

First Report of Sweet potato badnavirus A and Sweet potato badnavirus B in South Africa

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DISEASE NOTES

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Citation

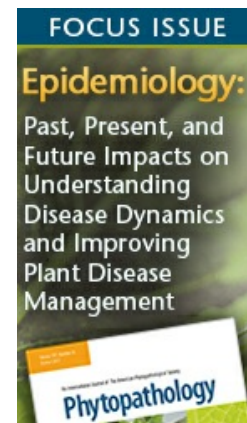
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Sweet potato is an important root crop, having significant nutritional and economic value in sub-Saharan countries such as South Africa. Sweet potato badnaviruses were first discovered in Peru using small RNA deep sequencing (Kreuze et al. 2009) and were later detected in Tanzania (Mbanzibwa et al. 2014), Honduras, and Guatemala (Kashif et al. 2012). Badnaviruses are pararetroviruses (family *Caulimoviridae*) with circular double-stranded DNA genomes (dsDNA) that range between 7.2 and 8.5 kb in size (Bhat et al. 2016). In this study we report the

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detection of sweet potato badnaviruses in plants collected during a survey in the Eastern and Western Cape provinces of South Africa. Symptomatic plants exhibited leaf curling, chlorotic spots, and chlorotic spots with purple rings. Small RNAs (sRNA) were isolated from five symptomatic and two asymptomatic plants using the Ambion mirVana miRNA RNA Isolation Kit (Ambion, Naugatuck, CT). The sRNA samples were prepared for sequencing using the Illumina TruSeq Small RNA Sample Preparation Kit (Illumina, San Diego, CA). The seven libraries were independently sequenced on the Illumina MiSeq platform (Illumina). Each of the seven libraries underwent quality trimming and downstream analysis. Over 6.9 million sequence reads from the seven libraries remained after quality control analysis. Sequence reads were assembled into contiguous (contigs) sequences using Velvet (Zerbino and Birney 2008). BLASTn and BLASTx searches against viral sequences revealed the presence of sweet potato badnavirus A (SPBVA) and sweet potato badnavirus B (SPBVB) in all seven libraries. The total number of SPBVA specific reads was 12,050, whereas 16,279 reads were identified as SPBVB. Both badnaviruses were detected in the symptomatic and asymptomatic samples as coinfections. The identity of the badnaviruses was confirmed by conventional Sanger sequencing of amplified polymerase chain reaction products. Virus-specific primers targeting the polyprotein gene of SPBVA and the ORF3b gene of SPBVB were designed using the CLC Bio Genomics Workbench (version 7.5.1) (CLC bio, Aarhus, Denmark). Amplification was achieved using the following primers: SPBVA-F (5'-TCCCACCTAAGGCTCAAGAA-3'), SPBVA-R (5'-GCAAAGTGTGCCCCCTGTAT-3'), SPBVB-F (5'-TGGGTGCAATTTTCATCAGAA-3'), and SPBVB-R (5'-GTGCATTTACCAGCCCAAAT-3'). The expected amplicons of 593 and 679 bp for SPBVA and SPBVB, respectively, were amplified and sent to Inqaba Biotechnical Industries for direct Sanger sequencing. The SPBVA sequence shared 100% nucleotide (nt) identity with the SPBVA isolate from China (GenBank accession no. KT448733), and the SPBVB sequence shared 99% nt identity with the Spanish isolate (GenBank accession no. KU511272). The sequences were submitted to GenBank under the accession numbers KY829453 and KY829454, for SPBVA and SPBVB, respectively. To our knowledge, this is the first report of sweet potato badnaviruses in South Africa. Future studies are necessary to determine what role



badnaviruses play in the etiology of sweet potato disease, because they are known to trigger infections and cause emerging diseases.

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