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COMPARATIVE GENOMICS

Blood, guts and vampire bats

The genome and gut microbiome of vampire bats are in a close evolutionary relationship as evidenced by adaptations to a blood-based diet, reports a study published in *Nature Ecology & Evolution*.

The common vampire bat, *Desmodus rotundus*, is one of only three obligate sanguivorous (blood-feeding) mammalian species. A blood-based diet is uncommon as it provides high protein levels (~93%), which can have a negative impact on kidney function, and extremely low levels of vitamins and carbohydrates. Blood-borne pathogens also pose a threat.

Taking a ‘hologenomic’ approach — that is, looking at the genome of not only the host but also its associated microbiota — the researchers compared the vampire bat to three other bat species whose diets consist of either insects, fruit or meat, such as small birds or reptiles. While the taxonomic composition of the vampire bat gut microbiota was similar to that of insect- or meat-eating bats, the functional profile differed strikingly from all comparator species, and also showed the least intraspecies variation between samples.

The comparative genomic and metagenomic analyses revealed a number of adaptations to sanguivory in the vampire bat genome. Importantly, the team also identified several adaptational contributions to sanguivory within a hologenomic context. For example, the vampire bat genome showed signs of positive selection of the *LAMTOR5* gene, which has a role in the response to nutrient starvation. The microbiome also showed an enrichment in genes involved in the response to low nutrient availability. These findings suggest that both the metabolism of vampire bats and its microbiota have adapted to a low-nutrient diet.

The authors also discovered hologenomic solutions to non-nutritional challenges of a blood-based diet. For example, the antimicrobial gene *RNASE7* exhibited signs of positive selection and contained amino acid substitutions that could increase the antibacterial function of its protein product. Moreover, the gut microbiome comprised a large abundance of bacteria previously reported to produce antiviral compounds.

This study highlights the value of looking at an organism and its associated microbiota as a whole, as both host genome and microbiome experience selective pressures.

Linda Koch

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ORIGINAL ARTICLE Zepeda Mendoza, M. L. *et al.* Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. *Nat. Ecol. Evol.* <https://doi.org/10.1038/s41559-018-0476-8> (2018)