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Job Announcement ref. #12-23005

Postdoc Position in Comparative Genomics in Fruit Bats

The Hiller Lab at the LOEWE Center for Translational Biodiversity Genomics (TBG) in Frankfurt, Germany is looking for a Postdoc to investigate the genomic underpinnings of convergent dietary adaptations in bats.

The Project

While most bats feed on insects, several independent lineages adapted to fruit- or nectar-based diets that are rich in sugars. In contrast to humans, where a sugar rich diet is a major risk factor for metabolic diseases, these bats have metabolic and physiological adaptations to such highly-specialized diets. The postdoc will capitalize on more than 15 already-existing new bat genomes sequenced in the lab with HiFi and HiC, comprehensive comparative RNA-seq datasets and our powerful genomic methods repertoire (e.g. TOGA [1]) to comprehensively discover the genomic basis of adaptations to sugar-rich diets in bats (see [2] for a similar example in hummingbirds). The project aims at providing novel insights into fundamental questions concerning (i) the contribution of gene-sequence vs. gene-expression changes and (ii) the importance of convergent vs. lineage-specific molecular changes for phenotypic convergence.

Our lab

The mission of our group is to understand how nature's fascinating phenotypic diversity has evolved and how it is encoded in the genome. Work in the lab includes sequencing and assembly of reference-quality genomes, genome alignment and gene annotation, development and application of comparative genomic methods to discover differences in genes and gene expression, and the use of statistical approaches to link phenotypic to genomic changes [1-10].

Our lab is part of TBG (https://tbg.senckenberg.de/) and the Senckenberg Society for Nature Research (www.senckenberg.de), and is based near the city center of Frankfurt am Main, Germany. TBG provides access to cutting-edge computational (large HPC clusters, genome browser) and lab infrastructure to sequence genomes. English is the working language in our lab. Senckenberg and TBG provide flexible working hours, an annual special payment, a company pension scheme, the Senckenberg badge for free entry in museums, the zoo, botanical garden and Palmengarten, and a leave of 30 days per year. Frankfurt is a vibrant and highly-international city at the heart of Europe that combines a skyscraper skyline with ample park and green areas. The Economist 2022 index ranked Frankfurt among the top 10 most livable cities worldwide.

Your profile

- PhD degree in bioinformatics/computational biology, genomics or a related area
- Solid programming skills in a Linux environment and experience with shell scripting and Unix tools are required
- Previous experience in comparative genomics is an advantage

Place of employment:	**Frankfurt am Main**
Working hours:	**full time (40 hours/week) / part-time options are available**
Type of contract:	**initially limited for 2 years, but funding is available for an extension**
Salary and benefits:	**according to the collective agreement of the State of Hesse (pay grade E13)**

The start date is flexible but should ideally be in the beginning of 2024.

Senckenberg is committed to diversity. We benefit from the different expertise, perspectives and personalities of our staff and welcome every application from qualified candidates, irrespective of age, gender, ethnic or cultural origin, religion and ideology, sexual orientation and identity or disability. Applicants with disabilities ("Schwerbehinderung") will be given preferential consideration in case of equal suitability. Senckenberg actively supports the compatibility of work and family and places great emphasis on an equal and inclusive work culture.

How to apply

Please send us your application documents containing

- a CV with publication list and contact information for at least two references
- a summary of previous research experience (max 1 page)
- and copies of certificates, transcripts and grades)

in electronic form (as a coherent PDF file) by **October 8th 2023** to recruiting@senckenberg.de and Prof. Dr. Michael Hiller michael.hiller@senckenberg.de **quoting the reference number #12-23005**, or apply through the online application form on our homepage.

Senckenberg Gesellschaft für Naturforschung
Senckenberganlage 25
60325 Frankfurt a.M.
E-Mail: recruiting@senckenberg.de

For more information please contact Prof. Dr. Michael Hiller, michael.hiller@senckenberg.de or visit the lab webpage https://tbg.senckenberg.de/hillerlab/.

Recent publications

[1] Kirilenko BM, *et al.* Integrating gene annotation with orthology inference at scale. Science, 380(6643), 2023

[2] Osipova E, *et al.* Loss of a gluconeogenic muscle enzyme contributed to adaptive metabolic traits in hummingbirds. Science, 379(6628), 185-190, 2023

[3] Blumer *et al.* Gene losses in the common vampire bat illuminate molecular adaptations to blood feeding. Science Advances, 8(12), 2022

[4] Roscito *et al.* Convergent and lineage-specific genomic differences in limb regulatory elements in limbless reptile lineages. Cell Reports, 38(3):110280, 2022

[5] Jebb *et al.* Six reference-quality genomes reveal evolution of bat adaptations. Nature, 583, 578–584, 2020

[6] Huelsmann *et al.* Genes lost during the transition from land to water in cetaceans highlight genomic changes associated with aquatic adaptations. Science Advances, 5(9), 2019

[7] Hecker *et al.* Convergent gene losses illuminate metabolic and physiological changes in herbivores and carnivores. PNAS, 116(8), 3036-3041, 2019

[8] Roscito *et al.* Phenotype loss is associated with widespread divergence of the gene regulatory landscape in evolution. Nature Communications, 9:4737, 2018

[9] Sharma *et al.* A genomics approach reveals insights into the importance of gene losses for mammalian adaptations. Nature Communications, 9(1), 1215, 2018

[10] Nowoshilow *et al.* The axolotl genome and the evolution of key tissue formation regulators. Nature, 554(7690), 50-55, 2018