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MINING FUNGAL SECRETOME REVEALS CELLOBIOSE DEHYDROGENASE AS REDOX PARTNER FOR LYTIC POLYSACCHARIDE MONOXYGENASE

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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.

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