

Development and mechanisms of resistance to *Bacillus thuringiensis* endotoxin Cry1Ac in the American bollworm, *Helicoverpa armigera* (Hübner)

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The American bollworm, *H. armigera*, evolved 31-fold resistance to selection pressure of *B. thuringiensis* endotoxin Cry1Ac within six generations. The Cry1Ac selected larvae of *H. armigera* showed cross-resistance to Cry1Aa and Cry1Ab both in terms of mortality and growth reduction. Studies on mechanisms of resistance to Cry1Ac showed that proteases of resistant insects degraded Cry1Ac faster than those of susceptible insects, which led to the relative unavailability of toxin of about 58 kDa for binding and perforation of midgut epithelial membrane of the target insect. Besides, resistant and susceptible populations of *H. armigera* differed in the binding of their receptors with Cry1Ac toxin. These results suggest the possibility of both mechanisms existing in imparting resistance. These findings mandate the necessity of *B. thuringiensis* resistance management for usage of *B. thuringiensis* either as a conventional insecticide or through transgenic crops.

Keywords: American bollworm, *Bacillus thuringiensis*, Cry1Ac, *Helicoverpa armigera*, Resistance

The ever-increasing area of transgenic *Bacillus thuringiensis* (*Bt*) cotton, about 4.6 million hectare in 2002 in USA, China, Australia and other countries, including India, from that of about 1.7 million hectares in 1996 in USA, justifies utility of *Bt* transgenes against bollworm complex, a major constraint in cotton productivity. Transgenic *Bt* cotton has further helped in minimizing use of conventional insecticides and thereby reducing environmental pollution and associated health hazards^{1,2}. One of ecological concerns of cultivation of transgenic *Bt* crops, especially evolution of resistance in insects to *Bt* toxins, has mandated implementation of *Bt* resistance management tactics legally in the developed countries like USA³ and Australia⁴. The *Bt* resistance management essentially consists of high level expression of *Bt* Cry1Ac toxin, maintenance of refugia (non-*Bt* crop) and suitable alternate host crops and recently, the use of *cry1Ac* and *cry2A* genes as in Bollgard II. In China, because of complexity of small farm holdings and mixed cropping, *Bt* resistance management tactic like maintenance of structured refugia is considered unnecessary and impractical to enforce, and hence is non-mandatory for *Bt* cotton cultivation, in spite of lack of high dose of *Bt* toxin in

the currently available transgenic varieties⁵. In India, however, maintenance of structured refugia is considered necessary for *Bt* cotton. Further, cotton being a cash crop, farmers may be tempted to discard refugia to favour economics of its cultivation. Since *Bt* resistance management has to be based on the nature of resistance in the test insect, the study of its characteristics in the insect populations is essential to fine-tune management tactics for location specific needs.

American bollworm, *Helicoverpa armigera* (Hübner) is an important polyphagous pest of worldwide occurrence. In India alone, it causes about US \$ 1 billion worth of crop damage every year⁶. Being a key pest of cotton, many insecticides are used for its control. As a result of indiscriminate use, many insecticides have failed to achieve a desired level of *H. armigera* control due to its ability to evolve resistance⁷.

Cry1Ac toxin in transgenic *Bt* cotton has successfully proved lethal to the larvae of *H. armigera* due to its constitutive availability in various parts, especially terminal leaves, flowers and bolls. Contrarily, target insect populations have also shown an ability to tolerate a wide range of toxicity of *Bt* strains and toxins *per se*^{6,8,9} or *in situ* in cotton plants¹⁰⁻¹⁴. This variation in susceptibility of *H. armigera* may be due to genetic variation in the populations, cross-resistance between xenobiotics, agroecological conditions, and variation in expression of Cry1Ac toxin in *Bt* cotton itself. This ability of *H. armigera* to tolerate higher concentrations of Cry1Ac toxin was

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further confirmed by development of resistance under selection pressure in the laboratory^{15,16}. The mechanism of *Bt* resistance in insects mainly centers around altered processing of CryIAc protoxin and the binding of CryIAc toxin to receptors on brush border membrane vesicles (BBMV) of midgut epithelium in many insects¹⁷. Extensive investigations on mechanisms of resistance in insects to conventional insecticides have helped in developing diagnostic tools and appropriate resistance management tactics. However, very little information is available on mechanisms of resistance in *H. armigera* to *Bt* toxins. This communication therefore reports studies on evolution of resistance, cross-resistance, and the importance of proteases and toxin-receptor binding in CryIAc resistance in *H. armigera*.

Materials and Methods

Chemicals and *Bt* CryIA toxins—Azocasein, N- α -p-Tosyl-L-lysine chloromethyl ketone (TLCK), N-Tosyl-L-phenyl alanine chloromethyl ketone (TPCK), soybean trypsin inhibitor (SBTI), bovine serum albumin (BSA) (electrophoresis-marker grade) and bovine trypsin were purchased from Sigma Chemical Company, St Louis, MO, USA. Other chemicals and reagents were purchased from Bangalore Genie Pvt. Ltd., Bangalore, and Qualigens Fine Chemicals, Mumbai. *Escherichia coli* JM 103 strains (hyper-expressing recombinant plasmid vectors pKK223-3; BGSC ECE52 *cryIAa*, ECE53 *cryIac* and ECE54 *cryIab*) producing CryIAa, CryIAc and CryIAb toxins were kindly provided by *Bacillus* Genetic Stock Center, Ohio State Univ., Columbus, USA.

Toxins of CryIAa, CryIAb and CryIAc were prepared from recombinant *E. coli* strains as per Lee *et al.*¹⁸. Cells were grown in nutrient broth containing 50 μ g/ml ampicillin for 72 hr, harvested by centrifugation at 4500 g at 4°C and the pellet suspended in lysis buffer (50 mM Tris, pH 8; 50 mM EDTA; 15% sucrose, lysozyme @ 2 mg/ml) and incubated for 4 hr. After incubation, lysis buffer was replaced with crystal wash-1 (0.5 M sodium chloride and 2% Triton X-100) and sonicated for 3 min on ice. The pellet was collected by centrifugation at 4500 g and washed thrice with crystal wash-1, crystal wash-2 (0.5 M sodium chloride) and then, with distilled water. Finally, the pellet was dissolved in solubilizing buffer (50 mM sodium carbonate, 10 mM dithiothreitol, pH 10.5) at 37°C for 6 hr. Supernatant containing toxin was collected following centrifugation at 4500 g for

10 min and stored at -20°C till further use. The proteins in the supernatant were separated by SDS-PAGE¹⁹ and toxin band identified as per Mohan and Gujar²⁰.

