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## **Guano among bat species from two regions shows influence of geography and diet on bacterial community**

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Studies of bat guano have shown that the diversity and structure of associated microbial communities can be related to factors such as host phylogeny, life history and reproductive stage, geography, and diet. Many insectivorous bat species in the southeastern U.S. have generalist diets that may shift seasonally to take advantage of abundant prey species or maximize caloric intake. Seasonal shifts in prey availability or consumption should be reflected in a guano microbiome change. We also expected to detect distinct guano microbiomes within species. Within species, distinct microbial communities related to geography, and finally life history and reproductive stage. We compared the bacterial communities in bat guano collected directly from five species and two regions of the USA. Guano was collected opportunistically during netting events from May to October from the Appalachian foothills (Rome, GA), and the coastal plain (Bluffton, SC). DNA was extracted from 160 samples. DNA elutions were pooled for samples based on collection time and species ID. We sequenced the 16S rDNA barcode regions (V3, V4). Qiime2 was used to filter reads and assign taxonomy (green genes reference classifier). The bacterial community detected in the Rome samples showed a seasonal shift related to diet shift in big brown bat and red bat samples. Samples from Rome had greater bacterial diversity among species; whereas, samples from Palmetto Bluff were more similar to each other. Overall geography and diet were important factors related to the diversity and structure of the guano bacterial community.