

Antimicrobial Resistance As Ecological Public Goods: Mobility and Risk Assessment Via Genomic Analysis of >66000 Replicons

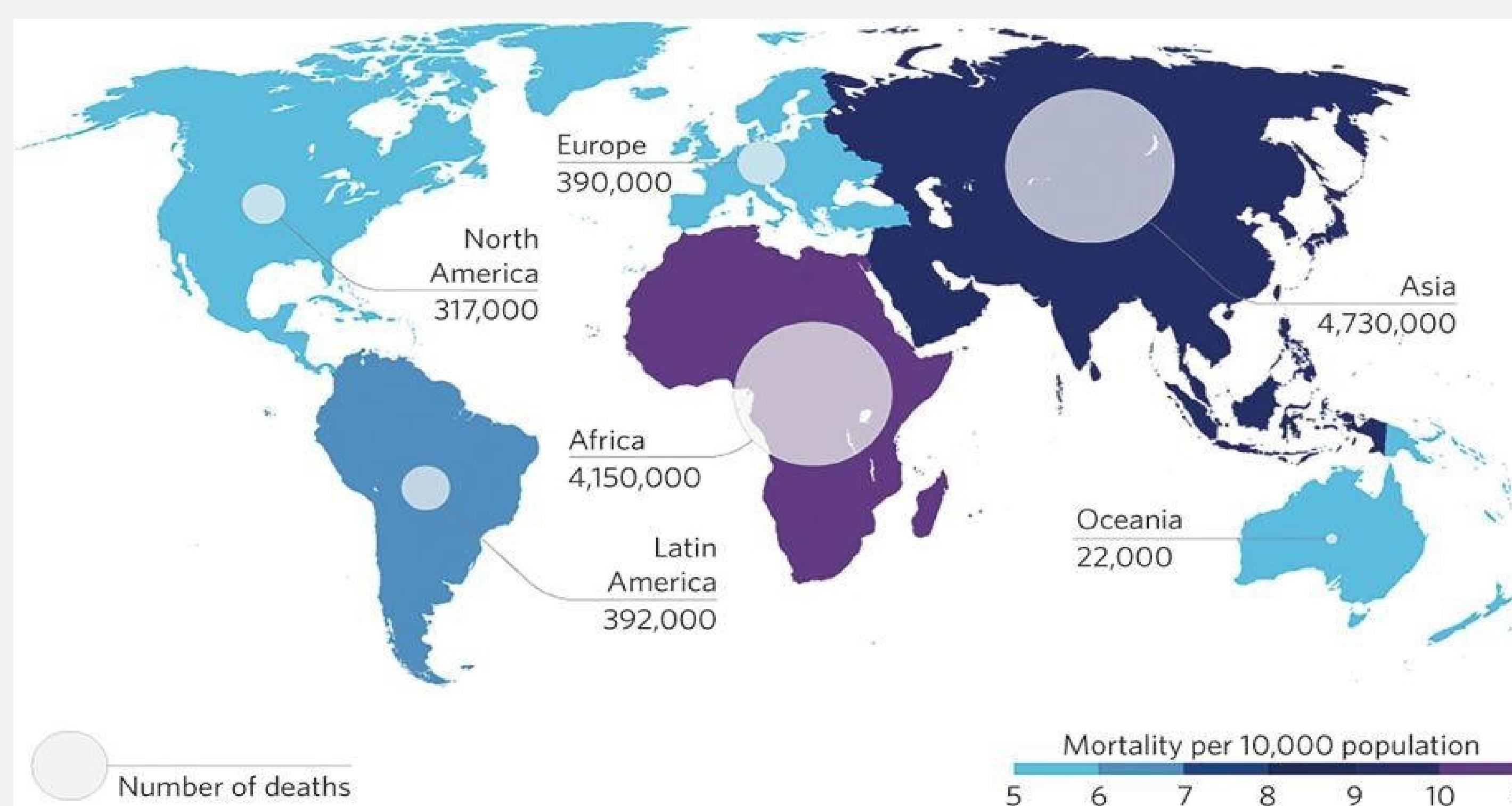
Bao Feng Jia¹, Claire Bertelli², Andrew G. McArthur³, Fiona .S.L. Brinkman¹

1. Department of Molecular Biology and Biochemistry, Simon Fraser University, Canada. 2. Lausanne University Hospital and University of Lausanne, Institute of Microbiology, Lausanne, Switzerland.

