Flowering at the right time: how do plants adapt to their local environments?

Miller Fellow Focus: Allison Gaudinier

A major tenet of evolutionary biology is that species have adapted to survive and reproduce successfully in their ecological niche. Within species, local adaptation often occurs such that populations consist of genotypes that are better suited for their specific habitats than populations from elsewhere. Such adaptation to environmental variation at a fine spatial scale is particularly critical for plants because they live their whole lives in one location. One route for local adaptation is the fine-tuning of the mechanisms by which plants sense environmental cues and respond by altering their development or physiology in order to thrive in ever-changing and at times unpredictable conditions. My research focuses on the genetic basis for local adaptation and explores how different populations of the same species have adapted to similar environmental conditions. Understanding how the adaptation has been accomplished historically will allow us to predict if and how plant species will adapt, or could be aided to adapt, through selection for genetic attributes that favorably adjust developmental programs as climate change alters their environments.

To investigate local adaptation, I study a species that has been used extensively in ecological research, the common yellow monkeyflower, *Mimulus guttatus*. This species of mon-

keyflower is native to western North America and is found across an incredibly diverse array of environments. Their habitats range from seaside cliffs to oak savannas in the Central Valley to montane meadows in the Sierra Nevada and Cascades ranges (**Figure 1**), and can include several challenging soil substrates like serpentine and copper contaminated mine tailings. The ecological pressures posed by these diverse environments have selected for patterns of genetic and trait differentiation among populations that adapt local individuals to their specific environmental challenges. I am interested in finding the genetic factors in these populations that contribute to local adaptation. My main projects are focused on how the variation in seasonal timing of flowering is regulated in these populations and how this timing adaptively evolves by rewiring of gene networks.

Call for Nominations

Miller Research Fellowship Nominations
Deadline: September 10, 2020

Miller Research Professorship Applications
Deadline: September 14, 2020

Visiting Miller Professorship Departmental Nominations
Deadline: September 15, 2020

Greetings From the Miller Institute

From all of us at the Miller Institute, we wish you health and wellness at this time of global pandemic. In our community, basic science research and interdisciplinary connections continue remotely. In this newsletter, we're sharing photos and stories of our members and how they have adapted their work, research and lives to this extraordinary time.

Are you researching COVID-19 or related topics? Let us know: email millerinstitute@berkeley.edu.

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miller.berkeley.edu

Call for Miller Professor Applications

Online Application Deadline: September 14, 2020

Miller Research Professorship AY 2021-2022

The Miller Professorship program is looking with a view to the future in announcing the call for applications for terms in the academic year 2021-2022. The objective of the Miller Professorship program is to provide opportunities for faculty to pursue new research directions on the Berkeley campus and to participate in the vibrant Miller Institute interdisciplinary scientific community. Appointees are encouraged to follow promising leads that may develop in the course of their research. In order to accommodate a range of faculty members, the Miller Professorship program offers appointees, in consultation with their Departmental Chair, the option of taking teaching relief or continuing to teach during their Miller Professorship term. Funds will be distributed differently depending upon the choice selected.

The primary evaluation criteria will continue to be research excellence. Proposals to write books are not viewed as competitive. Applicants are also encouraged to describe their interest in participating in the Miller Institute community and providing mentorship to the Miller Research Fellows.

Beginning in May 2020, applications will be accepted from UC Berkeley faculty for terms in the 2021-2022 academic year. Applications are judged competitively and are due by September 14, 2020. It is anticipated that between four and ten awards will be made.

For more information, and to access the application, visit miller.berkeley.edu/professorship.

Call for Visiting Miller Professor Nominations

Online Nomination Deadline: September 15, 2020

Visiting Miller Research Professorship AY 2021-2022

The Advisory Board of the Miller Institute for Basic Research in Science invites Berkeley faculty to submit online departmental nominations for Visiting Miller Research Professorships and the Gabor A. and Judith K. Somorjai Visiting Miller Professorship Award for terms in Fall 2021 or Spring 2022. The purpose of these Visiting Miller Professorships is to bring promising or eminent scientists to the Berkeley campus on a short-term basis for collaborative research interactions. It is required that awardees be in residence at Berkeley during their appointment term. Faculty members or research scientists from around the world are eligible to be considered for sponsorship. Non-US citizens must be eligible for J-1 Scholar visa status in order to be awarded. Faculty members at other UC campuses are eligible to be nominated for this program. The Miller Institute, as the sponsor and administrative department, will extend an invitation after advising the department of its selection.

