Arch Virol (1997) 142: 271–285

Archives of Virology

Divergence and conservation of the genomic RNAs of Taiwan and Hawaii strains of papaya ringspot potyvirus*

C.-H. Wang and **S.-D. Yeh**

Department of Plant Pathology, National Chung Hsing University, Taichung, Taiwan, Republic of China

Accepted September 17, 1996

Summary. The complete nucleotide sequence of the genome of a Taiwan isolate of papaya ringspot potyvirus (PRSV YK) was determined from three overlapping cDNA clones and by direct RNA sequencing. Comparison was made with the reported Hawaii isolate of PRSV HA. Both genomes are 10 326 nucleotides long, excluding the poly(A)-tail. They encode a polyprotein of 3 344 amino acids with a 5′ leader of 85 nucleotides and a 3′ non-translated region of 209 nucleotides. The two genomes share an overall nucleotide identity of 83.4% and an amino acid identity of 90.6%. The 3′ non-translated regions show 92.3% identity. The first 23 nucleotides of the leaders are identical, while the remaining parts of the leaders only show 51.6% identity. The P1 protein genes of the two isolates are very different, with 70.9% nucleotide identity and 66.7% encoded amino acids identity. However, the other viral proteins of the two virus isolates are similar, with a 82.5–89.8% nucleotide identity of their genes and 91.2–97.6% amino acid identity, indicating that they are strains of the same potyvirus. Analysis of the ratios of nucleotide differences to the actual amino acid changes revealed that there are only 2.63 nucleotide changes for each amino acid change in the P1 protein, whereas for the other proteins 4.0–16.4 nucleotide changes are required for each amino acid replacement. The P1 protein has 58% of all the differences of polyprotein. The unusual variation in the leader sequences and the P1 proteins suggests that the two PRSV strains were derived from different evolutionary pathways in different geographic areas.

Introduction

Papaya ringspot virus (PRSV) is a member of the *Potyvirus* genus of the family *Potyviridae* [11], with flexuous particles of 780 × 12 nm and a genome consisting

*The nucleotide sequence data reported in this paper has been deposited at EMBL under accession number X97251.

of a single stranded RNA of positive polarity [7, 33, 54]. PRSV has a single type of coat protein (CP) of 36 000 daltons (36 kDa) [16, 32] and induces both cylindrical inclusions [31] and amorphous inclusions [26] in the cytoplasm of host cells. The former consists of a 70 kDa cylindrical inclusion protein (CIP) [53] and the latter consists of a 51 kDa amorphous inclusion protein (AIP) [8].

PRSV isolates are either type P or W. Type P (papaya-infecting) isolates cause serious problems in papaya throughout the tropical and subtropical regions; while type W isolates, previously called as watermelon mosaic virus 1, are of economic importance to cucurbits throughout the world [33]. The host range of PRSV type W does not include Caricaceeae (papaya), but P isolates infect the papaya family [33, 56]. Most isolates of these two pathotypes are serologically indistinguishable when tested by the CP and CIP antisera [53, 56].

PRSV HA is an isolate originally from Hawaii and is a typical severe strain of type P [16]. This virus has been well characterized in host range [33, 56], serology [56], gene expression [54] and genetic organization [58]. In the late 1970s, PRSV spread throughout Taiwan area and severely destroyed most of the commercial papaya orchards [48]. Two major strains of PRSV type P infecting papaya were found in Taiwan, one causing mosaic symptom on papaya and the other causing wilt symptoms [5]. Wang et al. [49] reported that the mosaic strain was the most common strain in Taiwan. Although the severe Taiwan mosaic strain and Hawaii HA are distinct in pathogenicity, they cannot be differentiated by serology [56]. PRSV YK originated from Yung-Kang in Tainan area is a stable isolate with biological properties representing the most prevalent mosaic strain in Taiwan [5].

The complete nucleotide sequence and genetic organization of the RNA genome of HA has been reported [58]. The genetic organization of PRSV is similar to those of the other potyviruses except that the first protein processed from the N terminus of the polyprotein, the P1 protein, is 18 kDa to 34 kDa larger than those of all reported potyviruses. The sequence of the 2960 nucleotide residues at the 3′ end of YK RNA has recently been determined and compared with those of HA, a mild strain HA 5–1, and type W strains [47], and the results indicated that the N terminus of the CP of the Taiwan YK isolate is different from those of other three strains, and this variability of the CP gene is correlated with the cross-protection specificity of the mild strain HA 5–1 [47, 49, 52, 57]. In this study, the complete nucleotide sequence of the genomic RNA of Taiwan YK isolate was elucidated and compared with that of the published Hawaii HA strain [58]. The fact that the nucleotide sequence of the genomic RNA and the amino acid sequence of the polyprotein are closely similar indicates that they are the strains of the same potyvirus. However, the greater differences in the regions of the 5′ leader and the P1 protein suggest different evolutionary pathways for the derivation of the two strains.

Materials and methods

Virus purification and RNA extraction

PRSV YK, a typical mosaic strain from Taiwan, was propagated in *Cucumis metuliferus* (Naud.) Mey. [30]. The virions were purified by Cs_2SO_4 centrifugation according to the method of Gonsalves and Ishii [16]. Genomic RNA was extracted by SDS-proteinase K treatment followed by sucrose density gradient centrifugation as described by Yeh and Gonsalves [54].

cDNA cloning, screening and in vivo excision

Complementary DNA was synthesized by the method of Gubler and Hoffman [18]. Purified PRSV YK RNA was employed as the template for cDNA synthesis, using an oligo (dT) primer with an *Xho*I site and the ZAP-cDNA synthesis kit (Stratagene, La Jolla, CA). The dsDNA was blunted by T_4 DNA polymerase and then ligated with the *Eco*RI adaptor at both ends. After hydrolysis with *Xho*I, they were unidirectionally ligated to the *Eco*RI/*Xho*I site of the Uni-ZAP XR lambda phage vector (Stratagene). Recombinant phage DNAs were encapsidated with a Gigapack II XL packaging extract, plated on *E. coli* strain PLK-F′ and then amplified in *E. coli* strain XL 1-Blue according to the manufacturers' instructions.

Clones corresponding to the 3′ region of YK RNA were immunoscreened with the antisera to PRSV CP [56] according to the method of Huynh et al. [20]. Clones corresponding to other regions of YK RNA were selected by hybridization. Digoxigenin-labelled (Boehringer Mannheim, Germany) or ^{32}P-labelled probes nick-translated from the inserts of PRSV HA clones pCI15 [58] and pHA16 [46], which reflected the regions of nucleotide positions 3 804 to 5 334 and positions 9 062 to the poly(A)-tail of HA RNA, respectively, were used to screen the clones by hybridization.

