ANALYSIS OF THE MICROBIOME OF ORNATE BOX TURTLES AND THEIR ENVIRONMENT

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The ornate box turtle (*Terrapene ornata*) is a species of North American turtle known for its distinctive and intricate shell patterns, which vary among individuals. Due to their asocial and isolated lifestyle as well as the lack of non-gastrointestinal microbiome studies of reptiles, we are very curious where their nasal microbiomes' originate. The microbiome of an organism is classified as the assortment of microorganisms found on or within an organism's cells and/or biofluid. Shotgun metagenomic sequencing data from ten turtle nasal lavage samples and four samples of the air surrounding the turtles' burrows were run through a digital workflow in Kbase. We used the data generated by Kaiju, an application in Kbase used for sample comparison to graphically determine the correlation between microbiomes of different turtle samples and between the turtle samples and the aerobiome. Using R, we produced alpha diversity visualizations of Shannon and Simpson diversity indexes. Additionally, we created beta diversity metrics including Bray-Curtis dissimilarity-based dendrograms and PCoA charts to compare diversity between samples, all with the end goal of answering if the ornate box turtle possess a common nasal microbiome and whether or not the aerobiome surrounding these organisms play a factor in the microbiota present.