

# 5<sup>th</sup> Year Committee Meeting



Sarah Stevens  
@microStevens  
McMahon Lab

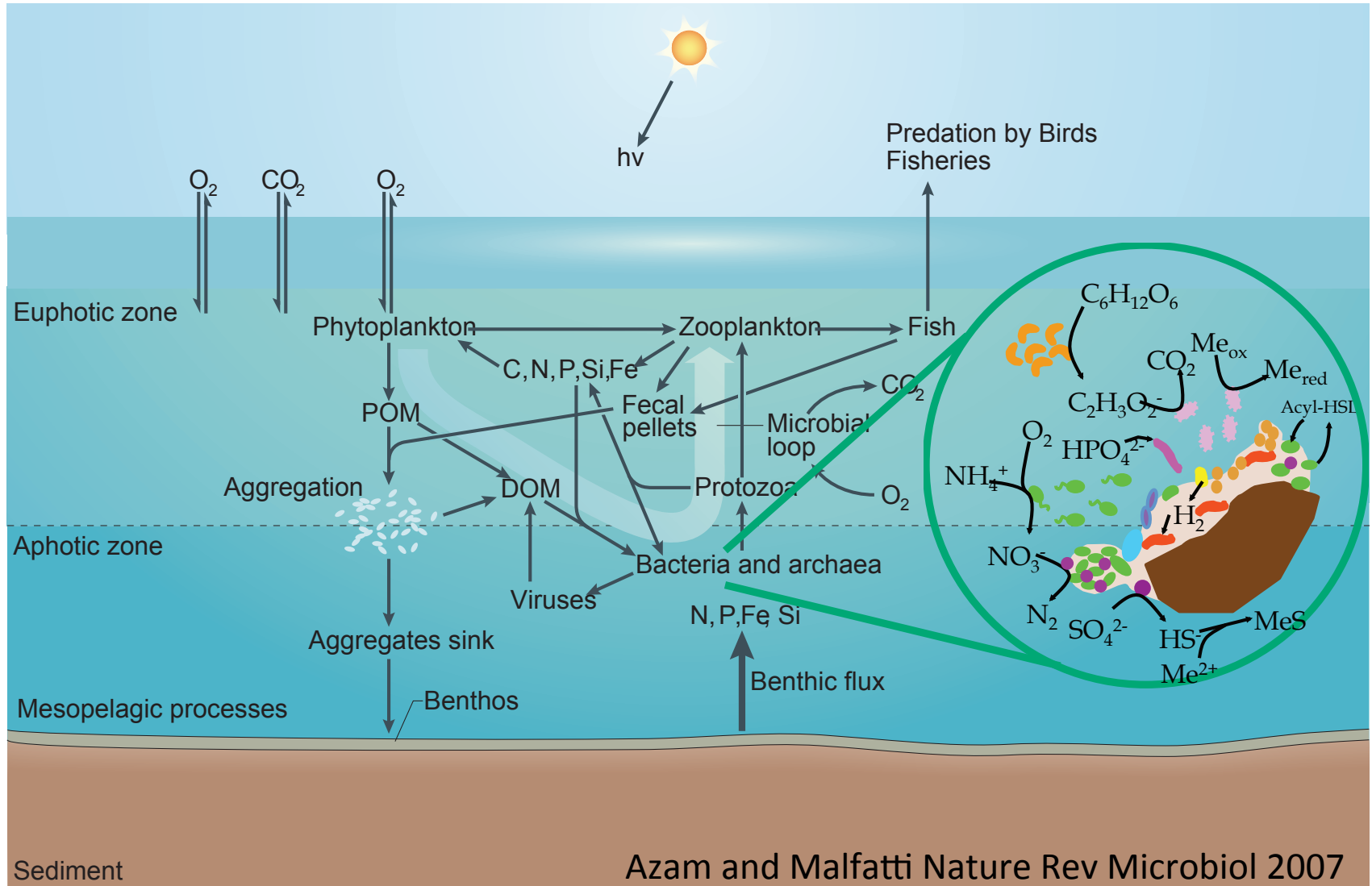
# Agenda

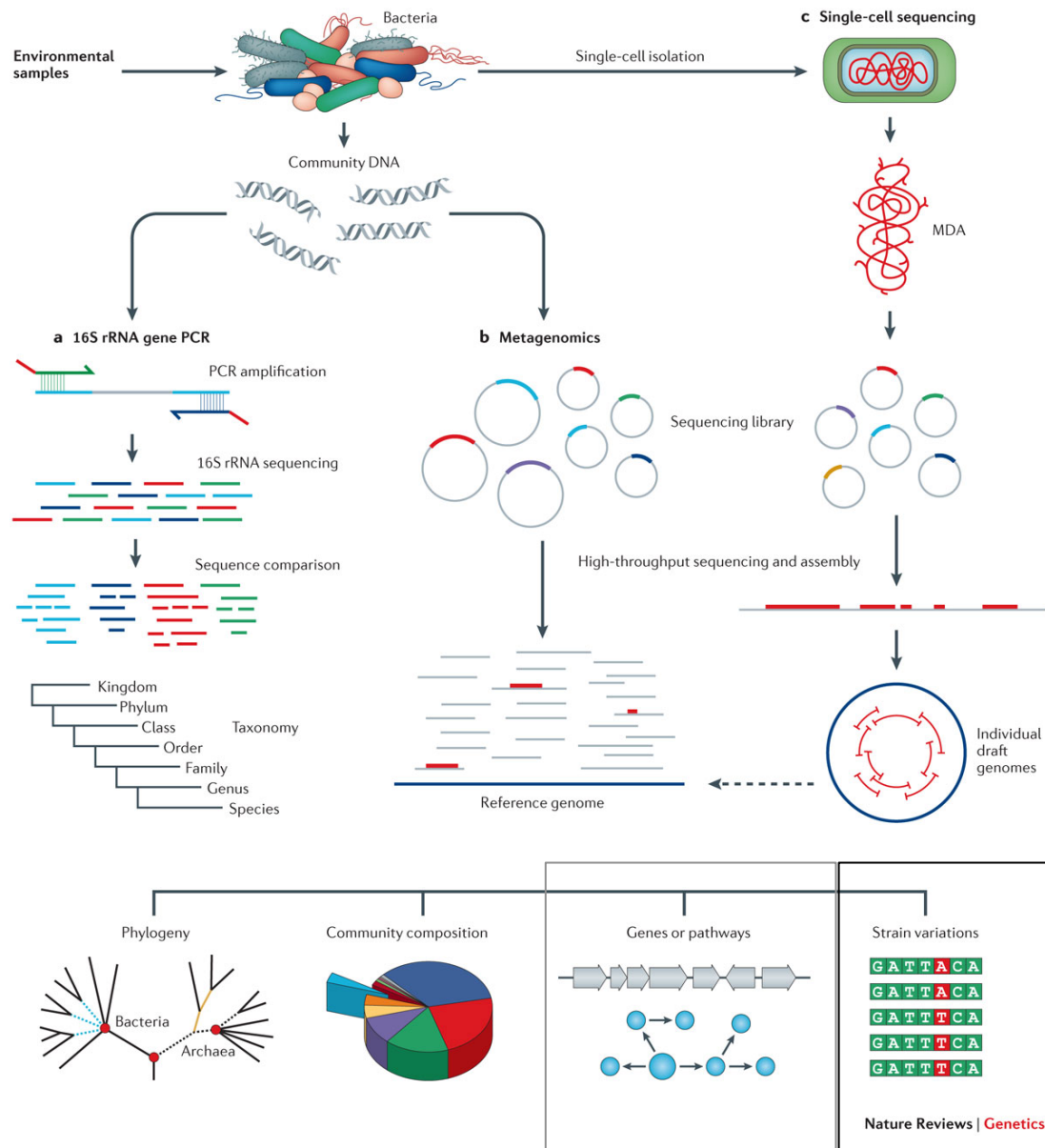
- Updates
- Short Intro
- Current Project
- Goals/Timeline

# Updates

- 2nd Paper accepted in ISME
  - Contrasting patterns of genome-level diversity across distinct co-occurring populations
- Taught 4 Data/Software Carpentry Workshops
- Attended Anvi'o Workshop
- Taught Anvi'o Workshop
- Attended Open Science Grid User School
- Attended Microbial Population Biology GRC
- 'Retired' from leading ComBEE