Insect rearing and bioassay—Larvae of *H. armigera* originally collected from chickpea on the Institute's farm in Delhi were reared on a chickpea based meridic diet similar to that of Nagarkatti and Prakaash²¹ at 27°C $\pm$ 2°C and 60-80% RH. Adults were fed with 10% honey solution and allowed to lay eggs on markin cloth used for covering jars. The eggs were collected daily by changing cloth and keeping them in humid conditions till they hatched.

Bioassays of Cry toxins were carried out by diet incorporation method as per Gujar *et al.*⁶. A series of dilutions of stock solution of Cry toxins (in water) was prepared and added to an aliquot of meridic diet, mixed thoroughly with pestle and mortar, and transferred into small plastic containers. Each container served as a replication. About 6 concentrations, ranging from 0.01 to 100 μ g toxin g⁻¹ diet, were used for each bioassay, with 3 to 5 replications per concentration. Neonate larvae (10) were released on treated diet per replication. The control consisted of normal meridic diet (without toxin). A minimum of 210 neonate larvae were used for each bioassay. The mortality was then pooled for each concentration. The concentrations showing corrected mortality between 20 and 80% at 96 hr were used for calculation of median lethal concentration (LC₅₀). The experiments with mortality of above 10% in control were discarded and repeated. All bioassays were carried out at 27°C $\pm$ 2°C and 60-80% RH. Ten 96 hr old surviving larvae from each of treatments and control were weighed individually and growth reduction was estimated for each treatment in comparison to that of control.

Resistance development under selection pressure—Selection of larvae of *H. armigera* originally collected from chickpea fields in Delhi for evolution of resistance was initiated with the release of 400 F₁ neonate larvae on a meridic diet treated with 0.5 μ g CryIAc g⁻¹ for 4 days till about 90% of larvae died. The surviving larvae were then transferred to the normal diet and maintained till pupation. Adults were allowed to lay eggs and the above process of selection was continued with the neonate larvae of next generation until 6 generations. First 3 generation larvae were fed on diet treated with 0.5 μ g toxin g⁻¹ for 4 days that proved lethal to about 90% larvae. For the fourth generation, the selection pressure was increased to 0.7 μ g toxin g⁻¹ for 6 days from egg-

hatch. For the fifth and sixth generations, toxin concentration was increased to 1.5 and 3.25 μg toxin g^{-1} diet, respectively for 6 days. Bioassays of Cry1Ac with a full range of concentrations were carried out on neonate larvae of F_1 , F_3 , F_4 and F_6 generations to estimate LC_{50} . The neonate larvae of the Cry1Ac selected F_6 generation were used for their response to Cry1Aa and Cry1Ab to determine development of cross-resistance.

Protease extraction and characterization—Ten larvae of final instar of *H. armigera* were immobilized on ice for 15 min and then dissected in an ice-cold 20 mM Tris-HCl buffer (pH 7) for midguts, which were later rinsed with Tris-HCl buffer to remove food particles. The midguts were, then, homogenized in Tris-HCl buffer and centrifuged at 4°C at 13,200 g for 15 min. The supernatant was made up to 1 ml with Tris-HCl buffer and stored at -20°C until use. The midgut protease activity was measured by azocasein digestion method²². Midgut homogenate (20 μl) was mixed with (130 μl) of Tris-HCl buffer (pH 9). To the above mixture, 100 μl of 2% azocasein was added and incubated for 1 hr at 35°C. The reaction was stopped by adding 500 μl of 5% ice-cold trichloroacetic acid (TCA). The mixture was centrifuged at 13,200 g for 15 min at 4°C. Supernatant (500 μl) was mixed with 500 μl of 1 N NaOH and absorbance was estimated at 420 nm. The protease activity of sample was calculated using trypsin standard curve in terms of tryptic unit (TU) as per Kunitz²³. For studies on inhibition of midgut proteases, PMSF, TPCK and TLCK were dissolved in methanol and SBTI in distilled water. Azocaseinolytic assay was carried out with gut homogenate (5×10^{-3} TU) incubated with different concentrations of each protease inhibitor separately in a total volume of 150 μl of 20 mM Tris-HCl (pH 9) for 1 hr followed by addition of 100 μl of 2% azocasein and 1 hr incubation²⁴.

Midgut protease of test insects was subjected to SDS-PAGE analysis on 12% gels under non-denaturing condition and processed for zymogram analysis²⁵. Midgut homogenate with a known protease activity (2×10^{-3} TU) was dissolved in non-reducing sample buffer without boiling (2% SDS, 25% glycerol, 60 mM Tris-HCl, pH 6.8, 0.1% bromophenol blue), and electrophoresis carried out at 4°C. Thereafter, the gel was washed for 10 min in 2.5% Triton X-100 to remove SDS and cut into strips. One gel strip was incubated with 100 mM Glycine-NaOH buffer (pH 10) containing 2% casein for 1 hr.

The second gel strip was incubated with Cry1Ac toxin (5 mg/ml) to identify the midgut protease responsible for its degradation. The gel strips were also stained with 0.5% Coomassie brilliant blue R250 and destained briefly with methanol-acetic acid-water (40:10:50) followed by treatment in 5% acetic acid overnight. Protease activity was revealed as zone of white clearing in a dark blue background.

Cry1Ab and Cry1Ac protoxins were incubated with protease preparations of resistant and susceptible populations of *H. armigera*. The samples (10 μl) were drawn at different time intervals, immediately boiled for a min, then SDS sample buffer added and boiled for 2 more min. The proteins of the samples processed at different time intervals were separated on SDS-PAGE.

Cry1Ac protoxin was converted into toxin by treating with trypsin. The complete conversion of protoxin to toxin was verified by loading the sample on SDS-PAGE and visualizing a single toxin band of molecular weight of 58 kDa. The midgut protease (1 TU) preparations from resistant and susceptible population were incubated with different concentrations of Cry1Ac toxin (4 to 30 μg) for 1 hr. After 1 hr incubation, samples were boiled for 1 min and then mixed with SDS sample buffer and boiled for 2 more min, and then separated on 10% SDS-PAGE. The protein content of toxin band was estimated by eluting Coomassie brilliant blue R250 dye, and comparing with a standard curve of BSA prepared by dye elution as above. The amount of toxin was then subtracted from the substrate to obtain the amount of toxin degraded.

