

## Nucleotide sequence of the coat protein gene of the Skierniewice isolate of plum pox virus (PPV)\*

Krzysztof Wypijewski<sup>a</sup>, Tadeusz Malinowski<sup>b</sup>, Wojciech Musiał<sup>a</sup>  
and Jacek Augustyniak<sup>a,c</sup>

<sup>a</sup>Department of Biopolymer Biochemistry, A. Mickiewicz University, Al. Fredry 10, 61-701 Poznań, Poland, <sup>b</sup>Research Institute of Pomology and Floriculture, Pomologiczna 18, 96-100 Skierniewice, Poland

Received 15 December, 1993

Key words: reverse-transcription — polymerase chain reaction, nucleotide sequence

**The coat protein (CP) gene of the Skierniewice isolate of plum pox virus (PPV-S) has been amplified using the reverse transcription — polymerase chain reaction (RT-PCR), cloned and sequenced. The nucleotide sequence of the gene and the deduced amino-acid sequence of PPV-S CP were compared with those of other PPV strains. The nucleotide sequence showed very high homology to most of the published sequences. The motif: Asp-Ala-Gly (DAG), important for the aphid transmissibility, was present in the amino-acid sequence. Our isolate did not react in ELISA with monoclonal antibodies MAb06 supposed to be specific for PPV-D.**

The plum pox virus (PPV<sup>1</sup>) [1, 2], belonging to a large potyvirus group of plant viruses [3] (for review of potyvirus molecular biology see [4, 5]), is responsible for a severe disease (sharka) of plums, peaches and apricots. Its occurrence has been reported from many European countries as well as from Egypt [6]. In Poland it was first reported by Szczygieł [7] on plum. The presence of PPV in peaches and apricots, as well as the susceptibility of particular plum and peach cultivars to PPV were reported by Zawadzka [8] and Zawadzka & Malinowski [9]. Since PPV causes heavy losses in orchards, there is a great demand both for the methods of sensitive and reliable detection of infection and for obtaining virus resistant or tolerant cultivars producing high quality fruit. Unfortunately, conventional methods of breeding have so

far failed to produce such cultivars. In the last years many reports on induction of the resistance to plant viruses in transgenic plants expressing viral coat proteins, have been published [10–12]. The initial step in construction of such plants is the isolation of the viral coat protein gene.

Particles of PPV contain plus-sense ssRNA of about 10 kb [13] coding for the polyprotein of  $M_r$  354000. One of the cleavage products of this large protein is the coat protein (CP) gene of  $M_r$  366000 [14]. The CP coding sequence is located at the 3' end of its precursor gene.

The aim of our study was the construction of plums expressing the PPV CP gene, thus preparing a molecular probe for detection of PPV in plants, as well as a comparison of the Skierniewice isolate of PPV (PPV-S) with the PPV

\*This work was supported by the State Committee for Scientific Research, grant no. 6 6074 92 03.

<sup>1</sup>Abbreviations: CP, coat protein; PPV, plum pox virus; RT-PCR, reverse transcriptase-polymerase chain reaction; PEG, polyethylene glycol.

<sup>c</sup>To whom correspondence should be addressed: Prof. J. Augustyniak, Zakład Biochemii Biopolimerów UAM, Al. Fredry 10, 61-701 Poznań, Poland.

strains from other countries. In this paper we describe the isolation, cloning and sequencing of CP gene of PPV-S. We also discuss possible application of the restriction fragment length polymorphism (RFLP) for characterisation of the PPV strains.

## MATERIALS AND METHODS

**PPV isolation and purification.** The plum pox virus (PPV-S) was isolated from the plum Dąbrowicka Prune grown near Skierniewice (central part of Poland). The culture of the virus was obtained by making repeated inoculations from single local lesions developed in *Chenopodium foetidum*. PPV was then propagated in pea. Virus particles were purified as follows. Infected pea leaves were homogenised in a mixture of 0.1 M Tris/thioglycolate buffer, pH 8.6, chloroform and carbon tetrachloride (100 g of leaves : 200 ml of buffer : 60 ml of CHCl<sub>3</sub> : 60 ml CCl<sub>4</sub>). The homogenate was centrifuged in glass tubes for 25 min at 3200 r.p.m. and the aqueous phase was collected and clarified (10 min at 10000 r.p.m.). Virus was precipitated by the addition of polyethylene glycol (PEG) 6000 and sodium chloride (4 g PEG 6000, 1.75 g NaCl/100 ml) followed by centrifugation (10 min at 10000 r.p.m.). Pellet was resuspended in 0.05 M borate buffer, pH 8.2, overnight. This mixture was clarified (10 min at 10000 r.p.m.) and virus was concentrated by centrifugation (60 min at 39000 r.p.m.). After the clarification in Eppendorf tubes (3 min at 12000 r.p.m.) the crude preparation was layered over 10%–40% sucrose density gradient and centrifuged in SW28 rotor at 27000 r.p.m. for 180 min. The fraction containing virus particles was diluted at least 3-fold with the borate buffer and centrifuged (45000 r.p.m. for 60 min). The final pellet was resuspended in borate buffer. Concentration of PPV particles in the solution was calculated from the UV absorption value at 260 nm, assuming that 0.1% solution of the virus gives  $A_{260} = 3.0$  [15]. If the preparation was not used immediately, it was mixed with glycerol (1:1) and stored at  $-20^{\circ}\text{C}$ .

