A New Functional Classification of Glucuronoyl Esterases by Peptide Pattern Recognition

Glucuronoyl esterases are a novel type of enzymes believed to catalyze the hydrolysis of ester linkages between lignin and glucuronoxylan in lignocellulosic biomass, linkages known as lignin carbohydrate complexes. These complexes contribute to the recalcitrance of lignocellulose. Glucuronoyl esterases are a part of the microbial machinery for lignocellulose degradation and coupling their role to the occurrence of lignin carbohydrate complexes in biomass is a desired research goal. Glucuronoyl esterases have been assigned to CAZymes family 15 of carbohydrate esterases, but only few examples of characterized enzymes exist and the exact activity is still uncertain. Here peptide pattern recognition is used as a bioinformatic tool to identify and group new CE15 proteins that are likely to have glucuronoyl esterase activity. 1024 CE15-like sequences were drawn from GenBank and grouped into 24 groups. Phylogenetic analysis of these groups made it possible to pinpoint groups of putative fungal and bacterial glucuronoyl esterases and their sequence variation. Moreover, a number of groups included previously undescribed CE15-like sequences that are distinct from the glucuronoyl esterases and may possibly have different esterase activity. Hence, the CE15 family is likely to comprise other enzyme functions than glucuronoyl esterase alone. Gene annotation in a variety of fungal and bacterial microorganisms showed that coprophilic fungi are rich and diverse sources of CE15 proteins. Combined with the lifestyle and habitat of coprophilic fungi, they are predicted to be excellent candidates for finding new glucuronoyl esterase genes.

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