Supplmentary Material for ‘Metabolic Network Analysis and Metatranscriptomics of a Cosmopolitan and Streamlined Freshwater Lineage’

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# Supplementary Methods

## A Freshwater Reference Genome Collection

This study relies on an extensive collection of freshwater bacterial genomes, containing MAGs obtained from two metagenomic time-series from two Wisconsin lakes, as well as SAGs from three lakes in the United States. Additional information about this genome collection can be found below.

### Single-Cell Genome Generation, Selection, and Sequencing

Water samples were collected from the top of the water column (depth <1m) from each of three lakes, Lake Mendota (Madison, WI, USA), Sparkling Lake (Vilas County, WI, USA), and Damariscotta Lake (Lincoln County, ME, USA), in 2009. Samples were cryopreserved and sent to the Single Cell Genomics Center at the Bigelow Laboratory for Ocean Sciences for sorting, as previously described (Martinez-Garcia *et al.*, 2012; Garcia *et al.*, 2013). Partial 16S rRNA genes amplified previously (Martinez-Garcia *et al.*, 2012) were phylogenetically classified using a controlled nomenclature for freshwater bacteria (Newton *et al.*, 2011) by insertion into references trees created in the ARB software package (Ludwig *et al.*, 2004).

Actinobacterial SAGs used in this study were then sent to the JGI for sequencing and assembly, also as previously described (Ghylin *et al.*, 2014). Briefly, shotgun libraries were constructed for each of the SAGs from re-amplified MDA products and sequenced on an Illumina HiSeq2000. All general aspects of and detailed protocols for library construction and sequencing can be found on the JGI website (http://www.jgi.doe.gov/).

For assembly, raw sequence data was first passed through a filtering program developed at JGI to eliminate known sequencing and library preparation artifacts. Assembly was then performed using Velvet (Zerbino and Birney, 2008) and ALLPATHS-LG (Gnerre *et al.*, 2011). Additional details of the assembly process have been previously described (Ghylin *et al.*, 2014) and are available through the JGI Genome Portal (http://genome.jgi.doe.gov) Genome sequences are available through IMG (https://img.jgi.doe.gov/cgi-bin/mer/main.cgi). Genome-specific information can be accessed in both databases by searching for the IMG Taxon OIDs given in Table 1.

### Metagenome Sampling, Sequencing, Assembly, and Binning

Water samples were collected from two lakes, Lake Mendota (Madison, WI, USA) and Trout Bog (Vilas County, WI, USA). For Lake Mendota, depth-integrated water samples were collected from the top 12 meters at 96 time points during ice-free periods from 2008 to 2011. For Trout Bog, depth-integrated water samples were collected from the epilimnion (44 samples) and hypolimnion (45 samples) layers during ice-free periods from 2007 to 2009.

Sample collection, DNA sequencing, and metagenomic assembly, have been described previously (Bendall *et al.*, 2016; Garcia *et al.*, 2016), as well as genomic binning for the Trout Bog samples (Bendall *et al.*, 2016). Similar genomic binning procedures were followed for the Lake Mendota samples. A summary is provided here.

All samples were filtered on 0.2 μm polyethersulfone filters (Supor, Pall Corp) prior to storage at -80°C, as described previously (Bendall *et al.*, 2016; Garcia *et al.*, 2016). DNA was extracted from these filters using the FastDNA kit (MP Biomedicals) and sent to the JGI for sequencing, as described previously (Bendall *et al.*, 2016; Garcia *et al.*, 2016).

Shotgun libraries were constructed for each of the samples and sequenced on an Illumina HiSeq2000, following a 2x150 indexed run recipe as previously described (Bendall *et al.*, 2016; Garcia *et al.*, 2016). All general aspects of and detailed protocols for library construction and sequencing can be found on the JGI website (http://www.jgi.doe.gov/). Metagenomic sequence reads are publicly available on the JGI Genome Portal (http://genome.jgi.doe.gov/) under Proposal ID 394. The full list of metagenomes is given in Table S12.

Raw sequence data was passed through a filtering program developed at JGI to eliminate known sequencing and library preparation artifacts. Prior to assembly, reads were merged with FLASH (Magoc and Salzberg, 2011), as previously described (Bendall *et al.*, 2016; Garcia *et al.*, 2016). Merged reads were pooled by lake and layer into three co-assemblies using SOAPdenovo (Luo *et al.*, 2012), and contigs from the resulting assemblies were assembled into a final assembly using Minimus (Sommer *et al.*, 2007), as previously described (Bendall *et al.*, 2016; Garcia *et al.*, 2016). Additional details of the assembly process are available through the JGI Genome Portal (http://genome.jgi.doe.gov) under Proposal ID 394. The full list of assemblies is given in Table S13.

Genomes were binned from each metagenomic co-assembly using MetaBat (Kang *et al.*, 2015), as described previously (Bendall *et al.*, 2016). Briefly, contigs were classified into bins using tetranucleotide frequency and coverage patterns across the time-series and then manually curated, as previously described (Bendall *et al.*, 2016). Genome sequences are available through IMG (https://img.jgi.doe.gov/cgi-bin/mer/main.cgi), and can be accessed by searching for the IMG Taxon OIDs given in Table 1.

