Boosting of enzymatic softwood saccharification by fungal GH5 and GH26 endomannanases

**Background:** Softwood is a promising feedstock for lignocellulosic biorefineries, but as it contains galactoglucomannan, efficient mannan-degrading enzymes are required to unlock its full potential.

**Results:** Boosting of the saccharification of pretreated softwood (Canadian lodgepole pine) was investigated for 10 fungal endo-β-(1→4)-mannanases (endomannanases) from GH5 and GH26, including 6 novel GH26 enzymes. The endomannanases from *Trichoderma reesei* (TresMan5A) and *Podospora anserina* (PansMan26) were investigated with and without their carbohydrate-binding module (CBM). The pH optimum and initial rates of enzyme catalysed hydrolysis were determined on pure β-mannans, including acetylated and deacetylated spruce galactoglucomannan. Melting temperature (Tm) and stability of the endomannanases during prolonged incubations were also assessed. The highest initial rates on the pure mannans were attained by GH26 endomannanases. Acetylation tended to decrease the enzymatic rates to different extents depending on the enzyme. Despite exhibiting low rates on the pure mannan substrates, TresMan5A with CBM1 catalysed highest release among the endomannanases of both mannose and glucose during softwood saccharification. The presence of the CBM1 as well as the catalytic capability of the TresMan5A core module itself seemed to allow fast and more profound degradation of portions of the mannan that led to better cellulose degradation. In contrast, the presence of the CBM35 did not change the performance of PansMan26 in softwood saccharification.

**Conclusions:** This study identified TresMan5A as the best endomannanase for increasing cellulase catalysed glucose release from softwood. Except for the superior performance of TresMan5A, the fungal GH5 and GH26 endomannanases generally performed on par on the lignocellulosic matrix. The work also illustrated the importance of using genuine lignocellulosic substrates rather than simple model substrates when selecting enzymes for industrial biomass applications.

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