Metalloprotease production by *Paenibacillus larvae* during the infection of honeybee larvae

Karina Antúnez, Daniela Arredondo, Matilde Anido and Pablo Zunino

Departamento de Microbiología, Instituto de Investigaciones Biológicas Clemente Estable (IIBCE), Avda Italia 3318, CP11600 Montevideo, Uruguay

American foulbrood is a bacterial disease of worldwide distribution that affects larvae of the honeybee *Apis mellifera*. The causative agent is the Gram-positive, spore-forming bacterium *Paenibacillus larvae*. Several authors have proposed that *P. larvae* secretes metalloproteases that are involved in the larval degradation that occurs after infection. The aim of the present work was to evaluate the production of a metalloprotease by *P. larvae* during larval infection. First, the complete gene encoding a metalloprotease was identified in the *P. larvae* genome and its distribution was evaluated by PCR in a collection of *P. larvae* isolates from different geographical regions. Then, the complete gene was amplified, cloned and overexpressed, and the recombinant metalloprotease was purified and used to generate anti-metalloprotease antibodies. Metalloprotease production was evaluated by immunofluorescence and fluorescence *in situ* hybridization. The gene encoding a *P. larvae* metalloprotease was widely distributed in isolates from different geographical origins in Uruguay and Argentina. Metalloprotease was detected inside *P. larvae* vegetative cells, on the surface of *P. larvae* spores and secreted to the external growth medium. Its production was also confirmed *in vivo*, during the infection of honeybee larvae. This protein was able to hydrolyse milk proteins as described for *P. larvae*, suggesting that could be involved in larval degradation. This work contributes to the knowledge of the pathogenicity mechanisms of a bacterium of great economic significance and is one step in the characterization of potential *P. larvae* virulence factors.

INTRODUCTION

American foulbrood is one of the most severe bacterial diseases that affects honeybee larvae. It has a worldwide distribution, causing significant losses to honeybee populations and the beekeeping industry (Hansen & Brødsgaard, 1999). The causative agent is *Paenibacillus larvae*, a Gram-positive, spore-forming bacterium (Genersch et al., 2006).

Larvae become infected when they consume food contaminated with *P. larvae* spores. These spores germinate in the larval midgut; vegetative cells proliferate, move to the haemocoel and spread throughout the larval body (Yue et al., 2008). During proliferation, *P. larvae* secretes different proteins that may act as virulence factors (Antúnez et al., 2010, 2011). It has been proposed that among the mixture of secreted proteins, *P. larvae* secretes metalloproteases that could be responsible for the larval degradation that occurs after death (Antúnez et al., 2009; Dancer & Chantawannakul, 1997; Holst & Sturtevant, 1940; Hrabáková & Martinek, 2007). Larvae with late-stage infections show a strong proteolytic activity that can be seen when larval debris is inoculated into milk, when protein coagulation occurs in a few hours (Holst & Sturtevant, 1940). Since metalloproteases seem to be related to the pathogenicity of *P. larvae*, the aim of the present work was to identify the sequence that encodes a metalloprotease in the *P. larvae* genome, and to evaluate its expression during the infection of honeybee larvae.

METHODS

Bacterial strains and plasmids. Fifty Uruguayan *P. larvae* isolates obtained from bees, larvae and honey of different geographical regions of Uruguay were selected from the collection of the Department of Microbiology, IIBCE (Antúnez et al., 2004, 2007). Four Argentinian isolates corresponding to different genotypes (PL8, PL99 and PL63) (Alippi & Aguilar, 1998) and one additional isolate, PLP (formerly *P. larvae* subsp. pulvificiens) were also used, in order to complete the four different *P. larvae* genotypes described (ERIC I - BOX A; ERIC II - BOX C; ERIC II - BOX B; ERIC III - BOX PLP: Antúnez et al., 2007). *P. larvae* strain 44, isolated from honey (Durazno, Uruguay), was selected from further assays. *P. larvae* was routinely grown in J medium and incubated at 37 °C (Hornitzky & Nicholls, 1993).

