Área: **Microbiologia Geral e Meio Ambiente (Divisão L)**

CONSTRUCTION OF A SMALL-INSERT METAGENOMIC LIBRARY WITH AMAZON SOIL DNA.

Shelly Paluan (*UCB*); **Isabel Cunha** (*UCB*); **Thais Lemos** (*UCB*); **Rodrigo Santos** (*Embrapa*); **Cristina Machado** (*Embrapa*); **Ricardo Kruger** (*UnB*); **Eliane Noronha** (*UnB*); **Cristine Barreto** (*UCB*); **Betania Quirino** (*UCB*)

Resumo

The world's population is growing at a dramatic rate and the demand for fuel is greater than ever. This is rapidly destroying the planet and so it is utterly needed to find cheap and effective ways to produce biofuels that will not cause any more harm to the environment. Hence, microbial enzymes could be the solution to this dilemma. The Amazon is well known for its biodiversity of fauna and flora. Thus, it is expected that its microbial biodiversity is also immense. Since only about 1% of microbes can be cultured in a lab, another approach to investigating the microbiota of environmental samples, such as soil and water, is required. One of the most successful approaches currently used is that of metagenomics, in which the genetic structure of the whole microbial composition of a sample is assayed molecularly. The purpose of this study is to characterize the bacterial diversity of the Amazon soil utilizing the metagenome approach. For such, the total DNA from the soil was extracted. After extracting, cleaning and purifying the total DNA, the latter was quantified and then restriction digested with *Pst*I. The digestion process yielded varying sizes of DNA fragments; however, for the purpose of this study, only the 3-8kb insert size portion was excised from the gel and purified to construct an expression library of 50.000 clones. In order to confirm these clones indeed had the plasmid, the plasmidial DNA of a few randomly selected clones was extracted and restriction digested with *Pst*I. Using the linearized vector as a reference, these digested clones' plasmidial DNAs revealed a series of different plasmids with varying sizes of inserts when run on a TBE agarose gel. Currently, the library is being screened for enzymatic activities such as celullase, xylanase, lipase and amylase, which are the main enzymes that can be potentially used in the production of biofuels.

Acknowledgments:
CAPES, CNPq, Embrapa - Agroenergia, Brasília, DF, UCB and UnB.

Financial Support:
CNPq, CAPES, FAPDF and UCB.

Palavras-chave: Amazon soil, bacteria, bioprospection, metagenome