

Isolation and Characterization of *Plutella xylostella* Granulovirus Isolated in Korea

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(Received 11 September 2005; Accepted 13 October 2005)

We have first isolated and characterized a *Plutella xylostella* granulovirus (PxGV) from dead larvae of *P. xylostella* in Korea. The granule of PxGV was ovoidal shape with an approximate measure of 350 – 400 nm × 150 – 200 nm, and each granule contained one single rod-shape virion with a mean size of 150 – 180 nm × 20 – 30 nm. The major granule protein, granulin, had a molecular weight of approximately 29 kDa. Whereas the nucleotide sequence of the granulin gene was identical to that of previously reported PxGV, nucleotide sequences of two of three putative p10 genes were slightly different from those of reported PxGV. These results suggested that the PxGV isolated in this study was a novel isolate containing different genomic information.

Key words: Baculovirus, *Plutella xylostella* granulovirus, Granulin gene, p10 gene

Introduction

The diamondback moth, *Plutella xylostella* is a widely-distributed and serious pest of crucifers in subtropical areas including South Asia, South-East Asia and South America (Abdul Kadir *et al.*, 1999a). In most regions of the world where *P. xylostella* is a pest, control has been heavily dependent on chemical pesticides although some progresses have been made with biological and integrated

pest management approaches. The heavy dependence on chemical pesticides has created severe pesticide resistance problems (Abdul Kadir *et al.*, 1999a). These severe pesticide resistance problems have prompted considerable interest in biological methods for *P. xylostella* control, including the introduction and manipulation of parasitoids and pathogens, such as *Bacillus thuringiensis* (Zhao *et al.*, 2000). In recent years, *B. thuringiensis* products have been widely used for *P. xylostella* control but genetic resistance in populations to some *B. thuringiensis* strains, compounded by cross-resistance to several different *B. thuringiensis* toxins, has also been identified (Tabashnik *et al.*, 1997). Such recent resistance problems serve to emphasize the urgent need for alternative control agents and their use within an integrated pest management approach.

Baculoviruses have been used as agents for the biological control of certain insect pest species (Zhang *et al.*, 2005). Two different members have been accepted within the baculoviruses, nucleopolyhedroviruses (NPVs) and the granuloviruses (GVs), based on the structure of the occluded virus and the occlusion body (OB). Most of our knowledge on the baculoviruses relates to the NPVs. The GVs are less studied because of the limited availability of permissive insect cell lines. Several baculoviruses including *Autographa californica* NPV (AcNPV) and *Galleria mellonella* NPV (GmNPV) have been reported to be infective to *P. xylostella* (Vail *et al.*, 1972; Abdul Kadir *et al.*, 1999a, 1999b). Since GV infecting *P. xylostella* (PxGV) was first reported by Asayama and Osaki (1970), several reports have showed PxGV as a promise control agent for *P. xylostella* (Kao and Rose, 1976; Wang and Rose, 1978).

Although the complete nucleotide sequence of PxGV

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genome has been reported (Yoshifumi *et al.*, 2000), no research has been performed on characteristics of this virus. In this study, a PxGV isolated from Korea was identified and characterized.

Materials and Methods

Virus isolate

Homogenate of PxGV-infected *P. xylostella* larvae was filtered through sterile cheesecloth. The mixture was centrifuged at $5,000 \times g$ for 5 min, and then, the pellets were washed three times with distilled water. The viral occlusion bodies were layered onto 40% – 65% discontinuous sucrose gradient and were centrifuged at $80,000 \times g$ for 60 min. The OBs were collected by centrifugation at $10,000 \times g$ for 10 min. Then, they were re-suspended with 0.5 M NaCl (Shim *et al.*, 2003).

Electron microscopy

For scanning electron microscopy, the purified OBs were dried at the critical point in CO₂. The samples were sputtered with gold in a sputter coater SC502 (Polaron, UK) and observed using field emission scanning electron microscope JSM-6700F (JEOL, Japan).