Beginning in May 2020, nominations will be accepted from UC Berkeley faculty for Visiting Professorship candidates for the 2021-2022 academic year. Nominations are judged competitively and are due by September 15, 2020. It is anticipated that between four and ten awards will be made.

For more information, and to access the nomination form, visit miller.berkeley.edu/visiting-professorship.

:: **Nomination & Application details**: miller.berkeley.edu   :: **Questions?** millerinstitute@berkeley.edu

Call for Nominations: Miller Research Fellowship
2021-2024 Term

Nomination Deadline: September 10, 2020

The Miller Institute for Basic Research in Science invites department chairs, faculty advisors, professors and research scientists at institutions around the world to submit nominations for Miller Research Fellowships in the basic sciences. Through this program, the Miller Institute seeks to discover and encourage individuals of outstanding talent, and to provide them with the opportunity to pursue their research on the Berkeley campus. Fellows are selected on the basis of their academic achievement and the promise of their scientific research. Miller Fellows also have a keen curiosity about all science and share an appreciation for an interdisciplinary experience. The Miller Institute is the administrative home department for each Miller Fellow who is hosted by an academic department on the Berkeley campus. A list of current and former Miller Research Fellows can be found at: http://miller.berkeley.edu/fellowship/members/all-mf-by-name.

Miller Research Fellowships are intended for exceptional young scientists of great promise who have recently been awarded, or who are about to be awarded, the doctoral degree. Miller Fellows are expected to begin their Fellowship shortly after being awarded their Ph.D. A short period as a postdoctoral fellow elsewhere does not exclude eligibility, but applicants who have already completed more than two years of postdoctoral experience are not eligible for nomination. **A nominee cannot hold a paid or unpaid position on the Berkeley campus at the time of nomination or throughout the competition and award cycle which may extend into February 2021.** Nominees who are non-US citizens must show eligibility for obtaining J-1 Scholar visa status for the duration of the Miller Fellowship. Non-US citizens will be required to prove English language proficiency prior to award. The Miller Institute does not support H1B visa status. Eligible nominees will be invited by email by the Institute to apply for the Fellowship after the nomination has been reviewed. Direct applications and self-nominations are not accepted.

*All nominations must be submitted using the Online Nomination System at: **miller.berkeley.edu.**

Nominators will need the following required information to complete the online nomination process:
- Nominee's complete full and legal name (do not use nicknames)
- Nominee's current institution
- Nominee's complete, current, and active E-mail address that will be valid through March 2021, current mailing address with postal code and telephone number
- Nominee's Ph.D. Institution and (expected) Date of Ph.D. (month & year required)
- Letter of recommendation and judgment of nominee's promise by the nominator (saved in PDF format). Letter must be specific to the Miller Fellowship, have a current date, and be on institutional letterhead. The Executive Committee finds it helpful in the recommendation letter to have the candidate compared with others at a similar stage in their development.
- Nominator's current active E-mail address, title, and professional mailing address (include zip code/campus mail code)

The Institute provides a stipend of $68,000 with annual 2% increases and an annual research fund of $10,000, for total initial compensation of $78,000. There is provision for travel to Berkeley for incoming Miller Fellows and their immediate families and a maximum allowance of $3,000 for moving personal belongings. Benefits, including medical, dental, vision and life insurance are provided with a modest contribution from the Miller Fellow. All University of California postdocs are represented by the UAW. Fellowships are awarded for three years, generally beginning August 1, 2021 and ending July 31, 2024. Approximately eight to ten Fellowships are awarded each year. Candidates will be notified of the results of the competition starting in mid-December, and a general announcement of the awards will be made in the spring.

We are grateful for your thoughtful participation in this process and hope that you regard the time you may devote to this effort justified by the contribution you will be making to the careers of distinguished young scientists.

