

# Madeleine Becker

BeckerM@si.edu | @mabscientist

## EDUCATION

**George Mason University & Smithsonian Conservation Biology Institute** 2020-2025  
Ph.D. Student in Biosciences: Biocomplexity and Evolutionary Biology  
Co-advisors: Jesús Maldonado, Cody Edwards

**University of Southern California** 2015-2019  
B.S. Biological Sciences, minor in Classics, *cum laude*

## SCHOLARSHIPS AND AWARDS

**Smithsonian-Mason School of Conservation Fellowship** 2020-2025  
Full-tuition scholarship and stipend

**USC Biological Sciences SCynergy Award** 2020  
Award for most outstanding graduating senior pursuing biological sciences

**USC Women in Science and Engineering Fellow** 2019  
Research grant

**Wattis Dumke Undergraduate Fellowship** 2018  
USC biological sciences department research grant

**USC Dornsife Dean's List** 2016-2019  
Dornsife College award for maintaining a GPA of 3.5 or above

**USC Trustee Scholarship** 2015-2019  
Full-tuition merit scholarship

**USC University Scholarship** 2015-2019  
Merit scholarship

## RESEARCH EXPERIENCE

**American Society of Mammalogists** 2020-2021  
Mammal Diversity Database Student Research Assistant

- Update, validate, and organize mammalian taxonomy entries, focusing on synonymies.
- Code in R and Excel to automate the collection and formatting of taxonomic data.

**University of Southern California** 2017-2019  
Undergraduate researcher; Principal Investigator: Suzanne Edmands

- Analyzed fox mitochondrial genomes to infer haplotype networks and loss of diversity.
- Processed and denoised scat bacterial reads for quality, uniqueness; assigned taxonomy.
- Extracted bacterial DNA from fox scat samples, quantified DNA concentration, performed PCR, ran gel electrophoreses, used Ampure bead chromatography.
- Ran quality checks, trimmed, mapped reads from 96 fox individuals.

**Los Angeles County Natural History Museum** 2019  
Mammalogy volunteer; Supervisor: Kayce Bell

- Paired, assembled, aligned and generated phylogenetic trees for 69 chipmunk (*Tamias*) mitochondrial genomes.

# Madeleine Becker

BeckerM@si.edu | @mabscientist

## National Museum of Natural History, Smithsonian Institution

2019

NSF REU National History Research Experience intern; Mentor: Michael McGowen

- Assembled 87 mitochondrial genomes and aligned, annotated, and partitioned ~400 more from GenBank to reconstruct phylogenetic relationships among delphinine dolphins, with emphasis on the position of *Delphinus delphis* morphotypes.

## University of Southern California

2015-2016

Undergraduate research assistant; Principal Investigator: Joseph Landolph

- Performed cytotoxicity assays determining concentrations at which cysteine and chromium (VI) are most toxic to mouse embryo cells, and which induce transformations.

## PUBLICATIONS

Adams NE, **Becker MA**, and Edmands S. (2021) Geographic source largely shapes *Urocyon* scat bacterial communities, but sex, weight, age, and season also contribute. (In prep).

Adams NE, **Becker MA**, and Edmands S. (2021) Host genetic diversity influences bacterial composition in the island fox, *Urocyon littoralis*. (In prep).

## CONFERENCE PRESENTATIONS

**Becker MA**, Murphy K, Charles Potter C, Ndong I, Keith-Diagne L, McGowen M. Global Phylogeography of Delphinine Dolphins Using Mitogenomics. Poster presentation delivered at The Ocean Sciences Meeting, San Diego, CA, February 2020.

**Becker MA**, Adams NE, Edmands S. Fecal microbial communities differ by intrinsic and extrinsic variables in *Urocyon littoralis*. Poster presentation delivered at the 99<sup>th</sup> Annual Meeting of the American Society of Mammalogists, Washington, D.C., June 2019.

**Becker MA**, Adams NE, Edmands S. Environmental Impact on Gut Microbiome Diversity in *Urocyon littoralis*. Poster presentation delivered at the 20<sup>th</sup> University of Southern California Undergraduate Symposium for Scholarly and Creative Work, Los Angeles, CA, April 2018.

## WORKSHOPS AND PROGRAMS ATTENDED

### University of Washington Summer Institute of Statistical Genetics

NSF scholarship awardee and institute participant (Online) Seattle, WA, July 2020

### Association for the Sciences of Limnology and Oceanography Multicultural Program

Travel grant awardee and program participant San Diego, CA, February 2020

### A Roadmap to the De Novo Assembly of Mammalian Genomes

Workshop volunteer Washington, D.C., June 2019

### Genome Annotation

Workshop participant Washington, D.C., June 2019

# Madeleine Becker

BeckerM@si.edu | @mabscientist

## ANIMAL EXPERIENCE

**Los Angeles County Natural History Museum** 2018-2019

Mammalogy volunteer; Supervisor: Jim Dines

- Took tissue samples and prepared pelts, skeletons, and study skins for scientific use.

**Worldwide Opportunities for Organic Farming (United Kingdom & Ireland) 2018**

Farm volunteer

- Fed, transported, herded, monitored, and treated cows, sheep, pigs, and chickens.
- Assisted in artificially inseminating over 100 cows, shearing 300 sheep.

**Tony La Russa's Animal Rescue Foundation** 2017

Animal care intern

- Monitored, fed, socialized, exercised, administered medication to shelter dogs and cats.
- Reported animal symptoms, took fecal samples, and weighed animals in veterinary clinic.

**Lindsay Wildlife Rehabilitation Hospital** 2017

Extended volunteer

- Hand-fed and administered medications to numerous native species of juvenile birds.

## TEACHING/MENTORING EXPERIENCE

**USC Neighborhood Academic Initiative** 2019

9<sup>th</sup> grade Latin teacher

- Created lesson plans, course material with the Cambridge Latin course to teach a class of 18, first-time Latin students on a bi-weekly basis.

**USC Women and Youth Supporting Each Other** 2017-2019

Administrative Director, Mentor

- Mentored middle school girls, lead discussions on relevant topics such as personal identity, body positivity, social media, bullying, race, gender, and sex education.
- Organized, managed mentor attendance and performance; wrote weekly newsletter.

## SKILLS

### Bioinformatics

Languages: Bash for Unix, Java, MATLAB, Python, R, SQLite

Genomic Programs: ANGSD, BEAST, BEAUi, BWA, Clustal Omega, DADA2, FASTQC,

FreeBayes, Geneious, MAFFT, Miniconda, mothur, NovoPlasty, Partition Finder, Picard

Tools, PopART, Qiime1, Qiime 2, SAMtools, Trimmomatic

Phylogenetic programs: FigTree, MrBayes, PAUP, RAxML

### Laboratory

DNA processing (extraction, amplification, quantification, cleaning, library prep), gel electrophoresis

### Animals

Animal handling (small/large, mammalian/avian, wild/pet/livestock), specimen preparation (mammal skinning/skeleton cleaning), rodent trapping, animal behavior observation