

MATTHEW E. MACGILVRAY

3105 Stevens Street, Apt. 4 • Madison, WI 53705
585.520.5246 • macgilvray@wisc.edu

MOLECULAR BIOLOGIST

- Solutions-focused and technically skilled-research professional with a demonstrated history of organizing individuals to complete large, multitask assignments.
- Highly analytical; able to identify performance indicators and effectively communicate progress in written reports to management.
- Excellent experimental design skills that have been implemented to develop new methods for answering challenging questions.

AREAS OF EXPERTISE

- Systems biology
- Next generation sequencing
- Quantitative proteomics/phospho-proteomics
- NeuCode SILAC/ SILAC
- Gene expression-microarrays, RNA-seq
- Chemostat operation
- Northern, Southern, and Western blots

TECHNICAL PROFICIENCIES

Software: Microsoft Office Suite; MacVector; Freehand 10; Endnote; Mendeley; GraphPad Prism; Ape; Cluster; Java TreeView; R; PyMOL

PROFESSIONAL EXPERIENCE

Research Scientist

BAUSCH AND LOMB, Rochester, NY

MARCH 2012-JULY 2012

Elucidating the molecular characteristics of *Staphylococcus aureus* that are associated with ocular infection and that are potential targets for treatment of ocular disease. Towards this goal, I conducted molecular testing to identify toxin and antibiotic resistance genes in both methicillin resistant (MRSA) and susceptible (MSSA) ocular isolates of *Staphylococcus aureus*.

Key Achievements:

- Using a PCR-based strategy, screened over 1000 *Staphylococcus aureus* clinical isolates for presence of the Pantone-Valentine leukocidin (PVL) toxin, a distinguishing characteristic that identifies hospital acquired versus community acquired MRSA
- Classified MRSA isolates according to their SCCmec type, elucidating the types most prevalent in eye infection
- Performed antimicrobial susceptibility (MIC) testing to identify MRSA isolates and determine drug resistance profiles

Laboratory Technician IV

UNIVERSITY OF ROCHESTER SCHOOL OF MEDICINE AND DENTISTRY, Rochester, NY

2007-2011

Oversaw the design and execution of a multi-million dollar project focused on identifying genes involved in *Streptococcus mutans* environmental stress response. Towards this goal, I attempted to delete all non-lethal genes in the organism's genome. The knockouts were then subjected to various stresses to determine if the deletion leads to an effect on the survival of the strain after acid or oxidative conditions.

Key Achievements:

- Generated over 1200 *S. mutans* deletion strains
- Developed a new method for complement strain construction
- Collaborated with team members to troubleshoot problems and find creative, cost-effective, time-saving solutions, such as the implementation of a rapid gel electrophoresis system
- Developed and implemented databases to organize data
- Recognized for outstanding contributions; promoted from Laboratory Technician III to IV
- Trained and mentored colleagues and staff in molecular biology techniques

EDUCATION AND TRAINING

Doctor of Philosophy in Microbiology

August 2012 - Present

Advisor: Dr. Audrey Gasch

UNIVERSITY OF WISCONSIN-MADISON, Madison, WI

I am utilizing transcriptomic and proteomic approaches to better understand stress response in *Saccharomyces cerevisiae*. Although yeast alter the expression of ~1000 stress response genes upon environmental insult, the upstream signaling pathways that regulate their expression are poorly understood. To address this, I am using computational methods to construct inferred signaling networks that will be tested experimentally using deletion mutants. I hope to determine factors that act as "hubs" in yeast stress signaling while also identifying nodes unique to individual stresses.

Key Achievements:

- Designed a 3'-end RNA-seq protocol for gene expression quantification
- Helped develop and implement a protocol for metabolic labeling of yeast cultures using NeuCode SILAC, which permitted quantitative proteomics at high levels of multiplexing

Master of Science in Microbiology

October 2011

Advisor: Dr. Robert Quivey

UNIVERSITY OF ROCHESTER SCHOOL OF MEDICINE AND DENTISTRY, Rochester, NY

I used biochemical and genetic approaches to investigate the role of membrane lipids in *S. mutans* acid stress tolerance. I identified cardiolipin as a factor that contributed to the acid-adaptive response. Mass spectrometry revealed cardiolipin as a reservoir for unsaturated fatty acids, lipid components previously shown to confer acid resistance in other organisms.

Key Achievements:

- Designed and implemented fluorescence anisotropy and lateral diffusion protocols to determine how lipids affect membrane fluidity
 - Developed lipid extraction and mass spectrometry methods to determine lipid composition of *S. mutans*
-

Bachelor of Arts

Major: Biology

May 2007

STATE UNIVERSITY OF NEW YORK AT GENESEO, Geneseo, NY

PUBLICATIONS AND ABSTRACTS

Baker JL, Derr AD, Karuppaiah K, **MacGilvray ME**, Kajfasz JK, Faustoferri RC, Rivera-Ramos I, Bitoun JP, Lemos JA, Wen ZT, Quivey, Jr RG. *Streptococcus mutans* NADH oxidase lies at the intersection of overlapping regulons controlled by oxygen and NAD⁺ levels. J Bacteriol. Submitted 2014 Feb.

Anna E. Merrill, Alexander S. Hebert, Gregory K. Potts, **Matthew E. MacGilvray**, Christopher M. Rose, Emily A. Voigt, Derek J. Bailey, Joel C. Bradley, William W. Wood, Marwan ElMasri, Michael S. Westphall, John Yin, Audrey P. Gasch, Joshua J. Coon. NeuCode labels for relative and absolute quantification. Nature Biotechnology. Submitted 2014 Jan.

Deborah Chasman, Yi-Hsuan Ho, David B. Berry, Corey M. Nemecek, **Matthew E. MacGilvray**, James Hose, Anna E. Merrill, M. Violet Lee, Jessica L. Will, Aseem Z. Ansari, Joshua J. Coon, Mark Craven, Audrey P. Gasch. Coordination and interconnectivity in the inferred stress-activated signaling network from yeast. MolSysBio. Submitted 2014 Jan.

MacGilvray ME, Lapek JD, Friedman AE, Quivey RG. Cardiolipin biosynthesis in *Streptococcus mutans* is regulated in response to external pH. Microbiology. 2012 Aug; 158(8):2133-2143.

Santiago B, **MacGilvray M**, Faustoferri RC, Quivey RG. The branched-chain amino acid aminotransferase encoded by *ilvE* is involved in acid tolerance in *Streptococcus mutans*. J Bacteriol. 2012 Apr; 194(8):2010-9.

Association for Research in Vision and Ophthalmology, Seattle, WA. May 5–9, 2013. Prevalence and characteristics of MRSA from clinical conjunctivitis trials versus ocular surveillance studies. Timothy W. Morris, Christine M. Sanfilippo, Christine K. Hesje, **Matthew E. MacGilvray**, and Wolfgang Haas. Bausch & Lomb, Inc., Rochester, NY, USA.

Association of Dental Research, General Session, Barcelona, Spain. July 14-17, 2010. The role of lipids in acid adaptation of *Streptococcus mutans*. **M. MacGilvray**, R. Faustoferri, R. Quivey Jr.

American Society for Microbiology 108th General Meeting (ASM), Boston, MA. June 1-5, 2008. Branched chain fatty acids in the membrane of *Streptococcus mutans* deficient for *fabM*. M. Courtney, R. Faustoferri, C. Hubbard, **M. MacGilvray**, R. G. Quivey.