Towards a better understanding of oxidative biomass deconstruction

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Introduction

The breakdown of waste plant material, in the form of lignocellulose, for subsequent fermentation into biofuels holds tremendous promise for securing humankind's future energy needs. Though research over several decades has provided many details of how fungi and microbes are able to degrade these materials, the industrial production of lignocellulosic biofuels has remained too costly to compete with fossil fuels. The discovery of lytic polysaccharide monooxygenases (LPMOs) in 2010/11 was, therefore, a key breakthrough. These enzymes oxidatively induce chain breaks into the crystalline region of hard to degrade polysaccharides such as cellulose and chitin, thereby augmenting the ability of other enzymes to degrade biomass. Indeed, the inclusion of LPMOs in enzymatic cocktails for cellulose degradation provides considerable improvements in the efficiency of saccharification, so there is now a worldwide drive to ensure that these enzymes are used effectively in industry. Our research is focused on the electron transfer processes that might be used to activate LPMOs.

Results

CAZy (www.CAZy.org) is a comprehensive database of structurally-related, catalytic and non-catalytic modules from enzymes involved in the degradation, modification or synthesis of carbohydrates. Using this resource we have identified a range of target proteins that contain domains of unknown funtion, denoted X-domains, appended to carbohydrate binding modules. Sequence analysis of these X-domains suggests that they may well play an electron transfer function and so we have selected a subset of targets to be characterised (Figure 1A).

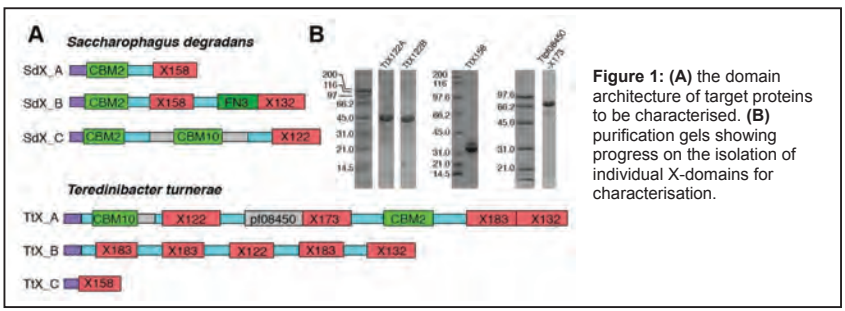

Figure 1: (A) the domain architecture of target proteins to be characterised. **(B)** purification gels showing progress on the isolation of individual X-domains for characterisation.

We are currently working on expressing and purifying these domains (Figure 1B) with the aim of combining structural studies together with biochemical, spectroscopic and redox analyses to gain a thorough understanding of X-domain function. We will then seek to exploit the knowledge gained through enzyme engineering to ensure maximal enzyme turnover during biomass degradation whilst also investigating other potential applications for these domains.

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Collaborators

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