Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat - DTU Orbit (14/11/2018)

Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat

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.

General information
State: Published
Organisations: Department of Bio and Health Informatics, University of Copenhagen, Chinese Academy of Sciences, Leibniz Institute for Zoo and Wildlife Research, University of Oxford, University of Glasgow, Stanford University, Animal-INIFAP, BGI-Shenzhen, San Diego Zoo’s Institute for Conservation Research, Universidad Nacional Autonoma de Mexico, National Autonomous University of Mexico, Copenhagen Zoo, Curtin University of Technology, Norwegian University of Science and Technology
Pages: 659-668
Publication date: 2018
Peer-reviewed: Yes

Publication information
Journal: Nature Ecology & Evolution
Volume: 2
ISSN (Print): 2397-334X
Ratings:
Scopus rating (2017): SJR 0.123 SNIP 0
Web of Science (2017): Impact factor
Original language: English
Electronic versions:
Hologenomic_adaptations_underlying_t.pdf
DOIs: 10.1038/s41559-018-0476-8

Bibliographical note
Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. Common license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this license, visit http://creativecommons.org/licenses/by/4.0/.
Source: FindIt
Source-ID: 2396551089
Research output: Research - peer-review ; Journal article – Annual report year: 2018