The size of the inserts of the selected clones was determined by *Eco*RI and *Xho*I digestion of purified recombinant lambda DNA, followed by ^{32}P-end-labeling and agarose gel electrophoresis. The selected lambda recombinants were converted to phagemids by in vivo excision [37], with coinfection of a helper phage R408 or VCSM13 (Stratagene) to excise the phagemid containing the cDNA insert from the lambda DNA. Bacterial colonies containing pBluescript recombinants were recovered by plating the phagemid-infected XL 1-Blue cells on ampicillin plates. Plasmid preparation was according to the method of Davis et al. [6], and the purified plasmids were digested with *Not*I and *Kpn*I to reconfirm the size of cDNA inserts.

Nucleotide sequencing and direct RNA sequencing

The cDNA inserts in the lambda ZAP II vector were digested with *Not*I and *Kpn*I, and the digested fragments were subcloned in pBluescript II SK(+) or KS(+) (Stratagene) to create clones of different orientations. Subclones were selected and terminally deleted by exonuclease III/mungbean nuclease treatment [17, 19, 34]. DNA was sequenced by the dideoxynucleotide chain termination method [36], using ssDNA templates generated from the terminally deleted plasmids using the helper phage VCSM13 [37]. As the 5′ end sequence of PRSV YK RNA was not obtained from the library constructed in the lambda ZAP vector, it was determined by direct RNA sequencing [59] using Moloney murine leukemia virus reverse transcriptase (Boehringer Mannheim) with the unlabeled synthetic oligonucleotide primers 5′d(GACGGTCTTTTAGTGCTATT), 5′d(CCCTCCAGGAAGGCCCTGCC),

5′d(CCGCAGTCGCATTTCTTGAA), corresponding to YK nucleotide positions 112 to 131, 278 to 297 and 422 to 441, respectively.

Sequence analysis

Sequence data were assembled and analyzed by the PC/Gene software (IntelliGenetics, Inc., Mountain View, CA), the MicroGenie software (Beckman Instrument, Palo Alto, CA) and the GCG package (Version 7-UNIX, Genetics Computer Group Inc., Madison, WI) [9, 10]. The complete nucleotide sequence of YK was compared with the published nucleotide sequence of PRSV HA [58]. GAPSHOW program was used to display an alignment of nucleotide or amino acid sequence by making a graph that shows the distribution of similarity and differences [9, 10].

Results and discussion

Complete nucleotide sequence of YK RNA

Three cDNA clones, pYKD9, pYKW63 and pYKW40, were selected from the lambda ZAP library by immunoscreening or hybridization, and they contained inserts of 2.2 kb, 6.3 kb and 4.0 kb, respectively. These three clones represented 99.7% of the PRSV YK genome. Sequence data were obtained from both orientations of the subclones and from the orderly deleted clones. The 34 nucleotide residues at the 5′ terminus were absent from the clone pYKW40, they were therefore determined by direct sequencing of the RNA using the oligonucleotide primers described in Materials and methods.

Comparison of the primary structures of the genomic RNAs of Taiwan and Hawaii strains

The assembled PRSV YK RNA sequence contained 10 326 nucleotides, excluding the poly(A) tail, and the length was identical to the published PRSV HA RNA (Fig. 1). Computer translation of the YK RNA revealed a single large open reading frame (ORF) that starts at the first AUG at the nucleotide position 86 and terminates with a UGA codon at position 10 118, followed by a 3′ non-translated region (NTR) of 209 nucleotides. The large ORF of YK encodes a polyprotein of 3 344 amino acids with a calculated molecular weight of 380 629 (381 kDa) (Fig. 2). The base composition of YK RNA is 31.4% adenine, 23.5% guanine, 18.4% cytosine and 26.6% uracil, which is similar to that of HA (31.2% adenine, 23.8% guanine, 18.0% cytosine and 27.0% uracil) and also similar to those of the other potyviruses [58].

Comparison of the complete nucleotide sequence of YK with that of the published Hawaii strain HA [58] indicated that they share an overall 83.4% nucleotide identity and a 90.6% amino acid identity for the polyproteins. A total of 1 711 nucleotide residues was found to be different between RNAs of YK and HA, resulting in 315 amino acid changes in the polyprotein (Figs. 1 and 2).

The 5′ leader sequence of YK RNA is 85 nucleotides long and has a significantly different base composition (43.5% A, 23.5% C, 5.9% G, 27.1% U) from that of the complete sequence. This is similar to the leader sequences of several

