

Announcements

See EEB's fall seminar series schedule [here](#).

EEB Graduate Student Research Grant call for proposals is now open. Submit your proposals to Nick Jacobsen by Nov. 12th!

Texas A&M's 2021 Genome Editing Virtual Symposium is Oct. 28th. Register [here](#)!

Congratulations to Amanda Beckman (@funcaption) on their proposal defense! 🎉 🎉



Want to submit a story or announcement for the *News fEEB*?

Let us know by [clicking HERE](#)

News fEEB

Ecology and Evolutionary Biology Monthly Newsletter

October 2021 · Volume 4 · Issue 2

Author: Mason K. Clark
masonclark93@tamu.edu

[@Mason_K_Clark](#)

EEB New Faculty Spotlight

Dr. Courtney Fitzpatrick



Dr. Fitzpatrick joined the Biology Department and EEB program this Fall 2021. Dr. Fitzpatrick received their BA in visual art from University of North Carolina Chapel Hill before working in the non-profit sector at The Hetrick-Martin Institute. Dr. Fitzpatrick then completed their PhD in Biology at Duke University in collaboration with the Amboseli Baboon Research Project followed by completing two Postdoctoral Fellowships at the National Evolutionary Synthesis Center (NESCent) and at Indiana University as part of the NIH funded Common Themes in Reproductive Diversity research group. Their research combines field-based empirical methods with mathematical modeling to understand how the ecology of social environments influences trait evolution with a focus on reproductive traits, often behavioral ones.

Check out [Dr. Fitzpatrick's website](#)

for more information!

Follow us on Social Media!

Twitter: [@TAMUEEB](#)

[Facebook](#)

And updates on our [website](#)!

You or a colleague accomplish something? Let us know by tweeting #TAMUEEB



For more information visit:
eeb.tamu.edu

TAMU 2021 Genome Editing Symposium Speakers

2021 GENOME EDITING
SYMPOSIUM SPEAKER
SPOTLIGHT:

DR. REBECCA BART

Donald Danforth Plant
Science Center



Editing the genome and epigenome of cassava to promote disease resistance

Cassava (*Manihot esculenta*) is an important food security crop in much of the world. Although cassava is prized as a highly productive crop even when grown without irrigation or fertilizer, it suffers from several microbial pathogens that can significantly impact yield. In this talk, I will cover two of the most important diseases of cassava: Cassava Brown Streak Disease caused by an RNA viral pathogen, and Cassava Bacterial Blight, caused by *Xanthomonas*. In both cases, we have identified important host susceptibility genes (S genes). S genes are encoded in the host genome and are required by the pathogen to complete its lifecycle. I will describe our work on exploring the biology of these unique pathosystems. Further, I will share recent data using various genome and epigenome editing tools to prevent the pathogens from accessing their cognate S genes and how, generally, these approaches can be used to promote host resistance.

2021 GENOME EDITING
SYMPOSIUM SPEAKER
SPOTLIGHT:

DR. PHILLIP A. CLEVES

Carnegie Institute for
Science - Department
of Embryology,
Baltimore, MD.



Using Transcriptomics and Reverse Genetics to Understand Mechanisms of Cnidarian-dinoflagellate Bleaching

