

Introduction

Arsenic (As) is the most ubiquitous toxic element and is naturally present in soils. Exposure to As is linked to many diseases.¹ Globally, an estimated 150 million people are exposed to unsafe levels of As in their drinking water.²

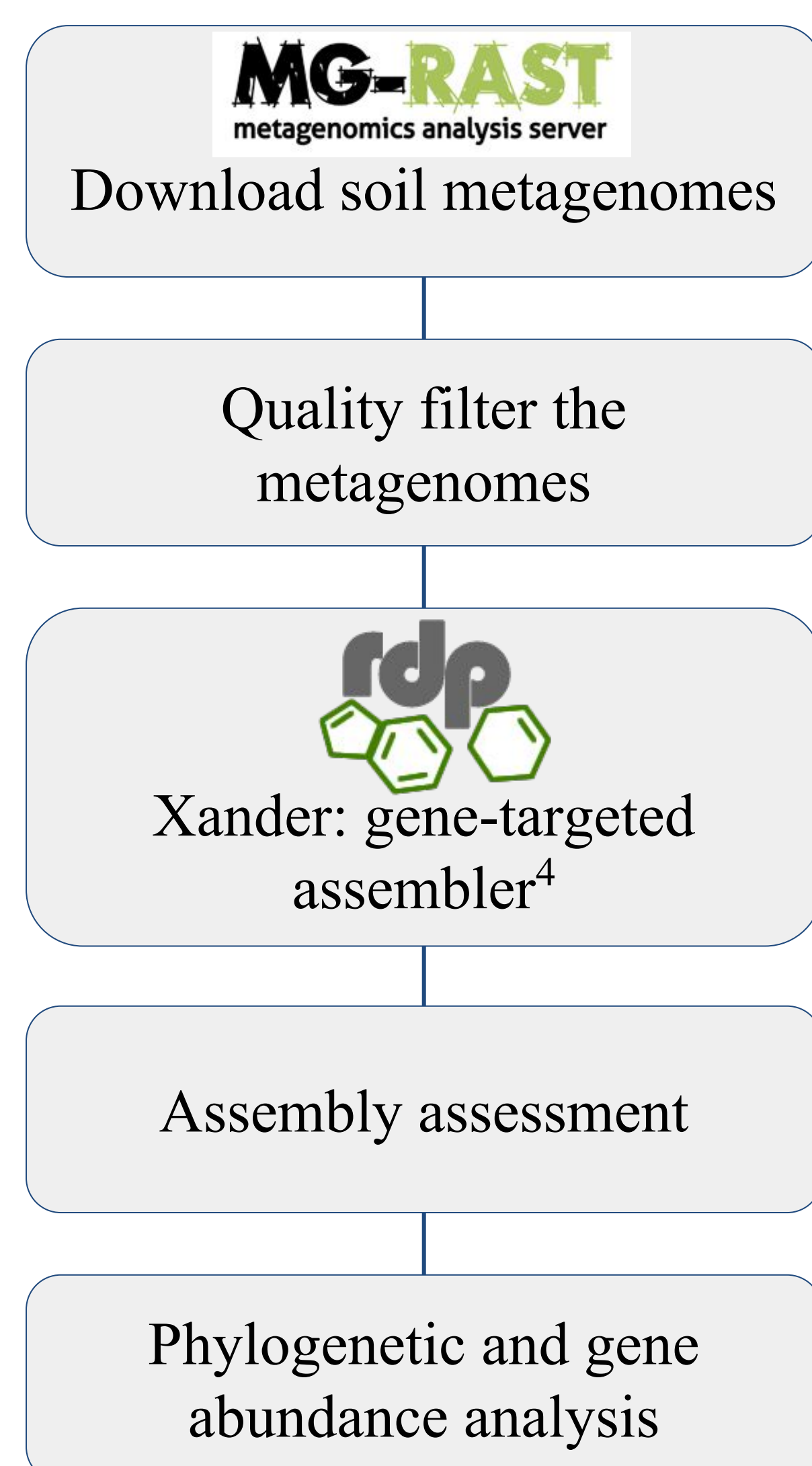
Bacteria play a key role in the As biogeochemical cycle by facilitating As biotransformation. The toxicity and mobility of As depends on its oxidation state; arsenite (As(III)) is more toxic than arsenate (As(V)).³

Arsenic resistant genes (AsRG) are well-studied in cultivated bacteria. However, there is an increasing number of soil metagenomes available, making it possible to identify phylogenetic distribution and diversity. A more integrated understanding of bacterial AsRG sheds light on the potential impact of microbial communities on the As cycle and the risk to humans.