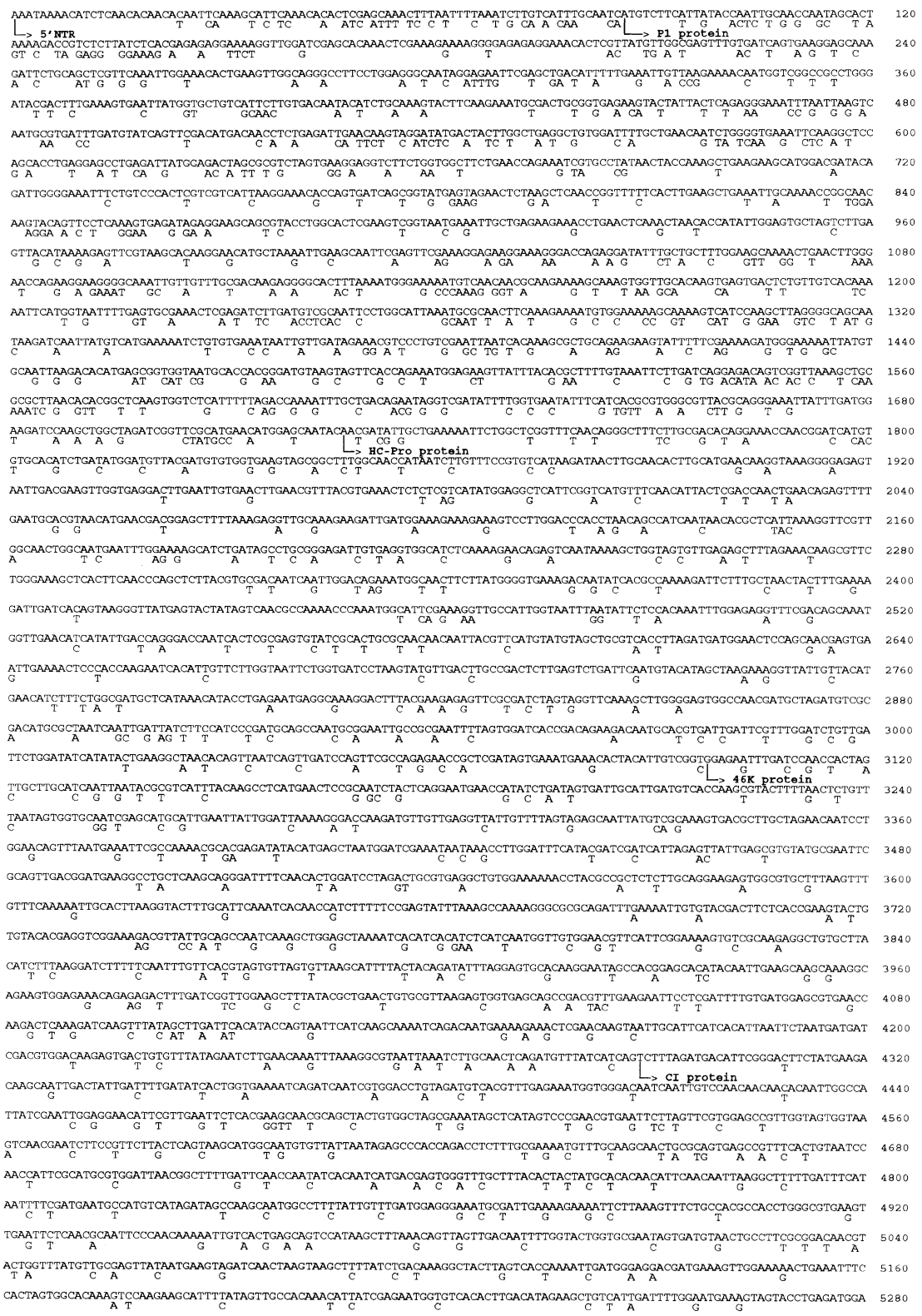

Fig. 1 (*continued*)

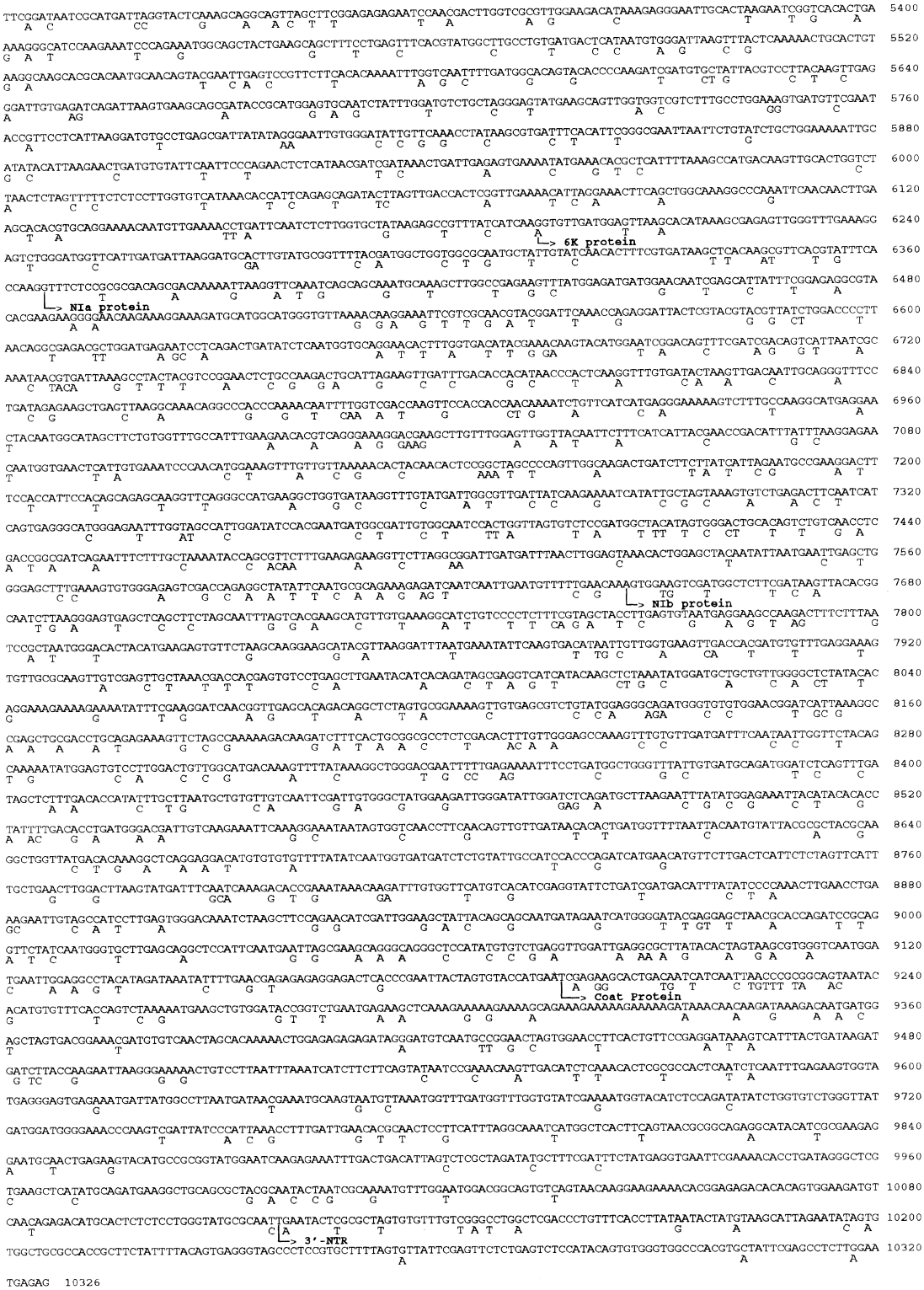

Fig. 1. Comparison of nucleotide sequences of PRSV YK (a Taiwan isolate) and HA (a Hawaii isolate). The complete sequence of the YK isolate is presented. Nucleotides of HA that differ from YK are shown below the YK sequence. Arrows indicate the initiation site of the open reading frame, the cleavage sites of viral proteins and the beginning of the 3′ non-translated region of PRSV RNA. The nucleotide sequence of HA strain was from Yeh et al. [58]