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Miller Research Fellowship Awardees 2020-2023

The Miller Institute is pleased to introduce the 2020-2023 Miller Research Fellows. Each year, the Miller Research Fellowship program seeks to discover individuals of outstanding talent and to bring young scholars of great promise to the Berkeley campus. The Fellows will be working with Berkeley faculty hosts for a three-year term beginning in the 2020 academic year. A full list of all past and present Miller Fellows is available on our website.

Adair Borges

Ph.D. - UCSF

Berkeley Dept. - ESPM / MCB/ BIOENG

Faculty Hosts: Jillian Banfield, Dave Savage, Adam Arkin

Bacteria and the viruses that infect them – bacteriophages (phages) – are locked in an ancient battle for survival. A phage replicates by converting a bacterial cell into a phage production factory, while bacteria try to destroy infecting phages. As a graduate student, I studied how bacteriophages survive being attacked by the bacterial CRISPR-Cas immune system. As a Miller Fellow, I will study how bacteriophages take control of the bacterial protein synthesis machinery and enact their own protein production program.

Anna Ho

Ph.D. - Caltech

Berkeley Dept. - Astronomy

Faculty Hosts: Eliot Quataert, Daniel Kasen

The fate of a star — how it lives, how it dies, and the corpse it leaves behind — depends primarily on its mass. High-mass stars explode as supernovae and leave behind a neutron star or a black hole. In rare cases, the corpse acts as an "engine" that launches a relativistic jet. These "engine-driven" explosions are the focus of my research: I use robotic telescopes to discover them as they are happening in the night sky, then use telescopes around the world and in space to watch them unfold.

Grayson Chadwick

Ph.D. - Caltech

Berkeley Dept. - MCB

Faculty Host: Dipti Nayak

I am interested in understanding the evolution of energy metabolism in microbes at multiple scales, from the interactions of organisms with their physical environment down to the modifications of individual bioenergetic protein complexes. I focus on organisms that are important sources and sinks of methane on Earth. Much of my previous work was conducted on uncultured organisms in complex environments, allowing us to understand broadly which biogeochemical processes are carried out by which organisms. My work as a Miller Fellow at UC Berkeley will focus on the genetic manipulation of pure cultures to produce more mechanistic understanding of energy metabolism in understudied organisms within the Archaea.

Michael Kim

Ph.D. - Stanford

Berkeley Dept. - EECS

Faculty Host: Shafi Goldwasser

I am a theoretical computer scientist studying the mathematical foundations of responsible machine learning. Much of this work aims to identify ways in which machine learning systems can exhibit problematic behavior (e.g., unfair discrimination) and to develop algorithmic tools that provably mitigate such behaviors. More broadly, I am interested in how the theory of computation can help tackle emerging societal and scientific challenges.

Antoine Koehl

Ph.D. - Stanford

Berkeley Dept. - Statistics

Faculty Host: Yun Song

In the post-genome era, we continue to identify new proteins based on their sequence alone, but often struggle to identify their precise biological function. My research seeks to use recent advances in statistical and machine learning techniques to provide better functional predictions to these so-called "orphan" proteins. In particular, my work will focus on the G protein coupled receptor superfamily- despite its central role in human physiology, there remain ~80 "orphan" receptors whose biological role is unknown.

Emily Davis

Ph.D. - Stanford

Berkeley Dept. - Physics

Faculty Host: Norman Yao

For my doctoral work, I built an experiment to generate and image nonlocal interactions in a cold atomic ensemble trapped in an optical cavity. At Berkeley, I look forward to working in Prof. Norman Yao's group studying many-body physics and high-pressure sensing in nitrogen vacancy centers in diamond.

Vayu Maini Rekdal

Ph.D. - Harvard

Berkeley Dept. - BIOENG/IB/PMB

Faculty Hosts: Jay Keasling, Britt Koskella, Michi Taga & Matt Traxler

Much of food processing is not performed by humans alone, but by microorganisms living outside and inside the body. I explore molecular interactions between these microbes and food components in fermented foods and the gut microbiota. This understanding will enable engineering of microbial chemistry to improve human food consumption and production and ultimately address challenges in sustainability, nutrition, and gastronomy.