3. Department of Biochemistry & Biomedical Sciences, McMaster University, Hamilton, Ontario, Canada

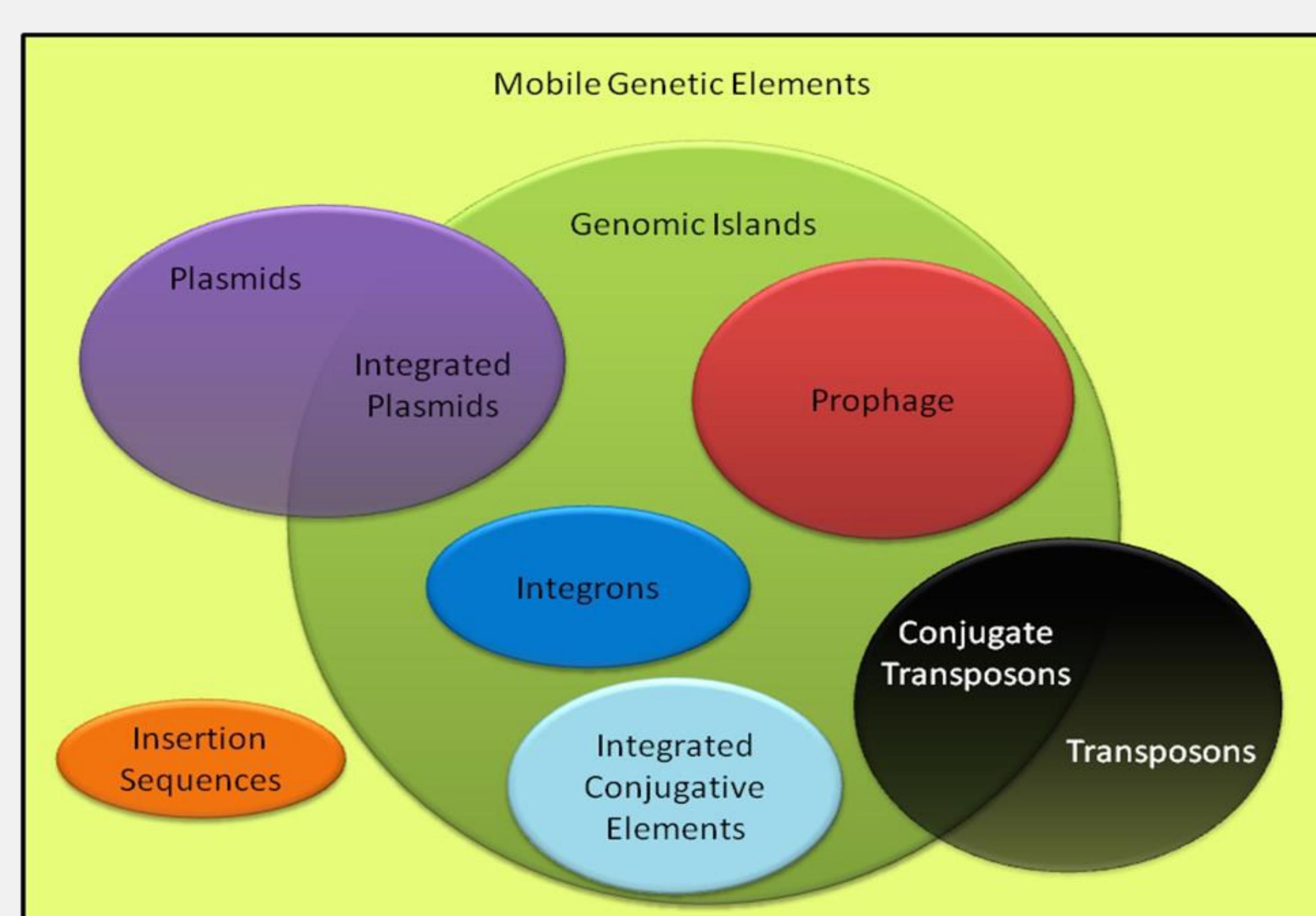
INTRODUCTION

- Antimicrobial resistance (AMR) and emergence of pan resistant superbugs – over 10 million deaths by 2050¹



- Need for research in understanding AMR mobility - Improving public health AMR risk assessment and prevention

- Genomic islands – clusters of genes of probable horizontal origin >8kb in length



- Virulence factors are disproportionately associated with mobile elements, including plasmids and genomic islands² – evolutionary advantage to remain mobile

Hypothesis:

Similarly to VFs, AMR genes are disproportionately associated with mobile sequences but differences should exist for certain AMR gene classes.