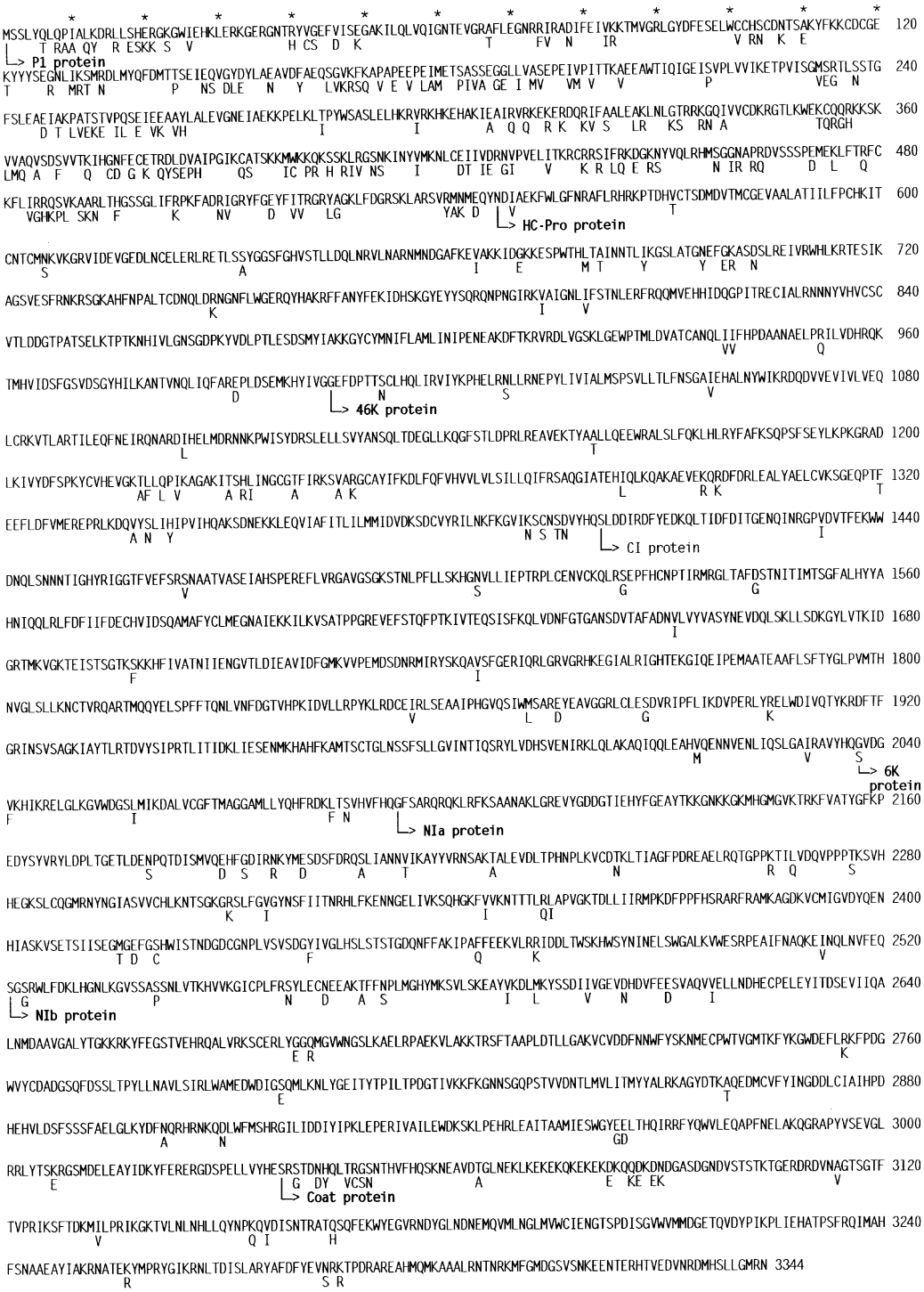

Fig. 2. Comparison of the deduced amino acid sequences of PRSV YK (a Taiwan isolate) and HA (a Hawaii isolate). The complete sequence of YK is presented. Amino acids of HA that differ from YK are shown below the HA sequence. The arrows indicate the N terminus of individual putative protein processed from the polyprotein. The amino acid sequence of HA was from Yeh et al. [58]

potyviruses which contain only 6.2 to 13.1% guanine [23]. The low content of guanine in the 5′ leader is a typical feature for potyviruses and other plant viruses [14]. The leader sequence of YK RNA has high AU content (70.6%), it has been proposed that this high AU content facilitates the melting of secondary structures of RNA for efficient translation [1, 22].

The 3′NTR of YK RNA contains 209 nucleotides with a poly(A) tail. A comparison of the 2 960 nucleotides of the 3′ region of YK RNA with those of the Hawaii severe strain HA, the mild mutant HA 5–1 and the non-papaya-infecting strain W has been previously reported [47].

The conserved and variable regions of the 5′ leader sequence

Comparison of the 5′ leader sequence of YK RNA with that of HA showed that they share a 64.7% nucleotide identity. The first 23 nucleotides of both RNAs are identical and this consensus sequence was also conserved in other potyviruses [40, 58]. This highly conserved sequence may play a common and important role for potyviruses, such as the binding of VPg, the assembly initiation site of virus particle, or the polymerase recognition signal for RNA replication.

Gallie et al. [15] reported that the 5′ leader of turnip yellow mosaic tymovirus (TYMV) did not enhance its translation in tobacco protoplasts, and suggested that the TYMV 5′ leader is host dependent in its ability to enhance translation. Petty et al. [29] investigated the systemic movement of barley stripe mosaic hordeivirus which is influenced by a single mutation in the 5′ leader sequence of the genome. They found that the systemic pathogenicity of the virus may be determined by the efficiency of translation of a viral gene in vivo and is not determined by the primary sequence of the encoded protein. Recently, the 5′ leaders of the two potyviruses, PSbMV and TEV, were found to enhance GUS activity to a similar level as the 5′ leaders of TMV [4, 28]. This effect on translation seems to be equivalent to the enhancing effect mediated by the TMV omega sequence, which consists of a $(CAA)_n$ motif of 25 nucleotides. This motif is responsible for the translational enhancement associated with the omega sequence, and two copies of $(CAA)_n$ alone are sufficient to confer a high level of enhancement [13]. This kind of motif is also present in the 5′ leaders of YK and HA strains of PRSV, with 7 and 10 repeats of CAA motif respectively. Especially, four repeats of the CAA triplet (CAACACAACACAATTCAA) were found in positions 14–31 of the PRSV leaders (Fig. 1). This association may enable the leaders of PRSV to have the same effect of translational enhancement mediated by TMV omega sequence. Comparison of the 5′ leaders of YK and HA from nucleotide positions 24 to 85 showed that they share only 51.6% identity (Figs. 1 and 3). This highly variable sequence may be related to a special function of PRSV, such as efficiency of translation, host determination, or pathogenicity.

