XIII SIMPÓSIO BRASILEIRO DE MICROBIOLOGIA APLICADA

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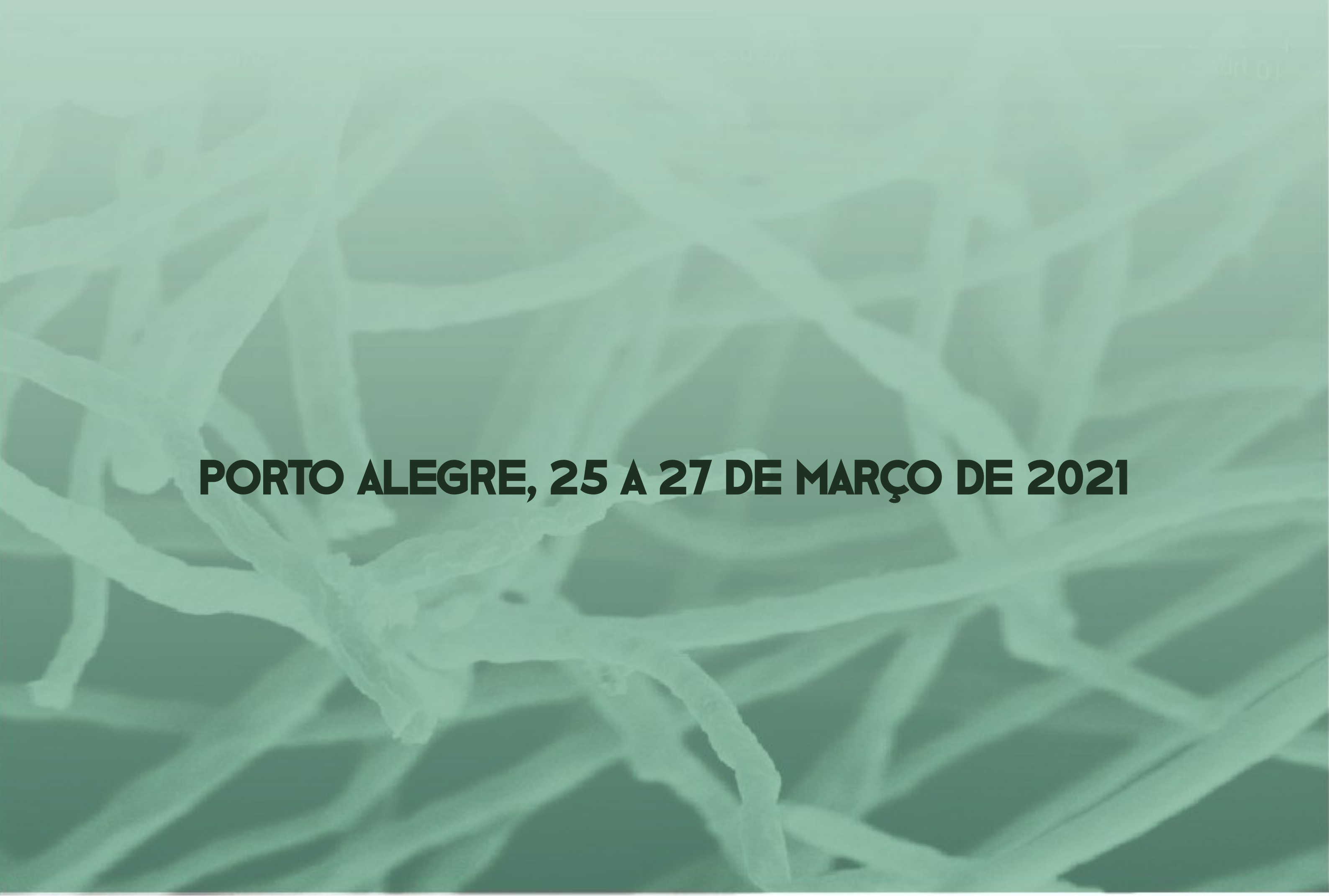

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PREDICTION OF METABOLIC PATHWAYS FROM FECAL MICROBIOTA OF WILD BLACK CAPUCHIN MONKEYS (*Sapajus nigritus*) FROM ATLANTIC FOREST BIOME IN SOUTHERN BRAZIL

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Intestinal microbiota diversity and composition can potentially influences the host nutrition, health, and behavior. Black capuchin monkeys (*Sapajus nigritus*) are an endangered endemic species to the Atlantic Forest Biome. Their population is reducing by habitat degradation, due to urban areas invasiveness, loss, fragmentation and disconnection of the habitat, increase in roads and energy matrix, hunting and hybridization. Furthermore, many nonhuman primates live in proximity to humans, and primate populations are influenced by human interaction, for example, captured and feeding. These interactions have important consequences to the primate since bringing them into contact with a wide diversity of microorganisms that might affect their health and species conservation. Computational methods, such as the use of metabolic network reconstructions, may provide a real situation of microbiota’s impact on host health and physiology. We studied the gut microbiota metabolic pathways of ten wild black capuchin monkeys using high-throughput amplicon sequencing of *16S rRNA* (V4 region) performed with Ion Torrent Personal Genome Machine (PGM). A predictive functional profile of the fecal bacterial community was conducted using PICRUSt2 software (v2.3.0). Briefly, the OTU sequences were executed using the script picrust2_pipeline.py. This script run each of the four key steps: sequence placement, hidden-state prediction of genomes, metagenome prediction, pathway-level predictions. The functions predicted were categorized using the mappings table from the KEGG database. We correlated the microbial functional features with habitat, proximity to humans, and diet of the wild black capuchin monkeys. A total of 42 level three KEGG pathways were identified using PICRUSt2 software program. Microorganisms associated to infectious diseases transmission from humans and domestics animals were related to anthropogenic human activities. Xenobiotic biodegradation, secondary metabolites and microbial resistance could be related to food web interactions, environmental pollutants, and/or antibiotic resistome. This knowledge may help better understand wild species' ecology and biology and help prevent future zoonoses (and can avert global pandemics), and contribute to the animal, environmental, and human health. To date, however, little is known on the composition and biosynthesis of gut microorganisms, which limits our understanding of the functionality of microbiomes.

Keyword: *Sapajus nigritus*; metabolic pathways; food plasticity; gut microrganisms

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