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New Disease Reports

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NEW DISEASE REPORT

First report of maize streak Reunion virus infecting rice in Burkina Faso

M. Bangratz[1] | M. Barro[2] | N. Fouad[1] | D. Sérémé[3] | D. Filloux[1] | E. Fernandez[1] | C. Julian[1] | A. I. Kassankogno[2] | A. K. Guigma[2] | P. Roumagnac[1] | I. Wonni[2] | C. Tollenaere[1] | N. Poulicard[1]

[1]PHIM, Univ Montpellier, IRD, INRAE, CIRAD, Institut Agro, Montpellier, France

[2]INERA, Institut de l'Environnement et de Recherches Agricoles du Burkina Faso, Laboratoire de Phytopathologie, Bobo-Dioulasso, Burkina Faso

[3]INERA, Institut de l'Environnement et de Recherches Agricoles du Burkina Faso, Laboratoire de Virologie et de Virologie Végétale, Kamboinsé, Burkina Faso

Correspondence
PHIM, Univ Montpellier, IRD, INRAE, CIRAD, Institut Agro, Montpellier, France. Email: nils.poulicard@ird.fr

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KEYWORDS
Africa, experimental agroinoculation, *Geminiviridae*, *Oryza* species, viral metagenomics, wild *Poaceae*

Among the 19 viruses reported to infect rice, only rice stripe necrosis virus (RSNV; *Benyvirus*, *Benyviridae*) and rice yellow mottle virus (RYMV; *Sobemovirus*, *Solemoviridae*) have been characterised in Africa (Wang *et al.*, 2022). To expand our knowledge of viruses infecting rice in Africa, we used a virion-associated nucleic acids (VANA) Illumina HiSeq approach (Moubset *et al.*, 2022; Fouad *et al.*, 2024) on 85 pools of 16 rice plants each, collected at random (without regard to disease symptoms) in 2016 and 2017 from 57 rice fields across six sites in Burkina Faso (Barro *et al.*, 2021). From the 288,971,924 raw sequences produced by Illumina sequencing, we first identified maize streak virus (MSV, *Mastrevirus*, *Geminiviridae*) (Fouad et al., 2024). We also obtained 63 contigs sharing a mean of 96.7% nucleotide identity with maize streak Reunion virus (MSRV, *Mastrevirus*, *Geminiviridae*). All of these contigs were identified in a pooled sample collected in 2017 from a field at the Karfiguela site in Burkina Faso (field/sample hereafter referred to as 17KA02). After total DNA extraction using the CTAB protocol and a rolling circle amplification (RCA) step (Fouad *et al.*, 2024), a PCR to detect MSRV (MSRV-F613bp: 5′-TTGGCAAGACCCGTCTGTAC-3′ / MSRV-R613bp: 5′-GGAGCCTCTACATCGTTGGG-3′) was performed on 172 pooled rice samples (2016-2019) and 17 pooled or individual wild *Poaceae* collected within or nearby the previously sampled rice fields (https://doi.org/10.23708/1IPJAU). Although no rice field other than 17KA02 was positive for MSRV, we detected the virus at two other sites located in a 100 × 100 km region, one in a pooled wild *Poaceae* sample (17SZ07w) and the other a symptomatic plant of *Rottboellia exaltata* (17BM02w). Both plants were collected in 2017, at the Senzon and Bama sites, respectively.

Full MSRV genomes were obtained by Sanger sequencing (Azenta, USA) of two PCR overlapping fragments done with specific primers (MSRV2F: 5′-ATACTGCTTAGGGCGAAGAGACAGC-3′/MSRVqPCR1R: 5′-TCCAGAGGTACTTTCATTCCCAGAG-3′; MSRVqPCR1F: 5′-CTTGCTGGTTGTGGTTTCGATAATG-3′/MSRV4R: 5′-AACTCCCTGCCATCGGTCTCGTA-3′) using RCA products as template. Complete genome sequences were assembled and deposited in GenBank (Accession Nos. PQ424982-PQ424984). A phylogenetic tree showed that all three MSRV isolates obtained in this study were genetically related to two isolates from wild species reported from Nigeria (Figure 1).