Nayeli Rodriguez Briones

Ph.D. - University of Waterloo

Berkeley Dept. - Chemistry

Faculty Host: K. Birgitta Whaley

Quantum information science gives us an effective language to ponder and understand our universe by describing the laws of nature in terms of the evolution of information. In this context, the question at the heart of my research is how quantum information science can be used to explore and discover new phenomena in the quantum regime and to deepen our understanding in several areas of science, such as quantum many-body theory, thermodynamics/statistical mechanics, and even biology and quantum gravity. In recent years I have been exploring several directions for applying the tools of quantum information science to cool quantum systems in an algorithmic way. These algorithmic cooling techniques are not only of theoretical interest for quantum physics, but they are also at the core of the practical applications in quantum technologies - from the preparation of pure states for quantum computation to the supply of reliable ancilla qubits in quantum error correction.

Veronika Sunko

Ph.D. - University of St. Andrews

Berkeley Dept. - Physics

Faculty Host: Joseph Orenstein

I am interested in understanding how observable properties of solid-state materials arise as a consequence of their structure and constituent elements. It is a question of both practical and fundamental interest; the former because such materials are critical for the development of novel technologies, and the latter because they represent an accessible window onto the underlying quantum many-body problem. As a Miller Fellow I will combine bespoke and sensitive spatially resolved optical probes of symmetry with external tuning parameters to investigate how symmetry and topology collaborate to yield material properties as we know them, both at microscopic and macroscopic length scales. I will do this on a range of promising new quantum materials, which I intend to synthetize, therefore creating novel quantum playgrounds.

Alfred Zong

Ph.D. - MIT

Berkeley Dept. - Chemistry

Faculty Host: Michael Zuerch

Order formation is typically defined in thermal equilibrium, yet new states of matter are found to emerge in many out-of-equilibrium contexts. I am interested in creating and studying non-equilibrium phases that are otherwise impossible to realize. Using attosecond spectroscopy and diffraction, I hope to understand how microscopic interactions govern phase transitions at the fundamental timescale of electrons, spins, and lattice. The goal is to achieve better control over ordering dynamics even in strongly correlated systems.

IN THE NEWS

Omar Yaghi (Visiting Miller Professor 2009) was awarded the **German Chemical Society Gold Medal** for his contributions to Reticular Chemistry, which includes metal-organic frameworks (MOFs), covalent organic frameworks (COFs), and molecular weaving. Professor Yaghi was also named as the **2019 Innovator of the Year** by *Innovation & Tech Today*.

Marla Feller (Miller Fellow 1994-1996, Executive Director 2017-present) was honored with a **2020 UC Berkeley Distinguished Teaching Award**.

Jennifer Doudna (Miller Senior Fellow 2017) was awarded the **2020 Vanderbilt Prize in Biomedical Science** for "*the invention of groundbreaking genomic technology that fundamentally changed the landscape for how we are able to approach the treatment of many devastating diseases and a host of other challenges facing mankind. Her work continues to create great promise for the future.*" Professor Doudna was also awarded the **2020 Guggenheim Fellowship in Biology.**

Jason Stajich (Miller Fellow 2006-2009) was elected a **Fellow of the American Academy of Microbiology.**

Two Former Miller Fellows, **Peter Hintz** (Miller Fellow 2015 - 2017) & **Sung-Jin Oh** (Miller Fellow 2013-2016), were named **2020 Sloan Research Fellows in Mathematics**.

Naomi Ginsberg (Miller Professor 2017-2018) received the **American Chemical Society 2020 early-career award** in Experimental Physical Chemistry.

Scott Tremaine (Visiting Miller Professor 2013) was awarded the **2020 Henry Norris Russell Lectureship** for his "*lifelong contributions to our understanding of the dynamics of natural cosmic systems on scales ranging from comets to clusters of galaxies, and for his mentoring of junior colleagues and leadership of major astronomical research institutions.*"

Gabor Somorjai (Miller Professor 1977-1978, Miller Senior Fellow 2009-2014) was awarded the **Helmholtz Medal** "*for his outstanding scientific achievements in the fields of humanities, social sciences, mathematics and natural sciences, biology, medicine and engineering sciences.*"

NEXT STEPS

Seyedeh Mahsa Kamali (first year Miller Fellow) will start as a **Research Scientist at Apple** in May.