BBMV extraction and characterization—BBMV from midguts of final instar larvae of *H. armigera* were prepared as per Wolfersberger *et al.*²⁶. Alkaline phosphatase²⁷ and leucine aminopeptidase²⁸ of BBMV preparations were estimated. The specific activity of alkaline phosphatase was 184.1 and 241.3 $\mu\text{moles}/\text{min}/\text{mg}$ protein, and that of leucine aminopeptidase was 0.48 and 0.52 $\mu\text{moles}/\text{min}/\text{mg}$ protein, respectively for resistant and susceptible populations. BBMV (10 μg) was boiled with SDS sample buffer at 95°C for 5 min and separated on 8% PAGE at a constant voltage of 70 mA (Mini-dual model Electrophoresis system of Bangalore Genei). The BBMV, thus separated, was transferred and immobilized onto nitrocellulose membrane of 0.45 mm pore size using electrotransfer system at 25 V for 1 hr as per standard protocol (Genei Blot Electro-Transfer System of Bangalore Genei). The membrane was

removed and floated in Tris buffered saline (TBST) (10 mM Tris-HCl, 150 mM NaCl, pH 8 and 0.05% Tween-20) followed by brief rinsing. The membrane was incubated with blocking buffer (TBST + 1% BSA) for 2 hr, followed by incubation in Cry1Ab toxin in TBST buffer (20 µg/ml) for 2 hr, which were later challenged with toxin specific polyclonal antibodies in TBST buffer (1: 20,000 dilution) for overnight at 27°C. The unbound antibodies were removed by washing the membrane thrice with TBST buffer, 5-10 min each time, and then incubating in Goat's anti-IgG-alkaline phosphate conjugate at 1:50,000 dilution for 1 hr. The membrane was washed with TBST buffer thrice as above and then incubated with BCIP/NBT for 10 min and then washed with distilled water. The BBMV binding with Cry toxin was detected as a purple band and its molecular weight estimated as per Southern²⁹.

Cry1Ac toxin (50 µg) was labelled with I^{125} using I^{125} labelled sodium iodide ($Na I^{125}$) (in dilute NaOH) by following chloramine-T method³⁰. The specific activity of labelled toxin was determined as per Karim *et al*³¹. Labelled toxin was mixed with 100 µl each of 2% BSA and 20% TCA and the mixture incubated on ice for 10 min, and then, centrifuged at 13,500 g for 10 min. The radioactivity of the pellet was counted in a gamma counter (I^{125} counter, ECIL, Hyderabad). The protein content of pellet was determined as per Bradford³².

Saturation binding assays were performed using a fixed amount of labelled toxin for varying amounts of BBMV. Labelled Cry1Ac (1 µg) was incubated with an increasing concentration of BBMV (2.5 to 70 µg) in 100 µl of phosphate buffered saline (PBS)/binding buffer (58 mM $Na_2H_2PO_4$, 17 mM NaH_2PO_4 , 6.8 mM NaCl and 0.1% BSA). After 1 hr of incubation at 27°C, bound toxin was separated from unbound toxin by centrifugation at 13,500 g for 10 min. The pellet

was washed thrice with binding buffer to remove unbound toxin and the remaining radioactivity associated with pellet was then counted in a gamma counter.

Statistical analysis—The mortality and growth reduction data were analyzed by using maximum likelihood programme³³ for estimation of their respective LC_{50} and EC_{50} in terms of µg toxin g⁻¹ diet for 96 hr period. The difference between two LC_{50} or EC_{50} was considered significant only if their 95% fiducial limits did not overlap³⁴.

Results

Development of resistance and cross-resistance—Larvae of *H. armigera* population were susceptible to Cry1Ac with LC_{50} of 0.21 µg toxin g⁻¹ before selection. LC_{50} of Cry1Ac increased 4.2- and then 31.4-fold in the F_3 and F_6 generations, respectively (Table 1). Concurrently, LC_{50} of Cry1Aa and Cry1Ab, after 6 generations of selection with Cry1Ac, were 21.94 and 17.56 µg toxin g⁻¹ diet, respectively which were 8.4- and 25.4-fold higher than their respective LC_{50} of 2.6 and 0.69 µg toxin g⁻¹ diet before selection. Similarly, growth reduction was also affected with development of resistance. The EC_{50} for growth reduction increased from 0.21 to 4.29 µg toxin g⁻¹ diet for Cry1Ab (20.5-fold) and from 0.359 to 4.56 µg toxin g⁻¹ diet for Cry1Ac (12.8-fold). Cry1Ac selected insects of the F_6 generation did not show any growth reduction to Cry1Aa (Table 2).

Cry1Ac was about 12- and 3-fold more toxic to the neonates of unselected *H. armigera* than Cry1Aa and Cry1Ab, respectively. On selection, Cry1Ac was about 3-fold more toxic than Cry1Aa and Cry1Ab.

Characterization of midgut proteases—Six midgut proteases, 2 major bands with molecular weights of approximately 71.6 and 31.6 kDa and 4 minor bands of 44.6, 40.5, 35.7 and 29.7 kDa were observed in

Table 1—Resistance development in *H. armigera* to selection pressure of Cry1Ac toxin

Generation	No. larvae treated	Cry1Ac (µg g ⁻¹ diet)	No pupated	LC_{50} (µg g ⁻¹ diet)	Slope ± S.E	Fold resistance
1	400 *	0.5	25	0.21 (0.051–0.354)	1.08 ± 0.37	—
2	500	0.5	40	—	—	—
3	500	0.5	50	1.04 (*)	—	4.2
4	635	0.7	60	2.60 (*)	1.04 ± 0.53	12.4
5	560	1.5	50	—	—	—
6	700	3.23	56	6.59 (3.87 – 28.78)	1.0 ± 0.29	31.4

*Not possible to calculate

both susceptible and resistant populations of *H. armigera*, while only one protease band was visible with Cry1Ac protoxin incubation (Fig. 1).

