Diversity and Abundance of Arsenic Resistant Genes in Soil Microbiomes

Susanna Yeh iCER ACRES Presentation, 7/27/17

Arsenic is the most Ubiquitous Toxic Element

Arsenic (As) terrorizes the metabolism process

Arsenate (As(V)) is similar to phosphate and can substitute in pathways

Exposure is related to cancer, cardiovascular disease, diabetes, neuropathy

As is present in groundwater and soil

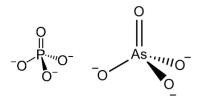
Bacteria influence the As cycle in the environment

As toxicity and bioavailability depends on oxidation and methylation states

Arsenate (As(V)): less mobile

Arsenite (As(III)): more mobile and toxic

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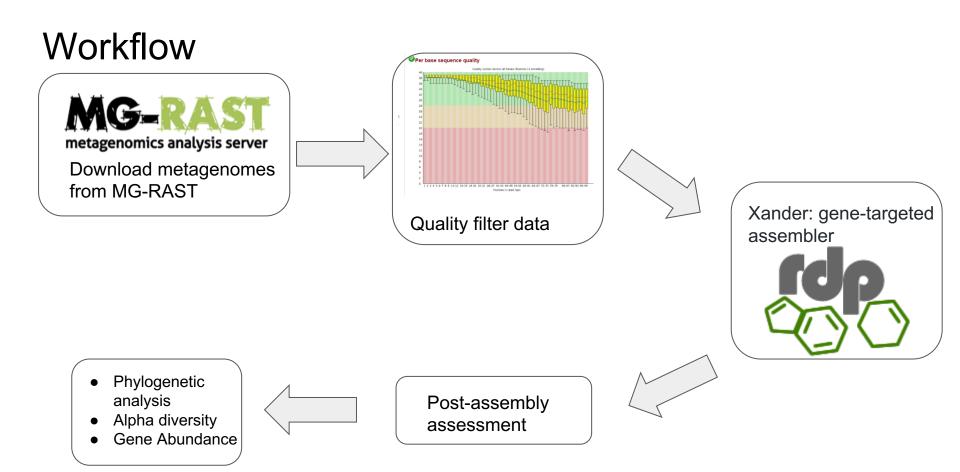


Not Much is Known about AsRG Diversity

Arsenic resistant genes (AsRG) are well-studied in cultivated bacteria
There is an increasing number of soil metagenomes available; it is possible to identify phylogenetic distribution and diversity
Better understanding of this diversity leads to improvement in As bioremediation process and risk assessment

Objectives:

- Compare AsRG in non-contaminated soil microbiomes
 - 12 sites, 2-3 samples per site, 5 countries
- Examine phylogeny of AsRG
- Expand the known diversity of AsRG
- Analyze abundance of AsRG in diverse soils



Diverse Datasets were Chosen

Sample ID	Coordinates	Sampling Date	Average Genome Size	Giga Base Pairs	MG-RAST Sample ID
lowa_corn22.3	41, -92	2009-06-28	5,248,659	8.19	4539522.3
lowa_corn23.3			5,208,064	8.12	4539523.3
lowa_agricultural00.3	42, -93	2012-07-19	6,203,490	24.98	4509400.3
Mangrove02.3	4, 100	2014-10-02	5,979,725	24.38	4603402.3
Mangrove70.3			6,005,221	24.54	4603270.3
Permafrost_Russia12.3	68, 161	2007-08-05	5,135,678	20.05	4546812.3
Permafrost_Russia13.3			5,131,959	19.2	4546813.3
Iowa_prairie75.3	42, -93	2009-06-28	6,994,965	18.79	4539575.3
Iowa_prairie72.3			7,169,200	17.58	4539572.3
Iowa_prairie76.3			7,088,957	17.43	4539576.3
Brazilian_forest95.3	10, 63	2010-01-01	5,787,131	13.27	4546395.3
Brazilian_forest39.3			8,789,768	9.04	4536139.3
Brazilian_forest54.3			8,371,924	9.69	4535554.3
Minnesota_creek46.3	45, -93	2013-06-05	6,504,862	10.65	4541646.3
Minnesota_creek45.3			6,057,590	9.77	4541645.3
Disney_preserve18.3	28, -81	2013-11-14	6,888,257	11.2	4664918.3
Disney_preserve25.3			7,230,169	4.14	4664925.3
California_grassland15.3	34, -118	2010-12-17	7,414,208	6.5	4511115.3
California_grassland62.3			12,981,156	5.77	4511062.3
Illinois_soil91.3	42, -88	2010-11-19	7,441,858	7.95	4653791.3
Illinois_soil88.3			6,954,025	7.14	4653788.3
Wyoming_soil22.3	48 -111	2013-07-16	5,354,164	0.82	4670122.3
Wyoming_soil20.3			5,350,858	6.41	4670120.3
Permafrost_Canada23.3	79, 91	2011-05-01	3,932,079	6.52	4523023.3
Permafrost_Canada45.3			4,719,216	5.52	4523145.3

