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Isolation and Molecular Characterization of Some Common *Bt*Cry Protein Receptor Genes from Certain Living Organisms.

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عزل وتوصيف جزيئى لبعض جينات مستقبلات Bt بروتينات الـ Bt من كائنات حيه معينة.

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ABSTRACT

Bacillus thuringiensis (Bt) crystal proteins are effective in controlling agriculturally harmful insects. However, the mechanism of Bt pesticidal action is fairly understood. It is assumed that the pesticidal protein has affinity for specific receptors in the midgut of the susceptible larvae and binds irreversibly to create holes in the gut leading to eventual death of the target larvae.

The main aim of the research is to identify and characterize Bt δ -endotoxin receptor in an important pest, Egyptian Cotton leafworm (*Spodoptera littoralis*).

Biological activities of crystal protoxins of BtkHD1 strain and Cry1C were determined by in vitro mortality assay on neonate larvae of S. littoralis. Also, Brush border membrane vesicles (BBMVs) were prepared from the 5th larvae of the same insect. Subsequently, immunoblotting experiments were performed using Cry1A Bt δ -endotoxins to detect the presence of specific toxin binding proteins on BBMVs. The toxin binds to proteins of 108.58 kDa on brush border membrane vesicles. It is therefore a strong candidate for in vitro S. littoralis Cry1 toxin receptor.

Specific primers for *S. littoralis* APN (*Sl*APN) were designed according to the nucleotide sequence of *Spodoptera litura* APN; GenBank accession number (AF320764). The full length of APN gene from that insect was obtained and it was cloned in pGEMT-easy vector and pET-30a and pPICZ A expression vectors.

The cloned gene was characterized through sequencing and studying expression in *E. coli* and *Pichia*

pastoris. The expressed protein was analyzed by Western blotting with anti- Cry toxin antibody. The Western blotting showed that the expression of target protein was detected by toxin. This analysis proved that APN protein exhibited binding properties towards Cry1A toxin. The sequence of *Sl*APN gene was deposited in GenBank under accession number JF509138.

The predicted amino acid sequence of *Sl*APN cloned gene encoded a putative 952 amino acid residues. The sequence possesses three conserved regions which are zinc-binding/gluzincin motif HEX₂HX₁₈E, the third zinc-binding ligand and gluzincin aminopeptidase motif GAMEN. Furthermore, five potential N-linked glycosylation sites (NXS/T) beside four highly conserved Cys residues are also observed. Finally, a highly conserved 64 amino acid residues from Leu 129 to Pro 193 was also detected.

Based on computational alignment, a theoretical 3-D model structure of *Sl*APN was obtained. Whereas, about 814 aa residues of whole suggested 3-D model were corresponded to residues 58-871 of the primary structure. The present *Sl*APN model contained four structural domains, which spread from N-terminal domain I to C-terminal domain IV over the regions Asn⁵⁸-Ile²⁶⁶; Ser²⁶⁷-Gly⁵⁰⁶; Asn⁵⁰⁷-Leu⁵⁸¹ and Ser⁵⁸²-Ala⁸⁷¹, respectively. The recorded overall dimensions of this model were 91A° x 55 A° x 65A° forming together a hook like structure.

Key words:

Bacillus thuringiensis; δ-Endotoxin; Aminopeptidase N receptor; Spodoptera littoralis; 3-D homology modeling; Pichia pastoris.

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LIST OF ABBREVIATIONS

| A260 | Absorbance at 260 nanometer |
|-------------|--|
| A280 | Absorbance at 280 nanometer |
| AlP | Alkaline Phosphatase |
| Amp | Ampicillin |
| APN | Aminopeptidase-N |
| APS | Ammonium peroxosulphate |
| ATP | Adenosine triphosphate |
| BBMV | Brush Border Membrane Vesicle |
| BCIP | 5-bromo 4-chloro 3-indolyl phosphate |
| BLAST | Basic local alignment search tool |
| BLASTn | Nucleotide blast (Search a nucleotide database using a nucleotide query) |
| BLASTx | Search protein database using translated nucleotide query |
| Bm | Bombyx mori |
| bp | Base pair |
| BmAPN | Bombyx mori Aminopeptidase-N |
| BSA | Bovine Serum Albumin |
| Bt | Bacillus thuringiensis |
| Btk | Bt subsp. krustaki |
| cDNA | Complementary DNA |
| Cry toxin | Crystal toxin |
| C- terminal | Carboxy terminal |

| DTT | Dithiothreitol |
|-------------------|---|
| DEPC | Diethylpyrocarbonate |
| dH ₂ O | Distilled Water |
| DNA | Deoxyribonucleic Acid |
| E. Coli | Escherichia coli |
| F1 SlAPN | A segment of <i>Sl</i> APN (from bp 1 to 2185) was excised from recombinant vector pGEM T-Easy/ <i>Sl</i> fl with <i>Eco</i> R1 |
| GPI | glycosylphosphatidyl-inositol |
| IPTG | Isopropyl-β-D-thiogalactopyranoside |
| Kb | Kilobase(s) |
| KDa | Kilodalton(s) |
| LB broth | Luria-Bertani broth |
| LC50 | 50% lethal concentration |
| μg | Microgram(s) |
| min | Minute(s) |
| MW | Molecular Weight |
| NBT | Nitro blue tetrazolium chloride |
| OD | Optical density |
| ORF | Open Reading Frame |
| PCR | Polymerase Chain Reaction |
| PEG | Polyethylene glycol |
| PFT | Pore-Forming Toxins |
| P. pastoris | Pichia pastoris |
| PM | Peritrophic Membrane |
| PMSF | Phenylmethylsulfonyl fluoride |
| Ppm | Part per million |

| PVDF | Polyvinylidene difluoride | | |
|----------|---|--|--|
| RE | Restriction Endonucleases | | |
| RNA | Ribonucleic Acid | | |
| rpm | Revolution per minutes | | |
| RT-PCR | Reverse transcription- PCR | | |
| SDS-PAGE | Sodium Dodecyl Sulphate Polyacrylamide Gel Electrophoresis | | |
| Sl | Spodoptera littoralis | | |
| SlAPN | Spodoptera littoralis APN | | |
| Slf1 | Full-length cDNA of SlAPN | | |
| Sl7 | 5'-truncated 1601 bp fragment of <i>Sl</i> APN | | |
| Sl8 | 3'- truncated 1359 bp fragment of <i>SlAPN</i> | | |
| TEMED | Tetramethylethylenediamine | | |
| U | Unit | | |
| UV | Ultraviolet | | |
| W/V | Weight Per Volume | | |
| X-gal | 5-bromo 4-chloro 3-indolyl β- D-galactopyrannoside | | |

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