



Quantification of a legume begomovirus to evaluate soybean genotypes for resistance to yellow mosaic disease



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ABSTRACT

Mungbean yellow mosaic India virus (MYMIV) infecting soybean and other legumes causes yellow mosaic disease (YMD). Evaluation of soybean genotypes for YMD resistance involves field screening at disease hot spots or in a protected environment using infectious clones or viruliferous whiteflies as sources of virus inocula. Development of efficient virus inoculation and quantification protocols to screen soybean genetic stocks against YMD is imperative for breeding resistant varieties. Binary plasmids harbouring complete, tandem dimeric genomic components DNA A and DNA B of MYMIV-soybean isolate were engineered. The infectivity of the clones was demonstrated in soybean genotypes JS335 and UPSM534 that display contrasting YMD resistance. As a follow-up, soybean germplasm lines, breeding lines, and representative cultivars that were initially screened at an YMD hot-spot were then subjected to *Agrobacterium*-based infection with MYMIV. Quantitative real time polymerase chain reaction (qRT-PCR) based copy number analysis of MYMIV genomic components allowed soybean genotypes to be classified into three discrete categories; resistant, moderately resistant and susceptible to the viral infection. Thus, a soybean germplasm disease screening system based on agro-infection and qRT-PCR based quantification of MYMIV was developed to facilitate breeding YMD resistant soybean. The implications of this study for obtaining YMD resistant soybean cultivars are discussed.

1. Introduction

The family *Geminiviridae* comprises a large group of phytopathogenic viruses (Fauquet and Stanley 2003; Fauquet et al., 2008; Brown et al., 2015; Zerbini et al., 2017) including begomoviruses infecting legumes (Ilyas et al., 2010; Qazi et al., 2007). Legume begomoviruses are transmitted by *Bemisia tabaci* and cause yellow mosaic disease (YMD) and are collectively known as yellow mosaic viruses (YMV). *Mungbean yellow mosaic India virus* (MYMIV) which infects legumes that include soybean belongs to the genus *Begomovirus*, family *Geminiviridae* and causes YMD. YMV infection in legumes causes an estimated annual crop loss of US \$ 300 million (Varma and Malathi, 2003).

Begomoviruses characteristically have circular, single stranded DNA (ssDNA) genomes encapsidated in twinned icosahedral virions of 18 nm × 30 nm (Stanley et al., 2005). The genomes of YMV infecting soybean have two ssDNA genomic components, known as DNA A and

DNA B, each approximately of 2750 nts in length. The genomic components encode proteins in virion-sense and complementary-sense strands (Usharani et al., 2004; Ramesh et al., 2013). DNA A encodes the coat protein (CP) (AV1) and the pre-coat protein (AV2) on the virion-sense whereas genes (AC1, AC2 and AC3) on the complementary-sense strand code for the replication associated protein (Rep), transcriptional activator protein (TrAP), replication enhancer protein (REn), respectively. Two further genes in the complementary-sense strand, AC4 and AC5, code for proteins that are symptom determinants and suppressors of RNA silencing (Li et al., 2015). Thus, genomic component DNA A, encodes proteins for viral ssDNA encapsidation, replication and suppression of RNA silencing. Component DNA B encodes the nuclear shuttle protein encoded in the virion-sense and the movement protein in the complementary-sense which are involved in intracellular and cell-to-cell movement of virus (Sanderfoot and Lazarowitz, 1996; Stanley and Gay, 1983; Ingham et al., 1995).

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