

## Characterization of a botybirnavirus in the phytopathogenic fungus *Leptosphaeria biglobosa*

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*Leptosphaeria biglobosa* is a worldwide pathogenic fungus that can cause black leg on many cruciferous crops, especially oilseed rape (*Brassica napus* L.). Here we characterize a double-strand RNA (dsRNA) virus, namely *Leptosphaeria biglobosa* botybirnavirus 1 (LbBV1), isolated from *L. biglobosa* strain GZJS-19 in China. The LbBV1 genome was sequenced by using conventional methods. The radial mycelial growth of *L. biglobosa* strains was determined on potato dextrose agar (PDA), and their pathogenicity assays were conducted on cotyledons of 14-day-old oilseed rape seedlings. LbBV1 has two dsRNA segments, namely dsRNA 1 and dsRNA 2, with the sizes of 6,190 and 5,900 bp, respectively. Each dsRNA segment contains one large open reading frames (ORF), putatively encoding a polypeptide of 202 and 192 kDa in size for dsRNA 1 and dsRNA 2, respectively. The polypeptide encoded by ORF2 (dsRNA 2) possesses several conserved domains including a protein-rich region and an RNA-dependent RNA polymerase (RdRp) domain. The cDNA sequences of dsRNA 1 and dsRNA 2 show high sequence identity of 78% and 81% to those of *Alternaria botybirnavirus* 1 (ABV1) at nucleotide level, respectively. The genomic organization and phylogenetic analysis supported that LbBV1 belongs to the genus *Botybirnavirus*. Purified spherical viral particles of LbBV1 are ~44 nm in diameter encompassing dsRNA 1 and dsRNA 2 and two structural proteins of 90 and 100 kDa, respectively. Strain GZJS-19 shows no significant difference in colony morphology, radial mycelial growth and pathogenicity compared with other LbBV1-free strains. However, introduction of LbBV1 virions into virulent strain HBtom-459 of *Botrytis cinerea* resulted in the reduced virulence and sclerotium formation of the derivative *B. cinerea* strains.