For transmission electron microscopy, the purified OBs were fixed for 2 hrs by 2% paraformaldehyde and 2% glutaraldehyde in 0.05 M sodium cacodylate buffer (pH 7.2). After post-fixation by 1% OsO₄ in the same buffer, the samples were dehydrated in ethanol/propylene oxide series and embedded in Epon-Araldite mixture. Ultra-thin sections were performed with a RMC MT-X ultramicrotome and photographed under the transmission electron microscope JEM-1010 (JEOL, Japan).

SDS-PAGE

The OBs were mixed with the 5 × sample buffer (60 mM Tris-HCl, pH 6.8, 25% glycerol, 2% SDS, 14.4 mM β-mercaptoethanol, 0.1% bromophenol blue) and were boiled for 5 min and were clarified by centrifugation ($15,000 \times g$ for 5 min). The total cellular lysates were separated on a 10% polyacrylamide gel containing SDS as described by Laemmli (1970).

PCR and oligonucleotide primers

The degenerate primers, Gr-F (5'-ATGGGATAYAACAR-AKCWYTRMGKTAYAGYMRHCAC-3') and Gr-R (5'-TTARTAVGCBGGDCCDGTRWAYARWGGYACRTC-3'), specific to granulin gene were designed based on the nucleotide sequences of previously reported granulin genes. Three pairs of oligonucleotide primers, Pxorf2-F (5'-CAAACGTCACATAATGC-3') and Pxorf2-R (5'-TG

TTGCTGAAACTGTTC-3'), Pxorf21-F (5'-TCGATAAC ATGTCCAGA-3') and Pxorf21-R (5'-TCTAGAATCTG CGCATA-3'), and Pxorf50-F (5'-CACAACGTGTATCT GGA-3') and Pxorf50-R (5'-GGGTTCGATTTACGATTT-3'), specific to three putative p10 genes of PxGV were also designed based on the nucleotide sequences of these genes reported by Yoshifumi *et al.* (2000). The PCR reaction was carried out with 250 ng of plasmid DNA, 100 pM of each primer and PCR PreMix (Bioneer Co., Korea) in a 20 μl PCR mixture for 33 thermal cycles (94°C for 1 min, 45°C for 1 min and 72°C for 1 min). Amplification was accomplished with the DNA Thermal Cycler (Perkin Elmer Cetus, USA).

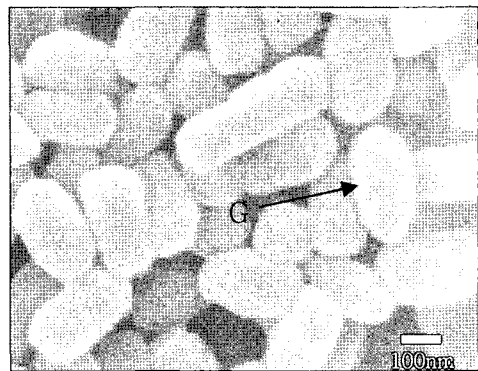
Cloning and sequence analysis

PCR amplified granulin and three p10 genes were cloned into pGEM-T Easy vector (Promega, USA), and their nucleotide sequences were determined on an ABI sequence Model 377 (ABI system, USA). The obtained sequences were compared with those of previously reported PxGV granulin gene and p10 genes using the BLAST.