**Estimation of serotype.** Serotyping of our isolate was made using the monoclonal antibodies MAb05 and MAb06 [16, 17] and positive controls PPV-W and PPV-A kindly given to us by Dr. Navratil. PPV-W and PPV-A represent

serotype PPV-D and PPV-M [18], respectively. MAb05 reacts with PPV of both serotypes PPV-D and PPV-M. MAb06 reacts with PPV-D but does not recognise PPV-M. DAS-ELISA tests were carried out according to a standard procedure [19].

**RNA extraction from virus particles.** Purified virus particles (about 1  $\mu\text{g}$ ) were suspended in proteinase K solution (0.1 M Tris/Cl, pH 7.4, 50 mM NaCl, 10 mM EDTA, 0.2% (w/v) SDS, 200  $\mu\text{g}/\text{ml}$  proteinase K), incubated for 2 h at  $37^{\circ}\text{C}$ , shaken for 10 min with the equal volume of phenol-chloroform mixture (500 g of phenol, 0.5 g 8-hydroxyquinolinone, 150 ml water mixed 1:1 with chloroform) and centrifuged for 10 min at  $4^{\circ}\text{C}$ . The aqueous phase was reextracted with the same mixture until no more protein appeared at the interphase, then twice with chloroform, and RNA was precipitated overnight with 2.5 vol. of ethanol at  $-20^{\circ}\text{C}$ .

**Primers for reverse transcription and PCR.** The following oligodeoxyribonucleotides were designed as the primers on the basis of two published PPV CP gene sequences [20, 21]:

primer PPVCP1 : 5' GAGATAT-  
**GGATCC**ctaCTACACTCCCCTCACAC 3'

primer PPVCP2 : 5' GTGAATA-  
**GGATCC**atgGCTGACGAAAGAGAAGAC 3'

The last 17 nucleotides of PPVCP1 (underlined) are complementary to the 3' end of the fragment of viral RNA coding for PPV polyprotein. Upstream to this sequence PPVCP1 contains an extra termination codon (cta) and restriction site (bold type) for *Bam*HI followed by 7 nucleotides which make possible recognition of the restriction site by the enzyme. Primer PPVCP2 consists of a 18-nucleotide segment (underlined) corresponding to the 5' end of the PPV RNA region coding for viral CP. Upstream to this segment PPVCP2 contains an initiation codon (atg), *Bam*HI restriction site (bold type) and extra 7 nucleotides.

**Reverse transcription and PCR.** RT-PCR was performed using an RNA PCR kit purchased from Perkin-Elmer Cetus. For reverse transcription about 0.1  $\mu\text{g}$  of PPV-RNA was used. The reaction was run in a buffer containing 10 mM Tris/HCl, pH 8.3, 50 mM KCl, 4 mM MgCl<sub>2</sub>, 1 mM each of dNTP, 20 U RNase inhibitor, 0.75  $\mu\text{M}$  PPVCP1 primer and 50 U M-MuLV reverse transcriptase. Final volume of the mixture was 20  $\mu\text{l}$ . The reaction mixture was incu-

bated at 42°C for 45 min followed by 10 min at 95°C and 5 min at 5°C. During incubation each sample was covered with 50 µl of mineral oil. After reverse transcription the sample was extracted with chloroform and transferred to a new tube for PCR. To the mixture were added: 8 µl of 100 mM Tris/HCl buffer, pH 8.3, 4 µl of 25 mM MgCl<sub>2</sub>, 1 µl of 15 µM PPVCP2 primer, 5 U of AmpliTaq DNA polymerase (Perkin-Elmer Cetus) and water up to 100 µl. The samples were then covered with mineral oil and incubated under the following conditions:

2 cycles	95°C	for 2 min
	50°C	for 1 min
	72°C	for 5 min
23 cycles	95°C	for 1.5 min
	63°C	for 1 min
	72°C	for 5 min
1 cycle	95°C	for 1.5 min
	63°C	for 1 min
	72°C	for 10 min

**Cloning and sequencing of the PCR product.** PCR product, extracted with chloroform, precipitated with ethanol and purified by Sea Plaque GTG agarose gel electrophoresis, was digested with *Bam*HI (Promega). The digested product was purified by gel electrophoresis and ligated to 50 ng of pBluescript II KS+ in the *Bam*HI site as described in [22]. The *E. coli* DH5αF' cells were then transformed with the recombinant plasmid using the rubidium procedure [23]. Four clones were selected for se-

quencing of the PCR product and the recombinant plasmids isolated by the alkaline method [24] and purified by two-step CsCl gradient centrifugation [25]. The purified plasmids were used for sequencing either directly or after sub-cloning.

Sequencing of the recombinant plasmids (containing either the whole PCR product or its fragments) was performed by the dideoxy method [26] using [ $\alpha$ -<sup>32</sup>P]dATP, 3000 Ci/mmol (Amersham) and Taq DNA polymerase (Promega) under conditions recommended by the supplier of the enzyme.

## RESULTS AND DISCUSSION

The results of ELISA (Fig. 1) clearly indicate that our PPV-S isolate reacted with the monoclonal antibody MAb05 but was not recognised by the MAb06 reacting with PPV-D. This means that PPV-S is different serologically from PPV-D. However, its similarity to PPV-M has not been checked with PPV-M specific antibodies.

