

MOLECULAR CHARACTERIZATION OF WHEAT STRIPE MOSAIC VIRUS: A NOVEL VIRUS-ASSOCIATED WITH SOIL-BORNE WHEAT MOSAIC DISEASE IN BRAZIL

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Resumo

Diseases caused by fungi, bacteria, nematodes and viruses affect wheat (*Triticum aestivum*). The soil-borne wheat mosaic disease (SBWMD) is one of the most common viral disease that causes economic losses in wheat in Brazil. The hypothesis that this disease is caused by the *Soil-borne wheat mosaic virus* or *Wheat spindle streak mosaic virus* in Brazil is based on biological characteristics, *in vitro* physical properties, particles morphology, as well as the ultrastructure of the affected cells. However, use of antisera or primers produced in other countries, resulting unsatisfactory reactions in diagnostic tests. Two possibilities may explain the unsatisfactory results, first: the virus-associated with SBWMD present high genetic variability; second: another viral species, not yet characterized, is infecting the wheat. The aim of this study was to characterize molecularly the viral species associated with wheat plants presenting SBWMD in Brazil. Wheat leaves and stems displaying mosaic symptoms were collected from different wheat cultivars in Passo Fundo, Rio Grande do Sul State, southern Brazil. Double-stranded RNA was extracted and submitted to next generation sequencing. The nucleotide (nt) sequence of a putative new member of the *Benyviridae* family was determined, and the name Wheat stripe mosaic virus (WhSMV) was proposed. Five primer pairs were designed to confirm the new virus infection from samples used to NGS. All primer pairs used in the PCR reactions resulted in amplifications of expected size fragments. WhSMV has a bipartite genome similar to RNA1 and RNA2 of the viruses belonging to the *Benyviridae* family. WhSMV RNA1 with size from 6583 to 6600 nts, contains a single open reading frame (ORF) encoding a 231.7 kDa polyprotein with putative viral replicase function. WhSMV RNA 2 with size from 4879 to 4901 nts, contains six ORFs: putative coat protein (CP); putative the major protein - readthrough (RT); putative triple gene block (TGB1, 2 and 3), possibly associated with viral movement; and a hypothetical protein of 2.8 kDa. In addition to the genomic organization and nt and amino acid sequence identities, phylogenetic analyzes showed that WhSMV is related to viral species of the *Benyviridae* family and distincted from the other species of the *Benyvirus* genus. Financial Support: BIOTRIGO Genética, UDESC, EMBRAPA, CAPES.

Palavras-chaves: *Triticum aestivum*, mosaic, NGS, virus, *Benyviridae*