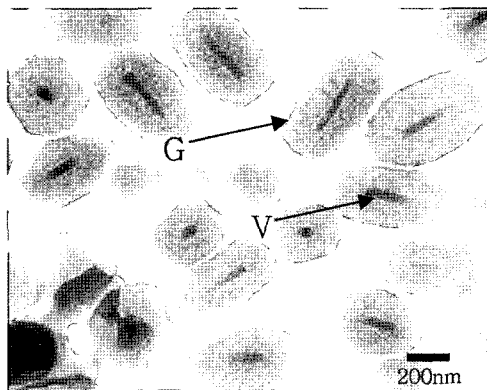
Results and Discussion

In this study, we isolated PxGV from dead larvae of *P. xylostella*, and named PxGV-K1. *P. xylostella* larvae infected with PxGV showed very distinct symptoms, exhibiting puffy, elongated integument and a change of color from dull green to pale yellow as previously reported (Asayama and Osaki, 1970). The gross pathologies of granuloviruses are similar to those of nuclear polyhedroses, but differences occur depending on the types of tissues infected. The first indication of infection in the larva is a loss of appetite and a progressive in the ventral side (Huger, 1963). The whiteness is due to the abundance of capsules in the hypertrophied fat bodies. When the infection is limited mainly to the fat body, the larva often increases in size, becomes white, opaque, and mottled at an advanced stage of infection, and later has a brownish discoloration (Hamm and Paschke, 1963). Infected larvae may live longer and become larger than an uninfected one. With the change in color, infected larvae usually become progressively weaker, sluggish, and flaccid.

The granule of the PxGV was observed as elliptical shape, but the shapes varied greatly (Fig. 1A), which are general features of GV (Tanada and Kaya, 1993). The approximate measure of the granule was 350 – 400 nm × 150 – 200 nm. Transmission electron microscopy revealed that each granule contained single rod-shaped virion with



(A)



(B)

Fig. 1. Scanning (A) and transmission (B) electron micrographs of the granules of PxGV-K1. The granules were purified by ultracentrifugation in linear 40% to 65% sucrose density gradients. Granule and virion were indicated as G and V, respectively.

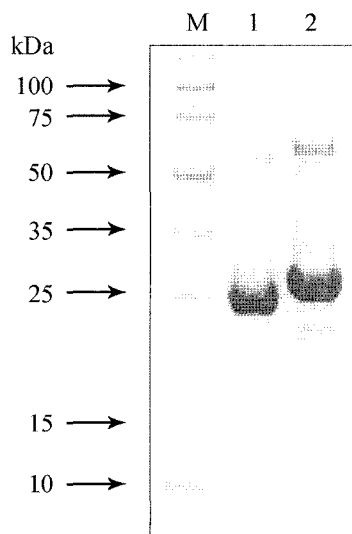


Fig. 2. SDS-polyacrylamide gel electrophoresis of the granulin protein of the PxGV-K1. Lane M: protein molecular weight marker; 1: granulin of PxGV-K1; 2: polyhedrin of AcNPV.

approximate size of 150 – 180 nm × 20 – 30 nm (Fig. 1B).

Granule of GV consisted of a major occlusion body protein, granulin, with a size of 27 – 31 kD (Tweeten *et al.*, 1981; Rohmann, 1992). Granulin of PxGV-K1 was about 29 kDa, which was estimated by the SDS-PAGE electrophoresis and smaller than polyhedrin of AcNPV (31 kDa) (Fig. 2). This result was consistent with previous reports that molecular weight of granulins were about 27 – 31 kDa (Tweeten *et al.*, 1981; Rohman, 1992).

The nucleotide sequence of PxGV-K1 granulin gene was completely same with that of previously reported PxGV granulin (Yoshifumi *et al.*, 2000). Whereas, when

