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NEW DISEASE REPORT

First report of a naturally occurring isolate of *Pepper yellow vein Mali virus* causing tobacco yellow leaf curl disease in Burkina Faso

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Begomovirus, disease surveillance, MinION

Pepper yellow vein disease (PYVD) has been reported to be associated with the African monopartite begomovirus *Pepper yellow vein Mali virus* (PepYVMLV) in West Africa (Tiendrébéogo et al., 2008; Zhou et al., 2008). Recently, vegetable isolates of PepYVMLV have also been shown to be associated with a DNA-B component in Burkina Faso (Ouattara et al., 2019) and Cote d'Ivoire (Soro et al., 2021).

In September 2021, severe leaf yellowing, curling and deformation symptoms (Figure 1), resembling those of pepper yellow vein disease were observed on tobacco (*Nicotiana tabacum*) bordering pepper and tomato fields in the locality of Tabtenga in Burkina Faso. Tobacco leaves with (n = 3) and without (n = 2) symptoms were collected. The samples were tested for the presence of begomoviruses using a PCR assay with degenerate primers designed to amplify the coat protein gene of Old World begomoviruses (Séka et al., 2016) followed by direct sequencing of PCR amplicons. PCR products of the expected size were only obtained from the three diseased tobacco plants. BLASTn analyses of the amplicon sequences (676, 687 and 694 base pairs (bp) in length; GenBank Accession Nos. OR483371 - OR483373) showed the highest pairwise identity (98 to 99%) with PepYVMLV isolates from Burkina Faso (MH778652; MH778653). To confirm these results, specific primers for the detection of both DNA-A and -B components of PepYVMLV were used for PCR testing (Ouattara et al., 2019). Both components were detected from the three diseased samples confirming the initial diagnosis. To obtain the complete sequences of DNA-A and -B components, samples were subjected to nanopore MinION sequencing as described by Ben Chehida et al. (2021). Global similarity search analysis resulted in 84/3076 and 99/3076 raw reads assigned to PepYVMLV DNA-A and DNA-B, respectively. Based on sequence assembly only one contig of 2781 bp (DNA-A component) was obtained (OR483374) with 96.7% identity to PepYVMLV isolated from Burkina Faso (MH778653, FN555171). A maximum-likelihood phylogenetic tree constructed with publicly

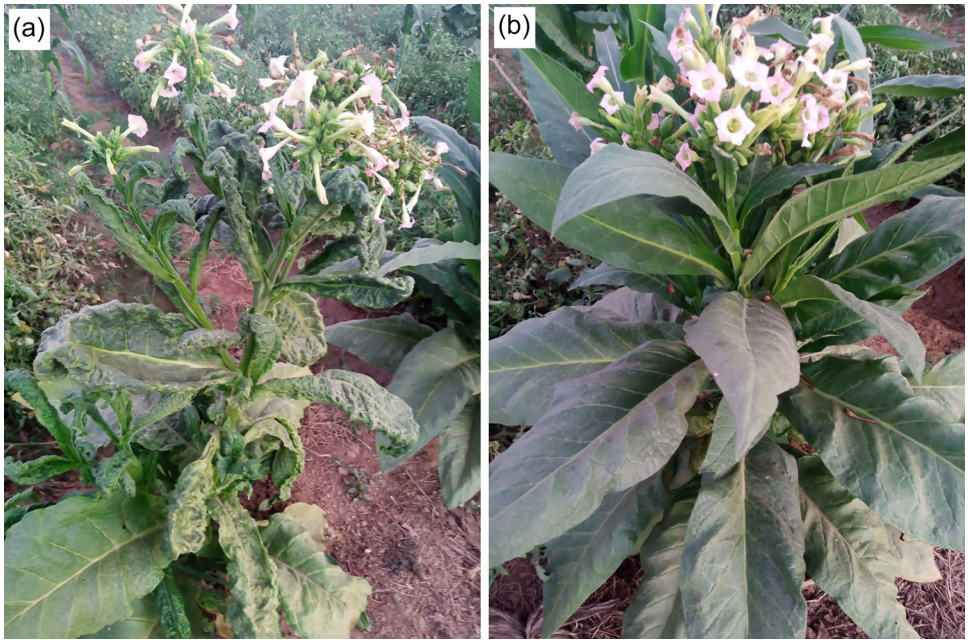

FIGURE 1 Diseased (a) and asymptomatic (b) tobacco plants (*Nicotiana tabacum*) observed around pepper and tomato fields in September 2021 in the locality of Tabtenga in Burkina Faso.