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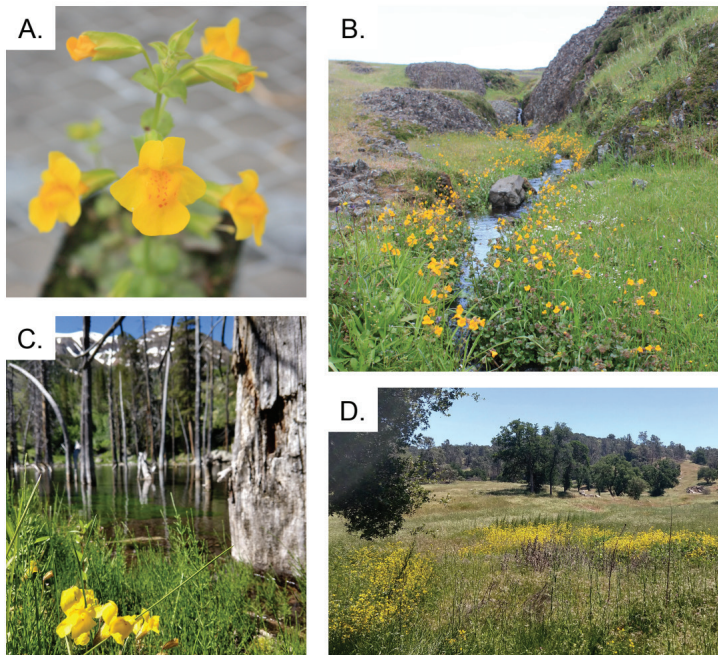UNIVERSITY OF CALIFORNIA

Figure 1: Monkeyflowers grow in diverse habitats.
A. A flowering monkeyflower **B**. Monkeyflowers in the Eastern Sierra Nevada Mountains near Mono Lake, CA (mid July 2019) **C**. Table Mountain Ecological Reserve near Oroville, CA (mid April 2017) **D**. Sierra Nevada foothills near Clovis, CA (late April 2019)

Annual plants, such as the monkeyflower populations I study, complete an entire life cycle from germination, vegetative growth, flowering and setting seed in less than 12 months. The timing of developmental transitions is highly regulated through genetic networks that sense environmental cues predictive of seasonal timing and then integrate this information with internal plant signals to ensure these transitions occur in favorable conditions and at an appropriate plant age or developmental stage. Monkeyflowers either germinate in the fall and pause growth over the winter, or they germinate in early spring. Similarly, populations vary when they begin flowering from early spring until midsummer. The timing of flowering for an annual plant is key to reproductive success - too early and the delicate flowers may succumb to late winter weather, too late and the plants risk encountering a lethal summer drought before they set seed.

Populations of monkeyflowers have adapted so that their flowering times reflect the seasonality of their locations. At low elevations, favorable spring flowering conditions occur much earlier in the calendar year than at higher elevations where snow may melt months later. Many plants, including monkeyflowers, use the length of the day, or photoperiod, as a key signal for the appropriate time to flower. Photoperiod is a consistent proxy for calendar date, as opposed to temperature or water availability as these factors on a given date can vary significantly from year to year. Monkeyflower populations will only transition to flowering after a specific day length threshold is reached, their critical photoperiod. When the photoperiod length is sufficient, genes in the pathway that initiate flower-

ing are upregulated and the transition from vegetative to reproductive growth begins. Because the growing season starts later at high elevation, high elevation populations tend to have longer critical photoperiods than low elevation populations.

In my research I am taking several experimental approaches to understand what genetic factors that vary among monkeyflower populations lead to adaptive variation in critical photoperiods. I am particularly trying to understand if high elevations populations with longer critical photoperiods from different locales across the broad geographic range evolved those differences relative to low elevation populations through changes in same gene(s) or if there are unique variants that have contributed to different populations independently reaching the same adaptive phenotype.

One method I am taking to find genes that may contribute to the differences in the critical photoperiod responses is using transcriptomics to quantify genome-wide gene expression under relevant day lengths. I am generating datasets that will allow me to know what genes are expressed and their expression levels at the time of tissue sampling. This snapshot can be further expanded by adding additional timepoints and additional populations, providing me the ability to look at temporal and evolutionary patterns. Using plants from populations with lower and higher critical photoperiods, I can compare the differences I see in the gene expression levels at specific timepoints and their patterns across the entire series and determine which genes may contribute to the critical photoperiod differences.

