Effect of anthropogenic presence on the fecal bacterial microbiome of cave bats (*Miniopterus schreibersii*)

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1 OBJECTIVES

1. Determine whether human presence in caves inhabited by the cave bat (Miniopterus schreibersii) can influence the composition of its fecal bacterial microbiome.
2. Determine the differences in bacterial type and abundance, based on the sampling areas.

2 ECOSYSTEM SERVICES

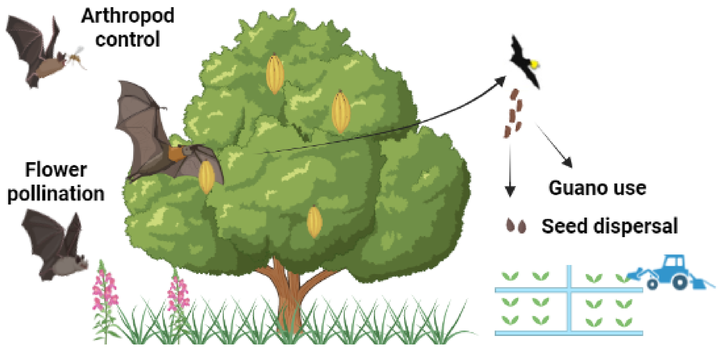


Figure 1: *Representation of bat ecosystem services*

3 ANTHROPOGENIC DISRUPTION

Over the past 20 years, there has been a progressive and widespread decline in biodiversity, up to a 25%.

Habitat degradation, climate change, and human activities are causing an impact on bat populations. Monitoring and addressing this anthropogenic disruption is crucial for preserving bat species and overall biodiversity.

4 MICROBIOME AS A HEALTH INDICATOR

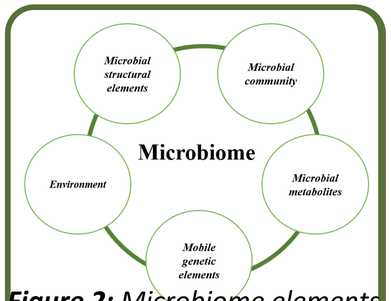
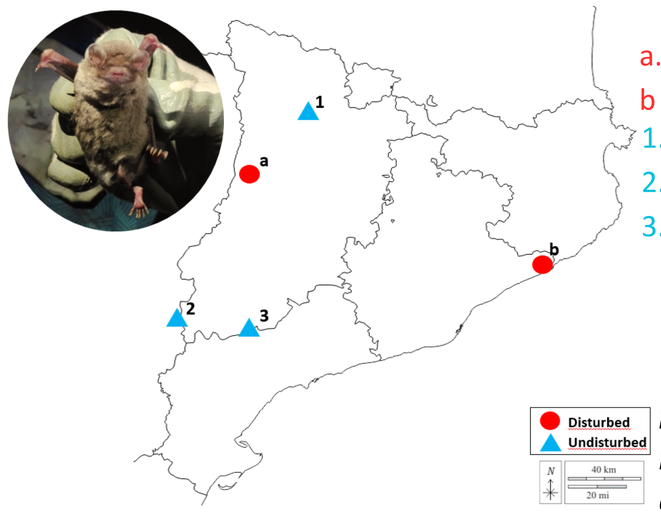


Figure 2: *Microbiome elements*

Anthropogenic pressure influences acute or cronic stress in animals.

The intestinal microbiome can be related to stress response through the gut-brain axis.

5 STUDY AREA



a. Colomera cave
b Malgrat de Mar mines
1. Savarneda cave
2. Mequinenza mines
3. Taverna cave

