PE 7 - Degradation of Chitosan with Chitinase G from Streptomyces coelicolor A3(2)

E.B. Heggset[1,2], M. Kristoffersen[1], I.A. Hoell[2], S.J. Horn[2], V.G.H. Eijsink[2], K.M. Vårum[1]

[1]NOBIPOL, Department of Biotechnology, Norwegian University of Science and Technology, 7491 Trondheim, Norway - [2]Department of Chemistry, Biotechnology and Food Science, Norwegian University of Life Sciences, 1432 Ås, Norway.

Chitinases are important in the degradation of chitin, and constitute families 18 and 19 of the glycoside hydrolases. Family 18 chitinases are retaining enzymes which operate via a unique substrate-assisted catalytic mechanism. This mechanism involves a nucleophilic attack of the N-acetyl group of the -1 sugar on the anomeric carbon which leads to formation of an oxazolinium ion intermediate. In contrast, family 19 chitinases are inverting enzymes, which operate according to a single displacement mechanism that does not require an N-acetylated sugar in the -1 subsite. We have previously used chitosans as soluble substrates to study the properties of family 18 chitinases, such as processivity, subsite specificity, and the production of specific oligosaccharides. Here we report studies on the degradation of chitosans with a family 19 chitinase, Chitinase G (ChiG), from Streptomyces coelicolor A3. Studies of the size-distribution of the product oligomers as a function of the extent of degradation suggest that ChiG operates according to an endo-type of action. The identities (acetylated/deacetylated) of the new reducing end sugar, the non-reducing end sugar and their nearest neighbors have been used to reveal information about the enzyme's preferences for acetylated/deacetylated units in its subsites. The different catalytic mechanism as well as different subsite preferences of ChiG, as compared to family 18 chitinases, results in production of oligosaccharides of very different composition as compared to those produced by family 18 chitinases.