



First report of Pineapple mealybug wilt-associated virus-1 and -3 in Ghanaian pineapple

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Mealybug wilt of pineapple (MWP) is a destructive viral-associated disease affecting pineapple (*Ananas comosus*) production in many growing regions worldwide, including Ghana (Sarpong *et al.*, 2017; Dey *et al.*, 2018). In Hawaii, MWP causes reduction in fruit yield by 30-55%, depending on the age of the plant at the onset of disease (Sether & Hu, 2002). In Ghana, fruit yield loss due to MWP has been estimated to be at about US\$248 per hectare (Sarpong *et al.*, 2017).

MWP is associated with one or a combination of *Pineapple mealybug wilt-associated virus-1* (PMWaV-1), PMWaV-2, PMWaV-3, PMWaV-4 and/or PMWaV-5 (Gambley *et al.*, 2008; Dey *et al.*, 2018). These viruses are members of the genus *Ampelovirus* in the family *Closteroviridae*, and transmitted by two types of mealybug, the pink pineapple mealybug (*Dysmicoccus brevipes*) and the gray pineapple mealybug (*D. neobrevipes*) (Sether *et al.*, 1998).

To further understand the association between viruses and MWP in Ghana, 24 pineapple plant samples showing typical symptoms of MWP (Fig. 1), including tip dieback, and descending curling, reddening, and wilting of the leaves which can prompt a complete breakdown of the plant, were collected during a survey of the Central region of Ghana in 2019. Total RNA was extracted from leaf tissues using a Quick-RNA™ Plant Miniprep Kit (Zymo Research Corp., USA). PMWaV-1 was detected in seven of the samples (29.2%), whereas PMWaV-3 was detected in two samples (8.3%) tested using reverse transcription polymerase chain reaction (RT-PCR) assays which targeted the HSP70h gene region of each virus (Sether *et al.*, 2005). All amplicons corresponding to PMWaV-1 (590 bp) and PMWaV-3 (495 bp) were purified and directly sequenced in both directions. Sequence comparison using BLASTn showed that the sequences of all the Ghanaian PMWaV-1 isolates (GenBank Accession Nos MN427634 - MN427639 and MN399973) shared 95.2% to 99.7% nucleotide identity with each other and 95.2-100% nucleotide identity with sequences of isolates previously published in GenBank (e.g. KT322152, KT322148, EF620774 and HE58322). The sequences of the two Ghanaian PMWaV-3 isolates (MN427640 and MN427641) shared 98.3% nucleotide identity to each other and 97.5- 99.3% nucleotide identity with sequences of isolates in

GenBank (e.g. NC043406, MH704742, GU563497 and JX508638).

To the best of our knowledge, this is the first report of the presence of the PMWaV-1 and PMWaV-3 in Ghanaian pineapple fields as well as in Africa. MWP is widely spread in Ghana (Sarpong *et al.*, 2017) and both viruses could be prevalent in Ghanaian pineapple fields. This supports the need to educate and train farmers on proper procedures for propagating pineapple materials from disease-free sources to reduce the impact and control spread of MWP disease on pineapple crops in Ghana.

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Figure 1

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