The general protease inhibitor, PMSF and trypsin specific inhibitors, TLCK and SBTI inhibited protease activity significantly. No inhibition of protease activity

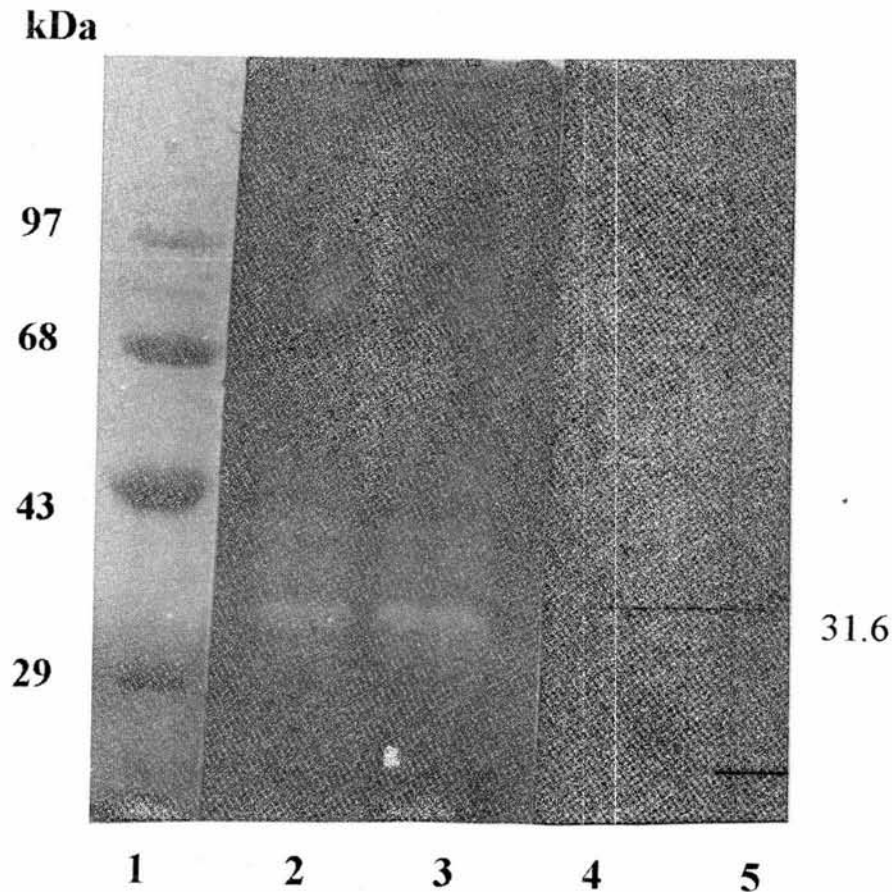


Fig. 1—Zymogram of midgut proteases of *H. armigera* on 12 % non-denaturing SDS-PAGE. [Lane 1: Protein molecular weight marker; Lane 2 and 3, midgut proteases of resistant and susceptible insects, respectively with casein as a substrate; Lane 4 and 5, midgut proteases of resistant and susceptible insects, respectively with Cry1Ac as a substrate]

Table 2 — Response of the Cry1Ac selected strain of <i>H. armigera</i> to <i>B. thuringiensis</i> toxins					
Toxin	Period of selection	LC ₅₀ /EC ₅₀ (µg g ⁻¹ diet)	Slope ± SE.	Fiducial limits	Fold resistance
Larval mortality (LC ₅₀)					
Cry1Aa	Before selection	2.59	1.29 ± 0.46	1.35-45.87	8.4
	After selection	21.94	0.39 ± 0.30	8.2-1955.0	
Cry1Ab	Before selection	0.69	1.63 ± 0.53	0.48-1.35	25.4
	After selection	17.56	0.39 ± 0.30	*	
Cry1Ac	Before selection	0.21	1.08 ± 0.37	0.05-0.35	31.4
	After selection	6.59	1.00 ± 0.29	3.87-28.78	
Growth reduction (EC ₅₀)					
Cry1Aa	Before selection	0.67	1.68 ± 0.24	0.54-0.92	**
	After selection	No growth reduction was observed			
Cry1Ab	Before selection	0.21	1.35 ± 0.20	0.15-0.26	20.5
	After selection	4.29	0.78 ± 0.19	2.70-12.90	
Cry1Ac	Before selection	0.36	1.76± 0.18	0.30-0.41	12.8
	After selection	4.56	1.33 ± 0.20	3.47-7.10	
**Not possible to calculate					

was observed with chymotrypsin specific inhibitor, TPCK even at a maximum concentration of 500 μ M (Table 3).

Activation of protoxins of Cry1Ab and Cry1Ac—Incubation of Cry1Ab protoxin with midgut proteases of susceptible population and also with trypsin for 2 and 4 hr led to the production of toxin. However, similar incubation even for only 2 hr with midgut proteases from

resistant population did not produce toxin suggesting the possibility of its rapid degradation (Fig. 2a). Similarly, the toxin of Cry1Ac protoxin was formed on the susceptible population and not in the resistant one on incubation for 2 and 4 hr with their respective midgut proteases (Fig. 2b).

The degradation of toxin was higher in treatment of toxin with protease from resistant insects than that from susceptible ones (Table 4).