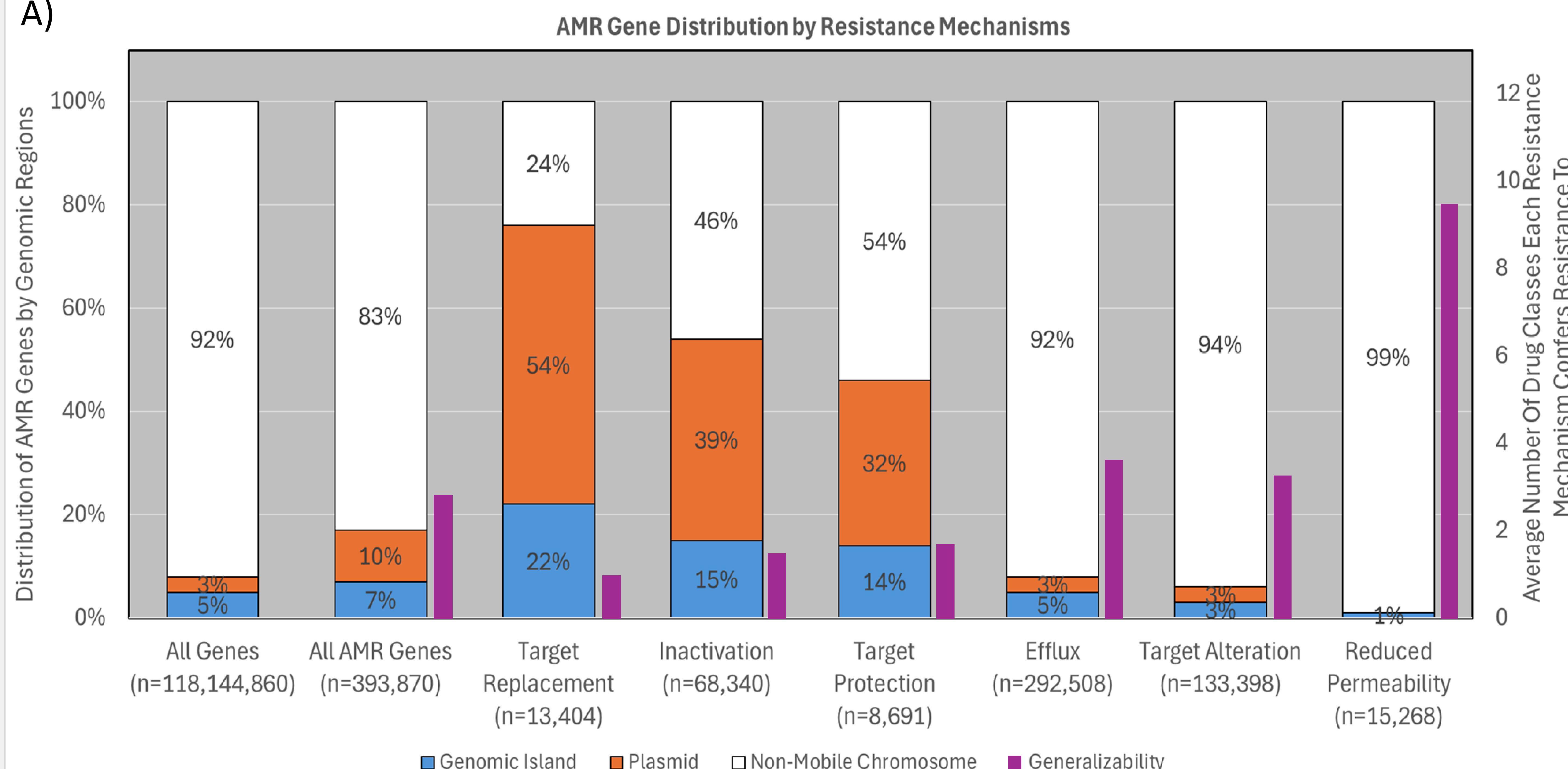


Funding & Acknowledgements

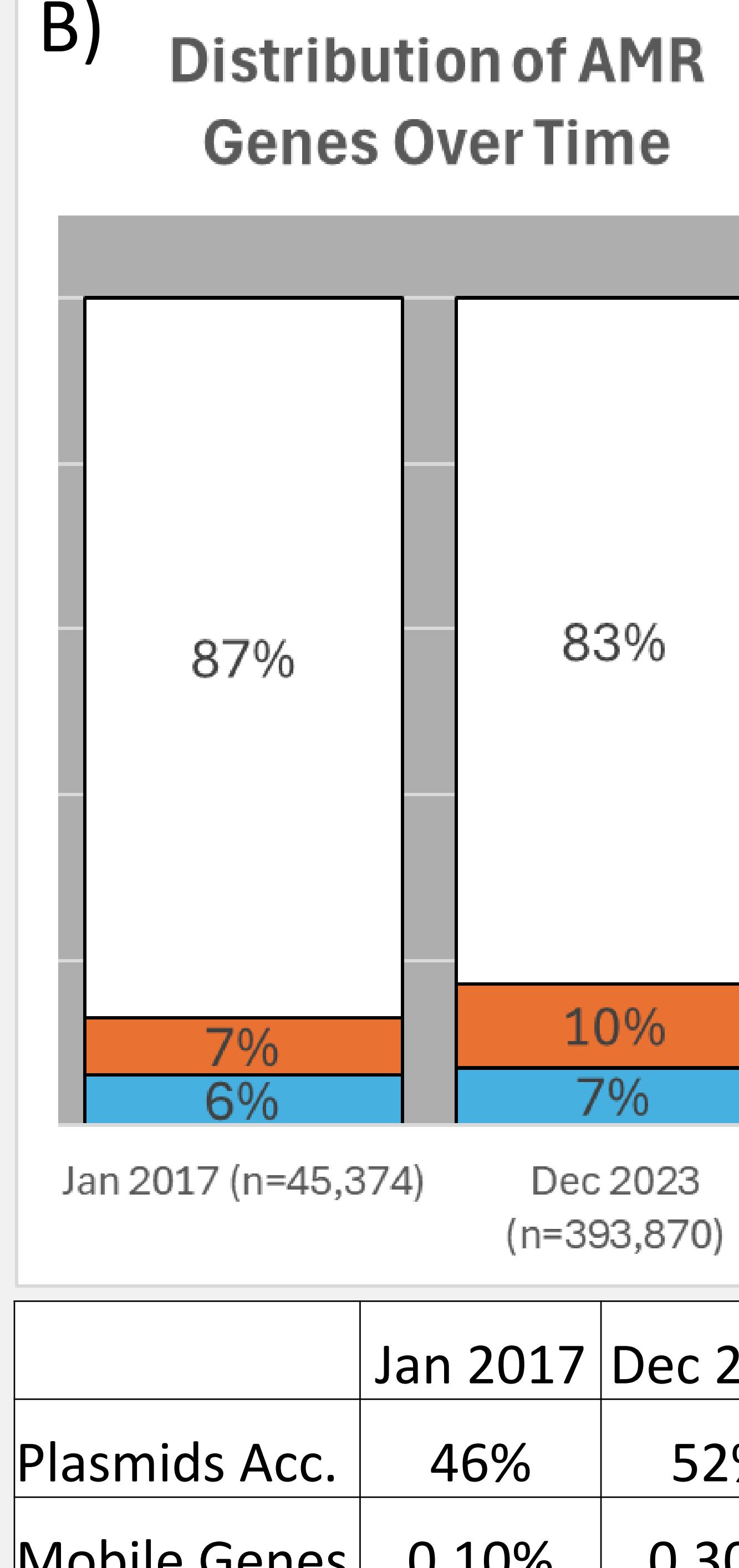


RESULTS

A)



B)

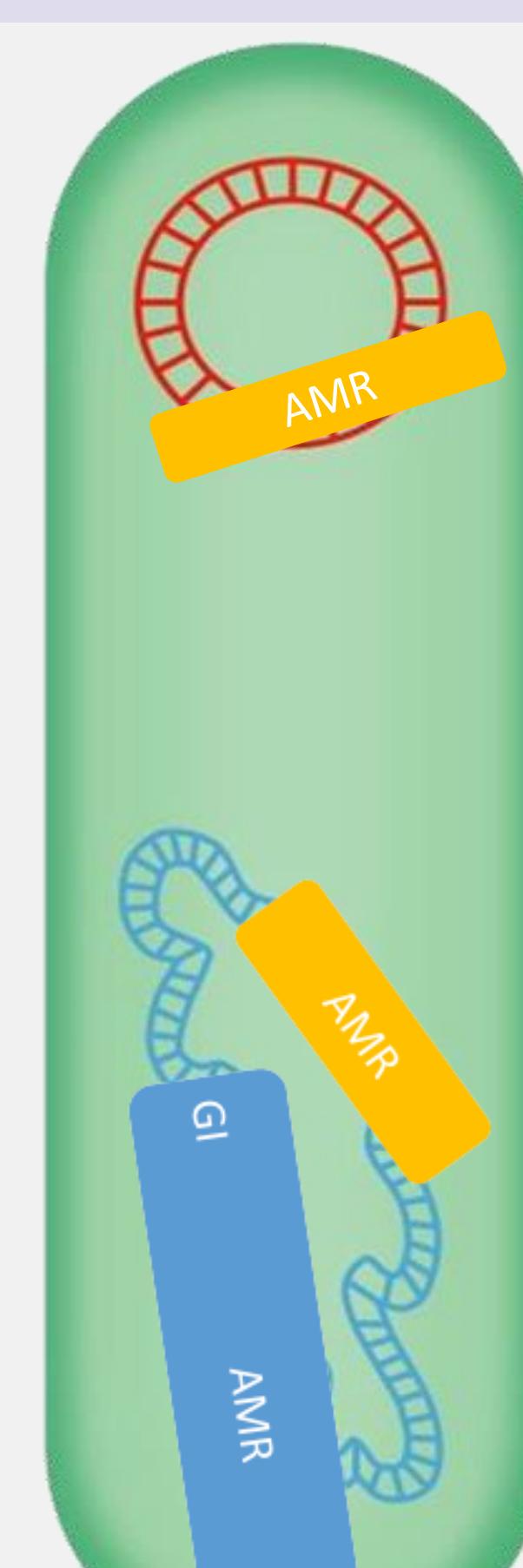
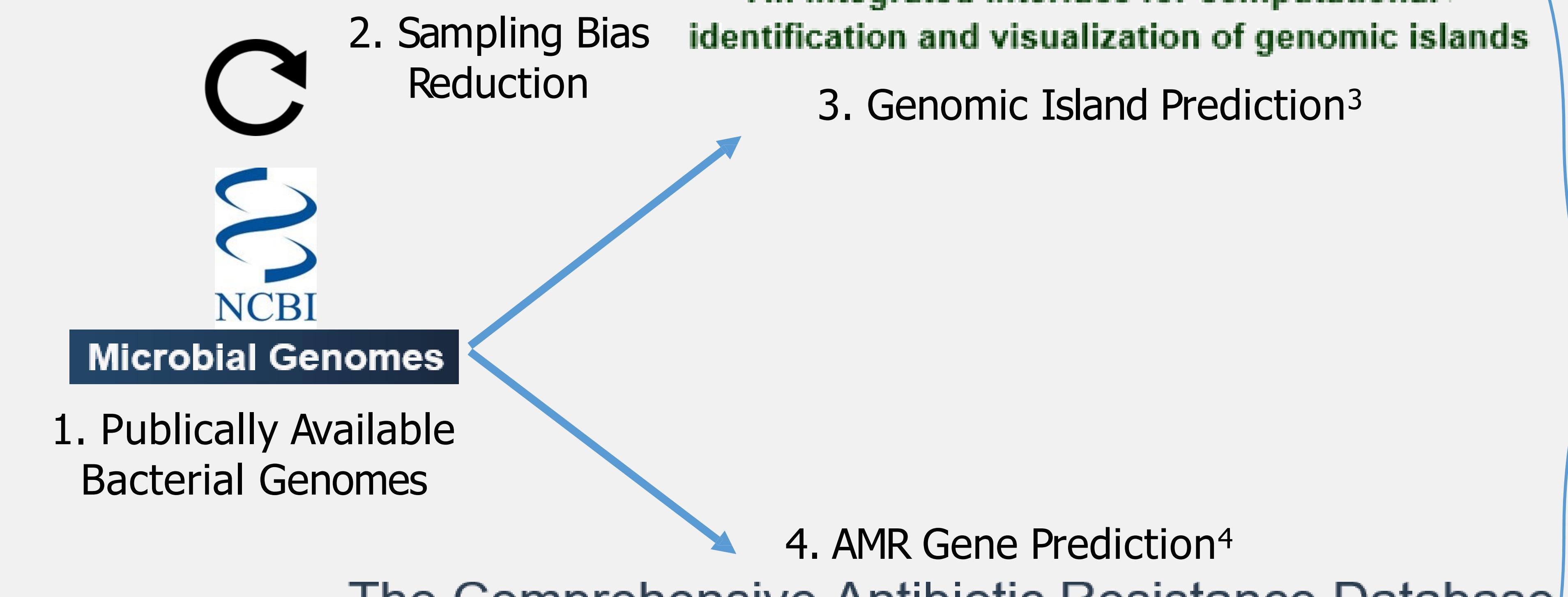


Distribution of AMR genes amongst the three regions of the bacterial genome

- A) AMR gene distribution varies based on resistance mechanism, and resistance generalizability (# of drug classes it confer resistance to).
- B) There's an increase in the number of genes (including AMR genes) on mobile elements over time in RefSeq.

METHOD

IslandViewer 4 An integrated interface for computational identification and visualization of genomic islands



Schematic of the AMR mobility trends analysis workflow.

Summary

- 1) Overall, AMR genes are disproportionately associated with mobile sequences. However, a strong predictor of mobility is how specific the resistance is.

2) Ecological "Public Goods":

- An AMR gene does not need to be present in all individuals in order to benefit all members of a community.

AMR Mobility:

$$\{ \text{Fitness Cost} + \text{Time Since Acquisition} + \text{Ecological Public Goods} + ??? \}$$

With better prediction and ecological sampling, an improved model for AMR gene transmission may be produced and exploited for future AMR surveillance and public health risk assessment.

References

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2. Ho Sui S, et al. The Association of Virulence Factors with Genomic Islands. *PLOS one*. 2009; 4(12): e8094.
3. Bertelli C, et al. IslandViewer 4: expanded prediction of genomic islands for larger-scale datasets. *Nucleic Acids Res*. 2017;
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