

Functional interpretation of APN receptor from *M. sexta* using a molecular model

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Abstract:

Insect pests are the major cause of damage to commercially important agricultural crops. The continuous application of synthetic pesticides resulted in severe insect resistance by plants. This causes irreversible damage to the environment. *Bacillus thuringiensis* (Bt) emerged as a valuable biological alternative in pest control. However, insect resistance against Bt has been reported in many cases. Insects develop resistance to insecticides through mechanisms that reduce the binding of toxins to gut receptors. Nonetheless, the molecular mechanism of insect resistance is not fully understood. Therefore, it is important to study the mechanism of toxin resistance by analyzing amino-peptidase-N (APN) receptor of the insect *M. sexta*. A homology model of APN was constructed using Insight II molecular modeling software and the model was further evaluated using the PROCHECK program. Oligosaccharides participating in post translational modification were constructed and docked onto specific APN functional sites. Post analyses of the APN model provide insights on the functional properties of APN towards the understanding of receptor and toxin interactions. We also discuss the predicted binding sites for ligands, metals and Bt toxins in *M. sexta* APN receptor. These data help in the development of a roadmap for the design and synthesis of novel insect resistant Cry toxins.

Key words: glycosylation, *Manduca Sexta*, post transnational modifications, aminopeptidase-N, Cry toxins

Background:

Gram positive bacteria *Bacillus thuringiensis* (Bt) is an environmentally safe biopesticide used against insects. It produces crystalline inclusions during the sporulation phase of its life cycle [1]. These Cry toxins are environmental friendly and provide protection against a wide range of insects like beetles, caterpillars, mosquito larvae etc. Pore formation takes place on the insect midgut brush border membrane after the receptor binds to the toxin. This leads to an osmotic imbalance for insect mortality [2]. Bt toxins binds with four different kinds of insect receptors through oligomerization [3]. The receptors include aminopeptidase-N (APN), cadherins, glycoproteins and alkaline phosphatase [4]. The APN receptor plays a major role with Cry toxin interactions. APN is a membrane protein and it undergoes post translational modifications (PTMs) through N and O-glycosylation process. N or O glycosylation is a post translational event that has implications on protein structure, stability, molecular recognition and signaling activities [5]. *M. sexta* aminopeptidase-N receptor attached to the midgut membrane with glycosyl phosphotidyl inositol (GPI) have anchoring function [4]. Moreover, mass spectrometric studies of the oligosaccharides were found to be Fuc2Hex3HexNAc3, Hex3HexNAc2, Fuc4Hex3HexNAc4 and Fuc3Hex3HexNAc3. These site specific oligosaccharides attached to different sites of APN are 295-297, 609-611, 623-625 and 752-754, respectively [6]. The cadherin receptor - toxin binding sites were identified by using phage display technique [7]. However, no such reports in APN receptor. Therefore, it is of interest to predict potential interaction sites with various ligands and peptides to understand receptor-toxin molecular interactions.

Methodology:

Sequence:

The APN protein sequence of length 990 amino acid was retrieved from Swiss Prot (ID-Q11001).

Template structure:

We used the template structure of Tricorn interacting factor from *Thermoplasma acidophilum* (PDB ID: 1ZIW) for modeling the APN protein.

Model refinement and evaluation:

The APN protein model was constructed by using Insight II (Accelrys) molecular modeller program and the structure is minimized by applying consistence valance force field (CVFF). Subsequent minimization was done using steepest descent and conjugated gradient algorithms in discovery program. The predicted 3-D structure was evaluated using the PROCHECK program.

Structural and topological studies:

Detailed domain topologies of APN was predicted individually by using the TOPS program [9] and number of sheets and helices in the domains were counted by using the PROF program [10]. Oligosaccharides binding motifs of APN were predicted by using NetOGlyc and NetNGlyc programs from ExPasy site [8].

Oligosaccharides 3-D structure prediction:

2-D Oligosaccharide structures were collected from experimental data provided elsewhere [6] and their 3-D structures were constructed by using Chemultra and ChemsKetch softwares. Moreover, file conversion was carried out using the OPEN BABLE software. Nevertheless, the above said structures, molecular weights and formulae were predicted with the help of ligand scout program and 3-D models were minimized by using the

TINKKER software [11, 12]. The best conformational structures were selected on the basis of minimum energies.

