



Short communication

Genetic diversity and population structure of *Sugarcane mosaic virus*

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ABSTRACT

Sugarcane mosaic virus (SCMV) is one of the causal pathogens of mosaic diseases on sugarcane, maize, sorghum and some other graminaceous species with worldwide distribution. The global genetic diversity and molecular evolution of SCMV capsid protein (CP) gene were investigated with the nucleotide sequences available in the GenBank database. Phylogenetic analyses revealed that SCMV isolates clustered in relation to their original hosts, and geographically distinct isolates from maize or sugarcane clustered differently. The populations between maize and sugarcane showed frequent gene flows; but within maize or sugarcane geography distinct isolates had infrequent gene flow. Recombination existed in the region of CP cistron and 3'-untranslated region (UTR). Most of the codons in the CP gene were under negative selection or neutral evolution except for codons 27 and 48, which were under positive selection. This study provided systematic analyses of the evolutionary processes contributing to the observed diversification of SCMV populations.

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RNA viruses have high mutation rates due to the error-prone replication attributed to the absence of proofreading activity in RNA-dependent RNA polymerases, short generation time and large population size (Domingo and Holland, 1997). RNA recombination between related or distantly related viruses, and even with host RNAs has been proposed to be one of the important evolutionary forces shaping genome evolution and divergence of plant RNA virus (Sztuba-Solińska et al., 2011). Therefore, plant RNA viruses exhibit high potential of genetic variation and diversity. The high level of genetic diversity enabled plant RNA virus to adapt to the changing environment including new or resistant hosts (Holmes, 2009). The knowledge of variability of genetic structure and diversity of the plant virus population is indispensable for the understanding of plant virus evolution and virus-plant interactions, in addition to developing durable strategies for the control of virus-induced diseases in plants (García-Arenal et al., 2001).

Sugarcane mosaic virus (SCMV) of the genus *Potyvirus* in the family *Potyviridae* is one of the causal pathogens of mosaic diseases in sugarcane, maize, sorghum and some other graminaceous species with worldwide distribution (Alegria et al., 2003; Achon et al., 2007) and causes great losses to crop yields. Once infected at an early stage of development, host plants would display symptoms of mosaic combined with chlorosis and dwarfism. Potyviruses have flexuous filamentous particles which contain a monopartite genome, a single-stranded positive-sense RNA of approximately 10,000 nucleotides that is covalently linked to a virus

genome-linked protein at its 5'-terminus and polyadenylated at its 3'-end (Revers et al., 1999). The genome encodes a single large polyprotein and a truncated frameshift product (Chung et al., 2008), which are proteolytically processed by three self-encoded proteases (Urcuqui-Inchima et al., 2001). The viral coat protein (CP) is multifunctional and involved in cell-to-cell and systemic movement, the regulation of viral RNA amplification (Urcuqui-Inchima et al., 2001), encapsidation of the RNA, vector transmission (Urcuqui-Inchima et al., 2001; Shukla et al., 1991), and perhaps host specificity (Shukla et al., 1991). The non-persistent transmission by aphids of potyvirus is the result of an interaction between the stylet of the aphid, the helper component protein (HC-Pro), and the conserved DAG (Asp-Ala-Gly) region of the CP (Pirone and Blanc, 1996). The highly variable N-terminus region of the CP is exposed on the surface and is thought to contain major virus-specific epitopes (Shukla et al., 1988). The core region and C-terminus are more conserved, although the last few amino acids of the C-terminus may be exposed on the viral surface (Shukla et al., 1988). CP sequences have been studied extensively to assess the difference within a potyvirus and between potyvirus species (Urcuqui-Inchima et al., 2001).

Numerous studies have been performed in recent decades on SCMV biology, genome characterization and sequence diversity (Alegria et al., 2003; Achon et al., 2007; Gao et al., 2011; Wang et al., 2010), but systematic research for SCMV genetic structure and diversity has been relatively scarce compared with other well-documented potyviruses including *Turnip mosaic virus* (TuMV) (Tomitaka and Ohshima, 2006), *Sweet potato feathery mottle virus* (SPFMV) (Tugume et al., 2010), *Watermelon mosaic virus* (Moreno et al., 2003) and *Potato virus Y* (Ogawa et al., 2008). To study the

