Mechanical pretreatment of grass for biogas production

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In the anaerobic digestion of lignocellulosic materials, the accessibility of microorganisms to the fermentable sugars is restricted by a layer of digestion-recalcitrant compound, lignin, which acts as an inhibitor restricting the degradation activity. In order to reduce the biomass particle size and to increase the feedstock’s specific surface area available to the microorganisms, and therefore improve the hydrolysis kinetics, lignocellulosic biomass should be mechanically pretreated before undergoing anaerobic digestion. A Hollander beater was successfully used for the comminution task of waste paper for methane production, in this research is proposed its use to treat grass for biogas conversion. The pretreatment time as well as the digestion time are studied using statistical methods and correlated to the methane and biogas yields resulting from the anaerobic digestion of grass. This assay provides information on how much and how fast the pretreated material can be degraded under optimal batch conditions, which are valuable parameters in the design and operation of biogas plants. Optimizing the parameters of the mechanical pretreatment, a more energy efficient process and better biomass exploitation can be achieved, improving the design and economic viability of a lignocellulosic biorefinery.

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Exploiting fungal diversity for optimized deconstruction and valorization of lignocellulosic biomass

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Filamentous fungi are an invaluable source of enzymes able to deconstruct the complex lignocellulosic plant cell wall. The wealth of genomic data obtained recently from wood-rotting fungi has revealed the diversity of lignocellulolytic enzymes they produce. The CIRM-CF collection hosted in our lab is dedicated to such fungi originating from specific temperate and tropical biotopes. This provides a unique tool to explore fungal functional biodiversity with applications in various fields of biotechnology, including the pretreatment and saccharification of biomass as well as the biotransformation of biomass-derived compounds into platform chemicals for food and non-food application. Beyond the comparison of genome portfolios, the analysis of transcriptome profiles in vivo allows identification of the sets of genes encoding the enzyme machineries expressed according to the organisms’ strategy for plant cell wall degradation/modification. These analyses reveal which enzymes are produced during the different stages of plant cell wall deconstruction, whether it will be drastic disruption or more subtle modifications, and under challenging environmental conditions, such as marine environments. Under the auspices of a Joint Genome Initiative-sponsored project from the US Department of Energy, we are currently establishing the genomic, transcriptomic and secretomic data from 40 Polyporales species grown on complex (Pine chips, Aspen chips, Wheat straw) and simple (cellulose, xylan, maltose) substrates. This compliments previous studies on selected fungi and the ligninolytic enzymes they produce and allows us to identify novel enzymes and try to elucidate the different mechanisms in nature involved in biomass deconstruction.

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