The highly variable P1 proteins

The site for hydrolyzing the P1 protein from the polyprotein of PRSV HA was previously predicted by Yeh et al. [58] to be Phe 547/Asn 548. Verchot et al. [45]

investigated the proteolytic domains of the 35 kDa P1 protein of TEV by mutagenesis analysis and concluded that His 214, Asp 223, Ser 256 and Asp 288 are required for optimal autoproteolytic activity. The P1 protein of potyvirus was shown to exhibit nonspecific RNA-binding activity, the FIVRG motif of the P1 protein of potyviruses is similar to the RNP2 motif found in the RNP-CS-type binding domain. Some proteins containing this motif interact with RNA during pre-mRNA processing [3, 41]. In a recent study, the N-terminal half of P1 was shown to be dispensable for proteolysis as well as genome amplification, cell to cell movement and systemic infection [43, 44]. The cleavage site Phe/Asn and the essential amino acids for autoproteolytic activity of the TEV P1 protein are also present in the polyprotein of the YK isolate (Fig. 2).

Comparison of the P1 protein of YK with that of HA showed that they share a 70.9% nucleotide identity and a 66.7% amino acid identity. This represents 58% of the overall changes in the polyprotein, indicating that the P1 protein is more variable than the other proteins of this virus. There are only 2.63 nucleotide changes for each amino acid change in the P1 protein, but for other proteins more than 4 nucleotide changes for each amino acid difference (Fig. 3). The small ratio for the P1 protein indicates that a greater proportion of the nucleotide changes lead to amino acid changes. The P1 protein region of YK RNA contains 1 641 nucleotides and coded for a 63 kDa protein. This 63 kDa P1 protein is similar in size to that of HA and is 18 kDa to 34 kDa larger than those of other potyviruses [58]. Although the P1 proteins of PRSV YK is distantly related to those of other potyviruses, of all the P1 protein of potyviruses compared, including PRSV YK, the functional domains for serine-type proteinase activity [58] are conserved and located at the C terminal part of this protein.

Shukla and Ward [38, 39] concluded that sequence identity of the CPs between different potyviruses ranged from 38% to 71%, whereas that between strains of each species ranged from 90% to 99%. When the CP cores of more viruses were compared, the highest level of sequence identity corresponds to strains of a potyvirus species are still in 90–99% [11]. The amino acid sequence is 93.5% identical for the P1 proteins of G2 and G7 strains of SMV [21], and an even greater identity of 96.8% was found between RAN and NAT strains of PPV [24, 25]. In this investigation, only 66.7% identity was found in the P1 proteins of YK and HA. This would indicate that the two isolates are two distinct potyvirus species if the threshold for the CP identity is applied to the P1 protein. However, the CP is much more conserved among potyviruses (identity of 53.2%–56.6%) than the P1 protein (identity of 10.4%–18.3%) [58]. Therefore, the threshold of sequence similarity of CPs for grouping strains as the same potyvirus is obviously not applicable to the P1 protein. Recently, similar results were obtained when the P1 protein was compared between strains of ZYMV and PVY [42, 50]. The P1 coding region of a ZYMV strain from Reunion Island had a low (53.3–57%) amino acid sequence identity to four ZYMV strains from Florida and California [50]. Tordo et al. [42] reported that the amino acid sequence identity between 12 PVY isolates ranged from 72.8–100% in the P1 coding region, and these isolates can be classified into three geographical groups.