	M	S	R	L	I	F	S	T	R	V	D	G	T	D	V	P	V	F	
PxGV-K1	TCGATAACAT	GTCCAGACTT	ATATTTTCGA	CGCGTGTGGA	CGGCACCGAT	GTCCCGGTTT	60												
AF270937													
PxGV-K1	FGG	APT	DKPY	VG	V	SEL	LNIL	120											
AF270937	TTTTGGTGG	TGCACCCACA	GATAAGCCCT	ATGTGGGAGT	CAGTGAGCTT	TGAACATTT													
PxGV-K1	GHS	KSH	AEEF	PRS	ETK	LWSE	180												
AF270937	TGGGACACAG	CAAGTCTCAC	GCCGAGGAGT	TCCCCAGGAG	CGAACTAAA	CTATGGTCCG													
PxGV-K1	LAP	GDT	TFFA	NKL	FTT	EVGF	240												
AF270937	AGTTGGCCCC	CGGAGACACC	ACGTTCCCCG	CCAACAAGCT	CITTACCACC	GAGGTCGGGT													
PxGV-K1	AVY	FGK	TKLN	NWA	CFK	RMFD	300												
AF270937	TCGCCGTGTA	CTTTGGGAAA	ACAAAGCTCA	ATAATTGGGC	GTGCTTTAAG	CGCATGTTTG													
PxGV-K1	TIE	SYI	LNPA	GCT	ATN	PLCM	360												
AF270937	ACACTATTGA	ATCCTACATT	TTAAACCCCG	CAGGDTGCAC	GGCCACAAC	CCCCGTGTGA													
PxGV-K1	IFP	GFN	TGCG	SNF	CNP	NNGD	420												
AF270937	TGATTCGCCCC	GGGTTTCAAC	ACCGGCTGCG	GATCCAACCC	TTGCAACCCC	AAACAACGGGG													
PxGV-K1	L G Q	V L A	L L Q Q	I L A	I I S	N P N P	480												
AF270937	ACCTCGGACA	GGTTTGGCT	CTGTTCGAGC	AAATTTTAGC	AATAATATCT	AACCCCAACC													
PxGV-K1	T N P	V D L	T P V L	D A I	A A L	A A Q V	540												
AF270937	CCACCAACCC	CGTGGATCTG	ACTCCGGTTC	TCGACGCCAT	AGCCGCTCTC	GCCGCTCAGG													
PxGV-K1	T A L	T T T	V N T I	N D N	V T A	L D G R	600												
AF270937	TCACCGCGCT	CACCACCCAC	GTCAACACGA	TAAACGATAA	CGTCAACCGCT	CTCGACGGCA													
PxGV-K1	I T N	L E T	T L N N	F V T	T T N	T S L L	660												
AF270937	GGATCACCAA	TCTGGAGACC	ACACTCAACA	ACTTCGTGAC	CACCACCAAC	ACGAGCCTGC													
PxGV-K1	T L Q	A D I	T N I L	D L L	T P L	T Q A L	720												
AF270937	TGACCTTACA	GGCAGACATT	ACAAACATCT	TAGATTGCT	AACACCGTTG	ACTCAGGCGC													
PxGV-K1	S N T	I N T	L N P F	V A G	I V A	A T P T	780												
AF270937	TATCCAACAC	TATCAACACG	TTAAATCCTT	TTGTGGCCGG	AATAGTGGCG	GCGACTCCGA													
PxGV-K1	F D S	T T Y	P V V P	I V N	P L L	N P P A	840												
AF270937	CCTTCGACTC	CACCACATAC	CCTGTGGTAC	CCATAGTGAA	TCCGTTACTC	AACCCCTCCG													
PxGV-K1	A R L	A S E	D V V D	T L D	T L Q	K E V K	900												
AF270937	CAGCCAGATT	GGCCTCGGAG	GACGTGTGCG	ACACGTTAGA	CACGCTGCAG	AAGGAGGTTA													
PxGV-K1	R F N	D Y T	D T F Q	Q L L	K N V	K I Q S	960												
AF270937	AGCGGTTTAA	CGACTACACC	GACACGTTTC	AACAGCTTTT	GAAAAACGTT	AAAATTCAT													
PxGV-K1	A N *						1020												
AF270937	CGGCAAAATTA	AACGTTAGCT	ATTCTCAATA	AGATRAATTA	ATGGCTAATA	TATGCGCAGA													
PxGV-K1	T T C T A G A						1027												
AF270937																		

Fig. 3. Nucleotide sequence of the putative p10 gene, PxORF21, of PxGV-K1. The nucleotide sequence of PxORF21 of PxGV-K1 (upper line) was compared with that of PxGV previously reported by Hashimoto *et al.* (2000). Dots indicate the same nucleotide sequence. The deduced amino acid sequence was indicated with one-letter code designations.

