



# Characterization and complete genome sequence of groundnut ringspot orthotospovirus in soybean in Brazil

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Soybean (*Glycine max* L.) is a major food crop in Brazil. To investigate the occurrence of new viruses in soybean, ten leaf samples from the Pedra Petra/MT, Planaltina/DF and Luis Eduardo Magalhães/BA regions in Brazil were collected in January 2018 and characterized as a pooled sample by high throughput sequence analysis. Total RNA extraction was performed with the PureLink Viral RNA/DNA kit (Invitrogen) followed by library preparation and transcriptome sequencing using the Illumina HiSeq2500 platform. *De novo* assembly of the 27,674,874 reads was carried out using the CLC Genomics Workbench software v7.0.3. The 6,074 contigs obtained were submitted to a BLASTn search using the Geneious software v9.1.5. Results revealed the presence of three contigs showing high identities with groundnut ringspot orthotospovirus (GRSV) segments L (94% identity - KY350136), M (98% - KY350137) and S (97% - L12048). RT-PCR using orthotospovirus universal primers BR60/BR65 (Eiras et al. 2001) confirmed the presence of the virus in soybean with a fragment of the expected size (453 bp) obtained for GRSV isolate LEM from plants of cultivar M8349-IPRO showing

crinkle/blistering leaves, mosaic and vein clearing in Luis Eduardo Magalhães/BA. Sanger sequencing of the amplicon showed a 99% nucleotide sequence identity with a GRSV isolate from peanut in Brazil (GenBank - KY400110). The complete nucleotide sequence of segments L, M and S was determined and consisted of 8,858 (MH686228), 4,847 (MH686227) and 3,040 (MH686229) bp, respectively. Further studies are necessary to evaluate the impacts of GRSV in soybeans in Brazil.

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## Reference

Eiras M, Resende RO, Missiaggia AA, Ávila ACD (2001) RT-PCR and dot blot hybridization methods for a universal detection of tospoviruses. *Fitopatol Bras* 26(2):170–175. <https://doi.org/10.1590/S0100-41582001000200009>

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