Members of the Blackman Lab grew and collected monkeyflowers from two low elevation populations and two high elevation populations in two field sites when days were 14½ hours long (at low elevation) or 15½ hours long (at high elevation). Plants were collected and flash frozen every four hours from 4am to midnight (**Figure 2**). With these samples, I am generating RNA-seq libraries to profile the gene expression, as previously described. This circadian time series will allow me to compare and contrast monkeyflower populations to see which gene expression and circadian patterns are best explained by population or origin, native site elevation, photoperiod, or most excitingly, an interaction between these factors in which gene expression in different populations responds differently to the same change in photoperiod.

From this expression profiling analysis, I will select genes that have different levels of expression or have different expression patterns either due to their population or native elevation for functional validation. Next, I will use genome editing methods, such as CRISPR-Cas9 (developed by former Miller Senior Fellow Jennifer Doudna), to mutate candidate genes. In order to understand the role a
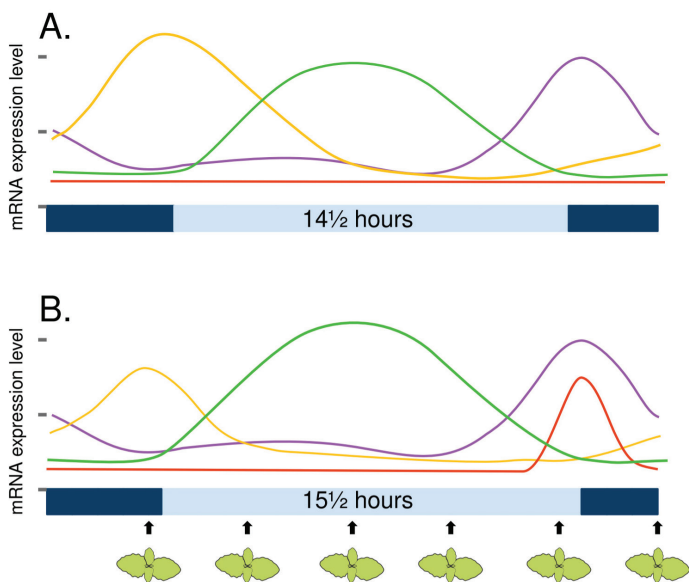
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Figure 2: Experimental design for circadian time course.
A. 14.5 hour days and **B.** 15.5 hour days plants were collected every 4 hours beginning at 4am. The lines display potential gene expression (mRNA) patterns and the differences in the two day lengths. Purple: Gene expression pattern and levels are consistent (peak occurs during the night in **A** and the day in **B**). Green: Gene expression pattern is consistent, the level is higher in **B**. Yellow: Gene expression is higher and the peak is wider in **A**. Red: Gene is only expressed in **B**.

gene (a component) plays in a plant (the system) you have to remove that gene to see how the system is perturbed. I will generate mutant lines for interesting candidate genes and determine what role the genes play in the plant's ability to sense critical photoperiod and the subsequent developmental responses.

Previous work in the Blackman Lab found that several genes that are part of the MADS-box transcription factor family are likely to be associated with differences in the critical photoperiod for flowering between low and high elevation populations. I used CRISPR-Cas9 gene editing to generate potential mutants of monkeyflower plants from this population. Preliminary results from one mutant has shown that this gene affects the transition from vegetative to reproductive growth (**Figure 3**).

Figure 3: Functional validation of a candidate MADS-box gene.
A. A wildtype monkeyflower. **B.** A mutant that cannot transition from vegetative growth to flowering.

After months of growing in conditions that meet critical photoperiod requirements, the mutant plant has still not flowered. I am carrying out further treatments of the plants, such as putting them in a cold room to simulate winter and/or treating with plant hormones that play a role in flowering induction. Because I am interested to see how this mutant has perturbed the gene network that regulates the flowering pathway, I also plan to perform expression profiling to understand what genes are misregulated in this mutant.

