## Analysis of a chitinase from EpapGV, a fast killing betabaculovirus

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Abstract The main function of baculoviral chitinase protein (V-CHIA) is to promote the final liquefaction of infected host larvae, facilitating the dispersion of occlusion bodies (OBs) in the environment. In this study, a v-chiA from Epinotia aporema Granulovirus (EpapGV) was identified and characterized. The 1,713 base pairs long open reading frame encodes a protein of 570 amino acids with a predicted molecular weight of 63 kDa. EpapGV V-CHIA sequence alignment resulted 62 % identical to Pieris rapae GV and Blastp search revealed a high conservation among all baculovirus chitinases. Amino acid sequence analysis indicated that the C-terminal KDEL present in most alphabaculovirus chitinases is absent in EpapGV V-CHIA, as well as in the rest of the betabaculoviruses. Phylogenetic analysis was performed with bacterial, lepidopteran, and baculoviral chitinase sequences available in databases. Using an AcMNPV bacmid (bAp-GOZA) a recombinant Ac-chiAEpapGV was obtained in order to overexpress EpapGV V-CHIA in cell culture. The presence of chitinase was detected in purified AcMNPV-

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M. L. Ferrelli · V. Romanowski Instituto de Biotecnología y Biología Molecular, Facultad de Ciencias Exactas, Universidad Nacional de La Plata, CONICET, La Plata, Argentina chiAEpapGV OBs. Peritrophic membranes of *Anticarsia gemmatalis* larvae fed with recombinant OBs showed an altered structure. The results presented in this study show that EpapGV chitinase overexpression in recombinant baculovirus can cause association of this protein with OBs, and suggest that this could be used to evaluate the protein role in early stages of baculoviral infections.

**Keywords** V-CHIA · Baculovirus · EpapGV · Chitinase · Peritrophic membrane

Chitin is an abundant polysaccharide in nature restricted to arthropods, nematodes, yeasts, and some other fungi [1]. In insects, chitin and covalently attached polypeptides are the primary components of their exoskeleton and the peritrophic membrane (PM) lining the midgut [2, 3]. Some organisms have developed the ability to degrade chitin by proteins known as chitinases. In insects, these enzymes play an important role in their growth and morphogenesis [4]. Most baculoviruses express chitinase, which participate in the liquefaction of infected larvae, late in infection. The degradation of the dead insect's cuticle facilitates the dispersal of the occlusion bodies in the environment [5, 6]. The first baculovirus chitinase (V-CHIA) was described in Autographa californica MNPV and classified as member of the family 18 of the glycohydrolase superfamily [7, 8]. Thus far, at least five chitinases from nucleopolyhedroviruses (NPVs, from Alphabaculovirus) were studied, but the information regarding betabaculovirus chitinases is scarce. A chitinase gene was identified in Cydia pomonella granulovirus (CpGV) by Kang et al. [9]. Later, in 2007, Daimon et al. characterized the V-CHIA of CpGV by constructing a recombinant Bombyx mori NPV (BmNPV) in which BmNPV v-chiA was replaced by CpGV v-chiA. They

demonstrated the CpGV V-CHIA endo- and exochitinase activities, its role in the liquefaction process and the early secretion of this protein, associated with the lack of KDEL endoplasmic reticulum retention motif [10]. Recently, another betabaculovirus chitinase, encoded in Pieris rapae GV, was also characterized [11].

Epinotia aporema granulovirus (EpapGV) is highly pathogenic for the bean shoot borer (Epinotia aporema Wals), a serious pest of soybean and other legume crops in South America. EpapGV causes a polyorganotropic infection and the liquefaction of the host after death [12]. Recently, the complete sequence analysis of EpapGV genome [13] revealed the presence of two genes known to cause the liquefaction effect in baculovirus: v-chiA (EpapGV ORF 32) and v-cath (EpapGV ORF 31), which encode a putative chitinase and a cysteine protease, respectively. Both genes are adjacent to each other in opposite orientations, as it is found in many baculoviruses, with an intergenic distance of 136 bp. Sequence analysis of EpapGV chitinase ORF revealed that it is 1,713 base pairs long and a hypothetic late promoter motif (TTAAG) was detected 6 nt upstream of the start codon. This gene encodes a predicted 570 amino acid long protein with a molecular weight estimated in 63 kDa. EpapGV chitinase had the highest identity (62 %) with PiraGV chitinase, followed by CpGV and ClanGV with 61 % identity. The amino acid sequence analysis showed that the C-terminal KDEL or related ER retention motif is absent. This characteristic is shared with all chitinases found in betabaculovirus genomes [11]. The catalytic domain was identified between positions 153 and 522 and the active site (FDGVDLDWE), between residues 301 and 309. A typical N-terminal domain found in bacterial and viral chitinases was located in the region spanning amino acid residues 15–148, and the putative signal peptide sequence, between amino acid positions 1 and 15 (online resource 1).

