# Kathleen Morrill-Pirovich, PhD

Computational biologist with a keen focus on comparative and evolutionary genomics, rooted in my dissertation on the genetic determinants of canine health and behavioral disorders that have parallels to human conditions. My rigorous approach to project management, enriched by cloud-based computational workflows, is evident from my pivotal roles in Darwin's Ark, a community science project on companion dogs, and the Dog Aging Project, a longitudinal study of healthy aging. These endeavors not only highlight my expertise in managing and analyzing expansive, multi-omic biobanks but also underscore my dedication to public-engaging scientific initiatives. As a senior scientist in genome analysis at Colossal Biosciences, I spearheaded approaches to modeling and predicting effects of non-coding, regulatory DNA sequence variants from data-constrained species, including ancient DNA from extinct taxa.

## Education

*Bates College*, Lewiston, ME, 2011 – 2015
Bachelor of Science in Biological Chemistry, minor in Mathematics, with distinction

*University of Massachusetts Chan Medical School*, Worcester, MA, 2016 – 2023
PhD in Biomedical Sciences at the Morningside Graduate School of Biomedical Science
Department of Bioinformatics and Integrative Biology | Program in Neuroscience

## Experience

### Research Roles

Senior Scientist
*Colossal Biosciences*, Dallas, TX
Computational Sciences Team
*kathleen@colossal.com*
2023 – present
The genetic basis for key phenotypes of long-extinct species is elusive. My role as senior scientist in genome analysis at Colossal Biosciences is to provide expertise on phenotypes and enable genotype-to-phenotype inference in target species through cross-species comparative genomics and transfer learning approaches.

Doctoral Student
*University of Massachusetts Chan Medical School*, Worcester, MA
Department of Bioinformatics and Integrative Biology
Research Advisor: Elinor Karlsson (*elinor@broadinstitute.org*)
2017 – 2023
The behavior of domestic dogs can be utilized as a natural neurogenetic system for human neuropsychiatric conditions. Dogs exhibit similar behavioral disorders of similar clinical presentation and therapeutic response, and behavioral selection in canine lineages has increased the prevalence of high effect, behavior-associated variants amenable to genomic investigations. My dissertation research focuses on the behavioral genetics of dogs and its relevance and utility towards human conditions.

Graduate Intern
*Cold Spring Harbor Laboratory*, Cold Spring Harbor, NY
Neuroscience Program
Research Advisor: Josh Dubnau (*joshua.dubnau@stonybrook.edu*)
2015 – 2016
The transposon storm hypothesis postulates that unregulated retrotransposon activity contributes to accumulation of DNA damage. By modeling the human neurodegenerative disease of amyotrophic lateral sclerosis (ALS) in *Drosophila*, we explored mechanisms behind impairment of siRNA silencing, retrotransposon activation, DNA damage, and non-cell autonomous death. When human TDP-43, a protein implicated in ALS, was over-expressed in glial cells, flies showed motor defects, early death, increased activity of endogeneous retrovirus "Gypsy", and DNA damage-signaled apoptosis.

Undergraduate Research Student
*Bates College*, Lewiston, ME
Undergraduate Senior Thesis in Biological Chemistry
Research Advisor: Larissa Williams (*lwillia2@bates.edu*)
2014 – 2015
Since 1996, the coverage of eelgrass (*Z. marina*) in the Frenchman Bay, ME, has declined from 3,174 to <200 acres. In 2013, major restoration areas disappeared. Genetic diversity was considered in explaining differences in survival between populations and resistance to disturbance. I isolated genomic DNA of 90 individual plants, amplifying and sizing six microsatellite loci, and quantified the genetic diversity of six distinct populations on the coasts of the Frenchman Bay and Mount Desert Island, ME. I correlated population genetics with factors of loss and resistance measured in field.

Summer Research Intern
*National Cancer Institute*, Frederick, MD
Molecular Control and Genetics Section
Research Advisor: Donald Court (*courtd@mail.nih.gov*)
2014 and 2015
The lambda phage Rex functions (*rexA* and *rexB* and their products) have been implicated in phage replication in and induction from *E. coli* hosts. I studied these functions and the induction of rexB's separate promoter, $P_{LIT}$, during DNA damage. I found this promoter dependent on host SOS response repressor protein, LexA, and confirmed this by mutation of the suspected binding site. This presents evidence of RexB having a role during prophage induction, perhaps in balance with RexA to temper the response of lambda to the degree of DNA damage in the host.