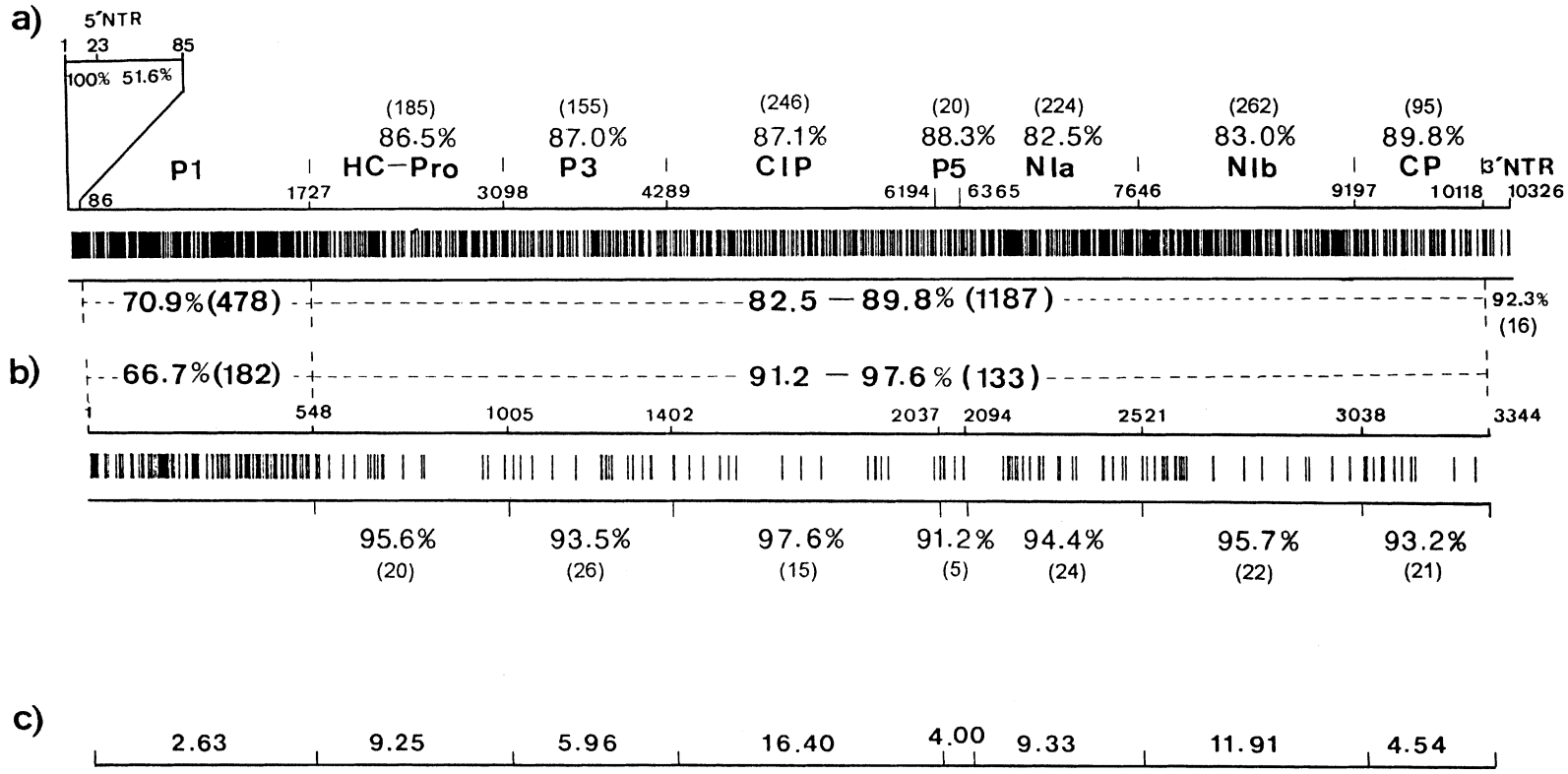

Fig. 3. The alignment of the nucleotide and amino acid sequences of PRSV YK and PRSV HA. The graphs display the alignment of nucleotide (**a**) and amino acid (**b**) sequences by the GAPSHOW program (GCG package, Version 7-UNIX) that showed the distribution of similarities and differences [9, 10]. The different nucleotides or amino acids are represented with vertical lines. The percentage of nucleotide (**a**) or amino acid (**b**) identity are shown and the numbers in parenthesis indicate the total residues of nucleotide or amino acid different in the compared region. Average numbers of nucleotide differences that result in one amino acid difference for each gene are indicated in (**c**). The nucleotide and amino acid sequences of HA strain are from Yeh et al. [58]

A new standard to distinguish different strains or viruses in the potyvirus group may have to be established when more sequence information for different P1 proteins becomes available. Nevertheless, the diversity of the P1 protein should be taken into consideration in work regarding taxonomy of potyviruses.

Other viral proteins

In previous studies of in vitro translation [8, 35, 51, 54] and the nucleotide sequence of PRSV HA, a tentative map of the polyprotein was proposed [58]. The cleavage sites in the polyprotein of YK were found to be similar to that of HA and other sequenced potyviruses (Fig. 2). Comparison of viral proteins of YK, excluding the P1 protein, with those of HA showed that they share 82.5–89.8% nucleotide identity and 91.2–97.6% amino acid identity (Fig. 3). There were 1 187 different nucleotides resulting in 133 different amino acids and a total of 42% different amino acids was found in the regions of the polyprotein excluding the P1 region. When the ratios of the number of nucleotide differences to the encoded amino acid changes were analyzed, it was found that an average of 8.92 nucleotide differences resulted in one amino acid change in regions of the polyprotein except for the P1 protein.

Comparison of the functional motifs of proteins of HA, except the P1 protein, with those of YK indicated that the motifs of the HC-Pro cysteine cluster of Cys-X_8-Cys-X_{13}-Cys-X_4-Cys-X_2-Cys (573–604) and the proteinase active sites of Gly- Tyr- Cys-Tyr (888–891) and His 963, and the CIP nucleotide-binding sites of GAVGSGKST (1 486–1 494) are identical. Motifs of other proteins were also conserved, as found in the VPg domain of the NIa protein (2 094 to 2 282), the protease domain of the NIa protein (2 283 to 2 520), the proteinase active sites of the NIa protein (His 2 327, Asp 2 362 and Cys 2 431) and the polymerase active sites of the NIb protein [YCDADGS(2763–2 769), GNNSGQQPSTVVDNT(S)-LMV (2 826–2 842) and NGDDL-X_{34}-K (2 869–2 908) (Fig. 2). The high degrees of conservation in the regions of the polyprotein, other than P1, and in its functional motifs indicated that YK and HA are strains of the same potyvirus.

Divergence and conservation of the genomic RNAs of YK and HA

Most of the nucleotide differences between YK and HA occurred in degenerate codon positions allowing the amino acid residues to be conserved. For example, more than 9 nucleotide changes resulted in only one amino acid change in HC-pro, CIP, NIa and NIb proteins. The extreme one is the CIP protein in which there were 246 nucleotide differences yet only 15 amino acid changes occurred (Fig. 3). It is likely that selection for essential functions of these proteins, such as aphid transmission, RNA replication and proteolytic processing is the cause.

Besides the P1 protein, the P3, the P5 proteins and CP are also much more variable than the HC-Pro, CIP, NIa and NIb proteins; only 4.0–5.96 nucleotide changes in the former three proteins for each amino acid change (Fig. 3). There are 155 and 20 nucleotide differences in P3 and P5 that resulted in 26 and

5 amino acid changes respectively. The changed amino acids are distributed rather randomly in different areas of the P3 and P5 regions (Fig. 3). The functions of the P3 and the P5 proteins of potyviruses are still not known. Alignment of the CPs of five sequenced PRSV strains was reported by our laboratory previously [47]. Differences in CP sequence among PRSV strains were located mostly at N-terminal regions of the CPs and the variation followed the differences in geographic origins rather than host specificity. Similar results were also noticed by Bateson et al. [2] who showed that variability of the CP genes among the W and P type isolates from Australia and those from other areas is not related to host specificity, such as papaya or non-papaya infecting, but corresponding to geographic distribution. Comparison of the predicted polyproteins of YK and HA of PRSV, determined by their nucleotide and amino acid sequences, demonstrated that the P1 protein is the most variable gene product, followed by P5, CP, and P3 in order. Whether the differences in the P1 proteins are related to host specificity or corresponding to geographic distribution remains to be further investigated.

