Complete nucleotide sequence of a viroid isolated from Etrog citron, a new member of hop stunt viroid group

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The complete nucleotide sequence of a viroid isolated citrus (<u>Citrus</u> <u>medica</u> L. USDCS 60-13), designated as isolate of hop stunt viroid (HSV-cit)(1), was established. single stranded circular molecules of citrus viroid RNA consists of 302 nucleotides, which can form a rod-like structure extensive base-pairing characteristic to the other Heterogeneity was found in the sequence No. 207-209. GAG when determined from sequence was cDNAs bу transcriptase dideoxy method usina viroid oligonucleotide primers (Fig.1 variant 1, major sequence). it was CGA when determined from two cDNA clones by M13 dideoxy method (Fig.1 variant 2, minor sequence).

Comparative analysis of the sequence of the four HSV isolates indicates that HSV-citrus is more closely related to HSV-c isolated from cucumber in The Netherlands (2,3) (sequence homology 99%) than HSV-hop and HSV-grapevine (4,5) from hop grapevine in Japan, respectively (sequence homology 96%).

variant 1





Fig. 1 Proposed secondary structures of HSV-citrus (variant 1 and variant 2). The sequence different from HSV-hop and HSV-cucumber are indicated by arrowheads ( $\triangleright$ ) and circles ( $\bullet$ ), respectively.

## REFERENCES

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