

Diversity of partial RNA-dependent RNA polymerase gene sequences of Soybean blotchy mosaic virus isolates from different host-, geographical- and temporal origins

Elrea Strydom^{a, b}

^aDepartment of Microbiology and Plant Pathology, University of Pretoria, Pretoria, 0002, South Africa;

^bForestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, 0002, South Africa.

elrea.appelgryn@fabi.up.ac.za

Gerhard Pietersen^{a, b, c}

^cGenetics Department, University of Stellenbosch, Stellenbosch, 7600, South Africa; ^aDepartment of Microbiology and Plant Pathology, University of Pretoria, Pretoria, 0002, South Africa; ^bForestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, 0002, South Africa.

Corresponding author at: Genetics Department, University of Stellenbosch, Stellenbosch, 7600, South Africa.

gerhard.pietersen@up.ac.za

+ (27) 12 420 3265

Abstract

Infection of soybean by the plant cytorhabdovirus Soybean blotchy mosaic virus results in significant yield losses in the temperate, lower-lying soybean production regions of South Africa. A 277 bp portion of the RNA-dependent RNA polymerase gene of 66 Soybean blotchy mosaic virus isolates from different hosts, geographical locations in South Africa, and time of collection spanning 16 years were amplified by RT-PCR and sequenced to investigate the genetic diversity of isolates. Phylogenetic reconstruction revealed three main lineages, designated Groups A, B and C, with isolates grouping primarily according to geographic origin. Pairwise nucleotide identities ranged between 85.7% and 100% among all isolates, with isolates in Group A exhibiting the highest degree of sequence identity, and isolates of Groups A and B being more closely related to each other than to those in Group C. This is the first study investigating the genetic diversity of SbBMV.

Keywords: Soybean blotchy mosaic virus; RNA-dependent RNA polymerase gene, maximum-likelihood analysis; pairwise nucleotide similarity