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NEW DISEASE REPORT

First report of *Pepo aphid-borne yellows virus* infecting watermelon (*Citrullus lanatus*) in Uganda

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Watermelon (*Citrullus lanatus*), a cucurbit of global importance, is a potential cash crop in Uganda (Masika et al., 2022). In December 2021, watermelon plants with extensive yellowing of mature leaves were observed in a field in central Uganda. Although farmers associated symptoms with nutritional deficiencies and moisture stress, biotic constraints like viruses can also induce such symptoms. For example, poleroviruses are associated with yellowing symptoms of mature leaves and reduction in watermelon yield. *Pepo aphid-borne yellows virus* (PABYV) is a polerovirus that has been reported in Côte d'Ivoire (Kone et al., 2015), South Africa (Ibaba et al., 2017), Tanzania (Desbiez et al., 2016) and Kenya (Kidanemariam et al., 2019). The virus, mainly transmitted by aphids, was first reported in Mali infecting summer squash (*Cucurbita pepo*) in 2008 (Knierim et al., 2014).

Three mature leaves of watermelon showing yellowing symptoms (Figure 1) were collected from a field in Mukono District in central Uganda. Samples were transported on ice to the National Crops Resources Research Institute, Namulonge, for total RNA extraction and RT-PCR amplification was done using primers designed targeting the coat protein region of the PABYV genome (forward 5'-GAATACGGTCGCGGTTAGATCTAGC-3', reverse 5'-GTTCTGGACCTGGCACTGGATGG-3'). Fragments of the expected size (588 bp) were produced and sent to Macrogen Europe B.V (Amsterdam, The Netherlands) for direct sequencing.

FIGURE 1 Yellowing symptoms of mature leaves on watermelon plant from Nakoosi, Mukono district, Central Uganda.

Sequence analyses showed that the isolates from this study (GenBank Accession Nos. ON650024-ON650026) shared between 95 to 99% identity between themselves. A BLASTn search revealed that these isolates were closely related to PABYV isolates in GenBank

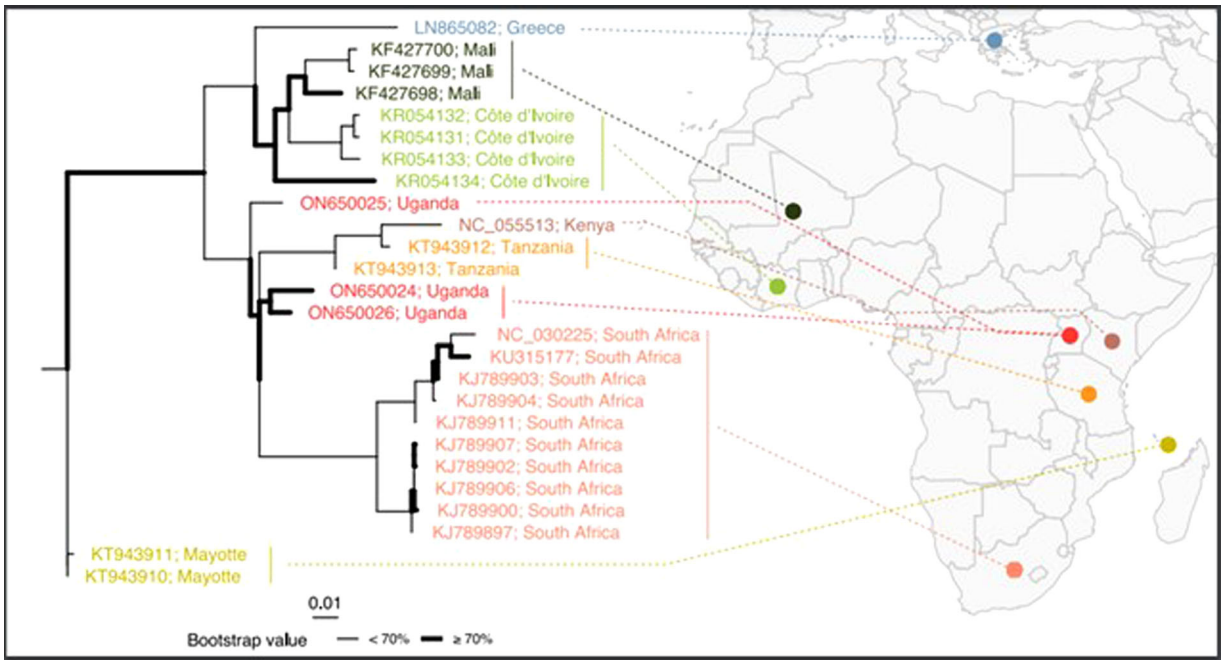

FIGURE 2 Maximum likelihood phylogenetic tree of partial coat protein nucleotide sequences of *Pepo aphid borne yellows virus* isolates under a TIM2e+I+G4 nucleotide substitution model in IQ-TREE v1.6.12, as determined as the best fit model by ModelFinder. Tree was rooted using a *Cucurbit aphid-borne yellows virus* (CABYV) isolate from Thailand (KF791040) as an outgroup (not shown). Branch thickness indicates bootstrap values (n = 1000) higher than 70%, as determined by ultrafast bootstrap and colours indicate the country of origin. Sequences from Uganda are indicated in red.

sharing between 98.3-98.7% identities with accessions KU315177, KJ789911, KJ789904, and KU315178. This is the first report of PABYV infecting watermelon in Uganda. The isolates from this study did not show any recombination as determined by RDP, GENECONV, Chimaera, MaxChi, BootScan, SiScan, 3Seq and LARD programmes implemented in the recombination detection programme 4 (RDP4) software. Phylogenetic clustering showed a close relationship between our isolates and those from other East African countries (Kenya and Tanzania) and from South Africa. Sequences from Côte d'Ivoire, Mali, and Greece formed another clade, suggesting a north/west versus south/east division in the genetic diversity of PABYV in Africa. Sequences from Mayotte, in the Indian Ocean, were more basal (Figure 2).

The identification of PABYV in multiple countries in Africa suggests that it might be widespread and well-established throughout the continent. Poleroviruses are transmitted by aphid vectors which multiply rapidly and can colonise new areas. In addition, the symptoms of infected plants may have been ignored or misdiagnosed, as illustrated by this report. The virus might therefore be more widespread than currently known. The diagnostic tools described here will help detection and hence the design of disease management strategies. In addition, breeding programmes should be developed to identify any sources of natural resistance, even in closely related family members.

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