O6.4

A simplified method for biobutanol production from corn stover

María Hijosa Valsero[1], Jerson Garita Cambronero[1], Ana Isabel Paniagua García[1,2], Rebeca Díez Antolínez[1,2]

[1]*Instituto Tecnológico Agrario de Castilla y León (ITACyL),* [2]*Instituto de Recursos Naturales (IRENA), Universidad de León*

Corn stover has been extensively studied as a feedstock for bioethanol production, and industrial technologies have been developed for this purpose. However, its transformation into biobutanol has only been assessed from a theoretical perspective or at laboratory-scale. Biobutanol is obtained by ABE bacteria which transform simple sugars into solvents. During the pretreatment of corn stover to release monosaccharides, inhibitory compounds that hinder ABE fermentation are generated. Therefore, detoxification steps prior to fermentation are generally needed.
A simplified method is proposed for the production of butanol from corn stover by acid hydrolysis with 0.9% H2SO4 during short times to reduce inhibitors generation, followed by enzymatic hydrolysis. Bacterial strain screening enables the production of about 6 g/L butanol from the hydrolysate without detoxification. Currently, hydrolysis and fermentation parameters are being improved to increase butanol concentrations.

O7.1

Discovery and engineering of pathways for conversion of lignin-derived aromatics to lipids by Cutaneotrichosporon oleaginosus

Allison Yaguchi[1], Michael Spagnuolo[1], Nicole Franaszek[1], Alana Robinson[1], Erin Mihealsick[1], **Mark Blenner**[1]

[1]*Clemson University*

Cutaneotrichosporon oleaginosus, previously known as Cryptococcus curvatus, is a non-model oleaginous yeast that is known for its ability to metabolize many alternative sugars, including xylose, and tolerate toxic lignocellulosic hydrolysate inhibitors such as 5-hydroxymethylfurfural and furfural. We discovered C. oleaginosus also tolerates and fully metabolizes lignin-derived aromatics including phenol, 4-hydroxybenzoic acid, p-coumarate, and resorcinol as sole carbon sources, as well as in co-utilization with glucose and xylose. We demonstrated lipid accumulation to over 69% of biomass by weight. RNAseq data revealed novel participating genes that were missed by BLAST analysis, facilitated aromatic metabolism pathway elucidation, and improved the existing genome annotation significantly. These pathways are being confirmed using metabolomics data. Finally, we will discuss the development of genetic tools to rapidly engineer this non-model system for the production of novel fatty acids such as ricinoleic acid and omega-3 fatty acids.