## Other Roles

*Darwin's Ark*, Team Member (darwinsark.org)
*Dog Aging Project*, Project II: Genetics, Team Member (dogagingproject.org)

# Awards and Honors

*Harold M. Weintraub Graduate Student Award*, 2023

*International Society of Psychiatric Genetics Early Career Investigator Program*, 2022

*Dean's Award for Outstanding Mid-Thesis Research*, 2022

*Diane M. Riccio Morningside Graduate School of Biomedical Sciences Travel Award*, 2022

*Anne D. Williams Family Prize in Population or Environmental Studies*, 2015

*Cancer Research Training Award*, 2014 & 2015

# Publications

**ORCiD**: 0000-0002-9139-453X

**Morrill, K.**, Chen, F., and Karlsson, E.K. Comparative neurogenetics of dog behavior complements efforts towards human neuropsychiatric genetics. (2023). *Human Genetics*. [Under Review].

Christmas, M.J., and 75 other authors, including **Morrill, K.** Evolutionary constraint and innovation across hundreds of placental mammals. (2023). *Science*. [Accepted for Publication].

Moon, K.L.†, Huson, H.J.†, **Morrill, K.†**, Wang, M., Li, X., Srikanth, K., Zoonomia Consortium, Svenson, G.J., Karlsson, E.K., Shapiro, B. Comparative genomics of Balto, a famous historic dog, captures lost diversity of 1920s sled dogs. (2023). *Science*. [Accepted for Publication].

Megquier, K., Turner-Maier, K., **Morrill, K.**, Li, X., Johnson, J., Karlsson, E.K., London, C.A., Gardner, H.L. The genomic landscape of canine osteosarcoma cell lines reveals conserved structural complexity and pathway alterations. (2022). *PLOS One*.

**Morrill, K.**, Hekman, J., Li, X., McClure, J., Logan, B., Goodman, L., Gao, M., Dong, Y., Alonso, M., Carmichael, E., Snyder-Mackler, N., Alonso, J., Noh, H., Johnson, J., Koltookian, M., Lieu, C.,

Megquier, K., Swofford, R., Turner-Maier, J., White, M.E., Weng, Z., Colubri, A., Genereux, D.P., Lord, K.A., Karlsson, E.K. Ancestry-inclusive dog genomics challenges popular breed stereotypes. (2022). *Science*.

Thomason, L., **Morrill, K.**, Murray , G., Court, C., Shafer, B., Schneider, T., Court, D. Elements in the $\lambda$ immunity region regulate phage development: beyond the 'Genetic Switch'. (2019). *Mol. Microbiol.*.

Megquier, K., Genereux, D., Hekman, J., Swofford, R., Turner-Maier, J., Johnson, J., Alonso, J., Li, X., **Morrill, K.**, Anguish, L., Koltookian, M., Logan, B., Sharp, C., Ferrer, L., Lindblad-Toh, K., Meyers-Wallen, V., Hoffman, A., Karlsson, E. BarkBase: Epigenomic Annotation of Canine Genomes. (2019). *Genes*.

Krug, L., Chatterjee, N., Borges-Monroy, R., Hearn, S., Liao, W.-W., **Morrill, K.**, Prazak, L., Rozhkov, N., Theodorou, D., Hammell, M., Dubnau, J. Retrotransposon activation contributes to neurodegeneration in a *Drosophila* TDP-43 model of ALS. (2017). *PLoS Genetics*.

**Morrill, K.**, Farrel, A., Dirks, A., Badger, M., Disney, J., Williams, L. Role of genetic diversity and water quality in the 2013 decline of eelgrass (*Zostera marina*) populations of the Upper Frenchman Bay, ME coastlines. (2015). *MDIBL Bulletin*.