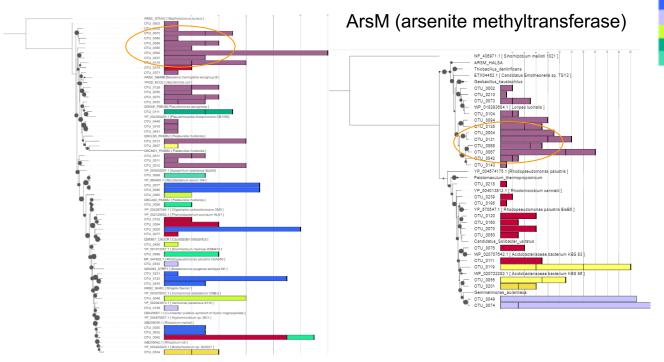
Full-length, High-Quality Sequences Assembled

Gene	Protein Function	Xander Max Length Assembled (aa)	Xander Model Length (aa)	Xander Max Percent Identity
aioA	Arsenite oxidase	815	837	97.619
arxA	Arsenite oxidase	508	831	95.652
arsM	Arsenite methyltransferase	217	269	96.154
acr3	Arsenite efflux pump	351	363	100
arsB	Arsenite efflux pump	266	430	100
arsC glut	Cytoplasmic arsenate reductase	116	117	100
arsC thio	Cytoplasmic arsenate reductase	83	133	100
arrA	Dissimilatory arsenate reductase	842	846	96.629
arsD	Arsenite metallochaperone	124	123	100
rplB	50S ribosomal protein L2	279	277	98.909

- aioA, acr3, arsC glut, arrA, arsD, rpIB have sequences >=90% of the HMM model length
- Each gene has a high maximum percent identity, giving more confidence to the model
- Xander can assemble near full-length sequences for each gene of interest

Potential Novel Diversity of AsRG

ArsC glut (arsenate reductase)

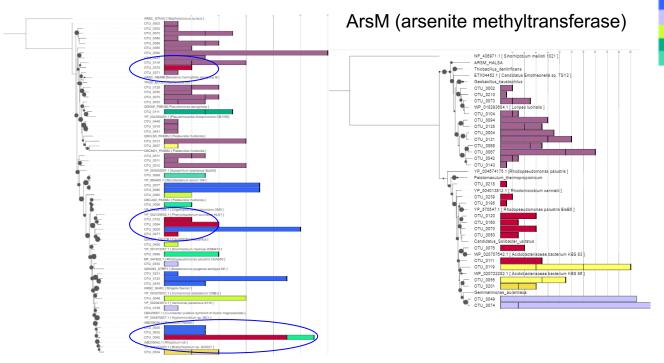


Iowa prairie Illinois soil California grassland Illinois soil Disney preserve Mangrove Permafrost Russia Permafrost Canada Wyoming soil Iowa corn Minnesota creek

- Sequences >= 90% of model length
- OTUs are assembled from metagenomes, clustered at 90% ID
- Accession numbers are from seed sequences and blast nr database
- Phylogeny is diverse within and across microbiomes

Phylogeny is diverse

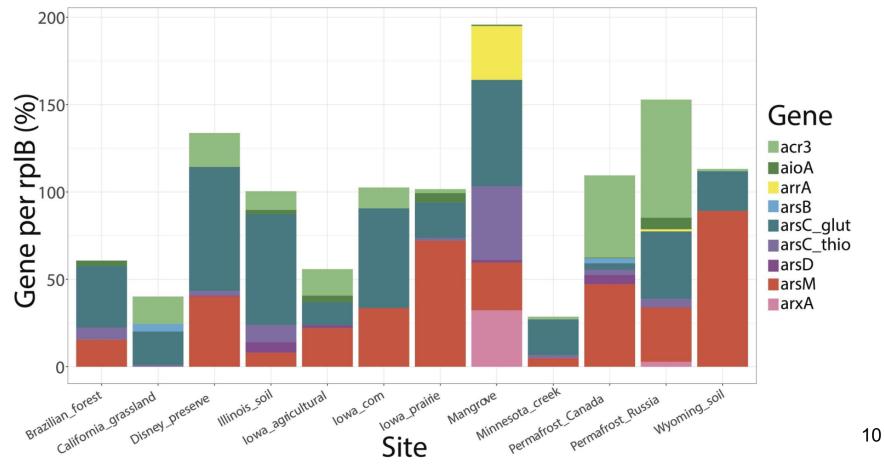
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Normalized AsRG Abundance Varies



Conclusions

Abundance and phylogeny of AsRG are diverse within and across microbiomes

Diverse microbiomes have the genetic potential to transform arsenic

Xander can assemble near full-length, high-quality contigs for AsRG

Future Direction

Include contaminated site for comparison

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