Nucleotide sequence of a full-length infectious clone of the Indonesian strain of tomato apical stunt viroid (TASV)

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ORIGIN

Using a two primer method similar to the one of Tabler *et al.* (1), we have obtained full-length monomeric clones of an Indonesian isolate of tomato apical stunt viroid (TASV). Infectivity of the cloned sequences was confirmed, by inoculation of double stranded recombinant plasmid DNA as shown previously for potato spindle tuber viroid (PSTV) (2). The complete nucleotide sequence of two independent infectious clones was determined using the chemical cleavage method of Maxam and Gilbert. No heterogeneity was found when comparing the sequences derived from the two clones.

SEQUENCE

10	20	30	40	50	60	70	80	90	100
CGGGAACUUU	CUUGAGGUUC	CUGUGUGUCU	CACCGACCC	UGCAGGCAUC	AAGAAAAG	AAUGGCGGGG	AGGAGAGAA	GUCCUUCAGG	GAUCCCCGGG
110	120	130	140	150	160	170	180	190	200
GAAACCGGA	GGAAGUCGAG	GUCGGGGGCU	UCGGAUACU	CCUUCGUGAG	ACAGGAGUAA	UCCCCGCGUA	AACAGGGUUU	UCACCCUCCU	UUCUUCGGU
210	220	230	240	250	260	270	280	290	300
UUCUUCGUC	UCGCGUGGAG	AGGUUCUGGG	CCUCGCGCG	GAGCUUCUCU	CUGGAGACUA	CCCCGUGGAA	ACAACUGAAG	CUUCAUCCCU	CACGCGCUU
310	320	330	340	350	360				
UUCUCUACU	UUGUUGCUCU	CCGGGCGAGG	GUGAAGCCCC	GUGGAACCCU	GGAAGGAGUC	CCU			

COMMENTS

The Indonesian isolate differs at 31 positions (nucleotide exchanges or insertions/deletions) from the published sequence of the type strain (3), giving an overall 91.5 % sequence homology. The secondary structure of the molecule is not extensively modified since most changes occur either in non base paired loops or as pairs of complementary changes. The differences are clustered and occur primarily in the so-called "Pathogenesis-Modulating" (PM) and "Variable" regions (4). There is only about 80 % homology with the type strain in these regions. We therefore suggest that the Indonesian isolate be regarded as a second strain of TASV. Eventhough the two strains have quite different PM regions, it should be noticed that they are of comparable pathogenicity on tomato.

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