Stanford

Elisa Mariel Visher

Postdoctoral Scholar, Genetics

Bio

HONORS AND AWARDS

- NSF Postdoctoral Research Fellowship, NSF (2022-2024)
- PRISM-Baker Postdoctoral Research Fellowship, PRISM-Baker (2022-2023)
- Philomathia Fellowship, Philomathia Foundation, UC Berkeley (2020-2022)
- George Gilchrist Student Research Award, American Society of Naturalists (2020)
- NSF Graduate Research Fellowship, NSF (2017-2022)

PROFESSIONAL EDUCATION

- Doctor of Philosophy, University of California Berkeley (2022)
- Bachelor of Science, Yale University (2016)
- PhD, University of California, Berkeley , Integrative Biology (2022)
- BS, Yale University , Biology (Intensive) and Anthropology (2014)

STANFORD ADVISORS

- Gavin Sherlock, Postdoctoral Faculty Sponsor

LINKS

- Personal Website: https://elisavisher.weebly.com/

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Elisa Visher is broadly interested in the (co)evolution of life history strategies, niche breadth, diversification, and adaptability. They use mostly experimental evolution methods in microbial systems to test the predictions and assumptions of theoretical literature. Currently, they are especially interested in understanding the genetics of trade-offs in microbes to better understand patterns of diversity in nature and constraints to adaptation.

Elisa recently completed their PhD in Integrative Biology at University of California, Berkeley. There, they worked with Professor Mike Boots on the ecology and evolution of infectious disease. Their dissertation used experimental evolution methods in a moth and granulosis virus model system to study trade-offs to resistance and viral host range. They were especially interested in how trade-offs interacted with each other and with ecological and environmental conditions to shape optimal strategies. They also contributed to work on eco-evolutionary theory and zoonotic disease emergence.

At Stanford, Elisa is exploring how trade-off shapes change over time, depend on evolutionary history, and determine coevolutionary diversification. A key goal of their project will be to understand how genetic processes determine phenotypic trade-offs, and how these processes might explain observed patterns in the conditionality of trade-offs. This will be achieved by using barcoding methods in two model systems (one evolutionary yeast system and one coevolutionary Pseudomonas and phage system) to conduct high-throughput fitness assays in multiple environments (or on coevolved partners) and track lineage dynamics. The research will therefore have consequences for understanding adaptation to changing environments, anti-microbial resistance evolution, and disease emergence.

LAB AFFILIATIONS

- Gavin Sherlock (9/1/2022)
- Dmitri Petrov (9/1/2022)