The mild strain HA 5–1 provided a high degree of protection in papaya against infection with the severe strain of PRSV in Hawaii [27]. However, different degrees of cross-protection effectiveness were observed when HA 5–1 was used against strains of PRSV in Taiwan [49]. When the mild strain HA 5–1 was used to protect papaya against the mosaic or wilt strains from Taiwan, high frequency of breakdown was observed [49, 57]. Recently, transgenic plants that expressed the CP gene of HA 5–1 [12] were tested against 13 isolates of PRSV. The results showed that the effect of strain-specific protection was similar to classical cross protection [55]. The high variations in the 5′ leader sequence, in the P1 protein and in the N-terminal sequence of the CP [47] represent the major different regions between YK and HA genomes. Whether these diverged regions play a role for the differences in pathogenicity or the strain-specific protection remains to be investigated.

Although YK and HA are different strains of PRSV from distinct geographic origins, selection seems to have kept most of the viral proteins highly conserved. On the other hand, the high variability in the 5′ leader region, the P1 protein and the N-terminal region of the CP suggests that the two strains may arise from different evolutionary pathways in different geographic regions. The host i.e. different papaya varieties may play an important role in providing different selection pressures for the divergence in the pathogen.

Acknowledgement

This study was supported by grants from the Council of Agriculture of the Republic of China.

References

1. Altmann M, Blum S, Wilson TMA, Trachsel H (1990) The 5′-leader sequence of tobacco mosaic virus RNA mediates initiation-factor-4E-independent, but still initiation-factor-4A-dependent translation in yeast extracts. Gene 91: 127–129

2. Bateson MF, Henderson J, Chaleeprom W, Gibbs AJ (1994) Papaya ringspot potyvirus: isolate variability and the origin of PRSV type P (Australia). J Gen Virol 75: 3 547–3 553
3. Brantley JD, Hunt AG (1993) The N-terminal protein of the polyprotein encoded by the potyvirus tobacco vein mottling virus is an RNA-binding protein. J Gen Virol 74: 1 157–1 162
4. Carrington JC, Free DD (1990) Cap-independent of translation by a plant potyvirus 5′ nontranslated region. J Virol 64: 1 590–1 597
5. Chang CA (1979) Isolation and comparison of two isolates of papaya ringspot virus in Taiwan. J Agric Res China 28: 207–216
6. Davis LG, Dibner MD, Batty JF (1986) Basic methods in molecular biology. Elsevier, New York, pp 89–104
7. De La Rosa M, Lastra R (1983) Purification and partial characterization of papaya ringspot virus. Phytopathol Z 106: 329–336
8. De Mejia MVG, Hiebert E, Purcifull DE (1985) Isolation and partial characterization of the amorphous cytoplasmic inclusions associated with infections caused by two potyviruses. Virol 142: 24–33
9. Devereux J, Haeberli P, Simithies O (1984) A comprehensive set of sequence analysis programs for the VAX. Nucleic Acids Res 12: 387–395
10. Devereux J (1989) The GCG Procedure Library Version 6.0. Genetics Computer Group, Inc, Madison, Wisconsin
11. Francki RIB, Fauquet CM, Knudson DL, Brown F (1991) Classification and Nomenclature of Viruses. Fifth Report of the International Committee on Taxonomy of Viruses. Springer, Wien New York (Arch Virol [Suppl] 2)
12. Fitch MMM, Manshardt RM, Gonsalves D, Slightom JL, Sanford JC (1992) Virus resistant papaya plant derived from tissues bombarded with the coat protein gene of papaya ringspot virus. Bio/Technology 10: 1 466–1 472
13. Gallie DR (1993) Posttranscriptial regulation of gene expression in plants. Annu Rev Plant Physiol Plant Mol Biol 44: 77–105
14. Gallie DR, Sleat DE, Watts JW, Turner PC, Wilson TMA (1987a) A comparison of eukaryotic viral 5′-leader sequences as enhancers of mRNA expression in vivo. Nucleic Acids Res 15: 8 693–8 711
15. Gallie DR, Sleat DE, Watts JW, Turner PC, Wilson TMA (1987b) The 5′-leader sequence of tobacco mosaic virus RNA enhances the expression of foreign gene transcripts in vitro and in vivo. Nucleic Acids Res 15: 3 257–3 273
16. Gonsalves D, Ishii M (1980) Purification and serology of papaya ringspot virus. Phytopathology 70: 1 028–1 032
17. Guo LH, Wu R (1982) New rapid methods for DNA sequencing based on exonuclease III digestion followed by repair synthesis. Nucleic Acids Res 10: 2 065–2 084
18. Gubler U, Hoffman BJ (1983) A simple and very efficient method for generating cDNA libraries. Gene 25: 263–269
19. Heniknff S (1984) Unidirectional digestion with exonuclease III creates targeted breakpoints for DNA sequencing. Gene 28: 351–359
20. Huynh TV, Young RA, Davis RW (1985) Construction and screening cDNA libraries in lambda gt 10 and lambda gt 11. In: Glover DM (ed) DNA cloning, a practical approach, vol 1. IRL Press, Oxford, pp 49–79
21. Jayaram CH, Hill JH, Miller WA (1992) Complete nucleotide sequence of two soyabean mosaic virus strains differentiated by response of soyabean containing the *Rsv* resistance gene. J Gen Virol 73: 2 067–2 077
22. Jobling SA, Gehrke L (1987) Enhanced translation of chimeric messenger RNAs containing a plant viral untranslated leader sequence. Nature 325: 622–625