Plasmid pET21(a) + was used for DNA cloning and protein expression (Studier & Moffatt, 1986). *Escherichia coli* XL-1 Blue was used for initial cloning of the DNA into plasmid vectors and for maintenance of the plasmids (Bullock et al., 1987). *E. coli* BL21 (DE3)
was used for final transformation and overexpression of recombinant proteins. E. coli was grown in Luria–Bertani (LB) medium at 37 °C. LB was supplemented with ampicillin (Amp, 100 mg ml⁻¹) when necessary.

**Preparation of P. larvae cells and protein suspensions.** A P. larvae vegetative cell suspension in PBS was incubated at 4 °C for 30 days to get a spore suspension. To confirm the absence of vegetative cells and determine the spore number, an aliquot was fixed with 4% paraformaldehyde (PFA) for 30 min, stained with DAPI (4',6-diamidino-2-phenylindole, Sigma) (1 μg ml⁻¹) for 5 min and visualized by fluorescence microscopy.

A P. larvae liquid culture was incubated at 37 °C with shaking for 72 h. It was centrifuged, and the pellet was resuspended in PBS and sonicated to obtain the whole bacterial proteins.

**Amplification of the metalloprotease gene.** The distribution of a metalloprotease gene among the different P. larvae isolates was evaluated by PCR using primers Prot1 (5'-GGCGTATCTTACGTAACG-3') and Prot2 (5'-GGGATCGTATCTTACGTAACG-3'), designed to amplify a 280 bp fragment of the unique nucleotide sequence published for this protein (GenBank accession number AF111421). Two different PCR products were selected and sequenced at Macrogen (Korea) in order to confirm their identity.

The partial nucleotide sequence encoding a P. larvae metalloprotease (GenBank accession number AF111421) was used to identify the complete gene that encodes this protein in the P. larvae genome (available at http://www.hgsb.bcm.tmc.edu; Qin et al., 2006). As the genome is not completely assembled, it was necessary to assemble two different contigs in order to get the complete sequence (Ctg01.584 and Ctg01.323). The sequence obtained was analysed using the Artemis program (available at www.sanger.ac.uk) in order to confirm ORFs. One ORF was identified as the metalloprotease gene (1590 bp).

Primers Met-F (5'-GGGCGCTTATGGAAGAAGG-3') and Met-R (5'-CCATTTAGTTAAGGAGAAGG-3') were designed in order to amplify the complete gene, and included restriction sites for NdeI and HindIII, respectively (restriction sites are underlined). A histidine tag was included in primer Met-R to facilitate protein purification (shown in italics).

**P. larvae DNA** was extracted from pure cultures using the Genomic DNA extraction kit from Sigma. PCR's were carried out as previously described (D'Alessandro et al., 2007; Piccini et al., 2002), using Platinum Taq DNA Polymerase High Fidelity (Invitrogen). Amplified DNA was analysed by electrophoresis on 0.8% agarose gels, stained with ethidium bromide (0.5 μg ml⁻¹) and visualized using a UV-transilluminator (Sambrook et al., 1989).

**Cloning and overexpression of the metalloprotease gene and purification of the recombinant protein.** PCR product was purified using the Gel Extraction DNA kit from Fermentas, digested with NdeI and HindIII (New England Biolabs) and cloned into plasmid pET21(a)+ (previously digested) using T4 DNA ligase (New England Biolabs). The ligation mixture was transformed into E. coli XL-1 Blue. Then the pET21(a)+ containing the P. larvae metalloprotease gene was moved into E. coli BL21(DE3) by transformation.

