Summary

The main focus of the present investigation was to predict the 3D structure of insecticidal toxins from *Photorhabdus luminescens* and receptors such as dynamin, synapsin, synaptotagmin and syntaxin from *Anopheles gambiae* and aminopeptidase N from *Helicoverpa armigera* using molecular modelling techniques. Attempt was also made to dock these predicted toxins structures with homology modelled receptors.

The output produced by the phylogenetic analysis suggest that TcaA, TcaB, TcaC and PirB toxins does not showed any evolutionary relationship with any of the cry toxins from *Bacillus thuringiensis*. Results obtained from the ProDom sever showed that TcaA, TcaB, TcaC and PirB sequences comprised of six, seven, ten and two domains respectively.

Each of these domains was later submitted to PSI-BLAST tool in order to find the best template sequence in PDB structural database, which could be considered for modeling purpose. Few of the subject sequences which were having E value better than the threshold were in turn selected for performing multiple sequence alignment through ClustalW server. ClustalW output revealed that all receptor sequences showed a good conservation with all the templates considered.

Receptor sequences from *Anopheles gambiae* and *Helicoverpa armigera* were modeled through homology modeling technique using SWISS Model server. Since there were no sequence homologs for the insecticidal toxin sequences from *Photorhabdus luminescens* in the PDB database during routine PSI BLAST search, 3D structure could not be generated through homology modelling approach. However, submission of the complete sequence of toxins to I-TASSER server generated 3D structure of toxins based on threading technique.
Modeled structures were then submitted to MODLOOP server for modeling the loop region. Validation of the loop modelled protein models through ERRAT, ProSA and Procheck suggest that modeled structures are of reasonable accuracy. An attempt was made to construct the fusion protein using PirB, Cry toxin and Garlic lectin. Two types of fusion proteins were constructed namely type I and type II.

Using Hex software, insecticidal toxins from *Photorhabdus luminescens* was docked onto the homology modeled receptors from *Anopheles gambiae, Helicoverpa armigera* and crystal structure of cadherin from *Drosophila melanogaster*. Overall topologies of both the fusion proteins were similar. Compared to type-I, type-II fusion protein appears to have better affinity with the cadherin receptor of *Drosophila melanogaster*. 