# Presentations

*World Congress on Psychiatric Genetics*, Oral Presentation (invitee), 2022, Florence, Italy
Available online: https://youtu.be/8SnauFP1cUQ

*The Biology of Genomes*, Poster Presentation, 2022, Cold Spring Harbor Laboratory, NY

*Society for Molecular Biology & Evolution*, Poster Presentation (virtual), 2021

*Medical and Population Genomics*, Primer Lecture, 2021, Virtual Broadcast
Available online: https://youtu.be/Yq1m1BJQbto

*Medical and Population Genomics*, Group Presentation, 2019, Broad Institute of MIT & Harvard

*2nd Annual Food Allergy Science Initiative Symposium*, Poster Presentation, 2019

*42nd Maine Biological and Medical Sciences Symposium*, Oral Presentation, 2015, MDIBL, ME

*Summer Poster Day*, Poster Presentation, 2014 & 2015, National Institutes of Health, Bethesda, MD

# Activities

## Outreach

"Every dog is an individual", Data Visualization Dashboard, 2022.
https://darwinsark.org/muttomics

"Envisioning Dogs in the Cloud" for Terra.bio, Blog Post, 2022.
https://terra.bio/envisioning-dogs-in-the-cloud/

"Dog and Human Genetics: Similarity and Difference" for Dog Aging Project, Blog Post, 2022.

"Using Genetics to Predict Physical Traits" for Dog Aging Project, Blog Post, 2021.

"July Pack Appreciation Event" for Dog Aging Project, Virtual Broadcast, 2020.
https://youtu.be/0vdsuO9K2VM

## Education

*Sacred Heart Upper School*, Greenwich, CT | Scientist Mentor, 2021 - 2022
Students placed 1st in the Team category of the 2021 CT-STEM science fair in (ctstemfoundation.org) and 3rd in the 2022 Connecticut Science & Engineering Fair.

*Broadie for a Week*, Cambridge, MA
"GWAS Gene Hunt" Module Developer and Mentor

*Experimental Design and Data Analysis Bootcamp*, Worcester, MA
Teaching Assistant, 2017 & 2019 | Course Instructor, 2020

## Interviews

Jeffrey M. Perkel, "Terra takes the pain out of 'omics' computing in the cloud", Nature
https://www.nature.com/articles/d41586-021-03822-7

Katherine J. Wu, "Humans Can't Quit a Basic Myth About Dog Breeds " , The Atlantic
https://www.theatlantic.com/science/archive/2022/04/dog-breed-personality-characteristics/629707/

Jack Tamisiea, "Dogs' Personalities Aren't Determined by Their Breed" , Scientific American
https://www.scientificamerican.com/article/dogs-personalities-arent-determined-by-their-breed/

## Illustration

Illustrations for print page summary. Christmas, M.J. *et al.* Evolutionary constraint and innovation across hundreds of placental mammals. (2022). *Science.*

Illustrations for figures. Chan, F. *et al.* Advancing genetic selection and behavioral genomics of working dogs through collaborative science. (2021). *Frontiers in Veterinary Science.*

## Events

2021 NIH Health Disparities Codeathon, "Cancer disparities through a genomic epidemiology lens"

# Skills

*Project Management.* Writing standard operating procedures (SOPs), designing workflows, workgroup leadership, research participant engagement (e.g., developing genomic report returns)

*Writing and Editing.* Experience writing SOPs and SOWs, LaTeX Typesetting Language

*2D and 3D Illustration.* Adobe Creative Suites, Corel Painter, Blender 3D, Autodesk Fusion 360

*Languages, Statistics, and Computing.* Python, R, Unix / Bash, workflow definition language (WDL), cloud-based computing (Terra.bio, Google), MATLAB, Maple Mathematics, GraphPad Prism, SigmaPlot

*Genomics and Bioinformatics.* Genome-wide association studies (GWAS), fine-mapping, heritability, global and local ancestry inference, GATK, PLINK, GCTA, VCFtools, SAMtools, BCFtools

*Molecular Biology.* DNA/RNA, PCR/qPCR, fragment analysis, next generation sequencing, protein chromatography, traditional and high-throughput Western blotting

*Cellular Biology.* reporter & activity assays ($\beta$-galactosidase, luciferase, GFP), genetic recombineering, cloning, FLP/FRT mitotic recombination, fluorescent imaging, confocal microscopy

*Model Organisms and Cell Culture.* Bacteria (*E. coli*), worm (*C. elegans*), fly (*D. melanogaster*), mammalian cell culture (primary and immortalized, mouse and human, cancer and non-cancer)