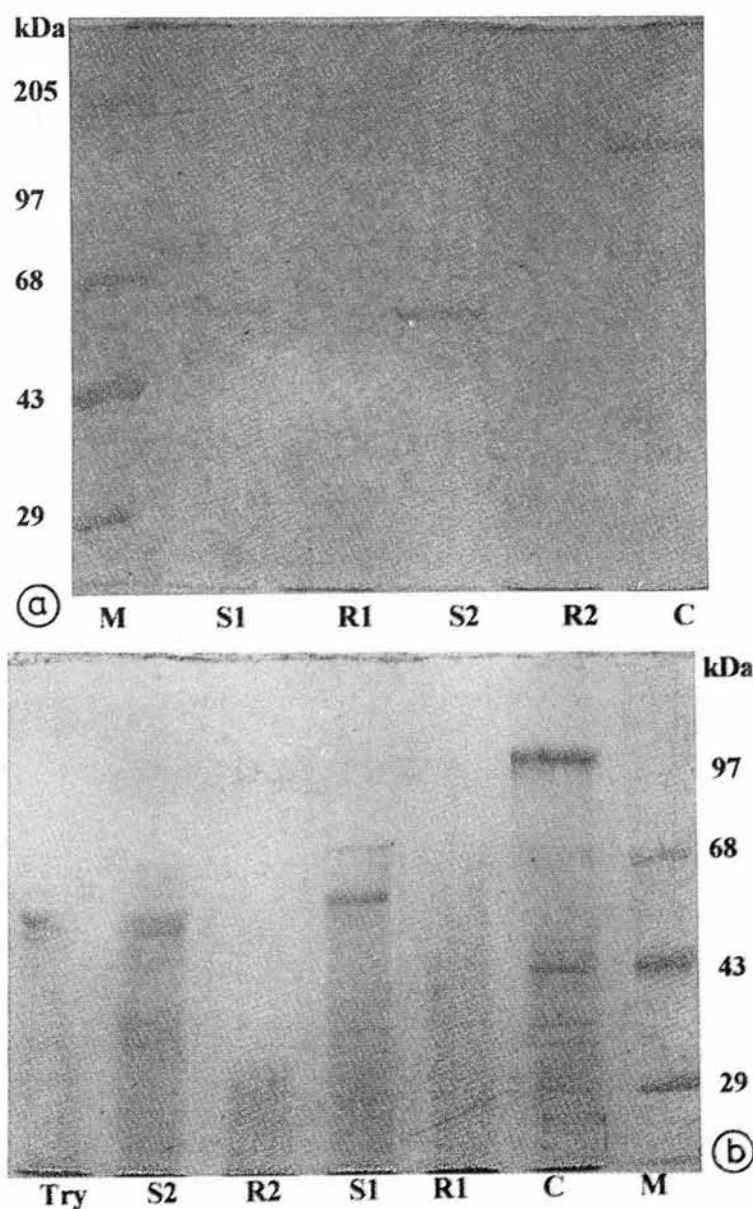


Fig. 2(a)—Proteolysis of Cry1Ab protoxin by midgut proteases of *B. thuringiensis* resistant and susceptible *H. armigera* [(Enzyme: 1 TU/2.5 μ g protoxin) M, Protein molecular weight marker, S1 and S2 Cry1Ab incubated with midgut protease of susceptible population for 2 and 4 hr respectively; R1 and R2 Cry1Ab incubated with midgut protease of resistant population for 2 and 4 hr respectively; C, Control without any protease incubation for 4 hr]. (b)—Proteolysis of Cry1Ac protoxin by midgut proteases of *B. thuringiensis* resistant and susceptible *H. armigera* [(Enzyme: 1 TU/2.5 μ g protoxin) Lane Try, trypsin; S1 and S2 Cry1Ac incubated with midgut protease of susceptible population for 2 and 4 hr respectively; R1 and R2 Cry1Ac incubated with midgut protease of resistant population for 2 and 4 hr respectively; C, Control without any protease incubation for 4 hr and M, Protein molecular weight marker]

Table 3—Inhibition of midgut protease activity of the *H. armigera* with protease inhibitors

Protease inhibitor	Inhibitor concentration	% inhibition of total proteolysis
PMSF	10 μ M	59.7 $\pm$ 4.7
	1 μ M	15.7 $\pm$ 4.72
	0.1 μ M	2.6 $\pm$ 2.1
TPCK	500 μ M	No inhibition
	50 μ M	No inhibition
	1 μ M	No inhibition
TLCK	500 μ M	34.2 $\pm$ 5.3
	50 μ M	15.3 $\pm$ 5.9
	1 μ M	No inhibition
SBTI	0.1%	58.7 $\pm$ 5.8
	0.05%	45.1 $\pm$ 8.1
	0.01%	24.3 $\pm$ 4.5

Table 4—Degradation of CryIAc toxin by midgut proteases of resistant and susceptible strain of *H. armigera*

Substrate (μ g) (CryIAc toxin)	Amount degraded (μ g /TU Enzyme/hr)	
	Resistant	Susceptible
4	Not detectable	0.17
8	5.2	0.32
12	6.2	1.15
16	5.4	1.82
24	4.7	1.56
30	4.0	0.95

Characterization of BBMV receptors—The CryIAb specific antibodies recognized a single receptor of about 77 kDa in BBMV preparation from both resistant and susceptible populations. Similar receptor was observed in both BBMV treated with Chaps buffer and untreated BBMV (Fig. 3). A difference was observed in binding of I^{125} labelled CryIAc toxin with receptors of resistant and susceptible population with resistance population showing saturation relatively at a lower concentration of BBMV (Fig. 4).

Discussion

Larvae of *H. armigera* developed many fold resistance to CryIAc depending up on the quantum and duration of its selection pressure^{16,35}. About 7-fold resistance in *H. armigera* was reported after 17-generations of selection of larvae fed on *Bt* cotton leaves *per se*¹². This ability of *H. armigera* to evolve resistance and lack of cotton varieties with high dose of Cry toxin expression may lead to evolution of resistance under field conditions. This possibility, simulated in northern China⁵, suggested the expected life of *Bt* cotton to be of about 7-10 years in areas under *Bt* cotton exceeding 70%.

H. armigera selected for resistance to CryIAc showed cross-resistance to CryIAb and CryIAa. The

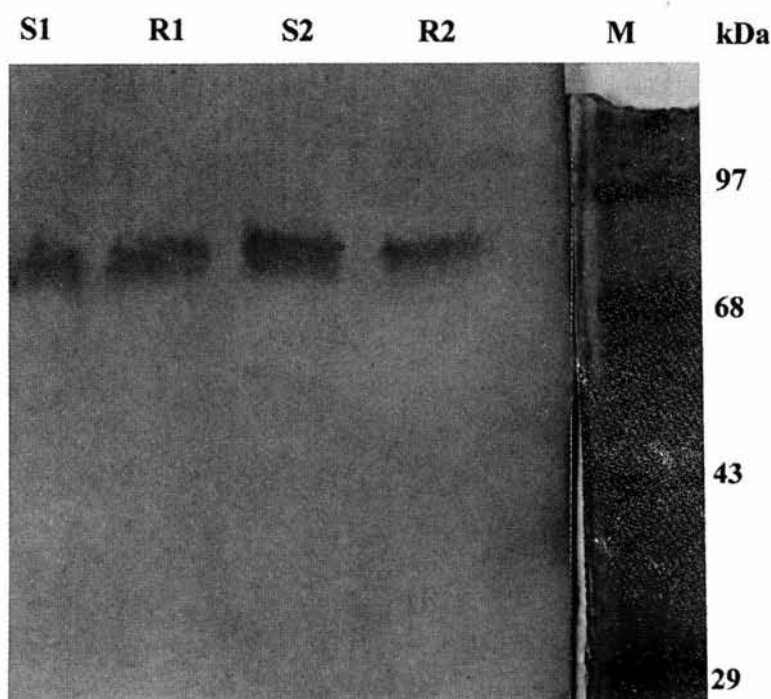


Fig. 3—Western blot of BBMV receptors of *H. armigera* for CryIAb. R1 and R2 BBMV of resistant population solubilized in Chaps buffer and non-solubilized, respectively, S1 and S2 BBMV of susceptible population solubilized in Chaps buffer and non-solubilized, respectively; M, Protein molecular weight marker

