

## PE 10 - Chitosanase from *Fusarium graminearum*

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Chitosan degrading activity was detected in the culture supernatant of the plant pathogenic fungus *Fusarium graminearum* using chitosans with different degrees of acetylation (DA) as a substrate. We have identified a chitosanase gene (fgcsa) in *F. graminearum* showing homology to the genes of the glycosyl hydrolase family 75. The fgcsa ORF encodes a polypeptide of 313 amino acid residues with a calculated molecular mass of 33.3 kDa including a putative 37 amino acid residues long signal sequence. Comparison between genomic and cDNA sequence revealed that two introns are present in the coding region. The fgcsa cDNA corresponding to the entire coding region excluding the putative signal sequence was obtained by reverse transcription-PCR amplification. The cDNA was cloned into the expression vector pGEX-4T-1 and introduced into *E. coli* BL21. The resulting *E. coli* transformants overproduce a 56 kDa GST-FGCSA fusion protein that was purified by affinity chromatography and is now being used for further characterization.