rep. 23:18, 2011.



Supplemental Figure 1: Maximum-likelihood tree based on the coat protein gene sequences of isolates from Burundi (Bu), Rwanda (Rw), Tanzania (Tz), Kenya (Ke) and Uganda (Ug) with their accession numbers. Strong bootstraps supports (>70%) of the strains are indicated by asterisks. Isolates from Burundi and Rwanda are indicated in red and blue respectively. The new sequences were deposited to GenBank as accessions HE654712 to HE654723.