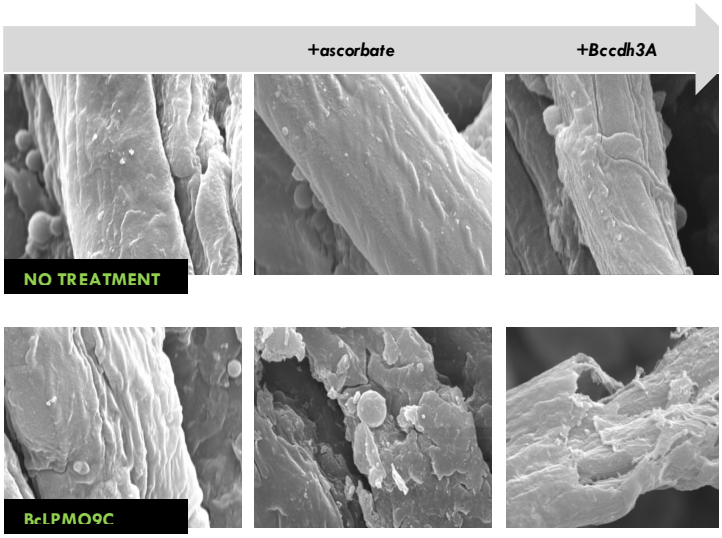
Mining fungal secretome reveals cellobiose dehydrogenase as redox partner for lytic polysaccharide monoxygenase

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Abstract (300 word limit)

Lytic Polysaccharide Monooxygenase (LPMO) are unconventional plant depolymerizing enzymes which catalyze oxidative disintegration of complex polysaccharides. These metalloenzyme utilize molecular oxygen and an external electron donor to cleave recalcitrant polysaccharide. Its distinctiveness in polysachharide degradation has surged interest in understanding the underlying mechanism, which led to discovery of several extrinsic electron donor partner. However, the knowledge of endogenous redox partner is still elusive and solely depends on speculative tendency of co-secretory protein to act as reductant. Therefore, the present study aims at mining the fungal secretome for probable redox partner. We investigated the secretome of Botrytis cinerea for the presence of enzymes belonging to CAZy superfamily. Comparative secretome data suggested preponderance of BcLPMO9C, LPMO belonging to GH61 superfamily, and as the major protein among rest of nine LPMOs harboured in the genome. Using Label transfer and pull down assays, we then investigated fungal secretome for BcLPMO9C interacting proteins and identified cellobiose dehydrogenase (BcCDH3A) as a probable redox partner, which was validated using various biochemical and biophysical assays including surface plasmon resonance and label-transfer studies. Further, the effect of Bccdh3A supplementation, into BcLPMO9C, on biomass disintegration was visualized using Scanning Electron Microscopy and X-ray diffraction studies. Overall, the current study provides for the first time a rationale and systematic approach to scrutinize the fungal secretome for deciphering endogenous redox partner for LPMO. This advancement in our knowledge on the molecular mechanisms of the LPMO-CDH interaction will provide insights into improving cellulolytic enzyme cocktails used in the biofuels industry.

Image



Recent Publications (minimum 5)

1. Pasari N, AdlakhaN,..,Yazdani SS.Impact of Module-X2 and Carbohydrate Binding Module-3 on the catalytic activity of associated glycoside hydrolases towards plant biomass. Scientific Reports (2017).
2. Gupta V, Chaudhary N, Adlakha N, Gulati P, Bhatnagar R. Functional analysis of BAS2108-2109 two component system: Evidence for protease regulation in Bacillus anthracis. The International Journal of Biochemistry & Cell Biology (2017).
3. Adlakha N, Pfau T, Ebenhoeh O, Yazdani SS. Insight into metabolic pathways of the potential biofuel producer, Paenibacillus polymyxa ICGEB2008. Biotechnology for Biofuels (2015)
4. Adlakha N, Yazdani SS. Efficient production of 2,3-butanediol from cellulosic hydrolysate using Paenibacillus sp. ICGEB2008 as a model organism. Journal of Industrial Microbiology and Biotechnology (2015).
5. Bashir Z†, Kondapalli V†, Adlakha N, Sharma A, Bhatnagar R, Yazdani SS. († first authorship shared) Diversity and functional significance of cellulolytic microbes living in the guts of termite, pill bug and stem borer. Scientific Reports (2013).



Biography (150 word limit)

I am, Nidhi Adlakha, a postdoctoral fellow at School of Biotechnology, at Jawaharlal Nehru University, New Delhi, India. I have nearly 10 years of experience in the field of Industrial Biotechnology which started with my PhD at Metabolic Engineering Group, International Centre for Genetic Engineering and Biotechnology, New Delhi (Thesis Supervisor: Dr. Syed Shams Yazdani) . Further, I have done my Postdoc at University of Aberdeen at Scotland: Supervisor Dr. Oliver

Ebenhoeh and at Jawaharlal Nehru University, New Delhi.

I have worked extensively on the cellulases and their role in the biomass degradation. I also remain engaged in developing efficient enzyme and microbial system for degradation of recalcitrant cellulose for biofuel production.

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Notes/Comments: