

Oral / Poster

1497-1 **Antibiotic resistance elements isolated from metagenomic libraries constructed with Cerrado soil samples**

Autores: Débora Farage Knupp dos Santos (UCB - Universidade Católica de Brasília) ; Alinne Pereira de Castro (UNB - Universidade de Brasília) ; Lucas S. Carvalho (UNB - Universidade de Brasília) ; Samuel Dias Araújo Junior (UCB - Universidade Católica de Brasília) ; Shelly de Fátima Paluan (UCB - Universidade Católica de Brasília) ; Betania Ferraz Quirino (EMBRAPA - Embrapa AgroenergiaUCB - Universidade Católica de Brasília) ; Ricardo Henrique Krüger (UNB - Universidade de Brasília)

Resumo

The collection of antibiotic resistance genes of an environment is denominated its resistome and the main reservoir of these genes is the soil, a biodiverse and unappreciated environment in this context. The consolidation of metagenomics allowed for the identification and description of new genes and functions of cultivable and not yet cultivable microorganisms. The description of the soil resistome and the elucidation of the antibiotic resistance mechanisms in this environment provide more data about the role of resistance genes – and of antibiotics – in nature. Small and large-insert metagenomic libraries were previously constructed with soil samples from Cerrado *stricto sensu*, a biome unique to Brazil. They were screened with the following β -lactamic antibiotics: amoxicillin, ampicillin, carbenicillin, cefalexin, cefamandole, cefoxitin, ceftazidime, penicillin G and piperacillin. In total, 62 resistant clones were isolated to five of the nine screened antibiotics. Of these, four clones from the small-insert library were selected for further tests. The selected clones were tested for multiresistance to the nine β -lactamic antibiotics and the minimum inhibitory concentration was determined in all antibiotics to which each clone was resistant. The inserts were sequenced and analyzed by the ORF Finder and Blastp programs. ORFs with functions related to antimicrobial resistance, bioremediation – roles in the degradation of aromatic compounds – and microbial signaling were revealed. They also identified hypothetical ORFs with unknown functions. In addition, two inserts exhibited ORFs similar to transposase enzymes, which correlate with the notion that resistance genes are indeed allocated in mobile elements. The identification of ORFs that are different from the “pattern” usually found in pathogenic isolates is compatible with the idea that environmental resistance genes possess diverse functions and that resistance per se is a secondary effect of these proteins. Such discoveries are promising as they can be raw data for assaying the role of some of these ORFs in microbial signaling and for their biotechnological applications in soil bioremediation. Furthermore, it can