

# Bioinformatic Analysis for Redesigning of Endochitinase 'Chic' as a Potential Biopesticide

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**Abstract** Agriculture has had to face the destructive activities of numerous pests like fungi, weeds and insects from time immemorial leading to radical decrease in yields. With the advent of chemical pesticides, this crisis was resolved to a great extent. However the over dependence on chemical pesticides and eventual uncontrolled use of them has necessitated for alternatives mainly for environmental concerns. Biopesticides or biological pesticides based on pathogenic microorganisms offer an ecologically sound and effective solution to pest problems.

Chitinolytic bacteria as biocontrol agents have showed potential antagonistic activity against pathogenic fungi by degrading the cell wall. *Serratia marcescens* has been reported producing multiple chitinases (ChiA, ChiB, and ChiC) and these enzymes are able to degrade the chitin in the cell walls of fungi and the exoskeletons of insects. In this study we are aiming to redesign endochitinase ChiC for enhanced catalytic activity. We have performed several bioinformatic analyses. To locate the key residues responsible to endochitinolytic activity, we did sequence alignment of several endochitinases by using ClustalW. We have identified four key residues W34, F66, W300 and E141 with the help of sequence alignment and structural analyses of chitinases. ChiC genes from *Serratia marcescens* (MTCC No. 7641) was cloned in bacterial expression vector and sequenced. We have done saturation mutagenesis at all the four positions and currently in a process to express the protein and their characterization. Changing the active site residues may enhance specificity and catalytic activity of the ChiC, which can be applied for the development of potential biopesticide.