

Titulo: METAGENOMICS ANALYSIS AND STUDY OF MICROBIOME SPECIES OF NATURAL BATS BORN IN PARÁ.

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Resumo:

Brazil is recognized as one of the richest countries in biodiversity, sheltering between 15 and 20% of the total number of species in the world. The country is home to about 15% of the planet bats, and much of this wealth is present in the Amazon biome, where Pará is the state with the highest number of recorded species (120). Most multi-cellular organisms have a closely associated microbial community that provides a variety of functions, from digestion to defense against pathogens. Plants and animals, including humans, can be considered superorganisms composed of many species of bacteria, archaea, and viruses. The metagenomics offers the opportunity to understand its physiological role and evolutionary significance. The goal of the project is to determine the bacterial diversity of different species of bats collected in the state. The study in question was conducted with samples pools (salivary gland, brain and intestine) collected bat species *Desmodus rotundus* and *Phyllostomus hastatus* captured in the city of Viseu, which is in the northeast of the state, in the localities Fazenda salina and Fernandez Belo. The taxonomic diversity and abundance of bacterial microbiota in each species of bat has been obtained through the use of data generated by next generation sequencing (NGS) platform Ion Torrent (Life Technologies) for each pool of samples. Data analysis was performed employing the first SORTMERA v.2.0 program aimed at filtering the data 16S, followed by *De Novo* assembly method using the MIRA v.4.02 and MEGAN as the graphic program for generating the bacterial diversity. As a result we obtained data of the bat *Phyllostomus hastatus* taking as given gross 987,600 readings, after SORTMERA against the database 16s SILVA remaining 43,463 filtered readings. Mounting the *De Novo* method used 98.61% of readings and generated 21 contigs, which were faced against the BLAST database (blastn), resulting in 5 contigs with identity for bacterial genomes, identified four species of bacteria: *Leadbetterella byssophila*, *Chryseobacterium sp*, *Acinetobacter sp* and *Flavobacterium*. And the species *Desmodus rotundus* raw data readings 1409806, after SORTMERA against the database 16s remained 61634 SILVA filtered readings. Mounting the new *De Novo* method used 98.13% of readings and generated 14 contigs, which were faced against the BLAST database (blastn), resulting in one contig with identity for bacterial genomes, we identified one species: *Clostridium histolyticum*.

Palavras-chave: Bats, Metagenomics, 16s, Biological diversity

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