Primers for the RT-PCR were constructed on the basis of the published sequences of the coat protein genes of PPV-Rankovic and PPV-D [20, 21]. If the sequence of the CP gene of PPV-S strain does not differ much from the previously known ones, the primers should enable us to amplify the region of 993 nucleotides of the PPV coding for 330 amino acids of the PPV CP. Gel electrophoresis of the PCR product (not shown) yielded only one band of the expected length. The product was cloned and its se-

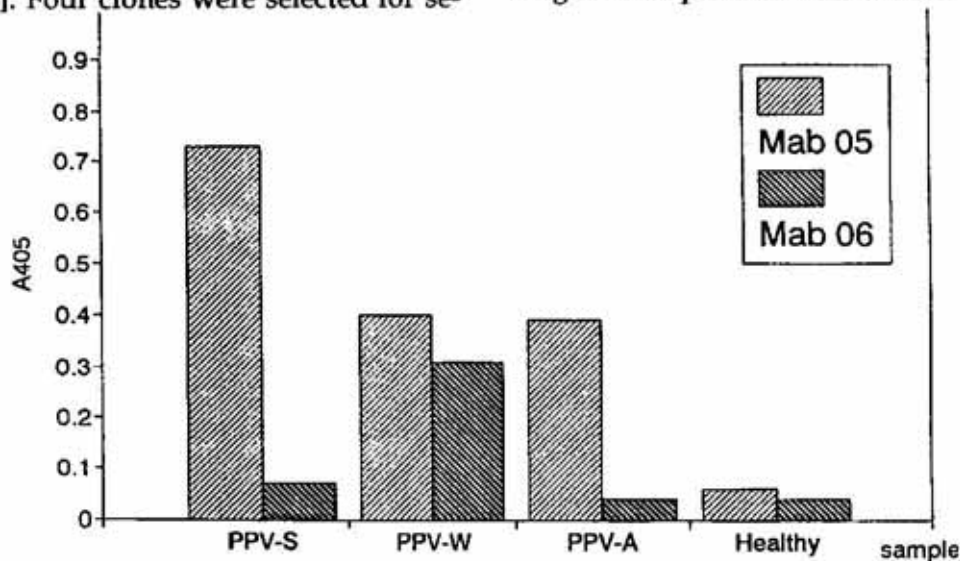


Fig. 1. The ELISA reaction of PPV-S with the monoclonal antibodies MAb05 and MAb06.

Table 1

*Nucleotide sequence of the coat protein gene of PPV-S and its comparison with CP genes of other PPV strains.*

Complete sequence is shown for the PPV-S isolate; for CP genes of other strains only differences are shown by letters, and identical nucleotides are marked with dots. Dashes denote deletions (PPV-NAT). Two 3-nucleotide long additions in the PPV-El Amar strain are indicated with arrow heads.

