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Sucrose bioconversion in linear and branched a-glucans by discovery and engineering of bacterial a-transglucosylases

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PURPOSE OF THE ABSTRACT

Polysaccharide-based materials are recognized as attractive alternatives to polymers derived from carbon fossil fuels, as revealed by their broad range of applications in food & feed, agriculture, health, or in chemical industries. In this context, some alpha-transglucosylases produced by lactic acid bacteria are of interest, as they catalyze the synthesis of high molar mass alpha-glucans, glucooligosaccharides or gluco-conjugates from sucrose[1], a low-cost and abundant renewable resource.

These alpha-transglucosylases are classified in GH70 family[2], which comprises today around 600 sequences for only about seventy enzymes biochemically characterized, that remains low. To accelerate the development of enzymatic glucosylation tools with desired properties, our work is focused on their structure-activity relationship studies and engineering. However, the natural diversity of GH70 enzymes is far from being fully explored, and the repertoire of our enzymatic tool-box enzymes could be expand by exploring the numerous lactic acid bacterial genomes sequences available in databases.

This presentation will describe our recent findings on several original GH70 enzymes isolated thanks to data mining or genome sequencing campaigns. Distinctive specificities in term of glucan molar masses (10 to 10^6 kg/mol), osidic bonds (alpha-1,2/alpha-1,3/alpha-1,6) and degree of branching will be reported, as well as their potential to produce novel block copolymers composed of various covalently-linked ?-glucans with contrasting structures and physicochemical properties. Moreover, the resolution of 3D structures of alpha-transglucosylases -free or in complex with oligosaccharides-, allowed us to decipher some of the molecular determinants involved in polymer elongation or in linkage specificity, opening promising strategies for GH70 enzyme engineering aiming at customize alpha-glucan architectures. Few examples on dextran size modulation will be given.

References :
[1] Leemhuis H et al. (2013) J. Biotechnol. 163, 250?272
[2] Lombard Vet al. (2013) Nucleic Acids Res. 42, 490?495

FIGURES

FIGURE 1

FIGURE 2

KEYWORDS

polysaccharide | white biotechnology | glycodiversification | enzyme structure-function relationship studies

BIBLIOGRAPHY

[1] Leemhuis H et al. (2013) J. Biotechnol. 163, 250–272

[2] Lombard Vet al. (2013) Nucleic Acids Res. 42, 490–495