The symbiosis between corals and dinoflagellate algae is essential to the energetic requirements of coral-reef ecosystems. However, coral reefs are in danger due to elevated ocean temperatures and other stresses that lead to the breakdown of this symbiosis and coral. Despite the importance of coral reefs, the molecular basis of how corals maintain a healthy symbiosis and avoid bleaching is poorly understood, in part because of the lack of a tractable genetic model system. The small anemone *Aiptasia* is symbiotic with algal strains like those in reef-building corals but has many experimental advantages, making it an attractive laboratory model for cnidarian symbiosis. To explore the transcriptional basis of heat-induced bleaching, we used RNAseq to identify genes that are differentially expressed during a time course of heat stress of symbiotic and aposymbiotic *Aiptasia* strains. We observed a strong upregulation of hundreds of genes at times long before bleaching begins in symbiotic anemones. The putative promoters of these early stress-response genes are enriched for binding sites for the NFkB and HSF1 transcription factors, suggesting that many of these genes share core transcriptional control. The overall expression patterns were similar between the symbiotic and aposymbiotic anemones, indicating that many of the expression changes are not specific to the presence of the algae. Nonetheless, reducing HSF1 activity with a pharmacological inhibitor resulted in more severe bleaching, suggesting that this symbiont-independent stress response is protective against bleaching. Genetic tools are needed to allow rigorous functional testing of the roles of candidate genes in symbiosis and bleaching. Recently, we have developed methods for knocking down and overexpressing genes of interest in *Aiptasia*. Meanwhile, we have successfully used the CRISPR/Cas9 technology to create genetic changes in embryos of the coral *Acropora millepora*. We used this technology to knock out HSF1 and demonstrated its role in coral heat tolerance. Through the establishment of both gain-of-function and loss-of-function methods in both *Aiptasia* and corals, it will be possible to exploit the year-round spawning of *Aiptasia* to perform initial tests of gene function in cnidarian-algal symbiosis and then further test the discoveries made using similar technologies in corals.



ECOLOGY and
EVOLUTIONARY
BIOLOGY

For more information visit:
eeb.tamu.edu

TAMU 2021 Genome Editing Symposium Speakers

2021 GENOME EDITING
SYMPOSIUM SPEAKER
SPOTLIGHT:

DR. ELIZABETH MAGA

Assistant Professor,
Department of Animal
Sciences, University of
California at Davis



Translating the use of lysozyme-rich milk from transgenic goats to fight diarrheal illnesses

Genetic engineering as applied to animal agriculture has the potential to benefit both animal and human health. For instance, human milk contains several factors that promote the growth of beneficial gut bacteria that help fight infection and maintain health; however, these factors are lacking in the milk of dairy animals. By producing these key antimicrobial components as part of the milk of farm animals, there is the potential to supply these health-promoting factors to human consumers throughout their lifetime. We have genetically engineered dairy goats to make one of these important antimicrobial factors, human lysozyme (hLZ) in their milk. Due to the purported role of human milk on gut microbiota formation, a source of milk rich in lysozyme could shift the microbial population of the gut during milk consumption to those microbes associated with beneficial activities for the host. Over the past 15 years, we have been using the pig as a human-relevant animal model to test the ability of hLZ goat milk to treat and prevent diarrhea which remains a leading cause of death of children under the age of five worldwide. Consumption of lysozyme-rich milk results in the modulation of gut microbiota in healthy, malnourished and E. coli-challenged pigs, promotes a healthier intestinal epithelium and can both resolve and prevent the symptoms of E. coli-induced diarrhea. These studies are paving the way for mechanistic studies on the role of gut microbiota modulation on intestinal and overall health and translational studies on the use of lysozyme-rich milk to treat and prevent diarrheal and intestinal diseases.



2021 GENOME EDITING
SYMPOSIUM SPEAKER
SPOTLIGHT:

DR. ARNAUD MARTIN

Assistant Professor,
Department of Biological
Sciences, The George
Washington University



Do butterflies dream of genetic tattoos? Exploring color pattern evolution using CRISPR

Understanding the generative mechanisms of morphological diversification requires the routine manipulation of genomes in a comparative context. I will present how current work using CRISPR mutagenesis illuminates how the wing color patterns of butterflies have radiated into an iconic example of biodiversity. CRISPR has indeed been a true revolution allowing the routine interrogation of gene function in insects that were previously difficult to manipulate in the lab. Gene knock-outs in butterflies reveal spectacular phenotypes that modify pattern shapes and colors, and for instance, we recently identified a gene that when removed, induces widespread ultraviolet-iridescence in butterflies normally devoid of this color. These experiments illustrate how evo-devo can delve into the genome-to-phenome relationship, and probe how evolution has been tinkering with a genetic toolkit of developmental genes involved in pattern and cell specification.



**ECOLOGY and
EVOLUTIONARY
BIOLOGY**

For more information visit:
eeb.tamu.edu