PPV-strain	Nucleotide sequence of CP gene					
	10	20	30	40	50	60
A: (PPV-S)	GCTGACGAAA	GAGAAGACGA	GGAGGAAGTT	GATGCAGGCA	AGCOGATTGT	AGTTACTGCA
B: (PPV-R)	.....	.....	.....	.....	.....G.....	.....
C: (PPV-D)	.....	.....G.....	.....	.....	.....	.....
D: (PPV-NAT)	.....	.....	.....	.....	.....	.....
E: (PPV-PS)	.....T.....	.....G.....G.....	.....T.....A.....	.....A.....	GA..T.C...	G..A.....
F: (PPV-oS)	.....T.....	AG..G.....	T..A.....	.....A.....	A..C.C..C	G..A.....
G: (El Amar)	.....T..G..	AG.....	A.....G	.....G	G..TTTA...	CACC..A..
		add(GAT)				
	70	80	90	100	110	120
A: (PPV-S)	COGGCAGCAA	CTAGCCCAAC	ACTTCAACCA	CCTCCAGTTA	TACAGCCTGC	ACCCAGACT
B: (PPV-R)	.....	.....	.....	.....C.....	.....	.....G.....
C: (PPV-D)	.....	.....	.....	.....C.....	.....	.....G.....
D: (PPV-NAT)	.....	.....	.....	.....C.....	.....	.....G.....
E: (PPV-PS)	.....	.....GTGG.....	.....GAC.....	.....G.....G.....	.....A.....	.....A..C
F: (PPV-oS)	.....	.....GTGG.....	.....A.C.....	.....G.....G.....	.....A.....	ATT..A..C
G: (El Amar)	A..CAGC...	T..GTTA...	..AC...G.A.	A.....A.A.	CGAGTA..A.	CTTA..AG..
		add (ACC)				
	130	140	150	160	170	180
A: (PPV-S)	ACGGCGCCAA	TGTTCAACCC	CATTTTCAAG	CCAGCAACAA	CTCAACCAGC	AACAAAACCA
B: (PPV-R)	.....T...	.....C.....	.....	.....	.....	.....
C: (PPV-D)	.....	.....C.....	.....	.....	.....	.....
D: (PPV-NAT)	.....	.....C.....	.....	.....	.....	.....
E: (PPV-PS)	..A..A.....	.....	.....T	.....	.....G..T..	GGT..G.....
F: (PPV-oS)	..A..A.....	.....	.....T	.....	.....G..T..	GAT..G.....
G: (El Amar)	..CA.G...T..T..	..C.....T	..G..G..	..G.G..GA.	C..T.GGA..	
	190	200	210	220	230	240
A: (PPV-S)	GTTTCACAGG	TGTCAGGACC	TCAACTGCAA	ACTTTTGGAA	CATATGGTAA	TGAGGATGCC
B: (PPV-R)	.....	.....	.....	.....	.....	.....A
C: (PPV-D)	.....	.....C.....	.....	.....	.....	.....A
D: (PPV-NAT)	.....	.....	.....	.....	.....A..C.....	.....A
E: (PPV-PS)	..C.T.CAA	T.....CA	CA..C..GG	T.....G	TT.....A..	..A..C..A
F: (PPV-oS)	..T.TA	T.....GG	..C..C..	T.....G	TT.A..A..	.....A
G: (El Amar)	..GC.T..CA	CAA..ACTA	..AC..CT.CT	T.....G	TGATC..G..	.....A..
	250	260	270	280	290	300
A: (PPV-S)	TCACCTAGCA	ACTCAAACGC	GCTAGTCAAC	ACAAACAGAG	ACAGOGACAT	CGATGCAGGA
B: (PPV-R)	.....	.....	.....	.....	.....G.....	.....
C: (PPV-D)	.....	.....	.....	.....	.....G.....	.....
D: (PPV-NAT)	.....	.....	.....	.....	.....TG.....	.....
E: (PPV-PS)	.....	C.....A	TT.G..G..T	..GGA..G..	T.....G..	.....
F: (PPV-oS)	.....	C.....A	TT.G..G..	..GGA..G..	T.....G..	.....
G: (El Amar)	G...C.ATG	CT..C..T.	AG...TCGA	..GGT...	..A..TG.	T.....G..T
	310	320	330	340	350	360
A: (PPV-S)	TCAATTGGAA	CTTTCACAGT	GCCACGTTTG	AAGGCAATGA	CITCGAAACT	ATCTTTGCCA
B: (PPV-R)	.....G.....	.....T.....	.....	.....	.....	.....C.....
C: (PPV-D)	.....	.....T.....	.....	.....	.....	.....C.....
D: (PPV-NAT)	.....C.....	.....T.....	.....	.....	.....	.....C.....
E: (PPV-PS)	..G.....	.....G.....	.....C..A	..AA.....	..A.....GT.	..C..A..G
F: (PPV-oS)	..G.....	.....	.....C..A	..AA.....	..A.....GT.	..C..A..G
G: (El Amar)	..C.....G..	.....	.....C..	..A.....	..A..A..G..	C..AC..T...
	370	380	390	400	410	420
A: (PPV-S)	AAGGTGAGGG	GAAAGGCCAT	TATGAACTTG	AACCATTGGG	CACATTATAG	TCCTTCACAG
B: (PPV-R)	.....A.....	.....T.....	.....	.....	.....	.....G.....
C: (PPV-D)	.....A.....	.....T.....	.....	.....	.....	.....G.....
D: (PPV-NAT)	.....A.....	.....T.....	.....	.....	.....	.....G.....
E: (PPV-PS)	.....ACC	.....A.....	.....A	..T.....	.....C.....	.....G...A
F: (PPV-oS)	.....AA	.....A..A..	.....A	..T.....	.....C.....	.....G...A
G: (El Amar)	.....AA	..G..A..A..	.....T.....	..T..CC...	TTTC..C..	.....G...A
	430	440	450	460	470	480
A: (PPV-S)	GTTGATTGTG	CAAACACAGG	AGCTCCGCAG	TCTTGTTC	AAACTTGGTA	TGAAGGAGTT
B: (PPV-R)	.....C.....	.....	.....	.....	.....	.....
C: (PPV-D)	.....C.....	.....	.....	.....	.....	.....
D: (PPV-NAT)	.....C.....	.....	.....	.....	.....	.....
E: (PPV-PS)	.....C.....	.....AC	.....A..A	..C..C.....	..G.....	.....
F: (PPV-oS)	.....A.....	.....AC	.....A..A	..C.....	..G.....	.....
G: (El Amar)	..G.....	..G.....C	.....A..	..C..C..T	.....A	.....