PxGV-K1 AF270937	CACAACGCGT ATCTGGACAC ATAACGGGAC AAGTATTTTA CGCACTGCGG AAACGGTTGC	60
PxGV-K1 AF270937	GATGTTATAG ATAATATATT ACAAAAAGCC ATGTGCGTCG TCGAAAGCAA TCCGACGTTT	120
PxGV-K1 AF270937 M S S I K	180
PxGV-K1 AF270937	AATAATTTTA AAAACAACA CAATTATACA TAAGAAGATT TACAAATGTC CTCGATTAAA	180
PxGV-K1 AF270937	D L Y N E I I K T Q Q D I A V T Y Q R V	240
PxGV-K1 AF270937	GATTATACA ACGAGATTAT CAAACTCAG CAAGACATAG CGGTGACTTA TCAGAGAGTG	240
PxGV-K1 AF270937 A A V E N E I K K K L Q E H A N S N T V	300
PxGV-K1 AF270937	GCAGCGGTAG AAAATGAAAT TAAGAAAAAA TTACAAGAGC ACGCCAATTC AAACACGGTA	300
PxGV-K1 AF270937 D Y K L D S V L T Q L G A T V P L L S K	360
PxGV-K1 AF270937	GATTACAAAC TGGACTCTGT GCTGACCAA TTGGAGCGA CGGTGCCATT GCTATCAAAA	360
PxGV-K1 AF270937 I V D S L K P K L D V P K V D V P K V D	420
PxGV-K1 AF270937	ATTGTAGATT CTCTAAACC CAAATTAGAT GTACCCAAG TCGATGTACC CAAAGTTGAT	420
PxGV-K1 AF270937 D V P K V D D V P K I D V P N V D D V P	480
PxGV-K1 AF270937	GACGTACCA AAGTTGATGA CGTACCCAAA ATTGATGTAC CCAATGTAGA TGACGTACCC	480
PxGV-K1 AF270937 K I D V D D T N V T D E T S N L N E V V	540
PxGV-K1 AF270937	AAATCGATG TAGATGACAC CAACCTAAT GACGAACGT CAAATTTAAA TGAATTTGTA	540
PxGV-K1 AF270937 V E S P N N H V E T *	600
PxGV-K1 AF270937	GTGGAATCG CTAACAATCA TGTAGAAACC TAACATCAGT TTAGATATA ATGTAACAAC	600
PxGV-K1 AF270937 T A A A A T T A T G T T A T T T T T T T T A T A T A T A T T A A A T T A G A G A A C	660
PxGV-K1 AF270937 T A A A A A A T C G T A A A T C G A C C	681

Fig. 4. Nucleotide sequence of the putative p10 gene, PxORF50, of PxGV-K1. The nucleotide sequence of PxORF50 of PxGV-K1 (upper line) was compared with that of PxGV previously reported by Hashimoto *et al.* (2000). Dots indicate the same nucleotide sequence. The deduced amino acid sequence was indicated with one-letter code designations.

the nucleotide sequences of three putative p10 genes, PxORF2, PxORF21 and PxORF50, were compared, the nucleotide sequence of PxORF21 of PxGV-K1 was different at 7 bases in coding region with that of reported (Fig. 3). Also, the nucleotide sequence of PxGV-K1 PxORF50 showed difference at 4 bases, 1 base in coding region and 3 bases in 3' untranslated region, respectively, with that of previously reported PxORF50 (Fig. 4). These results suggested that the PxGV-K1 isolated in this study is a novel isolate containing different genomic information with previously reported PxGV isolates.

In conclusion, the Korean isolate, PxGV-K1, was determined to be a novel GV isolate through the comparison of viral gene sequences, although it had the general characteristics of PxGV. In particular, our isolation study will increase the knowledge concerning geographical variation in PxGV and may aid in the development of more effective virus strains for biological control of *P. xylostella* and other lepidopteran pests.

Acknowledgement

This study was supported by Technology Development

Program for Agriculture and Forestry, Ministry of Agriculture and Forestry, Republic of Korea and by the Brain Korea 21 project.

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