



NEWSLETTER

WHO ARE WE?

Bat1K is an initiative to sequence the genomes of all of the approximately 1300 living species of bats. This, however, is not an easy task. This project is only possible by the mobilisation of bat researchers, volunteers, students, and bat lovers throughout the globe.

Hello and welcome to the first quarterly Bat1K newsletter. Our newsletters will be a place for our members to receive updates on our progress, find out more about any of our recent publications,

and to find out more about how you can contribute to the Bat1K movement and help us to uncover the secrets of the unique adaptations hidden in the bat genome.

BAT1K WHITE PAPER

The Bat1K White paper came out in late February with the aim to provide information about the Bat1K initiative; the goals and steps being taken to achieve them, encouraging participation from the scientific community and outlining the major areas of research that may benefit from our work.

We would like to take the opportunity to thank the Bat1K community for their commitments, and all those who have been circulating our paper on social media.

Annual Review of Animal Biosciences

Bat Biology, Genomes, and the Bat1K Project: To Generate Chromosome-Level Genomes for All Living Bat Species

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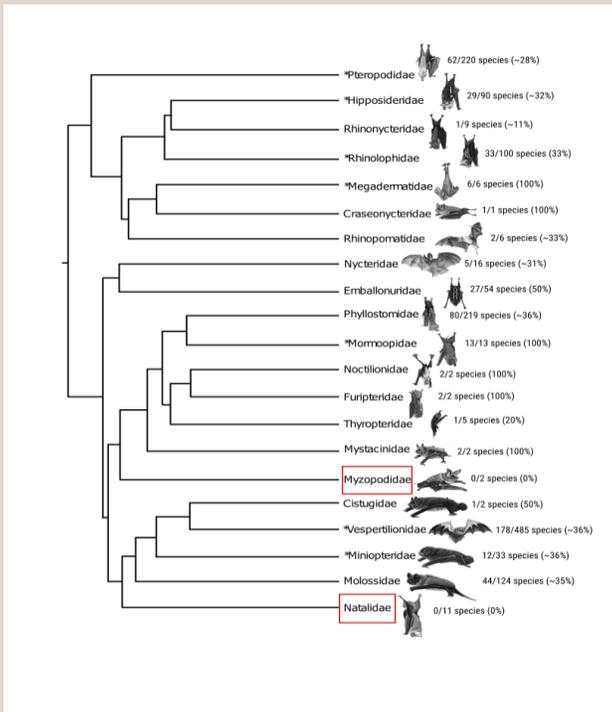
AVAILABLE AT: <https://doi.org/10.1146/annurev-animal-022516-022811>

Featured Paper: *Growing old but staying young: The role of telomeres in bats' exceptional longevity*



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Scientists have uncovered part of the molecular mechanism that gives a long-lived bat species its unprecedented lifespan. Work published in *Science Advances* led by Bat1k member Dr Nicole Foley and Bat1k Director Professor Emma Teeling point to telomeres, protective structures at the end of chromosomes, as playing a key role. While telomeres were found to shorten with age in two of the bat species studies, there was no detection in the longest lived species (*Myotis*; pictured left) that telomeres shortened with age. This suggests that long-lived bats have evolved better mechanisms to prevent and repair age induced cellular damage. Paper available at: <http://advances.sciencemag.org/content/4/2/eaa0926>



WHERE ARE WE NOW?

Since its foundation, Bat1K has received contributions from around the globe, with over 160 members including computational scientists, conservationists, and organizations pledging valuable resources such as bat tissues, bioinformatic expertise, and time. At current, Bat1K is on phase 1. As to date, we are in absence of a representative from both the Natalidae and Myzopodidae families (see left).

In order for stage 1 to be completed and for us to progress to stage 2, we must find representatives from the two missing families. We ask that anyone who has contacts working with these families of bats in these regions would please inform them of Bat1K and that we are in need of their contributions, be that living individuals, flash frozen tissue, or anything that is available to them.

STEERING COMMITTEE

The Bat1k directors would like to warmly welcome two new additions to the Bat1k steering committee; Dr Sébastien Puechmaille and Dr Burton Lim. Dr Puechmaille will act as a network liaison, advising and helping interactions within the Bat1k community. Dr Lim will aid with sample collection, ensuring Bat1k keeps with international/national guidelines and to aid with the progression of the Bat1k phases. Further information regarding members of our steering committee can be found at <http://bat1k.com/members/>.



Dr Sébastien Puechmaille



Dr Burton Lim

PILOT STUDY

A pilot study to test the methods proposed in the Bat1k paper was initiated by the Bat1k directors with six bat species were chosen based on their maximum lifespan (four species shown left). Sequencing and assembly is underway in Dresden, Germany under Dr Gene Myers (Co-director) and Dr Michael Hiller (Steering committee). Sequencing of tissues currently consists of PacBio, BioNano, Hi-C and 10X Genomics technologies. Funding to complete Phase 1 (a representative from each family) has been submitted with the goal to initiate the sequencing of 21 bat genomes covering all bat families.

Clockwise from top left:

Rhinolophus ferrumequinum
©Gareth Jones
MLS* 30.5 years

Myotis myotis
©Emma Teeling
MLS 37.1 years

Rousettus aegyptiacus
©Brock Fenton
MLS 22.9 years

Pipistrellus kuhlii
©Andrea Locatelli
MLS 8 years
*MLS: Maximum Lifespan