A single colony was inoculated into LB Amp and incubated with shaking until the OD₆₀₀ reached 0.6. Protein production was induced by IPTG addition (final concn 1 mM). To corroborate the protein production, samples were taken before and after different times after that, centrifuged, and the pellets subjected to SDS-PAGE. To evaluate the protein solubility, the pellet taken 4 h after induction was resuspended in PBS, sonicated, centrifuged again, and pellet and supernatant were subjected to SDS-PAGE. The recombinant metalloprotease was purified under denaturing conditions and renatured in the Unidad de Producción de Proteínas Recombinantes, Institut Pasteur Montevideo, Montevideo, Uruguay. Briefly, the culture pellet was used to extract the inclusion bodies under denaturing conditions using 6 M guanidine.HCl. Inclusion bodies were suspended and renatured in 50 mM Tris, 500 mM NaCl, 20% (v/v) glycerol, 0.7 M L-arginine pH 7.4, by the drop-by-drop method. The metalloprotease was dialysed in successive steps to eliminate the salts and concentrated (twice) with PEG 40000 at 6 °C overnight. It was purified using an anionic interchange column with DEAE TSKgel-5PW resin (TOSOH Biosep), packed in a XK 16/100 column (GE Healthcare).

Protein concentration was determined by the method of Bradford (1976) using BSA as a standard, and the protein was stored at 4 °C.

**Anti-metalloprotease serum preparation for immunofluorescence.** Female CD-1 mice, 6–8 weeks old, from the breeding facilities at the IIBCE were used. Mouse antiserum was raised using a four-dose immunization schedule with 100 μg recombinant metalloprotease per dose. The first dose was administered in Freund's complete adjuvant, and subsequent doses, at 2-weekly intervals, in Freund's incomplete adjuvant. The serum was collected 1 week after the last immunization. Animal experiments were conducted in accordance with procedures authorized by the IIBCE.

**Antiserum specificity evaluation.** Antiserum specificity was evaluated by SDS-PAGE and Western blotting. Whole P. larvae proteins were suspended in sample buffer, boiled for 5 min, subjected to 12% SDS-PAGE and stained with 1% Coomassie brilliant blue (Sambrook et al., 1989). Proteins subjected to SDS-PAGE were transferred to nitrocellulose membranes (Towbin et al., 1979) and Western immunoblots were performed using a 1:100 dilution in PBS/Tween 20/1% skimmed milk of mouse polyclonal antiserum raised against the recombinant metalloprotease.

Serum specificity was also tested using P. larvae-infected and non-infected larvae. Three P. larvae-infected larvae (collected in the field and with clinical symptoms of American foulbrood) and three non-infected ones were separately macerated in 500 μl PBS; an aliquot was mixture with sample buffer, boiled for 5 min and subjected to 12% SDS-PAGE (Sambrook et al., 1989). Proteins were stained with Coomassie brilliant blue and subjected to SDS-PAGE and Western blots using anti-metalloprotease serum, as described above.

**Detection of metalloprotease by immunofluorescence.** P. larvae vegetative cells or spore suspensions were fixed with 4% PFA for 20 min. P. larvae cells or sections of larvae were washed with PBS, blocked with 2% BSA in 50 mM PBS/NaCl for 20 min and incubated with the primary antibody, the anti-metalloprotease serum (at 1:100 dilution), for 60 min in 50 mM PBS/NaCl with 2% BSA. After PBS rinses, cells were incubated with a FITC-conjugated secondary antibody to mouse IgG (1:100 dilution; Molecular Probes) for 30 min and finally rinsed with PBS. Incubations were performed at room temperature. A negative control was performed by treating the cells only with the secondary antibody. Imaging analysis was performed using a confocal microscopy (Olympus Fluoview 300).