Objectives

- Compare AsRG in non-contaminated soil microbiomes
- Examine the phylogeny of AsRG
- Expand the known diversity of AsRG
- Analyze the abundance of AsRG

Methods



rplB Shows Community Structure Differs Among Sites

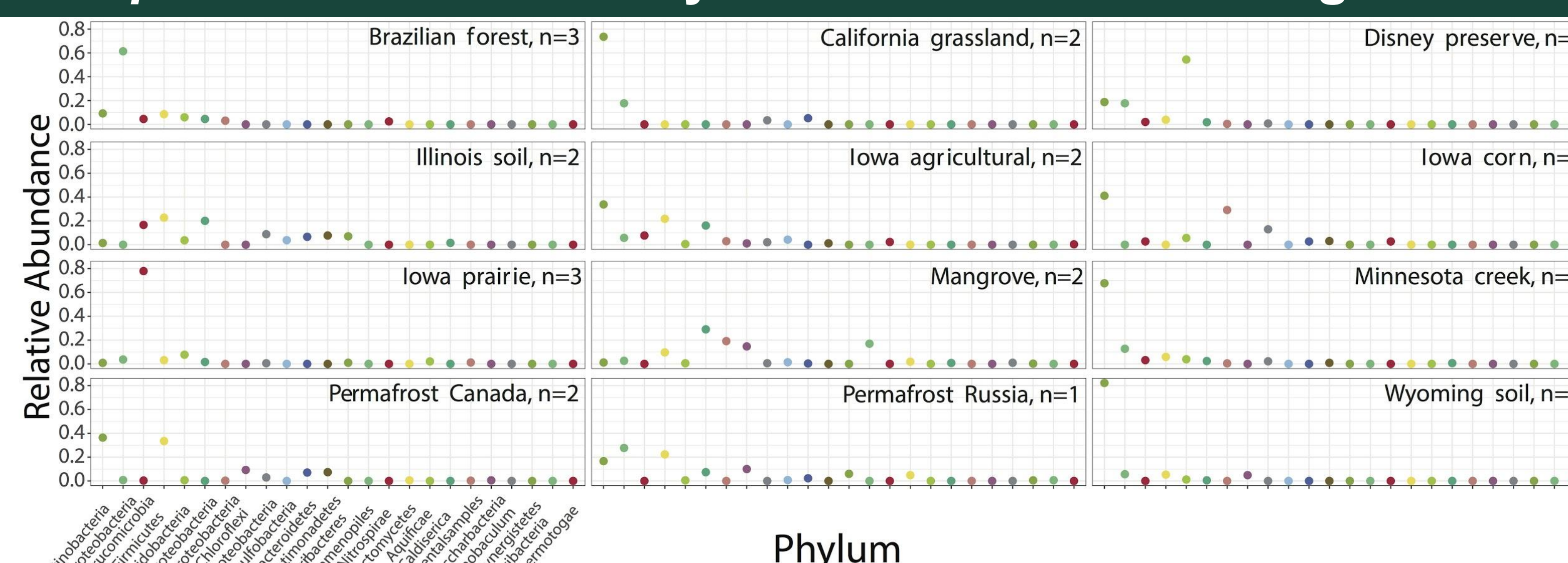


Fig 1. The metagenomes used vary in mean *rplB* abundance. Taxonomic assignment of *rplB* is indicated by color and n refers to the number of samples in each site.

Full-Length, High-Quality Sequences Assembled

Table 1. Xander assembled full or almost full-length sequences for every gene of interest. The maximum percent identities are all greater than 95%, giving confidence to the models used

Gene	Protein Function	Max Length Assembled (aa)	Model Length (aa)	Max Percent Identity (%)
<i>aioA</i>	Arsenite oxidase	815	837	97.6
<i>arxA</i>	Arsenite oxidase	508	831	95.6
<i>arsM</i>	Arsenite methyltransferase	217	269	96.1
<i>acr3</i>	Arsenite efflux pump	351	363	100
<i>arsB</i>	Arsenite efflux pump	266	430	100
<i>arsC glut</i>	Arsenate reductase	116	117	100
<i>arsC thio</i>	Arsenate reductase	83	133	100
<i>arrA</i>	Arsenate reductase	842	846	96.6
<i>arsD</i>	Arsenite metallochaperone	124	123	100
<i>rplB</i>	50S ribosomal protein L2	279	277	98.9

