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A plant virus satellite RNA exhibits a significant sequence complementarity to a chloroplast tRNA

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Submitted May 1, 1992

Cucumber mosaic virus (CMV) satellite RNAs (satRNAs) depend on CMV for their replication and share no significant sequence homology with CMV genomic RNAs. They can modify the symptoms induced by CMV in certain host plants. Our Y-satRNA (369 nucleotides) elicits bright yellow mosaics on tobacco which are quite distinct from those of other strains. It does not encode any functional polypeptides for biological activity and thus the molecule itself must trigger the yellow induction. Compared with other typical strains (~335 nucleotides), Y-satRNA has a unique domain (approximately residues 100–200: Y region) which was shown to be responsible for the yellow symptom expression (1, 2).

We have found that the Y-region had an intriguing sequence motif, exhibiting a significant sequence complementarity to a specific $tRNA^{Glu}$ (Figure) which functions as cofactor in the first step of chlorophyll biosynthesis (3). The free energy values for the $tRNA^{Glu}$ structure and the putative base-pairing between Y-region and $tRNA^{Glu}$ are −29.1 kcal/mole and −76.7 kcal/mole, respectively. Due to the remarkable sequence complementarity, it is proposed that the yellow chlorosis induced by Y-satRNA might result from antisense hybrid formation between Y-satRNA and the chloroplast $tRNA^{Glu}$.

It has been demonstrated that naturally occurring antisense RNAs regulate the expression of a variety of prokaryotic genes (4). Studies of their functions suggest that antisense regulation occurs at processing and transcription levels as well as translation level. Numerous reports have been also published on naturally occurring antisense RNAs in animals (5, 6) and plants (7). With respect to pathogenesis by antisense, Haas *et al.* previously found a sequence complementarity between viroids and plant 7S RNA and proposed that the pathogenic effects of viroids in plant on infection is due to the formation of a hybrid between the two molecules (8). While most of natural antisense RNAs are produced by the transcription of their individual target sites in the opposite direction to the target RNA transcription, an antisense RNA produced by an unlinked gene, which is not exactly complementary to its target RNA, have been also observed (9, 10). The possible hybrid formation of Y-satRNA and chloroplast $tRNA^{Glu}$ should be classified in the latter case.

ACKNOWLEDGEMENT

We thank Dr M.Miyano for establishing the computer programs for analysis of sequence complementarities on the VAX system.

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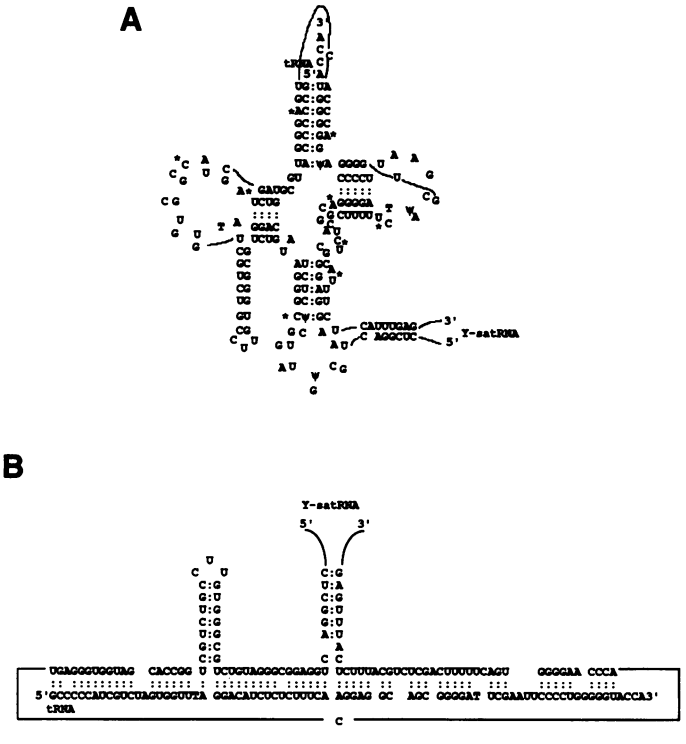

Figure. Possible complex formation between Y-region and chloroplast $tRNA^{Glu}$. The putative complex between the satRNA and $tRNA^{Glu}$ was determined by visual inspection of the sequences after computer-assisted analyses using the secondary structure prediction programs in IDEAS run on a VAX/VM and DANASIS (Hitachi, Japan) run on a NEC PC9801 in combination with a harrplot program for complementarity developed in our research institute. Free energy values were calculated according to the way compiled by Salser (11). The entire sequence of $tRNA^{Glu}$ was aligned with the sequence of Y-region (residues 112 to 204) in a secondary structure model (A) and in a linear form (B). The $tRNA^{Glu}$ sequence is the inner one in A and the lower one in B. Asterisks in A represent mismatched bases. Modified bases are not indicated in B.