	490	500	510	520	530	540
A: (PFV-S)	AAGCGAGATT	ATGATGTCAC	GGACGATGAA	ATGAGCATCA	TTTTAAATGG	TCTTATGGTT
B: (PFV-R)	.....	.....	.....	.....	.....	.....
C: (PFV-D)	.....	.....	.....	.....	.....	.....
D: (PFV-NAT)	.....C.....	.....	.....	.....	.....	.....
E: (PFV-PS)	.....T.....	.....	A..T..CC..	.....	.....G.....	CT.G.....
F: (PFV-oS)	.....T.....	..C.....	A..T..G...	.....	.....G.....	C..G.....
G: (El Amar)	..GA..C..C..	....C.....	T..T.....	.....T.....	.....G.....	G.....C.....
	550	560	570	580	590	600
A: (PFV-S)	TGGTGCATAG	AGAATGGAAC	ATCCCCGAAT	ATCAATGGAA	TGTGGGTGAT	GATGGATGGG
B: (PFV-R)	.....	.....	.....	.....	.....	.....
C: (PFV-D)	.....	.....	.....	.....	.....	.....
D: (PFV-NAT)	.....	.....	.....	.....	.....	.....
E: (PFV-PS)	.....C.....	..A..C.....	G..T....C	.....	.....	.....
F: (PFV-oS)	.....C.....	..A..C.....	G....T..C	....C.....	.....	.....
G: (El Amar)	.....T.....	.....	.....	..T.....	.....C.....	.....C.....
	610	620	630	640	650	660
A: (PFV-S)	GAAACACAAG	TGGAGTATCC	AATAAAGCCA	TIGTTGGATC	ATGOGAAACC	CACTTTTAGA
B: (PFV-R)	.....	.....	.....	.....	.....	.....
C: (PFV-D)	.....	.....C.....	.....	.....	.....	.....
D: (PFV-NAT)	.....	.....	.....	.....	.....	.....
E: (PFV-PS)	..G.....	.....	.....C.....	.....	..C.....	.....
F: (PFV-oS)	.....	.....	.....C.....	.....	..C.....	.....
G: (El Amar)	..G.....	.....	.....C.....	.....	.....	.....
	670	680	690	700	710	720
A: (PFV-S)	CAAATTATGG	CACATTTGAG	TAACGTGGCT	GAAGCGTATA	TTGAAAAACG	AAATTATGAA
B: (PFV-R)	.....	.....	.....	.....	.....	.....
C: (PFV-D)	..G....G...	..G.....	CG.....	.....G..G..	..G.....	.....C...
D: (PFV-NAT)	.....	.....	.....	.....	.....	.....
E: (PFV-PS)	.....	.....	.....	.....C.....	.....	.....G.....
F: (PFV-oS)	.....	.....	.....	.....	.....	G....C..G
G: (El Amar)	.....	.....	.....	.....	.....	G.....G.....
	730	740	750	760	770	780
A: (PFV-S)	AAAGCATACA	TGCCAAGGTA	TGGAATTCAG	CGCAACCTGA	CAGACTACAG	CCTCGCCAGA
B: (PFV-R)	.....	.....	.....	.....	.....	.....
C: (PFV-D)	.....	.....	.....	.....	.....	.....
D: (PFV-NAT)	.....	.....	.....	.....	.....	.....
E: (PFV-PS)	.....	.....	.....	.....	.....T.....	T..A.....
F: (PFV-oS)	.....	.....	.....	.....	.....T.....	.....
G: (El Amar)	.....	.....	..T.....	.....	..G..T.....	.....
	790	800	810	820	830	840
A: (PFV-S)	TATGCCTTIG	ATTTTACGA	AATGACTTCA	ACGACACCCG	TACGGGCACG	TGAAGCTCAT
B: (PFV-R)	.....	.....	.....	.....A.....	.....	.....
C: (PFV-D)	.....	.....	.....	.....	.....	.....
D: (PFV-NAT)	.....	.....	.....	.....	.....	.....
E: (PFV-PS)	..C.....	.....	.....	..A..G..T..	..G..T.....	.....
F: (PFV-oS)	..C.....G	.....	.....	..A....T..	..G..T.....	.....
G: (El Amar)	..C.....	.....	.....	.....T.....	..G..T.....	.....
	850	860	870	880	890	900
A: (PFV-S)	ATCCAGATGA	AGGCAGCAGC	ATTGAGAAAT	GCTCAAAATC	GTTTATTTGG	CTTGGATGGA
B: (PFV-R)	.....	.....	.....	..T.....	.....	.....
C: (PFV-D)	.....	.....	.....	..T.....	.....	.....
D: (PFV-NAT)	.....A.....	.....	.....	..T.....	.....	.....
E: (PFV-PS)	..A.....	.....	.....	..T.....	.....	.....
F: (PFV-oS)	..A.....	.....	.....	..T..G.....	.....	.....
G: (El Amar)	..A.....	.....G..	.....	..C..G.....	.....	.....
	910	920	930	940	950	960
A: (PFV-S)	AACGTCGGAA	CACAAGAAGA	GGACACAGAG	AGACACACCG	CTGGTGATGT	TAATCGCAAC
B: (PFV-R)	.....	.....	.....	.....	.....	.....
C: (PFV-D)	.....	.....	.....	.....G..A.....	.....	.....
D: (PFV-NAT)	.....	.....	.....	.....	.....	.....
E: (PFV-PS)	.....	.....	.....	..G.....	.....C.....	.....
F: (PFV-oS)	.....	.....	.....	..G.....	.....C.....	G.....
G: (El Amar)	..T..T.....	.....	.....	..G.....	.....	.....
	970	980	990			
A: (PFV-S)	ATGCACAACC	TCCTCGGTGT	GAGGGGAGTG	TAG		
B: (PFV-R)	.....	.....	.....	.....		
C: (PFV-D)	.....C.....	.....	.....	.....		
D: (PFV-NAT)	.....	.....A.....	.....	.....		
E: (PFV-PS)	.....	.....	.....	.....		
F: (PFV-oS)	.....	.....	.....	.....		
G: (El Amar)	.....T.....	.....A.....	.....	.....		

A: (PFV-S) - Skierniewice isolate of PFV, B: (PFV-R) - Rankovic strain of PFV [20],  
 C: (PFV-D) - PFV-D strain [21], D: (PFV-NAT) - PFV-NAT strain [13], E: (PFV-PS) [32],  
 F: (PFV-oS) [32], G: (El Amar) - PFV-El Amar strain [6].

quence was read in 4 independent experiments to avoid mistakes, possible when Taq DNA polymerase is used for DNA amplification. The nucleotide sequence of the PCR product and its comparison with the published sequences of CP genes of PPV is shown in Table 1. PCR amplification may occur even when there are some mismatches between the primer and the target sequence [27]. Therefore it should be stressed that the sequences of the first 18 and the last 17 nucleotides may actually originate from the sequences of primers. In preparing cDNA we have not used primers corresponding to the sequences outside the CP gene.