# Microbes Perform Many Nutrient Transformations in Lakes







## ORIGINAL ARTICLE

# Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations

Matthew L Bendall<sup>1,8</sup>, Sarah LR Stevens<sup>2,8</sup>, Leong-Keat Chan<sup>1</sup>, Stephanie Malfatti<sup>1</sup>, Patrick Schwientek<sup>1</sup>, Julien Tremblay<sup>1</sup>, Wendy Schackwitz<sup>1</sup>, Joel Martin<sup>1</sup>, Amrita Pati<sup>1</sup>, Brian Bushnell<sup>1</sup>, Jeff Froula<sup>1</sup>, Dongwan Kang<sup>1</sup>, Susannah G Tringe<sup>1</sup>, Stefan Bertilsson<sup>3</sup>, Mary A Moran<sup>4</sup>, Ashley Shade<sup>5</sup>, Ryan J Newton<sup>6</sup>, Katherine D McMahon<sup>2,7</sup> and Rex R Malmstrom<sup>1</sup>

<sup>1</sup>DOE Joint Genome Institute, Walnut Creek, CA, USA; <sup>2</sup>Department of Bacteriology, University of Wisconsin-Madison, Madison, WI, USA; <sup>3</sup>Department of Ecology and Genetics, Limnology and Science for Life Laboratory, Uppsala University, Uppsala, Sweden; <sup>4</sup>Department of Marine Sciences, University of Georgia, Athens, GA, USA; <sup>5</sup>Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI, USA; <sup>6</sup>School of Freshwater Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI, USA and <sup>7</sup>Civil and Environmental Engineering, University of Wisconsin-Madison, Madison, WI, USA

**Multiple models describe the formation and evolution of distinct microbial phylogenetic groups. These evolutionary models make different predictions regarding how adaptive alleles spread through populations and how genetic diversity is maintained. Processes predicted by competing evolutionary models, for example, genome-wide selective sweeps vs gene-specific sweeps, could be captured in natural populations using time-series metagenomics if the approach were applied over a sufficiently long time frame. Direct observations of either process would help resolve how distinct microbial**

# Current Project

**Table 1. Stages of microbial speciation under different rates of selection and homologous recombination<sup>a</sup>**

	(A) $r/s \gg 1$	(B) $r/s \ll 1$
Stage 1	New niche-specifying variant(s) acquired by mutation, homologous recombination, or HGT	
Stage 2	Ecological separation: new variant spreads in new niche by recombination	Ecological separation: new variant spreads in new niche by clonal expansion
Stage 3	Genetic separation driven by genome-wide depression in recombination between new and ancestral niches	Genetic separation driven by periodic selection and drift
Stage 4	Genetic separation maintained by genetic barriers to recombination, including sequence divergence and epistasis; otherwise lineages may merge back together	Genetic separation maintained by further periodic selection and drift events; lineages are permanently separate
Stage 5	Lineages remain ecologically and genetically distinct (at both adaptive and neutral loci, genome-wide) until extinction	

<sup>a</sup>The relative influence of selection [ $s$ , the average fitness difference experienced by a niche-specifying (adaptive) allele in different niches] and recombination ( $r$ , the recombination rate per locus per generation) is expressed as the  $r/s$  ratio. The stages represent rough, potentially overlapping, and potentially terminal steps (e.g., Stage 2 need not lead to Stage 3).



