

# Occurrence and Evolutionary Analysis of Coat Protein Gene Sequences of Iranian Isolates of *Sugarcane mosaic virus*

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**Table S1** Detection of recombination by seven different methods implemented in RDP4

Recombination ( host and site)	DQ315494/BR10 (Sugarcane/Brazil)	DQ315495/BR11 (Sugarcane/Brazil)	DQ315496/BR13 (Sugarcane/Brazil)	DQ315498/BR15 (Sugarcane/Brazil)	DQ925428/VN-SC4 (Sugarcane/Vietnam)	
<b>Major parent (host and site)</b>	DQ315497/BR14 (Sugarcane/Brazil)	AF006731/Isis7 (Sugarcane/Australia) <sup>a</sup>	DQ315497/BR14 (Sugarcane/Brazil)	DQ315497/BR14 (Sugarcane/Brazil)	DQ925430/VN-SC3 (Sugarcane/Vietnam)	
<b>Minor parent (host and site)</b>	AF006731/Isis7 (Sugarcane/Australia)	DQ315497/BR14 (Sugarcane/Brazil)	AF006731/Isis7 (Sugarcane/Australia)	AF006731/Isis7 (Sugarcane/Australia)	X98167/Bor (Maize/Germany)	
<b>P-values determined by seven different programs</b>	<b>RDP</b>	$3.299 \times 10^{-13}$	$3.944 \times 10^{-13}$	$5.418 \times 10^{-12}$	$6.698 \times 10^{-9}$	$1.574 \times 10^{-5}$
	<b>GENECONV</b>	$2.080 \times 10^{-12}$	$2.443 \times 10^{-12}$	$9.303 \times 10^{-11}$	$2.825 \times 10^{-5}$	ND
	<b>BootScan</b>	$2.314 \times 10^{-13}$	$2.771 \times 10^{-13}$	$1.874 \times 10^{-11}$	$8.994 \times 10^{-10}$	$2.510 \times 10^{-10}$
	<b>MaxChi</b>	$5.901 \times 10^{-06}$	$5.868 \times 10^{-06}$	$4.483 \times 10^{-10}$	$1.370 \times 10^{-09}$	$2.853 \times 10^{-06}$
	<b>Chimera</b>	$2.727 \times 10^{-05}$	$2.727 \times 10^{-05}$	$8.777 \times 10^{-05}$	$2.694 \times 10^{-05}$	$1.253 \times 10^{-01}$
	<b>Siscan</b>	$3.738 \times 10^{-11}$	$3.738 \times 10^{-11}$	$7.170 \times 10^{-13}$	$8.820 \times 10^{-11}$	$6.372 \times 10^{-10}$
	<b>3Seq</b>	$1.404 \times 10^{-13}$	$1.404 \times 10^{-13}$	$9.669 \times 10^{-18}$	$1.491 \times 10^{-18}$	$8.439 \times 10^{-10}$
<b>Beginning breakpoint (nt)<sup>b</sup></b>	462	462	393	393	748	
<b>Ending breakpoint (nt)<sup>b</sup></b>	734	733	790	755	1050	

<sup>a</sup> Sequence used to infer unknown parent

<sup>b</sup> These breakpoints were deduced from the alignment of all sequences by the software RDP4.

ND, recombination was not detected by this program.