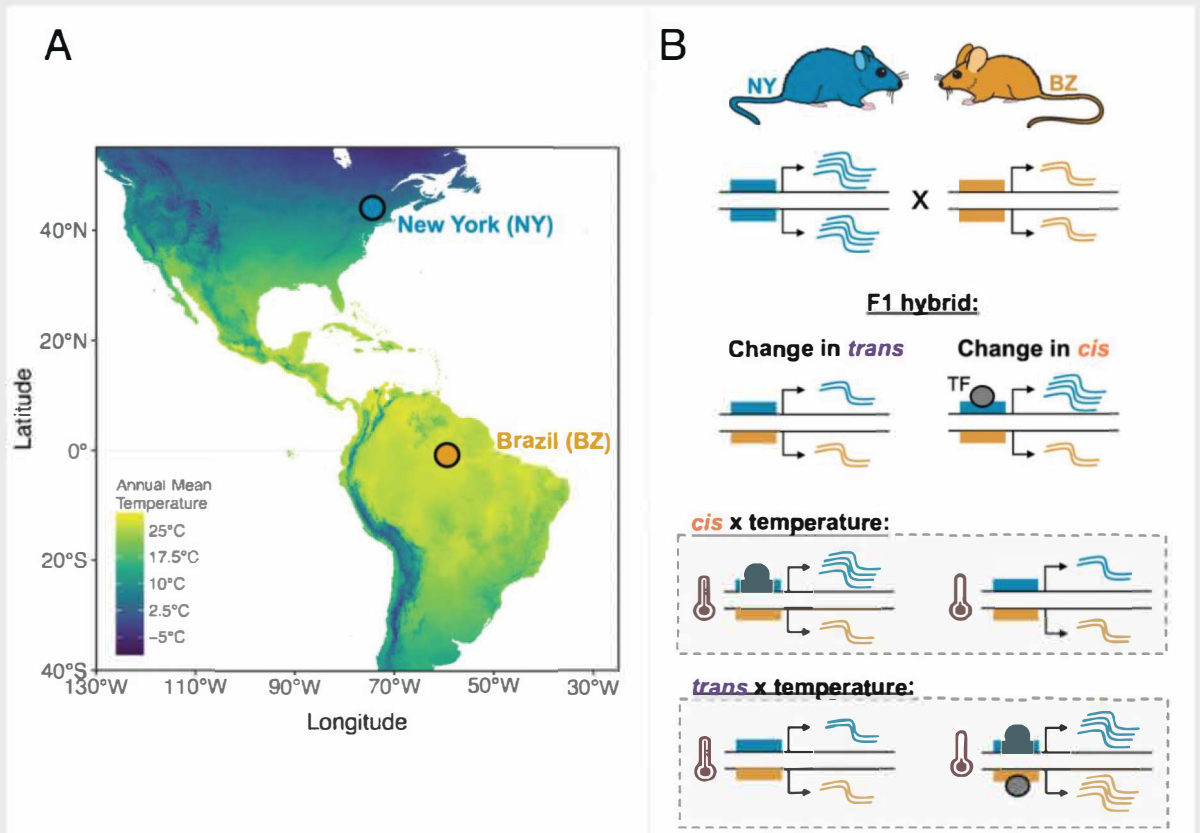


Featured Publication

Former MVZ Graduate Students Mallory Ballinger and Katya Mack, Former Postdoc Eric Riddell, Graduate Student Sylvia Durkin, and Professor Michael Nachman

Gene Regulation Helps Species Thrive in New Climates

Gene expression is shaped by genetic and environmental effects, yet these two factors are rarely considered together in the context of adaptive evolution. Gene expression can be controlled by mutations near to the gene of interest (*cis*-) or by mutations in distant genes (*trans*-). In a recent paper in [PNAS](#) former MVZ Graduate Student Mallory Ballinger and colleagues dissected the *cis*- and *trans*-regulatory impact on gene expression associated with the adaptation of house mice to temperate and tropical climates. By rearing cold-adapted and warm-adapted mice in cold and warm conditions and studying gene expression, Ballinger and colleagues showed how both genetic and environmental effects on gene expression allow species to thrive in new environments.



Above: A. Variation in mean annual temperature across North and South America. Wild-derived inbred lines originate from upstate New York (43°N) and equatorial Brazil (3°S). B. Schematic depicting how *cis*- and *trans*-changes can be inferred with F1 hybrids, and how environmental differences may result in *cis* x temperature and *trans* x temperature effects. Blue and gold boxes represent *cis*-regulatory regions for NY and BZ, respectively. Wavy lines depict transcript levels of an allele. TF = transcription factor.