**Larval infection assay.** Worker larvae from the progeny of a single wild-mated honeybee queen (Apis mellifera ligustica) maintained in a disease-free apiary at the IIBCE were used for this study. Larvae were collected and maintained as described by Evans (2004). Two groups of 12 larvae each were used. One larval group was fed with food supplemented with P. larvae at a final concentration of 1000 spores μl⁻¹ for the first 48 h; thereafter, normal larval diet was used for feeding. The second group, control larvae, was fed with normal larval diet throughout the experiment. Each day, the larvae were taken out of the incubator and examined. Surviving larvae were transferred to...
new wells filled with fresh food. The experiment was performed in triplicate. Infected and control (non-infected) larvae were sacrificed 5 days after infection, fixed by microinjection with 4% PFA and incubated overnight in 4% PFA. The larvae were extensively washed with PBS and embedded in a gelatin/albumin matrix. The matrix was prepared as follows. A mixture of 1 ml 4.5% albumin in saline buffer (0.15 M NaCl, 0.003 M NaNO₃), 0.5 ml 0.5% gelatin in saline buffer and 50 µl 25% glutaraldehyde was placed in a mould (1 x 1 cm) and larvae (previously dried with tissue paper) were placed in the middle of the mould. The mixture was air-dried for 5 min and then the matrix was removed from the mould. Histological sections (50 µm) were prepared using a vibratome and sections were mounted on glass slides previously covered with 2% agarose.

**RESULTS**

**Distribution of a *P. larvae* metalloprotease gene**

According to the PCR results, all Uruguayan and Argentinian *P. larvae* isolates tested carried the gene encoding the studied metalloprotease, indicating that this potential virulence factor is widely distributed (data not shown). Two PCR products were randomly selected and sequenced; they showed 99% identity with the published partial sequence (AF111421.1).

**Amplification, cloning and overexpression of a metalloprotease gene and purification of the recombinant protein**

The complete gene encoding a *P. larvae* metalloprotease was amplified, cloned into pET21(a) + and transformed into *E. coli* BL21 (DE3). The production of the recombinant protein was confirmed by SDS-PAGE, since the expected 59 kDa band was observed after protein expression induction. The highest production was obtained after 4 h incubation (Fig. 1a). Most of the recombinant metalloprotease was detected in the insoluble protein fraction (data not shown) and it was successfully purified (Fig. 1b). After several days at 4 °C, the 59 kDa purified protein suffered autoproteolysis, yielding a 40 kDa protein (Fig. 1c).

**Detection of the metalloprotease in *P. larvae* vegetative cells and spores by immunofluorescence**

Mouse polyclonal anti-metalloprotease serum was used to determine the localization of the metalloprotease in *P. larvae* vegetative cells and spores. The protein was detected inside vegetative cells and on the surface of spores, as shown by immunofluorescence images (Fig. 2). The initial vegetative cell and spore suspensions were washed several times in order to clean the cells, since when no washes were carried out the green signal corresponding to secreted metalloprotease was detected throughout the surrounding medium, indicating the secretion of metalloprotease (data not shown). *P. larvae* cells treated only with the secondary antibody did not show any fluorescent signal (data not shown).

In order to test the specificity of the antiserum against *P. larvae* metalloprotease, SDS-PAGE and Western blot assays were performed. Among the mixture of whole *P. larvae* proteins only one protein was recognized (Fig. 3). In order to confirm that the antiserum did not recognize larval proteins, total larval proteins were obtained from *P. larvae*-infected and

![Image](346x223 to 505x432)

**Fig. 1.** Overexpression of *P. larvae* metalloprotease and purification of the recombinant protein. The *P. larvae* metalloprotease gene was amplified, and cloned into the pET21(a) + system; expression was induced by IPTG addition and then evaluated by SDS-PAGE. Purification of recombinant protein was performed under denaturing conditions, and recombinant protein was incubated at 4 °C. (a) Overexpression of metalloprotease gene. Lanes: 1, Wide Range protein molecular mass markers (Bio-Rad); 2, before induction; 3, 4 h after induction. (b) Purification of recombinant metalloprotease. Lanes: 1, purified protein; 2, pre-stained protein markers, Broad Range (New England Biolabs). (c) Recombinant metalloprotease after incubation at 4 °C for several days. Lanes: 1, Wide Range protein molecular mass markers (Bio-Rad); 2, purified protein.
non-infected larvae and subjected to SDS-PAGE and Western blotting using anti-metalloprotease serum. When the mixture of total proteins of *P. larvae* infected larvae was analysed, only one protein was detected, while no band was detected when non-infected larvae were analysed (Fig. 4). These results confirm the expression of metalloprotease by *P. larvae*, and also confirm the specificity of the antiserum.

