



Multi-omic analysis of adaptation in experimental *Escherichia coli* populations by Dr. Megan Behringer

DATE

Monday,
November
26

TIME

2:00 - 3:00 PM

LOCATION

Health & Public
Affairs II, RM
345 - Video to Lake
Nona BBS 103

HOSTED BY

Faculty Cluster
Initiative, Genomics
and Bioinformatics
Cluster, and the
Burnett School of
Biomedical Sciences

Megan Behringer studies the genetic framework underling how microbial populations adapt to complex novel environments such as during infection or when new populations are established in nature. Upon colonization, competition for resources drives adaptation, which can result in innovation, diversification and even cooperation among individuals within the evolving microbial population.

Behringer uses laboratory populations of *Escherichia coli* K-12 which have been continuously evolving for over 40,000 generations in a spatially-structured, nutritionally-complex environment to examine the genetic mechanisms supporting within-species subpopulation structure. Utilizing a combination of population genomics, transcriptomics, proteomics, and metabolomics, she demonstrates the various strategies microbes utilize to colonize, adapt to, and eventually exploit new habitats and how these strategies are limited as nutrients become more scarce.



Megan Behringer Ph.D.

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