Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat - DTU Orbit (03/12/2018)

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Adaptation to specialized diets often requires modifications at both genomic and microbiome levels. We applied a hologenomic approach to the common vampire bat (*Desmodus rotundus*), one of the only three obligate blood-feeding (sanguivorous) mammals, to study the evolution of its complex dietary adaptation. Specifically, we assembled its high-quality reference genome (scaffold N50 = 26.9 Mb, contig N50 = 36.6 kb) and gut metagenome, and compared them against those of insectivorous, frugivorous and carnivorous bats. Our analyses showed a particular common vampire bat genomic landscape regarding integrated viral elements, a dietary and phylogenetic influence on gut microbiome taxonomic and functional profiles, and that both genetic elements harbour key traits related to the nutritional (for example, vitamin and lipid shortage) and non-nutritional (for example, nitrogen waste and osmotic homeostasis) challenges of sanguivory. These findings highlight the value of a holistic study of both the host and its microbiota when attempting to decipher adaptations underlying radical dietary lifestyles.

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