DISEASE NOTE



First report of maize yellow mosaic virus (MaYMV) on maize (Zea mays) in Tanzania

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Maize yellow mosaic virus (MaYMV) has been reported from China, Ecuador, Brazil and Burkino Faso on maize since 2016 and appears to be an emerging virus with a wide global distribution. Thirty-five maize samples with varying degrees of mosaic and stunting symptoms, were collected in May/June 2015 from the regions of Mara, Arusha, Manyara, Kilimanjaro, Morogoro and Pwani in Tanzania. Total RNA was extracted from leaf material, which was used to prepare RNAtag libraries according to Shishkin et al. (2015). Sequencing was carried out on an Illumina HiSeq2500 instrument. The reads from each dataset were taxonomically classified using the Kaiju software package (Menzel et al. 2016), with thirty datasets having reads showing homology to MaYMV, as well as either/both *Maize chlorotic mottle virus* and potyviruses. Trimmed

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datasets were assembled using CLC Genomics Workbench 9 de Novo assembly tool on default settings, with the exception of the following: "minimum contig length" (2000 bp), "length fraction" (0.9), "similarity fraction" (0.9). This yielded seven full/near full genomes with GenBank accession numbers MG664788 -MG664794, sharing 97.9-99.9% sequence homology. These sequences shared a 96.3-96.5% (KU291105) and 97-97.3% (KU291103) nucleotide identity with those from China. Seven positive samples were tested with RT-PCR, using the PCR primers MaYMV-F and MaYMV-R (Chen et al. 2016). Six samples produced the expected RT-PCR amplicon of 750 bp, with one potentially below the detection limit for RT-PCR. An RNA-seq negative sample did not produce the MaYMV amplicon but was positive for a maize control RT-PCR (actin), as expected. The identities of the amplicons were confirmed in four samples using Sanger sequencing. Next generation sequencing and PCR confirmed MaYMV positive samples in all sampled regions except Pwani. The broad geographical distribution of MaYMV in samples from this study suggests that the virus is well established in Tanzania.

References

Chen S, Jiang G, Wu J, Liu Y, Qian Y, Zhou X (2016) Characterization of a novel polerovirus infecting maize in China. Viruses 8(5):120. https://doi.org/10.3390/v8050120

Menzel P, Ng KL, Krogh A (2016) Fast and sensitive taxonomic classification for metagenomics with Kaiju. Nat Commun 7:11257

Shishkin AA, Giannoukos G, Kucukural A, Ciulla D, Busby M, Surka C, Chen J, Bhattacharyya RP, Rudy RF, Patel MM, Novod N, Hung DT, Gnirke A, Garber M, Guttman M, Livny J (2015) Simultaneous generation of many RNA-seq libraries in a single reaction. Nat Methods 12:323–325