Phylogeny of baculoviral chitinase sequences was analyzed in previous reports: Wang et al. [14] suggested the monophyletic relationship between baculoviral and bacterial chitinases, and Daimon et al. [15] proposed that the bacterial-type chitinase genes of lepidoptera might have been acquired from a bacterium or a baculovirus. Those phylogenetic studies contained little information on betabaculovirus chitinases since very few sequences of this genus were available. In order to further support the suggested relationship among baculoviral, lepidopteran, and bacterial chitinases, we report a comprehensive new phylogenetic analysis based on more sequence data by means of MEGA 5 program with default parameters [16] (Fig. 1a). A neighbor joining (NJ) tree was inferred, and the topology was analyzed using bootstrapping (1,000 replicates). The analysis showed that chitinase sequences were clustered in well-supported groups. Baculoviral (alphabaculovirus and betabaculovirus) chitinases formed a Fig. 1 a Phylogenetic analysis of chitinase sequences. Method: Neighbor-Joining, Bootstrap (1,000 replicates). Bootstrap numbers are shown. b SDS-PAGE and western blot analysis of cell lysates (cells) and growth media (GM) of High Five cells infected with recombinant and wild type (wt) viruses. c Western blot analysis of recombinant and wild type OBs. d Electron microscopy of PMs extracted from *A. gemmatalis* larvae fed with recombinant AcchiAEpapGV OBs and AcGFP OBs (used as a negative control)

monophyletic group that clustered with bacterial-type lepidopteran V-CHIAs, indicating that these chitinases had a common origin. This baculoviral and lepidopteran group clustered with one clade of bacterial chitinases but within a larger clade that include other bacterial sequences. These results are in agreement with previous studies [7, 9, 14, 15] reinforcing the hypothesis that baculovirus and lepidopteran chitinases have a bacterial origin, and were acquired by horizontal gene transfer.

In order to characterize the EpapGV V-CHIA protein a recombinant AcMNPV was constructed (Ac-chiAEpapGV) containing the complete EpapGV v-chiA ORF under the control of the polyhedrin promoter. In brief, v-chiA ORF was amplified with specific primers (5'-TGGTACCGTAT GAAACTAGCAATTGTGTC-3' and 5'-GGGAGCTCGC TATCCTTTACAGAACGCG-3') and cloned in pBacPak9 (Invitrogen). The resulting plasmid was cotransfected in High Five cells [17] with bApGOZA DNA [18]. bAp-GOZA is an AcMNPV bacmid that is nonviable if transfected alone because it is defective for the 1629 gene. It gains viability upon homologous recombination with the transfer plasmid which restores the 1629 deletion. It is worth noting that this bacmid retains the native chitinase gene of AcMNPV. As the parental genome is nonviable, only recombinant virions were recovered from the growth medium (GM). Recombinant V-CHIA expression was verified in SDS-PAGE, yielding a 63 kDa product, as expected from the predicted amino acid sequence and verified by western blot with anti-HaSNPV V-CHIA antibodies [14]. On the contrary, the native AcMNPV V-CHIA was not detected (Fig. 1b). The cross reaction of these antibodies with EpapGV V-CHIA evidences a close relationship between alpha- and betabaculovirus chitinases. Subsequently, the chitinase activity present in the growth medium of Ac-chiAEpapGV infected cells was evaluated under different conditions of temperature and pH (Online resource 2). The highest enzyme activity was detected at 27 °C. On the other hand, the data showed that the chitinolytic activity is maintained at pH values ranging from 5 to 10. The highest activity was observed at pH 7. The recombinant virus, which expresses both endogenous AcMNPV and EpapGV chitinases, showed higher activity than the wild type (wt) AcMNPV used as a control. Therefore, the difference observed can be attributed to an overexpressed active EpapGV V-CHIA. Similar western



Ac-chiAEpaGV

AcGFP

blot and activity results were obtained in a Spodoptera litura NPV chitinase study [19].