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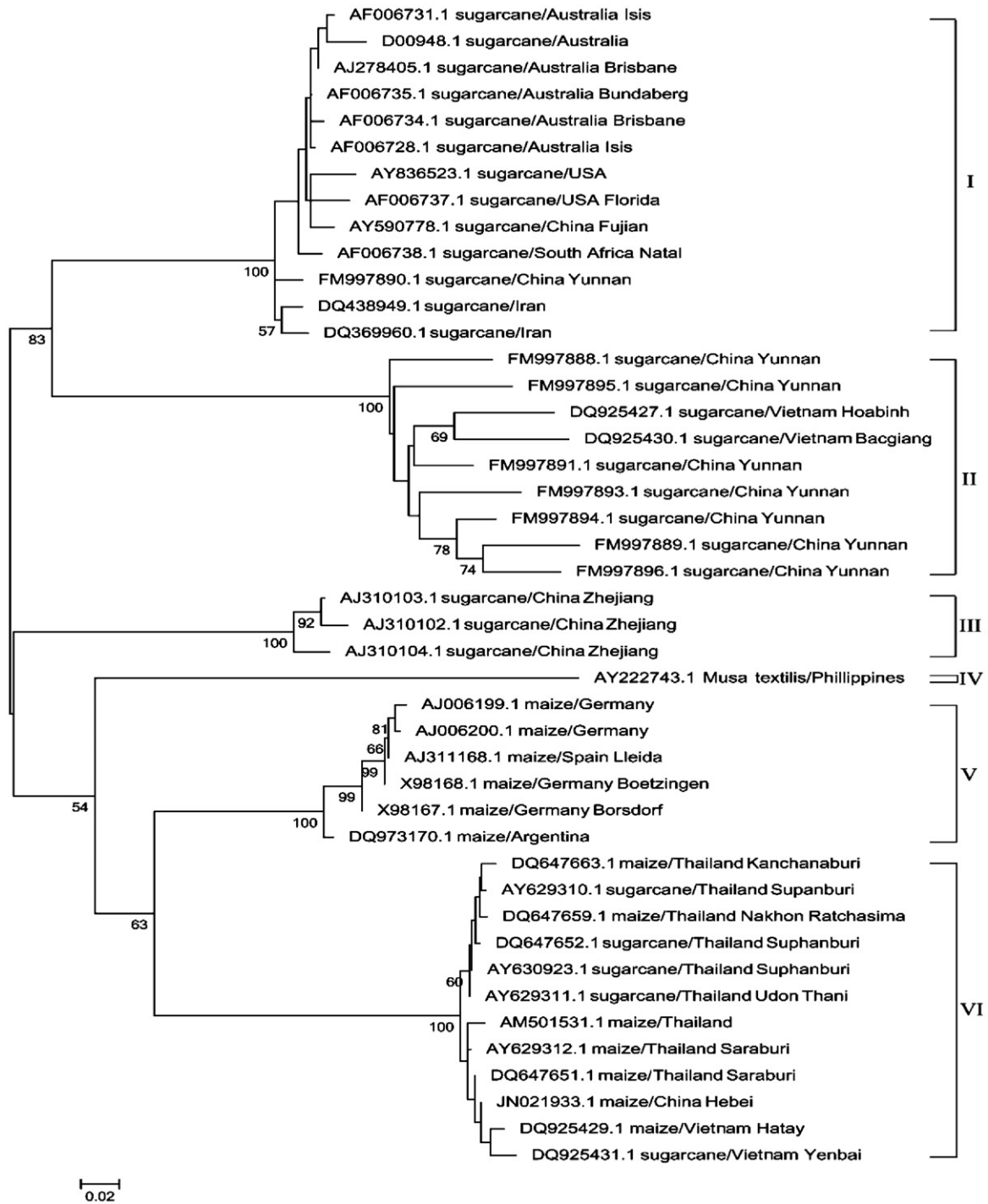


Fig. 1. Neighbor-joining tree generated based on the non-recombinant nucleotide sequence alignment of the CP cistron of different SCMV isolates depicting phylogenetic relationships. The bootstrapping replicates = 1000. Branches with bootstrap values of $\geq 50\%$ were shown. The scale bar represents genetic distance (substitutions per nucleotide).

genetic structure and elucidate potential factors that shape variation in SCMV population, a large number of host and geography distinct isolates of SCMV CP cistron and/or 3'-UTR were selected to assess the genetic structure of the population by analyses of their recombination, phylogeny, population demography and selection pressure acting on the CP gene.

Sequences of the SCMV CP cistron and/or 3'-UTR retrieved from the GenBank database (Supplementary Table 1) were processed and aligned using Clustal W (Thompson et al., 1994). The N-terminal of SCMV CP cistron had great diversity with the presence of

insertions and/or deletions, with the lengths ranging from 915 to 984 nt while most sequences were 939 nt (gaps are shown in Supplementary Figure 1). To evaluate the genotype profile of SCMV isolates, a phylogenetic tree was constructed by the neighbor-joining algorithm (1000 bootstrapping replicates) with the program MEGA 5.03 (Tamura et al., 2011) based on the non-recombinant CP cistron. The SCMV populations clustered into six groups distinguishable according to their genetic distances (Fig. 1) which were related to their original hosts, although different groups existed within the same host, in accordance with former

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