
Screening of a Moxotó Goat Rumen Small Insert Metagenomic Library for Cellulosic Activity for Biotechnological Use

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INTRODUCTION: The use of lignocellulosic biomass as feedstock in the process of fuel production is an alternative to revert the excessive dependence in nonrenewable energy. Bacterial enzymes are capable of degrading plant biomass and are widely used in industry as biocatalysts. Metagenomics techniques can be used to discover new enzymes from both culturable and not-yet-culturable bacteria for the development of tailor-made enzymatic cocktails. **MATERIAL AND METHODS:** A metagenomic library was screened for the ability to hydrolyse carboxymethyl cellulose (CMC) and 462 clones were found to possess this activity. Clones were also screened for activity activity in other substrates such as xylan and crystalline cellulose (Avicel®). **RESULTS AND DISCUSSION:** Restriction enzymes were used to obtain the restriction profiles of each clone to determine whether they were different from each other or not. Those clones whose DNA was different will be sequenced. Finished the sequencing, bioinformatics' analyses will help to choose the ORFs of interest for expression and protein purification followed by characterization. The enzymes available in the market have a high cost, thus showing the necessity to develop new biocatalysts with higher efficiency and lower prices, and also optimized to Brazilian biomass. **CONCLUSIONS:** It is hoped that this study reveals new genes responsible for the deconstruction of lignocellulosic biomass, which are of biotechnological interest.

Keywords: bioethanol, metagenomics, microorganisms

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