TLP-310. Brazilian microbial diversity as a source of new strains for deconstruction of lignocellulosic biomass

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Introduction. Despite the intense research efforts to increase the efficiency of *Lignocellulosic* biomass hydrolysis, there are only a limited number of microbial strains able to produce enzymes at industrial scale and with low cost. Therefore, the strain improvement coupled to strain/ genes discovery is central to warranty the economic viability of lignocellulosic biofuel production. Objective. The goal of this screening was to identify novel lignocellulolytic strains among a large collection of microorganism sampled from distinct Brazilian biomes.

Materials and methods. We screened a microorganism collection containing 8452 bacterial strains and 265 fungal strains. These microorganisms were previously isolated from soil and plants. The secretion of cellulase, xylanase and pectinase was assayed using solid medium containing *Carboxymethylcellulose (CMC)* and avicel, xylan and pectin, respectively. The enzymatic index (ei) was estimated in triplicate. Selected strains were growth by submerse fermentation, using sugarcane bagasse as unique carbon source. Selected bacterial and fungal strains were identified using the 16s rRNA and its1-5.8s-its2 sequences, respectively.

Results. From 8452 bacterial strains, 17.8%, 2.7% and 0.5% were able to use *CMC*, xylan and pectin, respectively. Twenty-two strains presented a high ei (6.0 to 16.4) on *CMC*. These strains were identified as *Bacillus* sp. and *Falsibacillus* sp. Among the 265 fungi screened, 36,7%, 65,2%, 55% and 96,2% were able to use cmc, xylan, pectin and avicel, respectively. These fungi were identified as *Fusarium* sp., *Penicillium* sp., *Microdochium* sp., *Trichoderma harzianum* and *Trichoderma ganense*.

Conclusions. Overall, it was possible to identify distinct strains/species of bacteria and fungi able to deconstruct lignocellulosic biomass. Further studies are being conducted at embrapa agroenergia.