**Detection of the metalloprotease during infection of larvae by immunofluorescence and FISH**

To evaluate the production of *P. larvae* metalloprotease during infection of honeybee larvae, the infection was reproduced in the laboratory and 5-day-old larvae were analysed by immunofluorescence and FISH. Metalloprotease was detected inside the larval midgut, as revealed by confocal microscopy images, confirming the production of this protein *in vivo* (Fig. 5). No metalloprotease production was detected in the midgut of non-infected larvae.

**Evaluation of the proteolytic activity of the metalloprotease**

Recombinant metalloprotease was able to hydrolyse milk proteins, as shown by the precipitation of proteins, confirming its proteolytic activity (Fig. 6). A negative control using PBS or protein elution buffer instead of the metalloprotease did not cause coagulation of milk.

---

**Fig. 2.** Detection of metalloprotease in *P. larvae* vegetative cells (a) and spores (b) by immunofluorescence (original images taken at ×1000 and ×2000 magnification, respectively; scale bar in panel b represents 10 μm). *P. larvae* vegetative cells and spores were incubated with mouse polyclonal antiserum raised against *P. larvae* metalloprotease and FITC-conjugated secondary antibody against mouse IgG, and visualized by confocal microscopy.

**Fig. 3.** Specificity of the antiserum used for *P. larvae* metalloprotease detection, using whole *P. larvae* proteins. The arrow indicates the recombinant metalloprotease. (a) SDS-PAGE analysis. (b) Western blot analysis. Lanes (both panels): 1, Wide Range protein molecular mass markers (Bio-Rad); 2, *P. larvae* whole bacterial proteins.
Metalloproteases have been described as virulence factors in a wide variety of micro-organisms, being involved in different mechanisms, including digestion of a wide variety of host proteins, attachment to host cells (Miyoshi & Shinoda, 2000), cytotoxicity (Kling et al., 1997), and evasion of the immune system by degradation of antibacterial peptides (Casteels et al., 1989).

Although the production of metalloproteases by P. larvae has been previously reported by several authors (Antúnez et al., 2009; Dancer & Chantawannakul, 1997; Holst & Sturtevant, 1940; Hrabák & Martinék, 2007) none of these studies identified the genes that encode these proteins. The P. larvae genome is being assembled and automatically annotated; 4955 proteins have been reported and only two are described as extracellular proteases (GenBank accession numbers ZP_02326503.1 and ZP_02326602.1). However, there is a lack of experimental evidence about the function and localization of these proteins. In the present paper, and based on a partial nucleotide sequence of a gene encoding a P. larvae metalloprotease, we report the identification of an ORF in the P. larvae genome that encodes this metalloprotease. The amino acid sequence of the reported ORF showed 100% identity with a P. larvae protein annotated as peptidase M4 thermolysin (GenBank accession number ZP_02330830.1). However, the coverage is only 78%, since the first 116 amino acids have not been included in the annotation. This ORF also showed a high percentage identity (67%) with the P. larvae extracellular proteases previously described (GenBank accession numbers ZP_02326503.1 and ZP_02326602.1), and with extracellular neutral proteases from Paenibacillus polymyxa, Brevibacillus brevis and Bacillus megaterium (GenBank accession numbers D00861.1, AP008955.1 and CP001983.1, respectively); in all these cases the coverage was 99–100%. These results suggest that the identified sequence corresponds to a P. larvae metalloprotease.