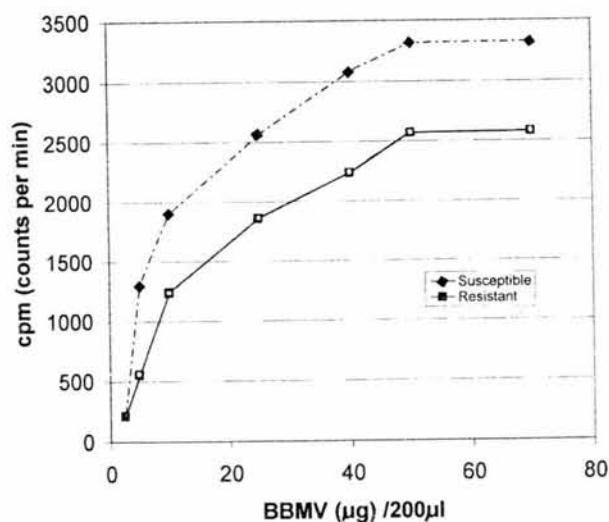


Fig. 4—Saturation binding of CryIAc with BBMVs of resistant and susceptible populations of *H. armigera*

CryIAc selected resistant *H. armigera* showed little cross-resistance to Dipel® which contains CryIAb, CryIAc and Cry2Aa toxins but showed high resistance to MVP formulation which contains only one CryIAc toxin¹⁵. However, this cross-resistance was not extended to CryIC and Cry2Aa³⁶. Liao *et al.*³⁷ reported significant differences in susceptibility of 3 strains of *H. armigera* to CryIAc and Cry2Aa. There was a small but significant negative interaction between these two Cry toxins. However, CryIAc selected strain of *Heliothis virescens* was found to be broadly cross-resistant to CryIAa, CryIAb, CryIBa, CryICa and Cry2Aa³⁸.

Growth reduction closely followed pattern of toxicity for CryIAb and CryIAc. However, CryIAc resistant insects showed very high tolerance to CryIAa. The cross-resistance between CryIA type toxins may be due to the presence of a common binding site on BBMVs, separate from that of Cry2A in *H. armigera*³¹. This is in contrast to non-saturable Cry2A binding with BBMVs and subsequent inhibition of labelled CryIAc in *Helicoverpa zea*³⁹. Similarly, Cry2A competed for the binding of CryIAa and CryIAb only slightly at high concentration of competitor, and CryIAc showed partial competition for binding of Cry2A only at high concentrations of the competitor in *H. virescens*⁴⁰.

Activation of CryIA protoxin with the midgut proteases of *H. armigera* is an essential step of mode of action, and also associated with resistance. Incubation of CryIA protoxin with midgut proteases at the ratio of 1 TU: 150 μg CryIAc protoxin for as long as 8 hr led to the formation of a stable toxin of about 58 kDa, similar to that of 65 kDa stable toxin

reported on incubation of protoxins of CryIAa, CryIAb, CryIAc and Cry2Aa with gut juice of *H. armigera*³¹. Of 6 proteases, the present studies report only one protease of about 31.6 kDa for CryIAc protoxin activation, probably in view of its high concentration, in contrast to 4 proteases of about 71, 49, 36 and 30 kDa sizes in the larvae of *H. armigera*⁴¹. Activation of CryIA protoxin with midgut proteases of *H. armigera* with 30 kDa protease⁴² and 46.6 kDa protease⁴³ has been reported. The midgut proteases of *H. armigera* were of serine kind, few chymotrypsin-like⁴⁴, but most trypsin-like, as they were inhibited by TLCK and SBTI and not by TPCK⁴¹. Involvement of midgut proteases in insect resistance has been reviewed⁴⁵; slower activation of CryIAc protoxin and faster degradation of CryIAc toxin in *H. virescens*^{46,47}. Liang *et al.*⁴⁸ found higher trypsin-like activity in the third instar larvae of resistant insects over the susceptible ones of *H. armigera*. Forcada *et al.*⁴⁹ reported that qualitative differences related to the presence or absence of proteolytic activity bands using PAGE could be responsible for the observed resistance in *H. virescens*. The present findings suggest that the absence of toxin formation with proteases of resistant insects may contribute to resistance in *H. armigera*. However, at a high concentration of Cry toxin; a toxin band was found in resistant insects too; which suggest that resistance may be partially due to the proteolytic degradation of toxin.

BBMV receptors, important sites for the binding of Cry toxins, are found to vary in insects; 5 binding sites with molecular weights ranging from 63 to 155-kDa in *H. virescens* and *H. zea*³⁰, 7 receptors for CryIAc with molecular weights ranging from 50 to 170 kDa in *H. virescens*⁵⁰, while the present study showed only one of about 77 kDa in the last instar larvae. The 120 kDa glycoprotein of BBMVs of *H. virescens* was found to have high homology with aminopeptidase N⁵¹, whereas 170 kDa aminopeptidase N purified fraction was considered functional receptor of *H. virescens* for CryIAa, CryIAb and CryIAc toxins⁵². The reduced binding of toxin with BBMVs of midgut of resistant population is often a cause of insect resistance¹⁷. Binding of BBMVs with CryIAb and CryIAc of the resistant strain was similar to that of susceptible strain but totally lacked for CryIAa in resistant strain of *H. virescens*⁴⁰. The differences in BBMVs binding in the present investigations may not be completely responsible for resistance. The report of post-binding event like transport of ions across the epithelial membrane in

H. zea may also contribute to resistance⁵³. The present studies call for more detailed investigations on the mechanisms of resistance and other characteristics, so as to develop *Bt* resistance management for *H. armigera* regardless of the fact that *Bt* is either used conventionally or through transgenic technology.