Based on the rice MSRV isolate, an infectious MSRV clone (pCAMBIA0380::MSRV) was synthesized (Azenta, USA) and agroinoculated into 200 plants of *Oryza sativa* spp. *indica* cv. IR64 and of *O. glaberrima* cv. Tog5673 as described by Fouad *et al.* (2024). Light to moderate

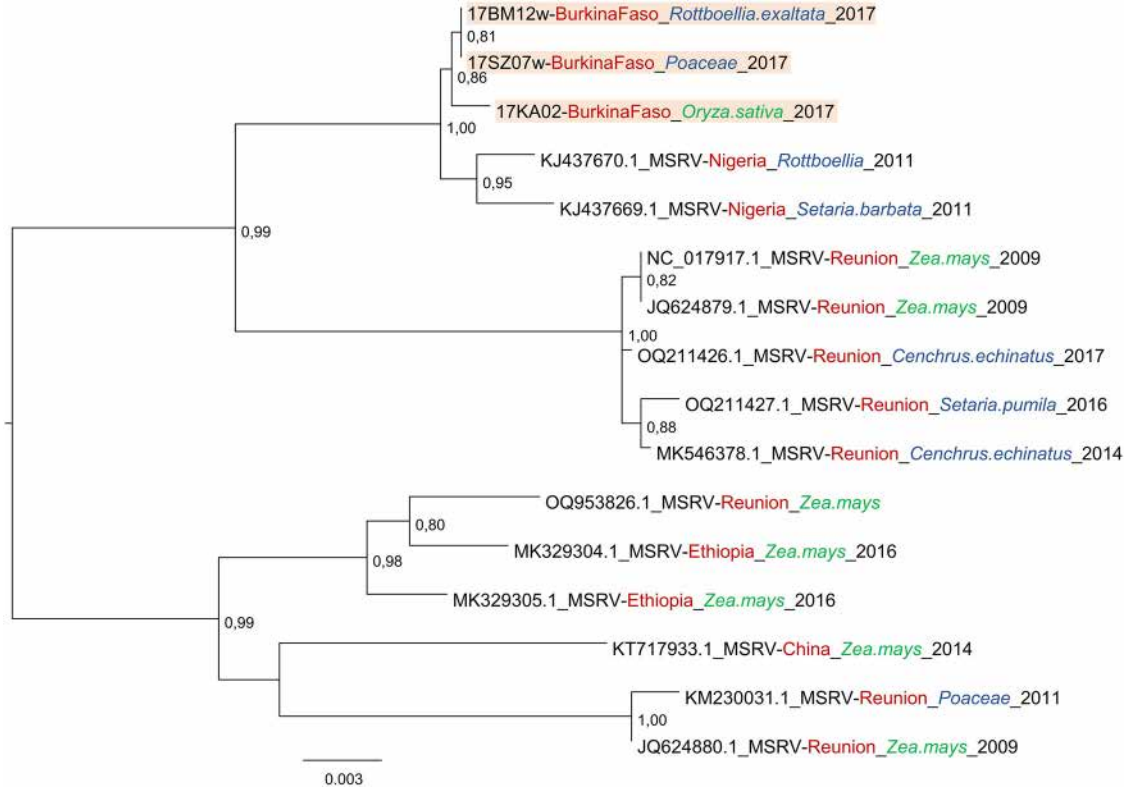

FIGURE 1 Phylogenetic tree constructed by maximum likelihood (K2+G) based on 16 complete MSRV genome sequences from Burkina Faso obtained during this study (three genomes highlighted in red) and from public databases. Only bootstrap values above 0.70 are reported. The country (in red) and the host (cultivated in green, wild in blue) origin of these sequences are indicated

