Título: Metagenomic data of microbially-driven nitrogen processes in two biodiversity conservation parks in the Brazilian savannah biome

Autores: E. C.P. Catão^{1*}; F.A.C. Lopes¹, R. H. Santana², M. M. C. Bustamante³, R. H. Krüger¹

Instituição: ¹Department of Cellular Biology, University of Brasília, Brasília -DF, Brazil, ² Genomic Sciences and Biotechnology Program, Catholic University of Brasília, Brasilia – DF, Brazil, ³Department of Ecology, University of Brasília, Brasília - DF, Brazil

*elisaccp@gmail.com

The Brazilian savannah presents a range of vegetation in which soil characteristics influence the microbial community structure. These savannah soils are nitrogen-limited, the major nitrogen input being biological fixation and with high ammonia concentration and low levels of nitrate. Due to their different water, gravimetric carbon and nitrogen contents, we hypothesized that vegetation and soil physicochemical parameters would influence the relative rates of different microbially mediated nitrogen ecosystem processes. To test our hypothesis, we sampled eight areas with different vegetation cover and soil characteristics in triplicate in two conservation parks that are 500 km from each other and at different altitude. Metagenomes, sequenced using the 454pyrosequencing, were obtained from the 24 native soil samples and annotated in MG-RAST. STAMP analysis pointed significant differences between areas, but not between the two parks, in the compositions for nitrogen metabolism functional genes. This result indicates that the different vegetation cover in the areas sampled within each park masked the effects of altitude and location. Soils with high and low water content presented the greatest α -diversity, possibly through greater evenness of species to overcome the less favorable conditions. Genes associated with nitrogen fixation, nitrosative stress, and nitrate and nitrite reduction to ammonia differed significantly between the phytophysiognomies sampled. Of the nitrogen cycle, functional gene subsystems related to ammonia assimilation were the most abundant across all soils. Genes associated with denitrification were also annotated but functional genes associated with nitrification were not detected, possibly because of sequencing depth, since nitrifiers abundance is low in these savannah soils. The nitrogen cycle processes differ between the areas of Brazilian savannah, as the results suggest. Whether vegetation cover or other soil parameters are associated with these differences were also tested according to the neutral or niche theory.

Palavras-chave: Cerrado, microbial diversity, metagenome, nitrogen cycle, biome conservation

Agência de Fomento: Capes, CNPq