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References

- Edge J M, Benedict J H, Carroll J P & Reding H K, Bollgard Cotton: An assessment of global economic, environmental and social benefits, *J Cotton Sci*, 5 (2001) 121.
- Huang J & Pray C E, Economic impact of Bt cotton in China. in *Proc. 7th Int. Symp. Biosafety of genetically modified organisms*. Beijing, China, Oct. 10-16, 2002. Int. Soc. Biosafety Research, Peking University, Beijing (www.worldbiosafety.net), (2002) 121.
- Environment Protection Agency, *Bt Cotton Refuge Requirements for the 2001 Growing season* http://www.epa.gov/pesticides/biopesticides/pips/bt_cotton_refuge_2001.htm
- Australian Cotton Growers Research Association, *Transgenic and Insect Management Strategy Committee*, Brisbane, Australia, (<http://cotton.crc.org.au/Publicat/Pest>), 2001.
- Ru L-j, Zhao J-z & Rui C-H, A simulation model for adaptation of cotton bollworm to transgenic Bt cotton in North China, *Acta Entomol Sinica*, 45 (2002) 153.
- Gujar G T, Archana Kumari, Kalia V & Chandrashekar K, Spatial and temporal variation in susceptibility of American bollworm, *Helicoverpa armigera* (Hübner) to *Bacillus thuringiensis* var. *kurstaki*, *Curr Sci* 78 (2000) 995.
- McCaffery A R, Resistance to insecticides in heliothine Lepidoptera: A global view. in *Insecticide Resistance from mechanisms to management*, edited by I Denholm, J A Pickett and A L Devonshire (CABI & Royal Society, London) 1999, 59.
- Kranthi K R, Kranthi S & Wanjari R R, Baseline susceptibility of CryIA toxins to *Helicoverpa armigera* (Hübner) (Lepidoptera: Noctuidae) in India, *Int J Pest Man* 45 (2001) 141.
- Fakrudin B, Badari Prasad P R, Prakash S H, KrishnaReddy K B, Patil B V & KuruvinaShetti M S, Baseline resistance to CryIAc toxin in cotton bollworm, *Helicoverpa armigera* (Hübner) in South Indian cotton ecosystem, *Curr Sci*, 84 (2003) 1304.
- Sims S R, Berberich S A, Nida D L, Segalini L, Leach J N, Ebert C C & Fuchs R L, Analysis of expressed proteins in fiber fraction from insect protected and glyphosate-tolerant cotton varieties, *Crop Sci* 36 (1996) 1212.
- Sachs E S, Benedict J H, Stelly D M, Taylor J F, Altman D W, Berberich S A & Davis S K, Expression and segregation of genes encoding CryIA insecticidal proteins in cotton, *Crop Sci*, 38 (1998) 1.
- Zhao J-Z, Zhao K-J, Lu M-G, Fan X L & Guo S, Interactions between *Helicoverpa armigera* and transgenic Bt cotton in North China, *Sci Agric Sinica*, 31 (1998) 1.
- Adamczyk J J Jr, Hardee D D, Adam L C & Sumerford D V, Correlating differences in larval survival and development of bollworm (Lepidoptera: Noctuidae) and fall armyworm (Lepidoptera: Noctuidae) to differential expression of CryIA(c) δ -endotoxin in various plant parts among commercial cultivars of transgenic *Bacillus thuringiensis* cotton, *J Econ Entomol*, 94 (2001) 284.
- Adamczyk J J & Sumerford D V, Potential factors impacting season-long expression of CryIAc in 13 commercial varieties of Bollgard[®] cotton, *J Insect Sci*, 1 (2001) 13.
- Akhurst R & Liao C, Protecting an investment-managing resistance development to transgenic cotton by *Helicoverpa armigera*. in *Proceedings of the Eighth Australian Cotton Conference*, 1996, Broadbeach, Queensland, Australian Cotton Growers Research Association, Brisbane (1996) 299.
- Kranthi K R, Kranthi S, Ali S & Banerjee S K, Resistance to CryIAc δ -endotoxin of *Bacillus thuringiensis* in a laboratory selected strain of *Helicoverpa armigera* (Hübner), *Curr Sci*, 78 (2000) 1001.
- Ferré J & Van Rie J, Biochemistry and genetics of insect resistance to *Bacillus thuringiensis*, *Annu Rev Entomol*, 47 (2002) 501.
- Lee M K, Milne A, Ge & Dean, D H, Location of *Bombyx mori* receptors binding region of a *Bacillus thuringiensis* δ -endotoxin, *J Biol Chem*, 267 (1992) 3115.
- Laemmli U K, Cleavage of structural proteins during the assembly of the head of bacteriophage T₄, *Nature*, 227 (1970) 680.
- Mohan M & Gujar G T, Characterization and comparison of midgut proteases of *Bacillus thuringiensis* susceptible and resistant diamondback moth (Plutellidae: Lepidoptera), *J Invertebr Pathol*, 83 (2003) 1.
- Nagarkatti S & Prakaash A, Rearing of *Heliothis armigera* (Hübner) on an artificial diet, *Tech Bull Commonwealth Institute of Biological Control Bangalore, India*, 17 (1974) 169.
- Marchetti S, Chiaba C, Chiesa F, Bandiera A & Pitotti A, Isolation and partial characterization of two trypsins from brush border membrane vesicles of *Leptinotarsa decemlineata* (Colorado Potato beetle), *Pestic Biochem Physiol*, 54 (1998) 115.
- Kunitz M, Crystalline soybean trypsin inhibitor II. General properties, *J Gen Physiol*, 30 (1947) 291.
- Milne R & Kaplan H, Purification and characterization of a trypsin-like digestive enzyme from spruce budworm (*Choristoneura fumiferana*) responsible for the activation of δ -endotoxin from *Bacillus thuringiensis*, *Insect Biochem Molec Biol*, 23 (1993) 663.
- García-Carreño F, Dimes L & Haard N, Substrate gel-electrophoresis for composition and molecular weight of proteases or protease inhibitors, *Anal Biochem*, 214 (1993) 65.
- Wolfersberger M, Luethy P, Maurer A, Parenti P, Sacchi F V, Giordana B & Hanozet G M, Preparation and partial characterization of aminoacid transporting brush border membrane vesicles from the larval midgut of cabbage butterfly (*Pieris brassicae*), *Comp Biochem Physiol*, 86A (1987) 301.
- Lowry O A, Roberts R N R, Wu M L, Hixon, W S & Crawford E J, The quantitative histochemistry of brain II. Enzyme measurements, *J Biol Chem*, 207 (1954) 19.
- Valaitis A P, Gypsy moth midgut proteases: Purification and characterization of luminal trypsin, elastase and brush border membrane leucine aminopeptidase, *Insect Biochem Molec Biol*, 25 (1995) 139.
- Southern E M, Measurement of DNA length by gel electrophoresis, *Anal Biochem*, 100 (1979) 319.