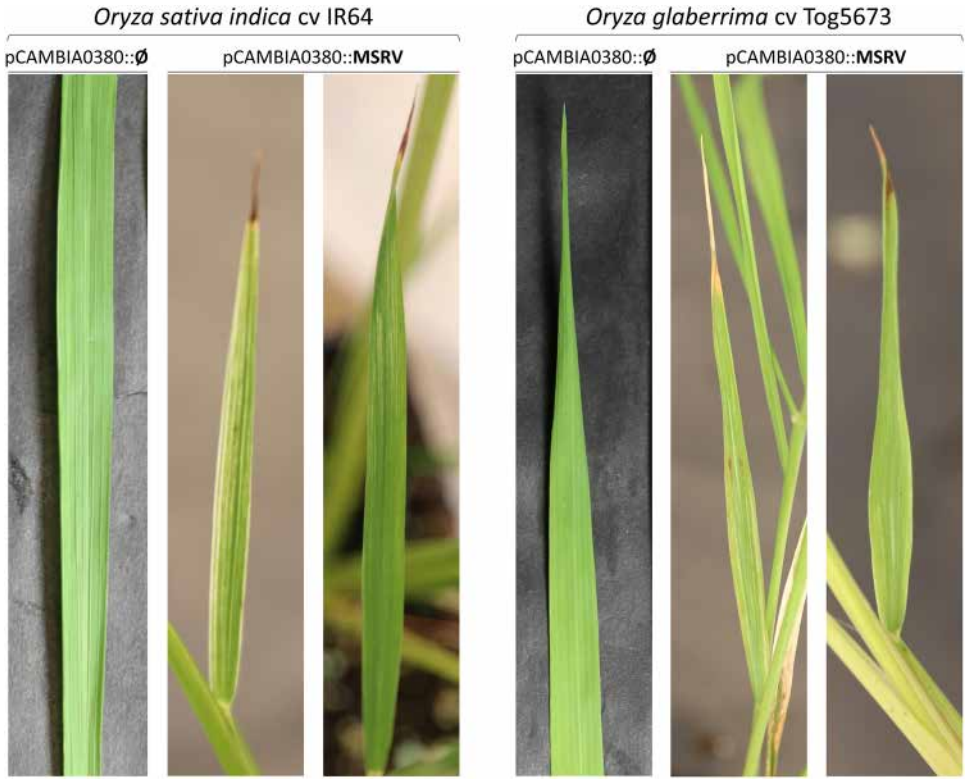

FIGURE 2 Symptoms associated with MSRV infection observed in two rice species (*Oryza sativa* L. spp. *indica* cv. IR64 and *Oryza glaberrima* Steud. cv. Tog5673) 28 days after agroinoculation with the pCAMBIA0380::MSRV infectious clone (negative control: pCAMBIA0380::Ø)

streaks (Figure 2) appeared 28 days after inoculation (dpi) on a few leaves of four IR64 plants and three Tog5673 plants. However, these symptoms never developed into clear and distinct streaks on whole plants, and no reduction in the plant growth was observed at 60 dpi. MSRV presence was confirmed in the symptomatic leaves by PCR and Sanger sequencing.

Although MSRV has so far only been described on maize and wild grasses (Kraberger et al., 2017), our study shows that rice is an alternative host for this virus. However, our results suggest that MSRV infection of rice is less frequent than MSV infection (Fouad et al., 2024). Nevertheless, MSRV has been described in African and Asian rice-producing countries and our results are important to consider when undertaking disease surveillance of rice fields worldwide.

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ORCID

M. Bangratz https://orcid.org/0009-0000-7653-9561
N. Fouad https://orcid.org/0009-0007-9601-3701
P. Roumagnac https://orcid.org/0000-0001-5002-6039
C. Tollenaere https://orcid.org/0000-0003-2045-2824
N. Poulicard https://orcid.org/0000-0003-3969-2131

REFERENCES

Barro, M., Kassankogno, A.I., Wonni, I., Sérémé, D., Somda, I., Kaboré, H.K. *et al.* (2021) Spatiotemporal survey of multiple rice diseases in irrigated areas compared to rainfed lowlands in the western Burkina Faso. *Plant Disease*, 105, 3889–3899. https://doi.org/10.1094/PDIS-03-21-0579-RE

Fouad, N.M.I., Barro, M., Bangratz, M., Sérémé, D., Filloux, D., Fernandez, E. *et al.* (2024) Old foe, new host: epidemiology, genetic diversity, and pathogenic characterization of maize streak virus in rice fields from Burkina Faso. *Phytobiomes Journal*, PBIOMES-08-23-0085-FI. https://doi.org/10.1094/PBIOMES-08-23-0085-FI

Kraberger, S., Saumtally, S., Pande, D., Khoodoo, M.H.R., Dhayan, S., Dookun-Saumtally, A. *et al.* (2017) Molecular diversity, geographic distribution and host range of monocot-infecting mastreviruses in Africa and surrounding islands. *Virus Research*, 238, 171–178. https://doi.org/10.1016/j.virusres.2017.07.001

Moubset, O., François, S., Maclot, F., Palanga, E., Julian, C., Claude, L. *et al.* (2022) Virion-associated nucleic acid-based metagenomics: a decade of advances in molecular characterization of plant viruses. *Phytopathology*, 112, 2253–2272. https://doi.org/10.1094/PHYTO-03-22-0096-RVW

Wang, P., Liu, J., Lyu, Y., Huang, Z., Zhang, X., Sun, B. *et al.* (2022) A review of vector-borne rice viruses. *Viruses*, 14, 2258. https://doi.org/10.3390/v14102258

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