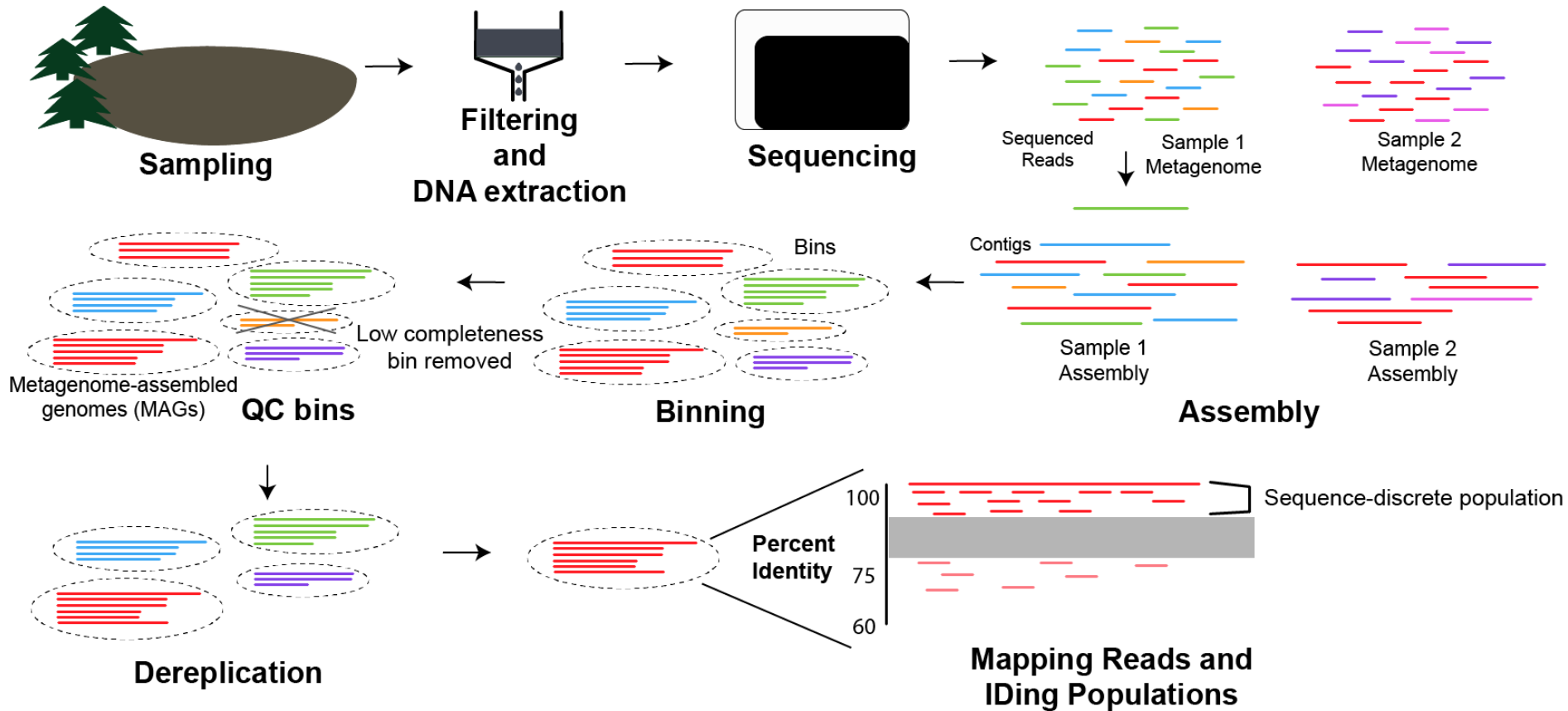
# Questions

- Are there ecologically distinct strains/genotypes within previously defined sequence-discrete populations?
- What stage of speciation are these distinct strains/genotypes at in their separation?
- Is there a barrier to recombination between co-existing strains?

# Stats on Metagenomes

- Crystal Bog
  - 2007-2009
  - 82 metagenomes
  - 20 Gbp assembled
- Mary Lake
  - 2009, 12 depths
  - 12 metagenomes
  - 11 Mbp assembled
- Mendota
  - 2008-2012
  - 94 metagenomes
  - 11 Gbp assembled
- Trout Bog
  - epilimnion
    - 2007-2009
    - 47 metagenomes
  - hypolimnion
    - 2005, 2007-2009, 2012-2013
    - 82 metagenomes

# Data Processing



# Stats on MAGs so far

- Crystal Bog
  - 2505 bins, 564 passed filtering
  - Phyla with > 10 bins:
    - Actinobacteria(342), Proteobacteria(267), Verrucomicrobia(113), Bacteroidetes(41), Candidatus Saccharibacteria(31), Chlorobi(29), Parcubacteria (10),
- Mary Lake
  - 352 bins, 104 passed filtering
  - Phyla with > 10 bins:
    - Proteobacteria(99), Actinobacteria(34), Planctomycetes(21), Verrucomicrobia(18), Bacteroidetes(18), Cyanobacteria(11)

# Goals/Timeline