- 30 Garczynski S F, Crim J W & Adang M J, Identification of putative insect brush border membrane binding molecules specific to *Bacillus thuringiensis* delta-endotoxin by protein blot analysis, *Appl Environ Microbiol*, 57 (1991) 2816.
- 31 Karim S, Riazuddin S & Dean D H, Interaction of *Bacillus thuringiensis* delta-endotoxins with midgut brush border membrane vesicles of *Helicoverpa armigera*, *J Asia Pacific Entomol*, 2 (1999) 153.
- 32 Bradford M M, A rapid and sensitive method for the quantification of microgram quantities of protein utilizing the principle of protein-dye binding, *Anal Biochem*, 72 (1976) 248.
- 33 Ross G E S, *Maximum likelihood programme* (Rothamsted Experiment Station, Harpenden, UK) 1977.
- 34 Litchfield J T & Wilcoxon F, A simplified method of evaluating dose-effect experiments, *J Pharm Exp Ther*, 96 (1949) 99.
- 35 Akhurst R, James W & Bird L, Resistance to Ingard® cotton by the cotton bollworm, *Helicoverpa armigera*, in *Proceedings of the 10th Australian Cotton Conference*, 16-18th Aug., 2000, Australian Cotton Growers Research Association, Brisbane, (<http://cotton.pi.csiro.au/Publicat/conf/coconf00/Areawide/25/25.htm>.) (2000) 1.
- 36 Zhao J-Z, Rui C, Lu MG, Fan X L, Ru L & Meng X-q, Monitoring and management of *Helicoverpa armigera* resistance to transgenic Bt cotton in Northern China, *Resist Pest Manage*, 11 (2000) 28.
- 37 Liao C, Heckel D G & Akhurst R, Toxicity of *Bacillus thuringiensis* insecticidal proteins for *Helicoverpa armigera* and *Helicoverpa punctigera* (Lepidoptera: Noctuidae), major pests of cotton, *J Invertebr Pathol*, 80 (2002) 55.
- 38 Gould F, Martínez-Ramírez A, Anderson A, Ferré J, Silva F J & Moar W J, Broad-spectrum resistance to *Bacillus thuringiensis* toxins in *Heliothis virescens*, *Proc Natl Acad Sci USA*, 89 (1992) 7986.
- 39 English L, Robin H D, Von Tarsch M A, Kulesza C A, Ave D, Coyle D, Jany C S & Slatin S L, Mode of action of Cry2A: A *Bacillus thuringiensis* δ -endotoxin, *Insect Biochem Molec Biol*, 24 (1994) 1025.
- 40 Lee M K, Rajamohan F, Gould F & Dean D H, Resistance to *Bacillus thuringiensis* Cry1A delta-endotoxin in laboratory selected *Heliothis virescens* strain is related to receptor alteration, *Appl Environ Microbiol*, 61 (1995) 3836.
- 41 Zhang J H, Wang C & Qin J D, The interactions between soybean trypsin inhibitor and δ -endotoxin of *Bacillus thuringiensis* in *Helicoverpa armigera* larva, *J Invertebr Pathol*, 75 (2000) 259.
- 42 Meenakshisundaram K S & Gujar G T, Proteolysis of *Bacillus thuringiensis* subspecies *kurstaki* endotoxin with midgut proteases of some important lepidopterous species, *Indian J Exp Biol*, 36 (1998) 593.
- 43 Brown D P, Wilkinson H S & Gatehouse J A, Midgut carboxypeptidase from *Helicoverpa armigera* (Lepidoptera: Noctuidae) larvae: Enzymes characterization, cDNA cloning and expression, *Insect Biochem Molec Biol*, 28 (1998) 739.
- 44 Xu G & Qin J, Extraction and characterization of midgut proteases from *Heliothis armigera* and *H. assulta* (Lepidoptera: Noctuidae) and their inhibition by tannic acid, *J Econ Entomol*, 87 (1994) 334.
- 45 Oppert B, Protease interactions with *Bacillus thuringiensis* insecticidal toxins, *Arch Insect Biochem Physiol*, 42 (1999) 1.
- 46 Forcada C, Alcácer E, Garcerá M D & Martínez R, Differences in the midgut proteolytic activity of two *Heliothis virescens* strains, one susceptible and one resistant to *Bacillus thuringiensis* toxins, *Arch Insect Biochem Physiol*, 31 (1996) 257.
- 47 Shao Z, Cui Y, Liu X, Yi H, Ji J & Yu Z, Processing of delta-endotoxin of *Bacillus thuringiensis* subsp. *kurstaki* HD-1 in *Heliothis armigera* midgut juice and the effects of protease inhibitors, *J Invertebr Pathol*, 72 (1998) 73.
- 48 Liang G, Tan W & Guo Y-Y, Comparison of some detoxification enzyme and midgut protease activities between resistant and susceptible cotton bollworm population to Bt, *Acta Phytophyl Sinica*, 28 (2001) 133.
- 49 Forcada C, Alcácer E, Garcerá M D, Tato A & Martínez R, Resistance to *Bacillus thuringiensis* Cry1Ac toxin in three strains of *Heliothis virescens*: Proteolytic and SEM study of the larval midgut, *Arch Insect Biochem Physiol*, 42 (1999) 51.
- 50 Cowles E A, Yunovitz H, Charles J F & Gill S S, Comparison of toxin overlay and solid-phase binding assays to identify diverse Cry1Ac toxin binding proteins in *Heliothis virescens* midgut, *Appl Environ Microbiol*, 61 (1995) 2738.
- 51 Gill S S, Cowles E A & Francis V, Identification, isolation, and cloning of a *Bacillus thuringiensis* Cry1Ac toxin-binding protein from the midgut of the Lepidopteran insect *Heliothis virescens*, *J Biol Chem*, 270 (1995) 27277.
- 52 Luo K, Sangadala S, Masson L, Mazza A, Brousseau R & Adang M J, The *Heliothis virescens* 170 kDa aminopeptidase functions as "receptor A" by mediating specific *Bacillus thuringiensis* Cry1A δ -endotoxin binding and pore formation, *Insect Biochem Molec Biol*, 27 (1997) 735.
- 53 Karim S & Dean D H, Toxicity and receptor binding properties of *Bacillus thuringiensis*-endotoxins to the midgut brush border membrane vesicles of the rice leaf folders, *Cnaphalocrocis medinalis* and *Marasmia patnalis*, *Curr Microbiol*, 41 (2000) 430.