It is obvious from the data shown in Table 1 that PPV-S is different from the other PPV strains, the CP genes of which have been sequenced so far. The smallest differences are observed between PPV-S and PPV-Rankovic strain: there are only 16 substitutions of nucleotides (homology 98.4%) of which 10 lead to substitutions of amino acids (Table 2). PPV-D strain differs in the CP gene from PPV-S by 27 substitutions (homology 97.3%). In both cases the substitutions are distributed non-uniformly along the gene. There is an about 390 bp long stretch in the central part of the genes (positions 427–818) where the sequences of PPV-S and PPV-Rankovic are identical. PPV-NAT (not aphid transmissible) [28] is shorter than the aphid transmissible PPV-S, PPV-Rankovic and PPV-D by 45 nucleotides, and differs from PPV-S by 19 substitutions. Apart from this deletion, PPV-NAT shows 91.1% homology with PPV-S. The largest number of substitutions is observed in relation to the El Amar strain [6] (80.6% homology); in this case most of the changes are located in the 5'-end region of the CP gene (78% of all changes within 420 bp at the 5'-end), while the region corresponding to C-terminal part of the coat protein is much more conservative.

Wetzel *et al.* [27] showed that the restriction fragments length polymorphism of the 243 bp PCR product can be used as a tool for dividing PPV strains into two groups: strains with or without the *RsaI* restriction site in the amplified fragment (GTAC at position 820–823 in Table 1). They also suggested that the presence or absence of the *RsaI* restriction site is highly correlated with the particular PPV-D serotype group. The original definition of the PPV-D and PPV-M serotype was made [18] using polyclo-

nal antibodies and the agar double diffusion technique. We have not done this kind of experiments with PPV-S. Therefore we do not know whether our isolate is an exception from this rule (it possesses the *RsaI* site but its serological properties differ from those of PPV-D), or the classification based on the reaction with MAb05 and MAb06 does not fully correspond to the original distinction between the PPV-D and PPV-M type.

We suggest that the primers and method we have used for amplification of PPV-S CP gene can be applied to other PPV strains. It should thus be possible to distinguish either of each pair of PPV strains of known CP sequence by RFLP analysis of the PCR product. For example, PPV-S and PPV-El Amar, compared with PPV-Rankovic, PPV-D and PPV-NAT, lack *HincII* site at position 421 (due to substitutions C<sub>426</sub> → T<sub>426</sub> in PPV-S and T<sub>423</sub> → G<sub>423</sub> in PPV-El Amar) or *HpaII* site at position 114 (substitution G<sub>116</sub> → A<sub>116</sub>). This comparison might serve as a simplified version of the classification based upon sequence data [29], especially if the IC-RT-PCR method developed by Wetzel *et al.* [30] is used.

The amino-acid sequence of PPV-S coat protein (predicted from the sequence of the CP gene) differs less from the other PPV strains (Table 2) than does its nucleic acid sequence. Like other aphid-transmissible PPV-strains, PPV-S contains an Asp-Ala-Gly motif (positions 11–13) which was suggested to be important for aphid transmissibility [6], preceded by a conserved stretch of 10 amino acids at the N-end of CP. Within this stretch in PPV-PS and PPV-oS [32] there are substitutions Glu-7 → Asp-7, and in PPV-oS and El Amar Arg-4 → Lys-4, but obviously these substitutions do not alter the nature of this stretch and are not incompatible with the suggestion of PPV strains being transmissible by aphids.

We have not checked the aphid transmissibility of PPV-S in a controlled experiment. However, PPV-S was isolated from a tree which had been infested with aphids. It has also been reported by Smolarz & Zawadzka [31] in 1978 that PPV occurring near Skierniewice is aphid transmissible.

Similarly as in the whole potyvirus group [4] the C-terminal part of PPV-S coat protein is, in general, much more conserved than its N-terminal part but, surprisingly, it differs in the

Table 2

*Amino-acid sequence of the PPV-S coat protein predicted from the nucleotide sequence of the CP gene and its comparison with the CP proteins of other PPV strains.*

Complete sequence is shown for PPV-Skierniewice only; identical amino acids in other strains are marked with dots.

Deletion of 15 amino acids in PPV-NAT is marked with dashes. Addition of two amino acids in PPV-El Amar is indicated with arrow heads.