Oligosaccharide docking and refinements:

Specific Oligosaccharide molecules were docked on experimentally predetermined sites of APN. Docking was carried out using DOCK software version 6.0 and by applying AMBER force fields [13]. Oligosaccharides were docked one at a time to APN and the docking binding energies were calculated for four oligosaccharides.

Molecular interactions:

The Ligplot tool was used to generate molecular level interactions [14]. Xscore program was used to select the best conformations among the docked complexes.

Multiple sequence alignment and active site prediction:

Multiple sequence alignment was performed using CLUSTAL-W to assess sequence conservation and polymorphism.

Active site identification:

Interactive sites or motifs of APN were predicted using the POCKET program [16]. Active site analysis was performed using the ConSeq program which can identify the functional residues [15].

Solvent accessible surface area:

Solvent accessible surface area (SASA) is calculated using the POPS program.

Discussion:

Figure 1 shows four predicted domains. Domain-I is located at the N-terminal region and it was found that domain I (1-193 amino acids) consists of an alpha helix and nine beta strands. Domain-II (194 – 443) consists of

eight alpha helices, eleven beta strands and it has also been recognized as a catalytic domain. Domain-III (443-560) consists of four alpha helices and four beta strands. Domain-IV is located at the C-terminal region (565-995) consisting of nineteen alpha helices and seven beta strands. Experimental results show that oligosaccharides binding sites are located at various positions 295-297, 609-611, 623-625 and 752-754 [6].

Oligosaccharides 2D structures were converted into 3D structures and four potential oligosaccharides were docked to APN receptor at specific locations to develop glyco-protein models (Table 1). Oligosaccharide molecules are having different molecular weights. OS-1, OS-3 and OS-4 are fucosylated molecules, where as OS-2 is the only non-fucosylated molecule. Fuc2Hex3HexNAc3 is an oligosaccharide (OS-1) having molecular weight of 1563.76 with seven ringed structure. Hex3HexNAc2 is of (OS-2) five ringed structure with molecular weight of 1183.35. Fuc4Hex3HexNAc4 an eleven ringed structure (OS-3) and its molecular weight is 2334.77. The last oligosaccharide Fuc3Hex3HexNAc3 (OS-4) is a nine ringed structure with molecular weight of 2027.31.

The single oxygen atom of oligosaccharide OS-1 formed three hydrogen bonds with different residues of APN 295 N, 296 Y and 297 T with hydrogen bond lengths 17.3, 7.24 and 14.7, respectively and binding energy of 24976.2 Kcal/J. The insect motif 609NTT611 is highly conserved and it is commonly utilized for glycosylation [17]. When OS-2 is successfully docked on to 609NTT611 of APN, the single oxygen atom in it formed two hydrogen bonds with Asp609 and Thr610 of APN with bond lengths of 5.9 and 10.4, respectively. The final minimized structure of APN-OS-2 docked complex has a binding energy of 24770.6 Kcal/J.

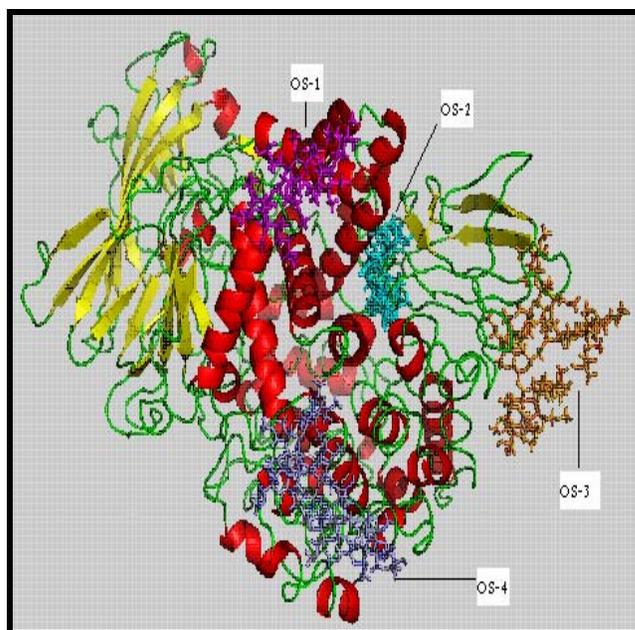


Figure 1: APN receptor 3D-model showing four docked oligosaccharides on their respective binding sites.

predicted model is given Table 2. The solvent exposed residues in the conserved regions are visualized using solvent accessible surface area data. Thus, the data presented here help in the development of a roadmap for the design and synthesis of novel insect resistant Cry toxins.