23. Johansen E, Rasmussen OF, Heide M, Borkhardt B (1991) The complete nucleotide sequence of pea seed-borne mosaic virus RNA. J Gen Virol 72: 2 625–2 632
24. Lain S, Riechmann JL, Garcia JA (1993) The complete nucleotide sequence of plum pox potyvirus RNA. Virus Res 13: 157–172
25. Maiss E, Timpe U, Brisske A, Jelkmann W, Casper R, Himmler G, Mattanovish D, Katinger HWD (1989) The complete nucleotide sequence of plum pox virus RNA. J Gen Virol 70: 513–524
26. Martelli GP, Russo M (1976) Unusual cytoplasmic inclusions induced by watermelon mosaic virus. Virology 72: 352–362
27. McMillan JRT, Gonsalves D (1987) Effectiveness of cross-protection by a mild mutant of papaya ringspot virus for control of ringspot disease of papaya in Florida. Proc Fla State Hort Soc 100: 294–296
28. Nicolaisen M, Jahansen E, Poulsen GB, Borkhardt (1992) The 5′ untranslated region from pea seedborne mosaic potyvirus RNA as a translation enhancer in pea and tobacco protoplasts. FEBS Lett 303: 169–172
29. Petty ITD, Edward MC, Jackson AO (1990) Systemic movement of an RNA plant virus determined by a point substitution in a 5′ leader sequence. Proc Natl Acad Sci USA 87: 8 894–8 897
30. Provvidenti R, Gonsalves D (1982) Resistance to papaya ringspot virus in *Cucumis metuliferus* and its relationship to resistance to watermelon mosaic virus. 1. J Hered 73: 239–240
31. Purcifull DE, Edwardson JR (1967) Watermelon mosaic virus tubular inclusion in pumpkin leaves and aggregates in leaf extracts. Virology 32: 393–401
32. Purcifull DE, Hiebert E (1979) Serological distinction of watermelon mosaic virus isolates. Phytopathology 69: 112–116
33. Purcifull DE, Edwardson JR, Hiebert E, Gonsalves D (1984) Papaya ringspot virus. CMI/AAB Descriptions of Plant Viruses No. 292
34. Putney SD, Benkovic SJ, Schimmel P (1981) A DNA fragment with an alpha-phosphorothioate nucleotide at one end is asymmetrically blocked from digestion by exonuclease III and can be replicated in vivo. Proc Natl Acad Sci USA 78: 7 350–7 354
35. Quiot-Douine L, Purcifull DE, De Mejia MVG (1986) Serological relationships and in vitro translation of a antigenically distinct strain of papaya ringspot virus. Phytopathology 76: 346–351
36. Sanger F, Nicklen S, Coulson AR (1977) DNA sequencing with chain-terminating inhibitors. Proc Natl Acad Sci USA 74: 5 463–5 467
37. Short JM, Fernandez JM, Sorge JA, Huse WD (1988) Lambda ZAP: a bacteriophage lambda expression vector with in vivo excision properties. Nucleic Acids Res 16: 7 583–7 600
38. Shukla DD, Ward CW (1988) Amino acid sequencing homology of coat proteins as a basis for identification and classification of the potyvirus group. J Gen Virol 69: 2 703–2 710
39. Shukla DD, Ward CW (1989) Identification and classification of potyvirus on the basis of coat protein sequence data and serology. Arch Virol 106: 171–200
40. Shukla DD, Ward CW, Brunt AA (1994) The Potyviridae. CAB International, Wallingford
41. Soumounou Y, Laliberte JF (1994) Nucleic acid-binding properties of the P1 protein of turnip mosaic potyvirus produced in *Escherichia coli*. J Gen Virol 75: 2 567–2 573
42. Tordo VMJ, Chachulska AM, Fakhfakh H, Ronancer ML, Robaglia C, Astier-Manifacier S (1995) Sequence polymorphism in the 5′ NTR and in the P1 coding region of potato virus Y genomic RNA. J Gen Virol 76: 939–949

43. Verchot J, Carrington JC (1995a) Debilitation of plant potyvirus infectivity by P1 proteinase-inactivating mutations and restoration by second-site modifications. J Virol 69: 1 582–1 590
44. Verchot J, Carrington JC (1995b) Evidence that the potyvirus P1 proteinase functions in *trans* as an accessory factor for genome amplification. J Virol 69: 3 668–3 674
45. Verchot J, Herndon KL, Carrington JC (1992) Mutational analysis of the tobacco etch potyviral 35-kDa proteinase: identification of essential residues and requirements for autoproteolysis. Virology 190: 298–306
46. Wang CH, Yeh SD (1992) Nucleotide sequence comparison of the 3′ terminal region of severe, mild, and non-papaya infecting strains of papaya ringspot virus. Arch Virol 127: 345–354
47. Wang CH, Bau HJ, Yeh SD (1994) Comparison of the nuclear inclusion b protein and coat protein genes of five papaya ringspot virus strains distinct in geographic origin and pathogenicity. Phytopathology 84: 1 205–1 210
48. Wang HL, Wang CC, Chiu RJ, Sun MH (1978) Preliminary study on papaya ringspot virus in Taiwan. Plant Prot Bull (Taiwan) 20: 133–140
49. Wang HL, Yeh SD, Chiu RJ, Gonsalves D (1987) Effectiveness of cross-protection by mild mutants of papaya ringspot virus for control of ringspot disease of papaya in Taiwan. Plant Dis 71: 491–497
50. Wisler GC, Purcifull DE, Hiebert E (1995) Characterization of the P1 protein and coding region of the zucchini yellow mosaic virus. J Gen Virol 76: 37–45
51. Yeh SD, Bih FY (1989) Comparative studies on in vitro translation of a severe strain and a mild strain of papaya ringspot virus. Plant Prot Bull (Taiwan) 31: 276–289
52. Yeh SD, Gonsalves D (1984a) Evaluation of induced mutants of papaya ringspot virus for control by cross protection. Phytopathology 74: 1 086–1 091
53. Yeh SD, Gonsalves D (1984b) Purification and immunological analyses of cylindrical inclusion protein induced by papaya ringspot virus and watermelon mosaic virus 1. Phytopathology 74: 1 273–1 278
54. Yeh SD, Gonsalves D (1985) Translation of papaya ringspot virus RNA in vitro: detection of a possible polyprotein that is processed for capsid protein, cylindrical-inclusion protein, and amorphous-inclusion protein. Virol 143: 260–270
55. Yeh SD, Gonsalves D (1993) Pratices and perspective of control of papaya ringspot virus by cross protection. Adv Dis Vector Res 10: 237–257
56. Yeh SD, Gonsalves D, Provvidenti R (1984) Comparative studies on host range and serology of papaya ringspot virus and watermelon mosaic virus 1. Phytopathology 74: 1 081–1 085
57. Yeh SD, Gonsalves D, Wang HL, Namba R, Chiu RJ (1988) Control of papaya ringspot virus by cross protection. Plant Dis 72: 375–380
58. Yeh SD, Jan FJ, Chiang CH, Doong TJ, Chen MC, Chung PH, Bau HJ (1992) Complete nucleotide sequence and genetic organization of papaya ringspot virus RNA. J Gen Virol 73: 2 531–2 541
59. Youvan DC, Hearst JE (1981) A sequence from *Drosophila melanogaster* 18S rRNA bearing the conserved hypermodified nucleotide: analysis by reverse transcription and high-performance liquid chromatography. Nucleic Acids Res 9: 1 723–1 741

Authors' address: Dr. S. D. Yeh, Department of Plant Pathology, National Chung Hsing University, 250 Kuo Kuang Road, Taichung, Taiwan 402, R.O.C.

Received February 5, 1996