QUANTITATIVE & SYSTEMS BIOLOGY COLLOQUIUM: Rapid Adaptation and Extinction Across Climates in Synchronized Outdoor Evolution Experiments of *Arabidopsis thaliana*

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Date:
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Time:
10:30 AM – 11:45 AM

Location:
SSM 116

About The Speaker:

Evolutionary biologist, plant ecologist and geneticist Moises (Moi) Exposito-Alonso is an Assistant Professor of Integrative Biology at the University of California Berkeley and Freeman Hrabowski Scholar of the Howard Hughes Medical institute. He is also investigator in the Innovate Genomics Institute, and faculty part of the Center for Theoretical Evolutionary Genomics and the Center for Computational Biology. Moi received a BSc. in biology from the University of Seville (Spain) in 2013, working as an evolutionary ecologist in the Doñana Biological Station (CSIC), and conducted a MSc in Quantitative Genomics in 2014 at the University of Edinburgh (Scotland, UK). After earning his Ph.D. in plant genomics in 2018 at the Max Planck Institute (Germany), he started his independent group in 2019 at the Carnegie Institute for Science at Stanford University. Since 2024, he joined the faculty at University of California Berkeley and HHMI to combine experimental ecology, computational genomics, and evolution-inspired gene editing to understand whether and how plants will evolve to keep pace with climate change.

Abstract:

Increased threats of climate change in the survival of plant species, has put a spotlight on evolutionary adaptive processes that could aid in short ecological timescales. Although the paradigm that genetic evolution is a slow process is breaking down with new genomic data of wild populations, long-term plant evolution experiments across climates that can test the speed of evolution or its predictability do not exist yet. Here we conduct a synchronized evolution experiment with the plant *Arabidopsis thaliana* in over 30 outdoor experimental facilities across Europe, the Levant, and US—we called this GrENE-net.org. Genome sequencing of >70,000 surviving plants across climates allowed us to detect clear signals of climate-driven rapid adaptation, map genetic loci involved in adaptation in different environments, and test the repeatability of adaptation. This work showcases the importance of understanding the genetic basis of environmental adaptation of species to anticipate the impacts of global change in nature.

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