

IN SILICO ANALYSIS TO COMPARE THE 18S rRNA GENE LIBRARIES AND ESTIMATE SPECIES RICHENESS WITHIN BIOME CERRADO.

Castro, A. P.^{1,2} Papas, G.^{1,2}, Quirino, B. F.^{1,2} and Kruger, R. H.^{1,2}

¹Pós-Graduação em Ciências Genômica e Biotecnologia, Universidade Católica de Brasília, DF, Brasil ²Ciências Biológicas, Universidade Católica de Brasília, DF, Brasil; Corresponding Author: kruger@pos.ucb.br

The Brazilian cerrado is the main savanna in America. Changes in fungal diversity associated with agricultural management have important implications for fertility and stability soil. Although it is known that fungal communities are affected by agricultural practices, the effects of agricultural intensification on fungal biodiversity remain unclear. A molecular approach was chosen to characterize cerrado *stricto sensu*, Soybean plantation, riverbank forest and pasture soil fungal communities. To assess the fungal diversity, sequencing of approximately 200 clones of 18S rRNA from each library was performed. In *silico* analysis using the computer program DOTUR and ?LIBSHUFF estimate the diversity and differences between libraries. DOTUR analysis showed that there are approximately 75, 85, 85 and 75 unique OTUs to cerrado, pasture, riverbank forest and soybean plantation. Comparison between the four rarefaction curves with a similarity cutoff value as low as 1% reveals that the number of OTUs for soybean plantation decreased by 50%, riverbank forest by 45%, pasture by 40% and cerrado by 35% demonstrating that microbial community soil cerrado is more diversity than others. The computer program ?LIBSHUFF show that the significant P-values obtained in both cases were < 0.0001, demonstrating strong evidence that the four libraries analyzed are significantly different.

keywords: DOTUR , OTUs, ?LIBSHUFF, 18S rRNA.
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