Conclusion:

A homology model of APN was constructed using Insight II molecular modeling software and the model was further evaluated using the PROCHECK program. Oligosaccharides participating in post translational modification were constructed and docked onto specific APN functional sites. Post analyses of the APN model provide insights on the functional properties of APN towards the understanding of receptor and toxin interactions. We also discussed the predicted binding sites for ligands, metals and Bt toxins in *M. sexta* APN receptor. These data help in the development of a framework for the design and synthesis of novel insect resistant Cry toxins.

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Supplementary material:

Table 1: Molecular interaction details of APN with different oligosaccharides. APN is docked with four oligosaccharides.

S. No.	Name of the Oligosaccharide	Interactive sites	Binding energy	Binding affinity	Hydrogen bond forming residue	Hydrophobic interactive residues	Non ligand residue involved in Hydrophobic interactions
1	Fuc2Hex3HexNAc3	295 NYT 297	-126.542	-81.5998	295N,296Y &297T	296 Y & 297 T	I257, N461, L465, R468 & V464.
2	Hex3HexNAc2	609 NTT 611	-81.8053	-68.3248	609N & 610T	609N, 617R & 651Q	R652, T612 & G 613
3	Fuc4Hex3HexNAc4	623 NRT625	-100.522	-94.941	621S, 624R & 625 T	621S & 625T	Q397, Q629, R 620, R632, V625, Q663, N654 & F662
4	Fuc3Hex3HexNAc3	751 NGS 753	-86.1063	-62.6317	752G, 754S & 761R	754S & 761R	F755, A800, S 809, Q798, R804, N749 C766 & R 751.

Table 2: Different conserved sites showing SASA values for various APN receptors

S. No.	Type of site	Mammal		Insect		Bacteria	
		Amino acid position in sequence	SASA value	Amino acid position in sequence	SASA value	Amino acid position in sequence	SASA value
1	GAMEN	GLY 316	112.3	GLY 323	111.4	GLY 316	212.3
		ALA 317	54.1	ALA 324	53.5	ALA 317	54.1
		MET 318	94.4	MET 325	92.9	MET 318	94.4
		GLU 319	124.5	GLU 326	123.4	GLU 319	124.5
		ASN 320	84.6	ASN 327	83.3	ASN 320	84.6
		TRP 321	213.5	TRP 328	210.4	TRP 321	113.5
		GLY 322	51.0	GLY 329	51.1	GLY 322	51.0
2	HEXXE	LEU 323	124.6	LEU 330	116.2	LEU 323	114.6
		HIS 352	226.6	HIS 359	226.9	HIS 352	226.6
		GLU 353	156.4	GLU 360	156.0	GLU 353	156.4
		LEU 354	192.7	ILE 361	189.7	LEU 354	176.7
		ALA 355	86.3	ALA 362	86.0	ALA 355	86.3
		HIS 356	237.0	HIS 363	236.7	HIS 356	237.0
		3	WWDNL	TRP 367	208.3	TRP 374	209.9
TRP 368	133.0			TRP 375	128.7	TRP 371	143.9
THR 369	97.8			ASP 376	110.4	TRP 372	114.0
HIS 370	116.1			ASN 377	93.6	ASP 373	98.9
LEU 371	59.9			LEU 378	60.2	ASN 374	76.4
TRP 372	112.5			TRP 379	111.2	LEU 375	48.9
LEU 373	65.4			LEU 380	64.8	TRP 376	104.3
ASN 374	78.4			ASN 381	78.1	LEU 377	50.6
GLU 375	130.1			GLU 382	129.9	ASN 378	43.5
GLY 376	43.6			GLY 383	43.3	GLU 379	94.5
PHE 377	132.3			PHE 384	131.3	GLY 380	26.5
ALA 378	110.3	ALA 385	110.0	PHE 381	73.6		