Normalized AsRG Abundance

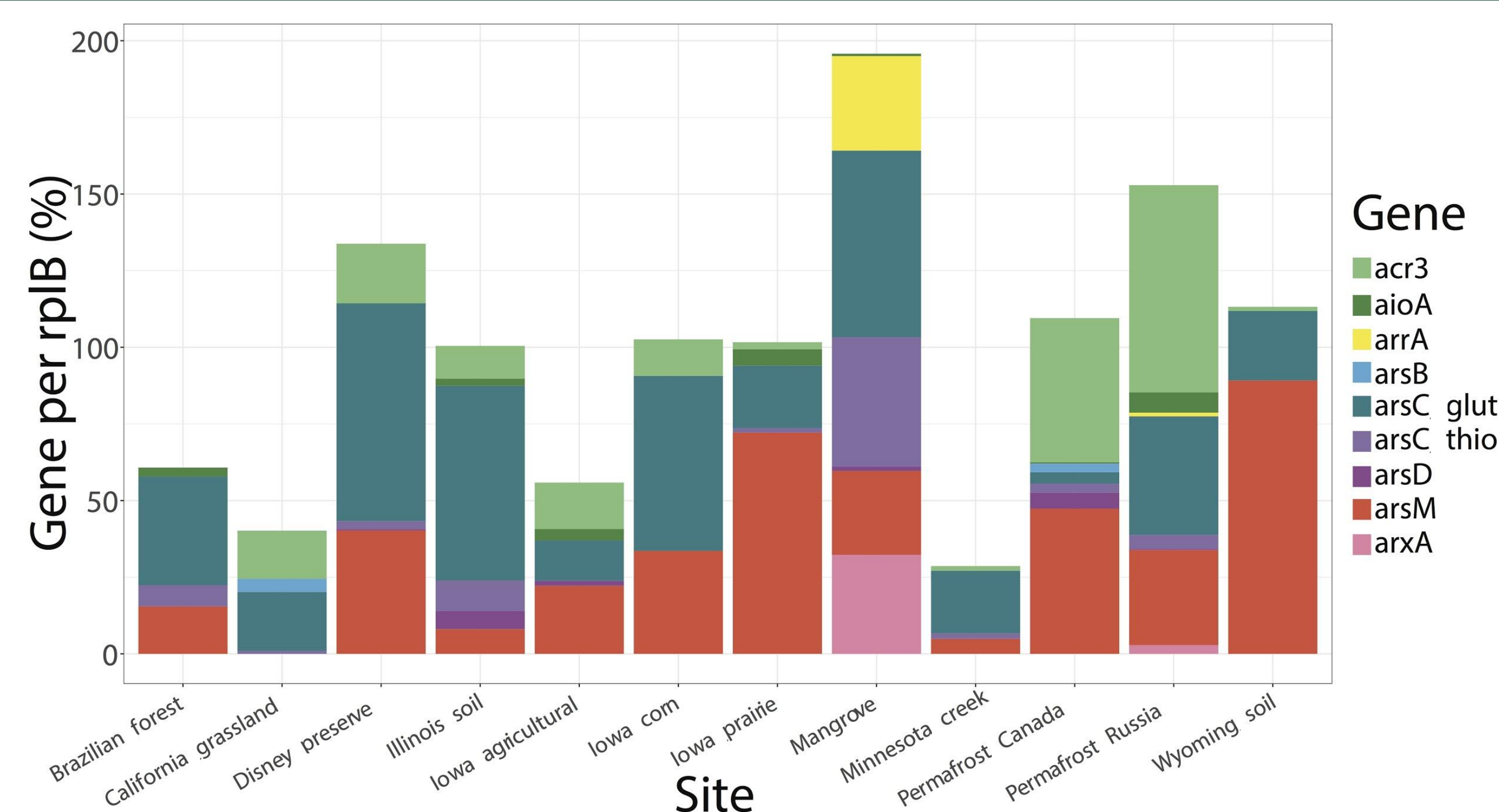


Fig 2. AsRG average abundances normalized to *rplB* vary widely among sites.

Potential Novel Diversity of *ArsC glut*



Fig 3. Maximum likelihood tree of near full-length assembled *ArsC glut* sequences clustered at 90% identity. Gene abundance per site is shown by the colored bars. Bootstrap values greater than 0.60 are indicated by grey circles.

Conclusion and Future Directions

- Diverse soil microbiomes have the genetic potential to transform arsenic
- The abundance and phylogeny of AsRG are diverse within and across microbiomes
- In the future, compare results with contaminated sites and examine beta diversity

References and Acknowledgements

1. Zhu, Y. *et al.* (2015). *Ann. Review of Earth and Planetary Sci.*
2. Brammer & Ravenscroft. (2009). *Environ. Int.*
3. Bahar MM, *et al.* (2013). *Water Air Soil Poll.*
4. Wang, Q. *et al.* (2015). *Microbiome*