Fungal Cellobiohydrolases and the Degradation of Crystalline Cellulose

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Fungal cellobiohydrolases are very efficient degraders of highly ordered crystalline cellulose. The soft -rot fungus *Trichoderma reesei* produces two different cellbiohydrolases, Cel7A (CBHI) and Cel6A (CBHII), which degrade cellulose crystals from the reducing and non-reducing ends, respectively [reviewed in 1]. Both enzymes have extended, tunnel shaped active sites formed by loops on the enzymes surfaces and promoting so called multiple attack or proeessive mode of action. The endoglucanases in the glycosyl hydrolase families 6 and 7 have more open active sites favouring random action in the middle of the cellulose chains. While the possibility of occasional opening and closing of the cellobiohydrolase active site loops cannot be excluded, structural, biochemical and mutagenesis studies of Cel6A and Cel7A support a model where a glucan chain end is introduced at the tunnel entrance and threaded through the entire tunnel for subsequent hydrolysis and release of products from the opposite end [2-4].

The white-rot fungus *Phanerochaete chrysosporium* also produces the two different types of cellobiohydrolases but - unexpectedly - has six different isoenzymes of the family 7 cellobiohydrolases (Cel7A-1 to -6) [5]. While the family 6 enzyme is apparently very similar to the corresponding Cel6A enzyme of *T. reesei* [6], there are interesting differences in both the sequences and expression patterns of the six different family 7 cellobiohydrolases in *P. chrysosporium* [7]. In addition, no endoglucanase genes have so far been identified in *P. chrysosoporium* although enzymes with endoglucanase activity have been isolated from its culture media. The indicates that different fungi may have developed slightly different strategies for crystalline cellulose degradation. The genes of all of the six isomzymes have now been cloned and sequenced permitting the development of heterologous expression systems and detailed analysis of the putative difference in their enzymatic function.

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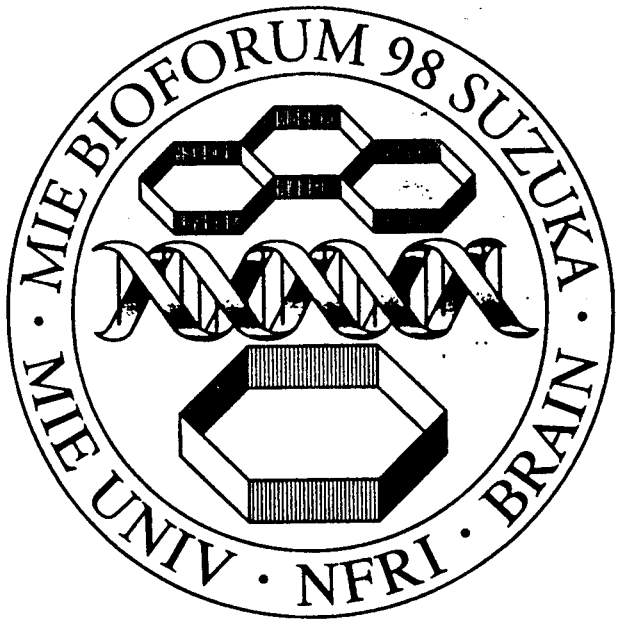

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