Characterizing the degradation of cellulose by combinations of cellulolytic enzymes

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Project Goals: To study the dynamics and interactions of cellulases during the degradation of cellulose. The overarching goal is to create biochemical models that describe the synergistic interactions between cellobiohydrolases and accessory enzymes as they create cellobiose from cellulose.

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Abstract Text:

To better understand factors that hinder cellulose degradation by cellobiohydrolases, we characterized accessory enzymes that act on cellulose in combination with *Trichoderma reesei* Cel7A, a cellulase that targets the reducing ends of glucan chains in cellulose to produce soluble cellobiose. These accessory enzymes include endo-1,4-beta-D-glucanase (Cel7B) from *Trichoderma longibrachiatum* and Cel6A, a cellobiohydrolase II. Cel7B is known for its ability to randomly cleave cellulose to produce additional binding sites for other cellulases, whereas Cel6A cleaves cellobiose units from the nonreducing ends of glucan chains in cellulose. By measuring reducing end production in reactions between cellulose from *Acetobacter* and these enzymes, we found that although Cel7B significantly increases cellulose hydrolysis by Cel7A, the enzyme appears to act in an additive manner rather than a synergistic one. Conversely, Cel6A appears to act synergistically with Cel7A at varying concentrations, contributing to more cellulose hydrolysis than either of the two enzymes alone. Future experiments will involve testing three-enzyme cocktails containing each of the previous enzymes to test whether these combinations allow for greater synergy in degrading cellulose. These data will be used to develop biochemical models to help explain single-molecule observations made for each enzyme acting on cellulose made using a newly developed SCATTIRSTORM microscope.

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