TITLE: FLOODED FORESTS AND FLOWING WATERS: THE ROLE OF THE AMAZON RIVER TYPES IN SHAPING MICROBIAL DIVERSITIES IN FLOODPLAIN SOILS

AUTHORS: MONTEIRO, G. G. T. N. ¹; BARROS, D. J.²; THIERRY, A.P.¹; VENTURINI, A. M¹; NEU, V.³; TSAI, S. M.¹; NAVARRETE, A. A.⁴

INSTITUTION: 1. Cell and Molecular Biology Laboratory, Center for Nuclear Energy in Agriculture, University of São Paulo, Piracicaba, SP, Brazil; 2. Federal University of Tocantins; 3. Federal Rural University of the Amazon; 4. University Brazil – Graduate Program in Environmental Sciences.

ABSTRACT:

Floodplains and other wetlands occupy approximately 840,000 km² in the lowland Amazon basin and contain a complex network of interlinked lakes connected by many rivers and streams. These systems contain forests and agroecosystems that are seasonally flooded by the adjacent rivers and directly influenced by their chemical properties. Three main river categories occur in the Amazon basin, and were established based on their color (black, white, and clear). The different water types present different physicochemical parameters as a result of the geological differences of the basin. To better understand the influence of the water type on the floodplain soil biogeochemistry and microbial community composition, we analyzed the bacterial and archaeal microbial community of 36 soil samples from forests and agroforests from three floodplains seasonally inundated by black (Negro River), white (Tapajos River), and clear (Tocantins River) water rivers in both flooding and dry seasons. Total RNA was isolated using the RNeasy PowerSoil Total RNA Kit and complementary DNA (cDNA) was synthesized using a QuantiNova Reverse Transcription Kit. Amplicon libraries were prepared with specific archaeal and bacterial primers for the 16S rRNA genes. The final library was sequenced on a MiSeq Personal Sequencing System. All 16S rRNA gene sequence reads were processed and analyzed using QIIME2 v.3.5.3. with the SILVA database. Statistical analyses were carried out using R in the RStudio environment. Both bacterial and archaeal communities were strongly modulated by the flood pulse, but were also strongly influenced by the water type. In the anaerobic environment created by the flood pulse in the rainy season, the type of water was the main driver of changes in the chemical profile and microbial community composition highlighting the importance of the hydrological cycle and water chemistry in the modulation of the microbial communities of the Amazonian floodplains.

Keywords: Microbial ecology, Amazon floodplains, Biogeochemistry, rRNA sequencing

Acknowledgments: We thank Marília de Souza Bento and Leonardo Machado Pitombo for their overall support, Ivanildo L. S. Gaia, Glauber Altrão Carvalho, and Domickson Costa for their support during fieldwork. We also thank the Fundação de Amparo à Pesquisa do Estado de São Paulo, Brasil (FAPESP) for the grant that made this study possible (2016/16687-3).