Baculoviral chitinase from AcMNPV can cause damages in the peritrophic membrane: In a study by Rao et al. [20], the baculovirus chitinase expressed in bacteria was purified and used to evaluate the action on the insect chitinous PM, the first barrier that virions need to cross to infect midgut epithelial cells. The effects observed showed that the baculoviral chitinase altered the PM permeability in vitro in a dose-dependent manner using the E. coli expressed protein. In other study where the *v*-chiA gene is under the control of its native promoter, the AcMNPV chitinase activity was detected associated to polyhedra purified from infected larvae [21]. However, no significant effect was observed in bioassays performed with recombinant v-chiA defective AcMNPV and wt AcMNPV OBs. These observations might be due to a very low concentration of V-CHIA in AcMNPV polyhedra [21]. In our hands, EpapGV V-CHIA was detected in Ac-chiAEpapGV polyhedra probably due to the overexpression of the *v*-chiA gene under the control of the strong polyhedrin promoter (Fig. 1c). Taking into account these observations, we tested the EpapGV V-CHIA containing polyhedra for the ability to damage the PM of Anticarsia gemmatalis larvae. Scanning electron microscopy showed PM alterations on larvae treated with Ac-chiAEpapGV OBs. By contrast, larvae treated with OBs from a recombinant Ac-GFP (constructed using the same vector and bacmid as described for Ac-chiAEpapGV virus) showed no damage (Fig. 1d). This observation suggests that changes on the PM can be attributed to the overexpression of V-CHIA. Previous studies showed that the larvicidal activity of a nuclear polyhedrosis virus toward the gypsy moth larvae (Lymantria dispar) was increased fivefold when it was coadministered with bacterial chitinase [22]. In that case, chitinases were supposed to cause perforations in the gut PM [3]. Recently, Wang et al. [19] obtained a recombinant AcMNPV that overexpresses SpliNPV V-CHIA. Biossays performed using these recombinant OBs improved the insecticidal activity of AcMNPV against Spodoptera exigua larvae. Taken together, these results suggest that Ac-chiAEpapGV could have insecticidal activity associated to damages on the PM. More experimental data are necessary to elucidate this.

In our study, we demonstrated that EpapGV contains a functional chitinase in agreement with the observed liquefaction of infected *E. aporema* larvae [12]. The EpapGV V-CHIA was active under alkaline conditions similar to those found in lepidopteran midgut. This feature, together with the effect on the PM shown here, indicates that this protein could be included in viral formulations in order to increase the oral infectivity of baculoviral agents. Studies on alphabaculovirus chitinases focused on the potential use of these proteins to improve the viral activity applied to biological control [20, 22]. As an alternative to formulation of biopesticidal mixtures (OBs + chitinase), our results suggest that the overexpression of a protein allows its association with OBs. Therefore, genetic modifications could be designed to enhance the oral infectivity of baculoviruses including viral genes under the control of strong promoters.

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Virus Genes

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**Online resource 1** 

Gene sequence and structure. Sites and main domains presenti n predicted protein are depicted. Late promoter element is indicated in red.





Catalytic domain

N-terminal domain

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Online resource 2

## ChiA activity at different temperatures and pH

In order to evaluate the activity of EpapGV CHIA at different temperatures High Five cells were infected with recombinant Ac-chiAEpapGV (MOI of 5), using the wt AcMNPV virus as a negative control. At 72 hours p.i. the growth medium was collected and 1 ml of sample containing similar protein quantities (5 mg/ml) were mixed with 1 ml of 0.2 M sodium phosphate buffer (pH 6.5) and 5 mg of chitin-azure (Sigma). Mixture obtained was incubated at different temperatures for 5 days. The tubes were centrifuged and the supernatants were used for measurement of absorbance at 560 nm. Abs (560) of cell free medium was used for normalization.



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In order to evaluate the activity of EpapGV CHIA at different pH values High Five cells were infected with recombinant Ac-chiAEpapGV (MOI of 5), using the wt AcMNPV virus as a negative control. At 72 hours p.i. the growth medium was collected and 1 ml of sample containing similar protein quantities (5mg/ml) were mixed with 1 ml of cell culture medium at different pH values and 5 mg of chitin-azure (Sigma). Mixture obtained was incubated at 27° C for 5 days. The tubes were centrifuged and the supernatants were used for measurement of absorbance at 560 nm. Abs (560) of cell free medium was used for normalization.

