

## BIOPROSPECTING FOR $\beta$ -GLUCOSIDASE ACTIVITY IN A GOAT RUMEN METAGENOMIC LIBRARY

Nidia S.P.L. Ramos,<sup>1</sup> Isabel S. Cunha,<sup>2</sup> Betulia M. Souto,<sup>3</sup> Ricardo Krüger and<sup>5</sup> Betania Quirino

<sup>1</sup>Research analyst– Universidade Católica de Brasília, Brasília, DF, Brazil; <sup>2</sup>Graduate student – Universidade Católica de Brasília, Brasília, DF, Brazil. <sup>3</sup>Research analyst– Embrapa Agroenergia, Brasília, DF, Brazil; ; <sup>4</sup>Research scientist – Universidade de Brasília, Brasília, DF, Brazil; <sup>5</sup>Research scientist – Embrapa Agrienergy, Brasília, DF, Brazil

The metagenome can be described as the collective genome of the microbiota found in an environmental sample. From the metagenomics perspective, one can explore the biotechnological potential of uncultivated microorganisms by known techniques. This approach was applied to the ruminal microbiota of Moxotó goats native to the semi-arid region of caatinga in Brazil. In order to study this ecosystem, a small insert library was constructed using environmental DNA from microorganisms found associated with the solids of the rumen. Preparation of DNA by partial restriction digestion resulted in fragments as small as 100 bp to as large as 15 kb. DNA fragments with sizes ranging from 5-8 kb were excised from the gel and purified. This purified environmental DNA was ligated to an expression vector and transformed into *Escherichia coli*, where approximately 50,000 clones were obtained. Digestion of the plasmidial DNA from a sample of these clones confirmed the presence of inserts. Screenings can be performed on a metagenomic library aim in at the bioprospection for enzymes of biotechnological interest. One of the goals of this study was the ur uit of cellulases and hemicellulases, which could be used in the production of second generation ethanol. This library was subjected to screening tests for evaluation of beta-glucosidase activity. A total of 10, 39 clones were screened and three positives clones were confirmed after retransforming their plasmidial DNA. They are currently being sequenced and further characterized.