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DISEASE NOTES

First Report of Beet Soil-Borne Virus on Red Table Beet in Brazil

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Beet soil-borne virus (BSBV, genus *Pomovirus*) is a soil-borne virus transmitted by the protozoan Polymyxa betae (Adams et al. 2017; Henry et al. 1986). The BSBV is frequently detected in sugar beet samples infected with beet necrotic yellow vein virus (BNYVV), which is the causal agent of rhizomania (Meunier et al. 2003). In 2015, BNYVV was detected for the first time in Brazil in red table beet samples from the region of São José do Rio Pardo, state of São Paulo (Rezende et al. 2015), and then the near-complete genome sequence of BNYVV isolate from Brazil was reported (Camelo et al. 2019). In this study, the presence of BSBV is first reported in red table beet samples collected in November 2016, in the same region where BNYVV was previously found. Total RNA was extracted from 0.1 g of rootlets of red table beet cultivar Boro showing abnormal proliferation, using the Purelink viral RNA/DNA kit (Thermo Fisher Scientific, Waltham, MA). A cDNA library was prepared with the Illumina TruSeq Stranded mRNA Sample Prep LT Protocol (Illumina, San Diego, CA). The nucleotide sequencing was done in an Illumina HiSeq 2500 System at the Center of Functional Genomics (ESALQ/USP, Piracicaba, Brazil), using a HiSeq Flow Cell v4 and the HiSeq SBS v4 kit (Illumina) in paired-end mode, producing reads of 100 bp (2) × 100 bp). A total of 59,921,714 reads were generated, and 175,594 contigs were assembled by Velvet de novo assembler with 21 k-mer setting. The tBlastx result using Geneious 8.1 (https://www.geneious.com) showed 346 contigs as viral sequences, and 34 contigs had some identity to RNA-1 of BSBV, 20 with RNA-2, and 23 with RNA-3. The contig belonging to each genome fragment was extended using "map to reference" command of Geneious to get near-complete genome segment sequences. RNA-1 sequence was assembled with 45,616 reads, RNA-2 with 49,529 reads, and RNA-3 with 40,545 reads. The near-complete genome of RNA-1 (5,819 nt; MH106714), RNA-2 (3,448 nt; MH106715), and RNA-3 (3,004 nt; MH106716) for the BSBV isolate from Brazil was very similar to the corresponding sequences for the BSBV type isolate

Ahlum (NC003518 to NC003520) (Adams et al. 2017), with identities ranging from 95.26 to 99.39%. To confirm the presence of BSBV, total RNA extracted from symptomatic rootlets of red table beet cultivar Boro was further analyzed by reverse transcription PCR (RT-PCR) using specific primers BSBV2for and BSBV2rev as described by Meunier et al. (2003). The nucleotide sequence of the amplicons of the expected size revealed 96.99 to 99.25% identities with corresponding nucleotide sequences from different BSBV isolates (FJ971717, FN812749, and KT194050) deposited on GenBank. Additionally, 10 plants of each red table beet cultivar (Bohan and Boro) were inoculated with soil samples from a commercial red table beet field, located in the region of São José do Rio Pardo, with rhizomania history, as described by Camelo et al. (2019). The BSBV was detected in the rootlets of three out of 10 Bohan and two out of 10 Boro plants by RT-PCR as described above. The same samples were analyzed for the presence of BNYVV by nested RT-PCR using the specific primers described by Morris et al. (2001). The BNYVV was detected in nine Bohan and eight Boro plants. This is the first report of BSBV occurring in red table beets in Brazil. According to **Tamada** (2016), BSBV remains restricted to beet roots and generally causes no obvious symptoms in roots or leaves. It is very likely that BSBV was already present in the region of São José do Rio Pardo at the time BNYVV was detected (Rezende et al. 2015).

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Supplementary Table S1. Comparison of the nucleotide (nt) and deduced aminoacid (aa) sequences of *Beet soil-borne virus* (BSBV) isolated from *Beta vulgaris* subsp. *vulgaris* cv. Boro (MH106714 to MH106716) with the corresponding sequences of the BSBV type isolate Ahlum (NC003518 to NC003520).

RNA	Genome region	Identity (%)	
		nt	aa
1	p204	99.38	97.41
	p105	96.43	96.85
2	p104	97.06	97.09
	p19 CP	97.98	99.39
3	p48 TGB1	96.61	97.89
	p13 TGB2	97.44	99.14
	p22 TGB3	97.56	95.26