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NEW DISEASE REPORT

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First report of *Phasey bean mild yellows virus* in Kenya with a new host record

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Genome studies in Australia reported a novel virus, *Phasey bean mild yellows virus* (genus *Polerovirus*; PBMYV), in mixed infections with *Bean leaf roll virus*, *Faba bean polerovirus 1*, *Soybean dwarf virus* and *Turnip yellows virus* naturally infecting phasey bean (*Macroptilium lathyroides*) (Sharman et al., 2021). Transmission studies with *Aphis craccivora* and by grafting with infected scions identified fabaceous hosts including chickpea, faba bean and pea as additional hosts of PBMYV (Wilson et al., 2012). In general, poleroviruses have narrow host ranges restricted to members of one or a few plant families, although exceptions exist (King et al., 2012). Sharman et al. (2021) found PBMYV in one non-legume host (*Anagallis arvensis*) suggesting that hosts outside the Fabaceae may be found. Previous field surveys in Kenya on leguminous crops observed mild yellowing symptoms and PBMYV was detected in pooled samples from these plants (Mukoye et al., 2020).

Diseased leaves including those infested with aphids (*A. craccivora*, *A. gossypii*, *Macrosiphum euphorbiae* and *Myzus persicae*) were collected during an extensive field survey for virus diseases in the main groundnut (*Arachis hypogaea*) growing areas of western Kenya (Bungoma, Busia, Kakamega and Siaya counties) during the 2020 and 2021 long- and short-rains growing seasons. A total of 345 farms (comprising 628,513 hectares) in the four counties were surveyed by sampling at intervals of 3–8 km along roads that traversed each area. Viral symptoms were widespread across the surveyed counties and included mild chlorosis, chlorotic mottling and spots, interveinal chlorosis, reddening and thickening of the leaves, leaf curling and bunching, reduced leaf size and stunting (Figure 1). The mean incidence of symptoms across the surveyed counties was 51% in the long rains season and 71% in the short rains season. There was a significant difference in disease incidence among the counties ($p < 0.0001$) with Busia having the highest mean incidence (67%), significantly greater than Bungoma (61%), Siaya (57%) and Kakamega (56%).

A total of 673 leaf samples were collected, pooled into one sample then sequenced on the MiSeq platform (Illumina, USA). A quality check on reads was done using FastQC. Trimmed reads were used for de novo assembly and contigs aligned to the viral genomes database using the CLC Genomics Workbench 10.1.2. The assembled contigs were subjected to a BLASTn search against the GenBank database. Phylogenetic analyses and comparisons were performed using the MEGA X software (Kumar et al., 2018) (Figure 2). The sequences from Kenya (GenBank Accession Nos. LC709260 and LC709261) had the closest identity (91–95%) with PBMYV (KT963000.2, MT966033.1 and MT966038.1) and grouped together with other isolates of the virus (Figure 2). The PBMYV Kenyan isolate is genetically distinct from the PBMYV Australian isolates described by Sharman et al. (2021).

To the best of our knowledge, this is the first report of PBMYV in Kenya and the first report in groundnut globally. Further studies

FIGURE 1 Symptoms observed on groundnut in Kenya included mild chlorosis, chlorotic mottling and spots, interveinal chlorosis, reddening and thickening of the leaves, leaf curling and bunching, reduced leaf size and stunting

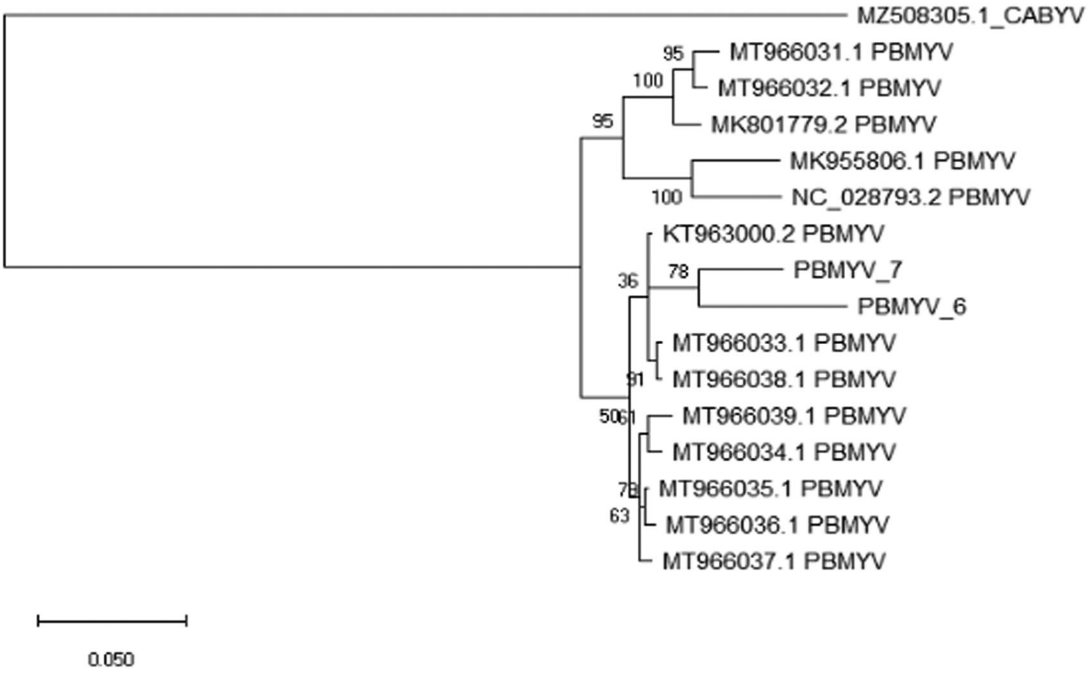

FIGURE 2 The PBMYV nucleotide sequences were aligned using the MUSCLE algorithm (Edgar, 2004) and MEGA X was used to calculate the pairwise distances between sequences and construct the Maximum-Likelihood phylogenetic tree using the Tamura-Nei model for nucleotide sequence alignments. *Cucurbit aphid-borne yellows virus* (MZ508305.1) was used as an outgroup

are needed to understand the distribution and molecular diversity of PBMYV in groundnut and other hosts, its persistence in the diverse agro-ecological zone pathosystems, economic impact, vector transmission and sequence diversity.

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