Recent Publication by MVZ Researchers

MVZ Graduate Student María José Navarrete Méndez and Professor Rebecca Tarvin

Neotropical Frogs Eye View

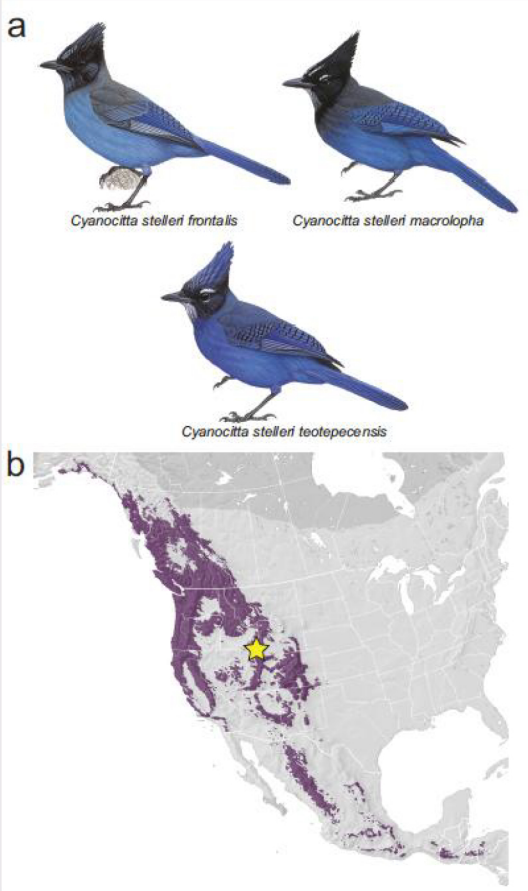
Frogs are taxonomically and ecologically diverse, constituting an ideal model for studying the evolution of visual systems. While most amphibians are nocturnal, those with daytime activity patterns are active in a broader and brighter light spectrum, suggesting that their visual systems may be evolutionarily adapted for better color vision. In a recent paper published in the journal of [Molecular Biology and Evolution](#) MVZ Graduate Student María José Navarrete Méndez and Professor Rebecca Tarvin investigated signatures of selection on visual opsin genes in five neotropical frog groups. The study evaluated signatures of selection on visual opsin genes across Neotropical anurans and focus on three diurnal clades that are well-known for the concurrence of conspicuous colors and chemical defense: poison frogs (Dendrobatidae), Harlequin toads (Bufonidae: *Atelopus*), and pumpkin toadlets (Brachycephalidae: *Brachycephalus*). In a remarkable finding, the authors discovered evidence of the loss of the SWS2 gene in the ancestor of poison frogs. The SWS2 opsin, usually expressed in the rod cells of amphibian retinas, is hypothesized to contribute to color vision at night. Interestingly, the absence of this pigment might have occurred after the origin of diurnality in poison frogs, potentially impacting their chemical ecology, biodiversity, and behavior. The results show how the diversification of visual opsin genes responds to shifts in ecology and life history in frogs and lays the foundation for future studies exploring how visual tuning alters the sensory landscape of animals.



MVZ Postdoc Phred Benham, Staff Curator Emerita Carla Cicero, Professor Michael Nachman and Professor Rauri Bowie

Steller's Jay Has Highest Quality Genome

A reference genome assembly is the complete sequence of a genome from one individual of a species. With a reference genome in hand biologists can ask questions about the genes that make a species unique, evolutionary relationships among different species, and multiple genomes of the same species can be compared to the reference to understand genetic diversity within that species. A recent paper in the [*Journal of Heredity*](#) by MVZ Postdoc Phred Benham, Staff Curator Emerita of Birds Carla Cicero, Professor Michael Nachman and Professor Rauri Bowie reports the generation of a reference genome for the Steller's Jay that is among the highest quality of any bird genome. This genome was generated with funding from the [**California Conservation Genomics Project**](#). Along with genomic data from 150 other species of California plants and animals this genome contributes to the project's mission to generate genetic resources for the management and protection of the state's biodiversity.



Above: a) Geographic variation among different Steller's jay (*Cyanocitta stelleri*) subspecies. *C. s. frontalis* is characteristic of the short-crested birds with blue forehead streaks found along the Pacific coast and in the Sierra Nevada of California. The *C. s. macrolopha* group of the Rocky Mountains and northern Mexico includes long-crested birds with white forehead stripes and a white line above the eye. Birds of Central American mountains possess bluer crests that are similar to *C. s. teotepecensis* illustrated here. b) Distribution map of the species (map data from <https://ebird.org/>). The yellow star marks the location of the contact zone between coastal plus northwest interior and Rocky Mountain populations.

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