Local adaptation plays a key role in the ability for a species to live in varied environments. Monkeyflowers are widely distributed and therefore are an excellent study system as they exhibit a great deal of local adaptation. Through genetic and molecular approaches, my research aims to explore what genes contribute to the differentiation of traits that foster adaptation to local climates.

Allie Gaudinier was born and raised in Alameda County, CA. She received a B.S. in Microbiology from UC Davis. After working as a laboratory technician for two years, she decided to go to graduate school. Allie was advised by Siobhan Brady for her Ph.D. in Plant Biology from UC Davis. Her graduate work focused on mapping transcriptional regulatory networks related to nitrogen metabolism and finding novel genes that regulate plant development in response to nutrient availability. Allie began her Miller Fellowship in the summer of 2019. She is a member of Ben Blackman's research group in Plant and Microbial Biology and is co-sponsored by Haiyan Huang in Statistics. Her hobbies include rock climbing, gardening, and hiking (and not being in quarantine at home!).

Contact: agaudinier@berkeley.edu
twitter: @a_gaudinier

ON THE FRONTLINES WITH COVID-19 TESTING

Miller Fellow **Cara Brook** (2017-2020) is one of a team of volunteers running the COVID-19 diagnostics pipeline out of the Innovative Genomics Institute, a joint UC Berkeley - UCSF venture directed by former Miller Senior Fellow, Dr. Jennifer Doudna. Daily, the team intakes and accessions new COVID-19-suspect samples from East Bay clinical settings, extracts RNA, and runs qPCR to test for the SARS-CoV-2 virus. In the past few weeks, the team has been moving towards a completely automated testing pipeline offering a 24-hour-turnaround for results. Cara is working to replicate a manual version of the IGI diagnostics pipeline with her collaborators abroad at Institut Pasteur of Madagascar.
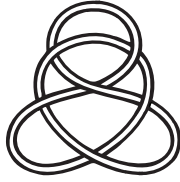
Contact Cara: cbrook@berkeley.edu

Learn more about IGI's work in their new medRxiv preprint at: https://www.medrxiv.org/content/10.1101/2020.04.11.20061424v1 or on the IGI website at: https://innovativegenomics.org/covid-19/.

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## RESEARCHING EMISSIONS DURING COVID-19

Miller Fellow **Alex Turner** (2017-2020) sends this update:

There has been quite a bit of speculation in the media on how the effects of this economic shutdown and shelter-in-place order on our carbon emissions. As a Miller Fellow, I've been involved with the Berkeley Environmental Air Quality & CO_2 Network (BEACO_2N; http://beacon.berkeley.edu). Our network has more than 60 instruments spread across the Bay Area measuring CO_2 and other trace gases. So I have spent quite a bit of my time at home delving into this data to quantify the impacts of this shelter-in-place on urban CO_2 emissions. Our preliminary data is showing fairly large changes to the diurnal cycle of CO_2.
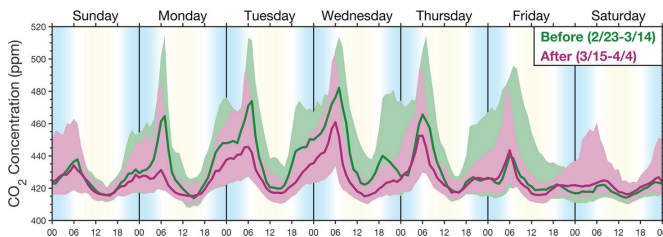
Contact Alex: alexjturner@berkeley.edu

MILLER MEMBERS DURING COVID-19

Qiong Zhang

Danqing Wang

with Pepper
Ekta Patel

baby mobile
Ruby Fu
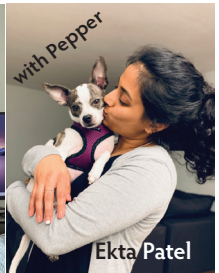
The Accelerating Universe, Dark Energy, and a New Surprise

Alex Filippenko
(alex@astro.berkeley.edu)

Miller Senior Fellow, and Professor of Astronomy, UCB

Miller Institute for Basic Research Zoom "Covid-19 Lunch"; 04/14/20

Empty Streets
by Yu He

Ambika Kamath & Yong Zheng

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