PPV strain	Amino acid sequence of CP					
	10	20	30	40	50	60
A: (PPV-S)	ADEREDEEEV	DAGKPIVVTA	PAATSPTLQP	PPVIQPAPQT	TAPMFPNPIFT	PATTQPATKP
B: (PPV-R)	.....	.....S.....	.....I.....	.....R.....	..S.L.....	.....
C: (PPV-D)	.....	.....	.....I.....	.....R.....	..L.....	.....
D: (PPV-NAT)	.....	.....	.....	.....R.....	..L.....	.....
E: (PPV-PS)	.....D.....	.....R.T.....	.....VA.T.....	A.....	..T.....	.....VR.
F: (PPV-oS)	...K..D...	...K.TA...	...VA.T...	A.....I..	..T.....	.....IR.
G: (El Amar)	...K.....	...R.L.T.T	QQPITT.T.	T.ITSTTL.A	QA.....	PA..E.T.RT
	add D <sup>^</sup>		add V <sup>^</sup>			
	70	80	90	100	110	120
A: (PPV-S)	VSQVSGPQLQ	TFGTIGNEDA	SPSNSNALVN	TNRDRDIDAG	SIGTFTVPRL	KAMTSKLSLP
B: (PPV-R)	.....	.....	.....	.....V.....	..V.....	.....
C: (PPV-D)	...F.....	.....	.....	.....V.....	.....	.....
D: (PPV-NAT)	.....	.....SH.....	.....	.....V.....	..T.....	.....
E: (PPV-PS)	..PPI..TKPR	S..V.....	...T.T...	..G...V...	.....A....	..T.....
F: (PPV-oS)	..L...ATP.	S..V.....	...T.T...	..G...V...	.....	..T.....
G: (El Amar)	..PHTTTTTP	S..VI...T	A.NA...V.R	..G...V...	.....	.....
	130	140	150	160	170	180
A: (PPV-S)	KVRGKAIMNL	NHLAHYSPSQ	VDLSNTRAPQ	SCFQTWYEGV	KRDYDVTDD	MSIILNGLMV
B: (PPV-R)	..K.....	.....A.....	.....	.....	.....	.....
C: (PPV-D)	..K.....	.....A.....	.....	.....	.....	.....
D: (PPV-NAT)	..K.....	.....A.....	.....	.....	.....	.....
E: (PPV-PS)	..K.....	.....A.....	.....	.....	.....E.....	.....
F: (PPV-oS)	..K.....	.....A.....	.....	.....	.....E.....	.....
G: (El Amar)	..K.....	.....F...A..	.....	.....	..R.....	.....
	190	200	210	220	230	240
A: (PPV-S)	WCIENGTSPN	INGMVMMDG	ETQVEYTIKP	LLDHAKPTFR	QIMAHFSNVA	EAYIEKRYNE
B: (PPV-R)	.....	.....	.....	.....	.....	.....
C: (PPV-D)	.....	.....	.....H.....	.....	..R.V.R..D..	..CV.....
D: (PPV-NAT)	.....	.....	.....	.....	.....	.....
E: (PPV-PS)	.....	.....	.....P.....	.....	.....	.....
F: (PPV-oS)	.....	.....	.....P.....	.....	.....	.....
G: (El Amar)	.....	.....	.....	.....	.....	.....
	250	260	270	280	290	300
A: (PPV-S)	KAYMPRYGIQ	RNLTDYSLAR	YAPDFYEMTS	TTFVRAREAH	IQMKAALRN	ACNRLFGLDG
B: (PPV-R)	.....	.....	.....	.....	.....	..V.....
C: (PPV-D)	.....	.....	.....	.....	.....	..V.....
D: (PPV-NAT)	.....	.....	.....	.....	.....	..V.....
E: (PPV-PS)	.....	.....	.....	.....	.....	..V.....
F: (PPV-oS)	.....	.....	.....	.....	.....	..V.....
G: (El Amar)	.....	.....	.....	.....	.....	.....
	310	320	330			
A: (PPV-S)	NVGTQEEDTE	RHTAGDVNRN	MEHLLGVRRG			
B: (PPV-R)	.....	.....	.....			
C: (PPV-D)	.....KQ...	...D.....	..TF.....			
D: (PPV-NAT)	.....	.....	.....M.....			
E: (PPV-PS)	.....	.....	.....			
F: (PPV-oS)	.....	.....	.....			
G: (El Amar)	.....	.....	.....M.....			

For designations of PPV see Table 1.

C-terminal half from CP of PPV-D by 12 amino acids, while in the N-terminal half only by 7 amino acids. On the contrary, in CP of PPV-El Amar, the N-terminal half of which differs largely from that of PPV-S, the C-terminal part (positions 161-330) is identical except for one substitution (Val → Met, pos. 327).

As shown in Fig. 1, PPV-S CP reacts well with antibody MAb05 but is not recognized by antibody MAb06. This indicates that PPV-S is serologically different from PPV-D which reacts with both MAb05 and MAb06.

Assuming that antibodies can recognise the external part of CP in intact viral particles and

knowing from aphid transmissibility that the N-terminal region of CP is externally oriented, it can be suggested that the different reactivity of MAb06 with PPV-S and PPV-D resulted from differences in amino acids 27, 39 and/or 45 (Ile, Arg and Leu in PPV-D substituted by Thr, Glu and Phe in PPV-S). Since other amino acids can also contribute to the reactivity against antibodies, it would be interesting to check the reactivity towards MAb06 of CP of PPV-PS, PPV-oS and El Amar, where these residues are the same as in PPV-S (although there are numerous other substitutions in the respective CP region). Unfortunately, during the present investigation these strains were not available for direct comparison.

We would like to thank to R. Adamiak (PAN Poznań) for synthesizing the primers.