The distribution of the gene that encodes this protein in P. larvae isolates of different geographical origins and belonging to different genotypes was assessed by PCR amplification. All isolates examined contained the gene, confirming that it is widely distributed.

The gene encoding P. larvae metalloprotease was over-expressed in E. coli and purified under denaturing conditions. A 59 kDa protein, corresponding to the predicted molecular mass of the preprometalloprotease, was obtained after purification. All extracellular bacterial neutral proteases are synthesized as inactive preproenzymes, consisting of a signal peptide, a prosequence and a mature sequence (Inouye et al., 2007). The signal peptide acts as a signal for translocation of preproenzyme to the membrane. The preproenzyme is processed into the proenzyme by the signal peptidase. The proenzyme then acts as a molecular chaperone leading to an autocleavage of the peptide bond linking the pro and mature sequences (Inouye et al., 2007). Some well-characterized examples are thermolysin and LasB, isolated from Bacillus thermodenitrificans and Pseudomonas aeruginosa, respectively (Kooi et al., 2005; McIver et al., 1995; O’Donohue & Beaumont, 1996). It has been reported that is necessary that metalloproteases are expressed as preproenzymes, to allow the correct folding and catalytic procedure (Kooi et al., 2005; McIver et al., 1995; O’Donohue & Beaumont, 1996). As for Bacillus thermodenitrificans, the P. larvae metalloprotease overexpressed in E. coli was obtained in inclusion bodies, and it should be purified to obtain the mature protein (Inouye et al., 2007; Marie-Claire et al., 1998).

After storage of preprometalloprotease (59 kDa) at 4°C the protein suffered autoproteolysis, giving a new protein of ~40 kDa.

Using the P. larvae recombinant metalloprotease generated in this study, a polyclonal mouse serum was produced. This antibody proved to be useful to identify the metalloprotease in the culture medium, showing that it is secreted outside the cells. This has been seen in the case of other insect pathogens such as Photorhabdus luminescens. This Gram-negative pathogen enters the haemocoel of...
infected hosts, producing a number of secreted proteins that promote colonization and subsequent death of the insect (Held et al., 2007).

The antiserum was also useful to confirm the expression of the metalloprotease by *P. larvae* vegetative cells and its presence on the spore surface. In some organisms, e.g. the fungal respiratory pathogen *Coccidioides posadasii*, expression of metalloproteases during spore differentiation has been reported (Hung et al., 2005). The authors also reported that the enzyme cleaved surface antigens, preventing host recognition of endospores. The antiserum was shown to be specific for *P. larvae* metalloprotease since no other *P. larvae* or larval protein was recognized when it was used for Western blotting.

When the anti-metalloprotease polyclonal mouse serum was used as the primary antibody in immunofluorescence-based microscopy assays, it was confirmed that the metalloprotease was expressed in vivo in the *P. larvae*-infected honeybee larval gut.

The images obtained using this approach also revealed clear damage of gut cells probably associated with the presence of bacteria expressing the metalloprotease, while the non-infected larvae showed a normal apparently healthy gut epithelium.

In conclusion, the present work reports the identification of a widespread *P. larvae* metalloprotease that is produced inside the cell, secreted to the external medium and could also be detected on the spore surface. It is produced in vivo during infection of honeybee larvae. This work contributes to the knowledge of the pathogenicity mechanisms of a bacterium of great economic significance and is one step in the characterization of potential *P. larvae* virulence factors.

**ACKNOWLEDGEMENTS**

The authors are grateful for the support from the DICYT-PDT (Uruguay) (research grant PDT 63/112) and a research fellowship financed by PEDECIBA-ANII (Uruguay). We thank Y. Mendoza (INIA) for providing honeybee hives and R. Cantera, S. Ruiz and P. Scavone (IIBCE) for assistance in bee processing and confocal microscopy imaging.

**REFERENCES**


Edited by: T. Msadek