Figure 2: *Geographical location of the study areas*

6 16S SEQUENCING

1. Fecal DNA extraction
2. Selective amplification of 16S rRNA (PCR)
3. Sequencing, bioinformatics

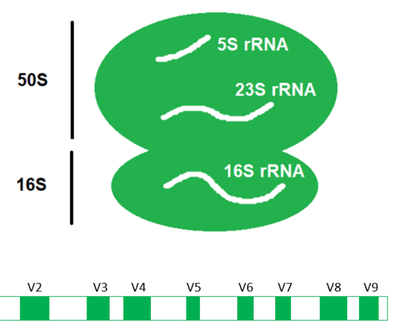


Figure 3: *Ribosomal complex and 16S gene*

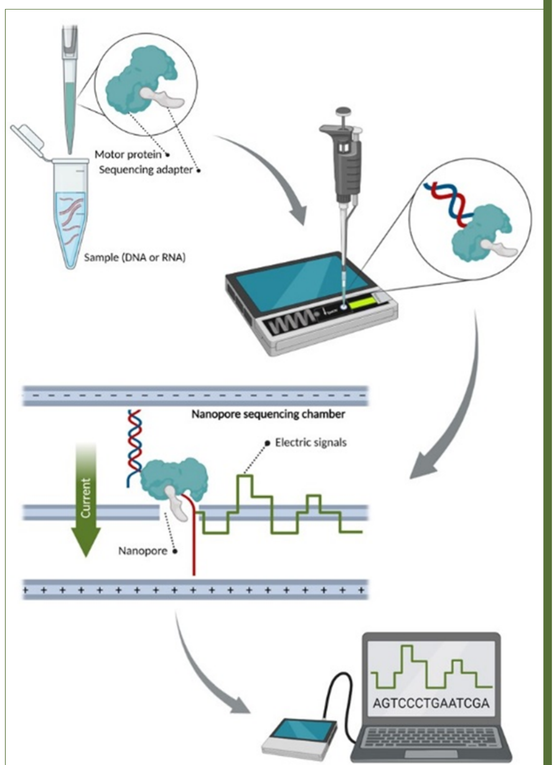


Figure 4: *Nanopore technology and data processing (Lobato-Bailón, L., 2023)*

7 RESULTS

Taxonomy description

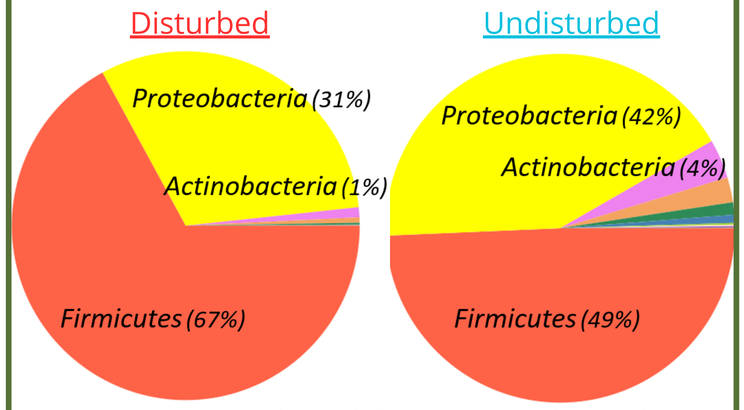


Figure 5: *Pie chart of the taxonomy observed*

- Disturbed: *Enterococcus > Escherichia Shigella > Bacillus > Candidatus Arthromitus > Klebsiella > Lactococcus*
- Undisturbed: *Bacillus > Escherichia Shigella > Streptococcus > Rickettsiella > Enterococcus > Lactococcus > Staphylococcus*

Alpha diversity

Beta diversity

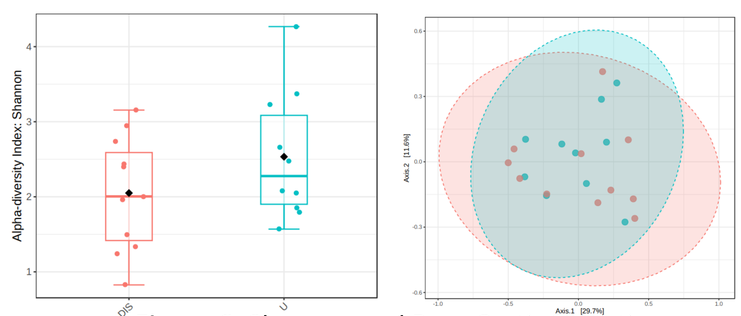


Figure 6: *Shannon and Bray-Curtis Statistics*

8 CONCLUSIONS

Bat microbiome is composed of a wide variety of microorganisms interacting with the host and its environment.

No significant differences have been observed between scenarios, although diverse bacterial composition has been described.

Monitoring bat populations is necessary to contribute on wildlife conservation and public health.

BIBLIOGRAPHY

Lobato-Bailón, et al. (2023). The fecal bacterial microbiome of the Kuhl's pipistrelle bat (Pipistrellus kuhlii) reflects landscape anthropogenic pressure. Animal Microbiome, 5, 7.