## REFERENCES

- Nemeth, M. (1986) Plum pox (Sharka); in *Virus, Mycoplasma and Rickettsia Diseases of Fruit Trees*; pp. 463–479, Akademiai Kiado, Budapest.
- Kegler, H. & Shade, Ch. (1970) Plum Pox Virus; C.M.I. A.A.B. *Descriptions of Plant Viruses*. No. 70
- Ward, C.W. & Shukla, D.D. (1991) Taxonomy of potyviruses: current problems and some solutions. *Intervirology* **32**, 269–296.
- Riechmann, J.L., Lain, S. & Garcia, J.A. (1992) Highlights and prospects of potyvirus molecular biology. *J. Gen. Virol.* **73**, 1–16.
- Shukla, D.D., Frenkel, M.J. & Ward, C.W. (1991) Structure and function of the potyvirus genome with special reference to the coat protein coding region. *Canad. J. Plant Pathol.* **13**, 178–191.
- Wetzel, T., Candresse, T., Ravelonandro, M., Delbos, R.P., Mazyad, H., Aboul-Ata, A.E. & Dunez, J. (1991) Nucleotide sequence of the 3' terminal region of the RNA from an atypical strain (El Amar) of plum pox potyvirus. *J. Gen. Virol.* **72**, 1742–1746.
- Szczygiel, A. (1962) Pojawienie się w Polsce groźnej choroby wirusowej szarki *Prunus virus 7*. (Appearance a severe viral disease sharka *Prunus virus 7* in Poland). *Ochrona Roślin* **6**, 14–17.
- Zawadzka, B. (1980) The response of several plum cultivars to infection with plum pox virus. *Acta Phytopathol. Acad. Sci. Hungar.* **15**, 215–221.
- Zawadzka, B. & Malinowski, T. (1989) Response of a few peach cultivars to infection with plum pox virus. *Plant Virology Proceedings of the 10th Conference of the Czechoslovak Plant Virologist*, 213.
- Ling, K., Namba, S., Gonsalves, C., Slightom, J.L. & Gonsalves, D. (1991) Protection against detrimental effects of potyvirus infection in transgenic tobacco plants expressing the papaya ringspot virus coat protein gene. *Biotechnology* **9**, 752–758.
- Gonsalves, D., Chee, P., Provvidenti, R., Seem, R. & Slightom, J.L. (1992) Comparison of coat protein-mediated and genetically-derived resistance in cucumbers to infection by cucumber mosaic virus under field conditions with natural challenge inoculations by vectors. *Biotechnology* **10**, 1562–1570.
- Wilson, T.M.A. (1993) Strategies to protect crop plants against viruses: pathogen derived resistance blossoms. *Proc. Natl. Acad. Sci. U.S.A.* **90**, 3134–3141.
- Maiss, E., Breyel, E., Briske, A. & Casper, R. (1988) Molecular cloning of DNA complementary to the RNA genome of plum pox virus (PPV). *J. Phytopathol.* **122**, 222–231.
- Ravelonandro, M., Varveri, C., Delbos, R. & Dunez, J. (1988) Nucleotide sequence of the capsid protein gene of plum pox potyvirus. *J. Gen. Virol.* **69**, 1509–1516.
- Moghal, S.M. & Francki, R.I.B. (1976) Towards a system for the identification and classification of Potyviruses. *Virology* **73**, 350–362.
- Navratil, M., Cikanek, D., Hilgert, I., Kristofova, H. & Karesova, R. (1992) Monoclonal antibodies against plum pox virus. *Acta Horticulturae* **309**, 169–173.
- Hilgert, I., Cikanek, D., Kristofova, H., Karesova, R. & Navratil, M. (1992) Monoclonal antibodies suitable for plum pox virus determination. *Hybridoma* (in press).
- Kerlan, C. & Dunez, J. (1979) Differentiation biologique et serologique de souches du virus de la Sharka. *Ann. Phytopathol.* **11**, 241–250.
- Clark, M.F. & Bar-Joseph, M. (1984) Plant virus enzyme immunosorbent assays. *Methods Virol.* **7**, 60–61.
- Lain, S., Riechmann, J.L. & Garcia, J.A. (1989) The complete nucleotide sequence of plum pox potyvirus RNA. *Virus Res.* **13**, 157–172.
- Teycheney, P.Y., Tavert, G., Delbos, R., Ravelonandro, M. & Dunez, J. (1989) The complete nucleotide sequence of plum pox virus RNA (strain D). *Nucl. Acids Res.* **17**, 10115–10116.
- Crouse, G.F., Frischauf, A. & Lehrach, H. (1983) An integrated and simplified approach to



- cloning into plasmids and single-stranded phages. *Methods Enzymol.* **101**, 78–89.
23. Hanahan, D. (1985) Studies on transformation of *Escherichia coli* with plasmids. *J. Mol. Biol.* **166**, 557–580.
  24. Sambrook, J., Fritsch, E.F. & Maniatis, T. (1989) in *Molecular cloning. A laboratory manual*, pp. 1.25, Cold Spring Harbor Laboratory Press.
  25. Gatger, S.J., Griffith, O.M. & Grill, L.K. (1974) Rapid purification of plasmid DNA by a single centrifugation in a two-step caesium chloride ethidium-bromide gradient. *Technical Bulletin of Beckman*, G-594.
  26. Sanger, F., Nicklen, S. & Coulson, A.R. (1977) DNA sequencing with chain-termination inhibitors. *Proc. Natl. Acad. Sci. U.S.A.* **74**, 5463–5467.
  27. Wetzel, T., Candresse, T., Ravelonandro, M. & Dunez, J. (1991) A polymerase chain reaction adapted to plum pox potyvirus detection. *J. Virol. Meth.* **33**, 355–356.
  28. Maiss, E., Timmpe, U., Briske, A., Jelkmann, W., Casper, R., Himmler, G., Mattanovich, D. & Katinger, H.W.D. (1989) The complete nucleotide sequence of plum pox virus RNA. *J. Gen. Virol.* **70**, 513–524.
  29. Ward, C.W., McKern, N.M., Frenkel, M.J. & Shukla, D.D. (1992) Sequence data as the major criterion for potyvirus classification. *Arch. Virol. (Suppl. 5)* 283–297.
  30. Wetzel, T., Candresse, T., Macquaire, G., Ravelonandro, M. & Dunez, J. (1992) A highly sensitive immunocapture polymerase chain reaction method for plum pox potyvirus detection. *J. Virol. Meth.* **39**, 27–37.
  31. Smolarz, S. & Zawadzka, B. (1978) Skuteczność mszyc w przenoszeniu wirusa ospowatości śliwy (szarki). (Efficiency of aphids in transmission of plum pox (sharka) virus). *Zesz. Probl. Post. Nauk Roln.* **214**, 51–58.
  32. Cervera, M.T., Riechmann, J.L., Martin, M.T. & Garcia, J.A. (1993) 3'-Terminal sequence of the plum pox virus PS and oS isolates: evidence for RNA recombination within the potyvirus group. *J. Gen. Virol.* **74**, 329–334.