Genomes were classified using taxonomic assignments from a set of 37 highly-conserved single-copy marker genes using Phylosift (Darling *et al.*, 2014), as previously described (Bendall *et al.*, 2016).

## Metatranscriptome Sampling and Sequencing

**Note: This material can be dropped since I do not use the internal standard. However, readers who consult the GitHub repo may be curious about the standard.**

This study used four metatranscriptomes obtained as part of a 24-hour sampling experiment designed to identify diel trends in freshwater microbial communities (unpublished study). Prior to RNA extraction, three samples were spiked with an internal standard to enable quantification of total transcript abundance, following an established protocol (Satinsky *et al.*, 2014). Briefly, a 970-nucleotide-long mRNA standard was synthesized using a a T7 RNA polymerase and the Riboprobe In Vitro Transcription System (Promega, Madison, WI), according to the manufacturer’s protocol. A fixed quantity of each standard (1.172 x 10^10 copies) was added independently to each lysis tube immediately prior to the addition of the sample filter. The DNA sequence of the internal standard follows.

### DNA Sequence of Internal standard

GGGTATTTTAACTTTACTAAGGAGAATTCATCATGGCAGAAATCGGTACTGGCTTTCCATTCGACCCCCATTATGTGGAAGTCCTGGGCGAGCGCATGCACTACGTCGATGTTGGTCCGCGCGATGGCACCCCTGTGCTGTTCCTGCACGGTAACCCGACCTCCTCCTACGTGTGGCGCAACATCATCCCGCATGTTGCACCGACCCATCGCTGCATTGCTCCAGACCTGATCGGTATGGGCAAATCCGACAAACCAGACCTGGGTTATTTCTTCGACGACCACGTCCGCTTCATGGATGCCTTCATCGAAGCCCTGGGTCTGGAAGAGGTCGTCCTGGTCATTCACGACTGGGGCTCCGCTCTGGGTTTCCACTGGGCCAAGCGCAATCCAGAGCGCGTCAAAGGTATTGCATTTATGGAGTTCATCCGCCCTATCCCGACCTGGGACGAATGGCCAGAATTTGCCCGCGAGACCTTCCAGGCCTTCCGCACCACCGACGTCGGCCGCAAGCTGATCATCGATCAGAACGTTTTTATCGAGGGTACGCTGCCGATGGGTGTCGTCCGCCCGCTGACTGAAGTCGAGATGGACCATTACCGCGAGCCGTTCCTGAATCCTGTTGACCGCGAGCCACTGTGGCGCTTCCCAAACGAGCTGCCAATCGCCGGTGAGCCAGCGAACATCGTCGCGCTGGTCGAAGAATACATGGACTGGCTGCACCAGTCCCCTGTCCCGAAGCTGCTGTTCTGGGGCACCCCAGGCGTTCTGATCCCACCGGCCGAAGCCGCTCGCCTGGCCAAAAGCCTGCCTAACTGCAAGGCTGTGGACATCGGCCCGGGTCTGAATCTGCTGCAAGAAGACAACCCGGACCTGATCGGCAGCGAGATCGCGCGCTGGCTGTCGACGCTCGAGATTTCCGGCGAGCCAACCACTGAGGATCTGTACTTTCAGAGCGATAACGCGATCGC

# Supplementary Results and Discussion

## Computation of Potential Seed Compounds

Metabolic network reconstructions for individual genomes contained between 110 and 339 genes, encoding between 241 and 587 reactions which interconvert between 374 and 699 metabolites (Table S14). On average, these genes account for 25% of the genes in the genome, a value consistent with metabolic network reconstructions for other organisms (see Supplementary Table 2 in Feist *et al.*, 2009). Clade-level composite metabolic network graphs were larger, with between 602 and 811 metabolites (Table S15).

These composite metabolic network graphs contained a large number of disconnected components (groups of nodes that are not connected to the bulk of the network, Figure S4). For simplicity, these components were dropped from the graph, and seed compounds were computed for the single largest component. In all cases, the single largest component contained at least 80% of the nodes in the original graph (Table S15).

Decomposition of the three metabolic network graphs into their strongly connected components (SCCs) resulted in a bow-tie structure, in which a single giant component contains a substantial fraction of the compounds (Figure S4). Across the three clades, the giant component contained 61% of the metabolites, a larger fraction than reported for other organisms (Ma and Zeng, 2003), which may be a consequence of the small and streamlined genomes of acI bacteria.

The total number of predicted seed sets (source components in the SCC condensation) ranged from 63 to 95, and the number of seed compounds ranged from 70 to 102 (Table S15). This discrepancy arises because some seed sets contain multiple compounds (Table S16). However, such seed sets were rare (4% of all seed sets), and contained at most six compounds (Table S16). The majority of seed compounds (96%) belonged to seed sets containing only a single compound (Table S16).

