

Faculté des sciences et de génie Département de biochimie, de microbiologie et de bio-informatique



C O N

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Linda Horianopoulos

DOE Great Lakes Bioenergy Research Center, Wisconsin Energy Institute, Center for Genomic Science Innovation, University of Wisconsin-Madison

Yeast metabolic diversity: Insights from comparative and functional genomics

Mercredi 23 octobre 2024 à 11 h 15

Pavillon Charles-Eugène Marchand, salle Hydro-Québec (1210)

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Abstract:

Foundational studies on eukaryotic functional genomics have focused on the model organism *Saccharomyces cerevisiae*. However, there is incredible diversity across over 1,000 species of budding yeasts which not only include ethanologenic yeasts, but also pathogens and yeasts used for industrial lipid and protein production.

Understanding the genetic basis and regulation of diversity can have applications that benefit humankind, including two examples my work has focused on: diversity of stress resistance and of metabolic rates. We identified yeasts with high stress resistance and rapid metabolic rates. Genes that may influence these phenotypes were uncovered using comparative genomics and transcriptomics. Specifically, we found gene family expansions associated with oxidative stress resistance and transcriptional rewiring in novel species with rapid glycolysis. The roles of these genes were validated using molecular genetics. Starting with diverse species has facilitated novel discoveries and generated testable hypotheses to advance our understanding of yeast biology, diversity, and genomics.

My research program will use this framework to study yeast tolerance to a broader range of stresses and to optimize acid tolerant yeasts for bioproduction. Ultimately, I will use phenotyping, comparative genomics, machine learning, synthetic biology, and molecular genetics to make fundamental and applied discoveries in yeast biology.

Hôtes: Steve Charette et Michel Guertin