

## **Abstract:**

Diverse forms of  $\delta$ -endotoxin gene of *Bacillus thuringiensis* (Bt) may offer novelty in their insect mortality potential and newer sensitivity range amongst the target insects. Thus they are always a welcome resource for insect control management strategies. To search for *cryIA* endotoxin gene known to be toxic to lepidopteran insect pests, a fairly large number of Bt isolates containing the  $\delta$ - endotoxin gene have been screened. Toxicity assays conducted against two major lepidopteran insect pests viz, cotton bollworm (*Helicoverpa armigera*) and yellow stem borer (*Scirpophaga insertulus*) revealed to the presence of a potential toxin contained in a *Bacillus thuringiensis* serovar *tolorthi* strain (S1). The potency of the toxin was higher than the known *cryIAb* toxin to cotton bollworm (CBW) and yellow stem borer (YSB). This finding figured as significant as a candidate gene for transgenic application. Thus, further studies for characterization of the gene was undertaken. Molecular characterization of the gene documented that the endotoxin gene to be carried out through southern analysis, depicted a difference at the genomic level. Subsequent, cloning and sequencing of the coding region of the gene documented it to match well with the reported sequence of *cryIAb* except an alteration of a single base at 668 position resulting the corresponding change of amino acid serine to phenylalanine at 223 position. This inclusion of a hydrophobic moiety at 223 position led to increased effective hydrophobicity of the toxin molecule. Theoretical homology modeling by Swiss-pdb Viewer (spdbv) revealed that it resulted centering this position with a local conformational change. It was suspected that these changes contributed enough towards the enhanced toxicity of the peptide molecule. The gene was thus reconstructed using indica rice preferred codons for high expression in rice tissue when transformed. It is expected that the highly toxic peptide will be effective against YSB even at moderate level of plant expression.