## Evaluation of Potential Seed Compounds

Here, we present a series of brief vignettes explaining why particular compounds were retained or discarded based on their biological (im)plausibility. For biologically plausible compounds, we also provide examples of manual curation efforts. These vignettes are not intended to provide a comprehensive explanation for all compounds, but to provide a flavor of the types of decisions that went into accepting or rejecting particular compounds.

**Carbamoyl phosphate**. Carbamoyl phosphate was predicted as a seed compound for all three clades. Carbamoyl phosphate synthase is the first step in arginine and pyrimidine biosynthesis, and catalyzes the reaction:

2 ATP + L-glutamine + hydrogen carbonate + H2O → L-glutamate + carbamoyl phosphate + 2 ADP + phosphate + 2 H+

This reaction contains a number of currency metabolites (ATP, ADP glutamine, glutamate), as well as the highly-connected metabolites carbonate, water, phosphate and protons. All of these metabolites were removed from the network during pruning. Thus, the reaction responsible for carbamoyl phosphate synthesis was effectively removed from the network, rendering carbamoyl phosphate a seed compound. Manual inspection of individual genomes revealed the gene for carbamoyl phosphate synthase, confirming carbamoyl phosphate is not an auxotrophy.

**R-enoyl-ACP**. A number of R-enoyl-ACP compounds were predicted to be seed compounds in clades acI-A and acI-B. These compounds were associated with a single COG annotated as an “Enoyl-[acyl-carrier-protein] reductase,” the enzyme which catalyzes the final step in fatty acid elongation. Many other seed compounds were predicted to participate in fatty acid and phospholipid biosynthesis, including a number of saturated fatty acids (associated with a COG annotated as a “long-chain-fatty-acid–CoA ligase”) and 1-acyl-sn-glycerol 3-phosphate compounds (associated with a COG annotated as an “1-acyl-sn-glycerol-3-phosphate acyltransferase”). Given the broad substrate specificity of these enzymes, KBase automatically assigns these enzymes to the catalysis of a number of reactions. Fatty acid and phospholipid biosynthesis pathways are often organism-specific and unlikely to be properly annotated by automatic metabolic reconstruction pipelines. Thus, these compounds were excluded from further consideration.

**L-Aspartate-4-semialdehyde, L-homoserine, and O-Phospho-L-homoserine.** Clade acI-C was predicted to have a seed set containing these three compounds. These three compounds can be interconverted via the following reactions:

homoserine dehydrogenase: L-aspartate-4-semialdehyde <–> L-homoserine

homoserine kinase: L-homoserine <–> O-phospho-L-homoserine

making the three compounds members of a SCC. The first reaction, homoserine dehydrogenase, is the final step in homoserine biosynthesis, so these compounds suggest an auxotrophy for homoserine. Homoserine biosynthesis proceeds via the following reactions:

aspartate kinase: aspartate –> L-aspartyl-4-phosphate

aspartate semialdehyde dehydrogenase: L-aspartyl-4-phosphate –> L-aspartate-4-semialdehyde

homoserine dehydrogenase: L-aspartate-4-semialdehyde –> homoserine

The presence of L-aspartate-4-semialdehyde as a seed compound suggests the reaction “aspartate semialdehyde dehydrogenase” is missing, and were unable to manually identify a candidate gene for this reaction. Furthermore, the acI-C composite genome contains the other two reactions in the pathway. Thus, on the evidence available, we conclude acI-C is auxotrophic for homoserine.

**L-arogenate.** This compound was predicted as a seed compound for clade acI-C, suggesting an auxotrophy for tyrosine. Tyrosine can be synthesized via the following reactions:

chorismate mutase: chorismate –> prephenate

prephenate aminotransferase: prephanate –> L-arogenate

arogenate dehydrogenase: L-arogenate –> L-tyrosine

L-arogenate was predicted to be a seed compound based on the presence of “arogenate dehydrogenase”, the final step in the pathway. The reaction “chorismate mutase” is also present, but we were unable to find a candidate gene for the reaction “prephenate aminotransferase,” suggesting an auxotrophy for tyrosine. However, L-tyrosine can be synthesized from chorismate via an alternative pathway:

chorismate mutase: chorismate –> prephenate

prephenate dehydrogenase: prephenate –> 4-hydroxyphenylpyruvate

tyrosine aminotransferase: 4-hydroxyphenylpyruvate –> L-tyrosine

All three genes in this pathway are present in the genome, indicating acI-C is not auxotrophic for tyrosine.

**Ala-Leu and gly-pro-L**. These di-peptides were predicted to be seed compounds for all three clades. The compounds are associated with the following reactions:

H2O + Ala-Leu –> L-Leucine + L-Alanine

H2O + Gly-Pro –> Glycine + L-Proline

These reactions were associated with four COGs, annotated as aminopeptidases. These seed compounds suggest the ability for the acI to degrade peptides, but the broad specificity of aminopeptidases means these particular di-peptides are unlikely to be the only substrates. Similarly, a number of seed compounds were associated with COGs annotated as gluco- and galactosidases, which also have broad substrate specificity. As a result, these genes were further investigated as described in the primary manuscript.

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