available begomovirus genome sequences and the sequences obtained in this study (OR483371 - OR483374) confirmed the genetic relationship of the isolates of PepYVMLV from tobacco with previously characterised isolates from West Africa (Figure 2).

To our knowledge, this is the first report of PepYVMLV naturally associated with tobacco yellow leaf curl disease in Burkina Faso and globally. Our results highlight the potential existence of alternative natural hosts for PepYVMLV.

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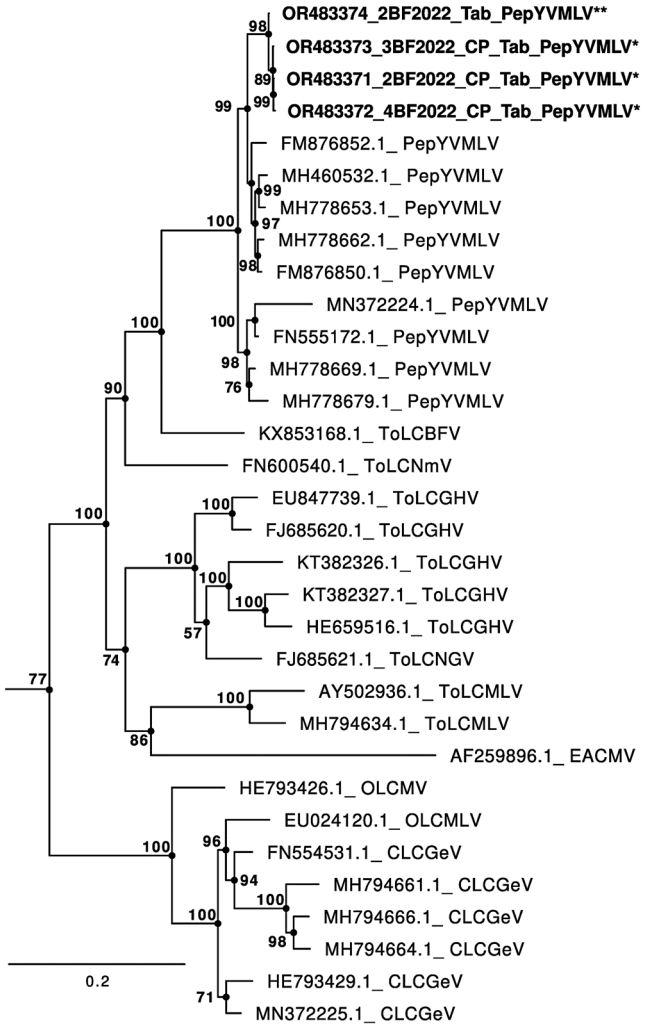

FIGURE 2 Maximum likelihood phylogenetic tree inferred from the alignment of DNA-A-like sequences of begomoviruses. The names of the sequences characterized in this study are in bold; ** and * indicate full sequence and coat protein sequences obtained from nanopore MinION and Sanger sequencing, respectively; PepYVMLV, *Pepper yellow vein Mali virus*; ToLCBFV, *Tomato leaf curl Burkina Faso virus*; ToLCNmV, *Tomato leaf curl Namakeli virus*; ToLCGHV, *Tomato leaf curl Ghana virus*; ToLCMLV, *Tomato leaf curl Mali virus*; EACMV, *East Africa cassava mosaic virus*; OLCMLV, *Okra leaf curl Mali virus*; and CLCuGeV, *Cotton leaf curl Gezira virus*. The horizontal scale indicates genetic distance. The outgroups were isolates of CLCuGeV.

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