

## FUNGAL CELLULASE SYSTEMS: THROUGH THE LOOKING GLASS

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The apparent chemical simplicity of cellulose, a polymer of  $\beta$ -1,4-linked D-glucopyranose units and the most abundant biopolymer of carbon on Earth, belies the elaborate, multi-component enzyme systems produced by microorganisms, such as fungi, to convert cellulose to its monomeric building block D-glucose. The most thoroughly investigated fungal source to date is the filamentous fungus *Trichoderma reesei*. A 'complete' fungal cellulolytic system generally contains multiple forms of three main types of enzyme activity, exocellobiohydrolase, endoglucanase and  $\beta$ -glucosidase, which act in synergy to bring about the depolymerization of cellulose. To date several theories have been suggested to explain (i) the roles of the individual cellulases in so-called 'complete' cellulase systems and (ii) the mechanisms involved in regulating the expression of different cellulases. The 'holy grail' of cellulase research is to identify the 'inducer/inducers' and mechanism of cellulase induction in organisms of biotechnological potential.

*Talaromyces emersonii*, a moderately thermophilic, aerobic fungus produces an array of  $\beta$ -glucan-modifying enzymes, including a potent extracellular cellulolytic enzyme system consisting of multiple endoglucanases, exocellobiohydrolases and  $\beta$ -glucosidases, many of which are significantly thermostable<sup>[1]</sup>. In this paper, we will present a detailed overview of the *Talaromyces emersonii* cellulolytic system at genome and proteome levels, in the context of the current theories on fungal cellulase systems. Factors that influence and regulate the expression of the individual enzyme components will be discussed and some of our most recent findings on the only cellulase produced by *T. emersonii* under conditions of catabolite repression and its potential role in cellulase induction will be presented. In conclusion, the question will be raised as to whether cellulase induction and regulation is equivalent in all fungal species, or if subtle differences have evolved to provide these eukaryotes with selective ecological advantages in Nature.

**Acknowledgements:** This work was funded by Enterprise Ireland Basic and Research Innovation awards to M.G.T.

[1] Murray, P.G.; Aro, N.; Collins, C.; Grassick, A.; Penttilä, M.; Saloheimo, M.; Tuohy, M. *Prot. Expr. Purif.* **2004.** 38, 248-257.