

Plasmid analysis and PanGWAS

Date etc

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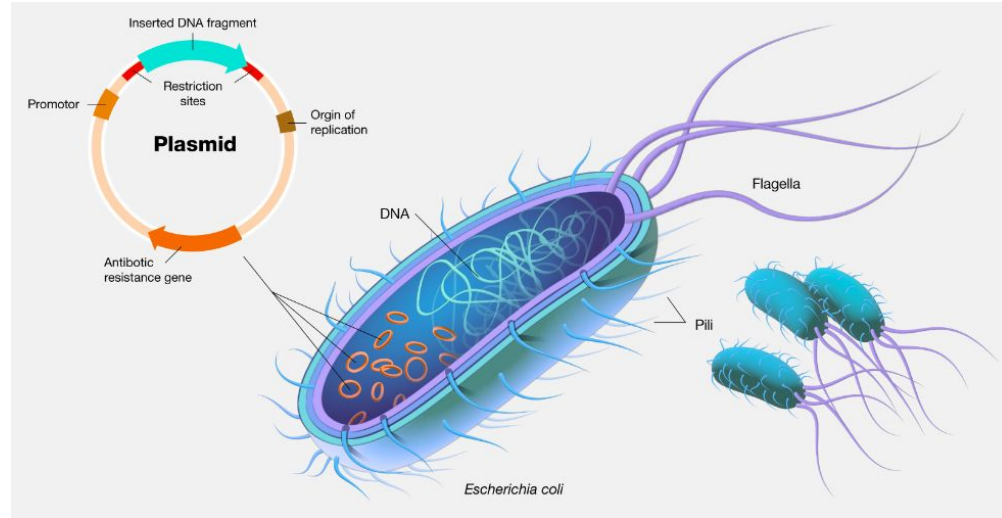


Infectious disease dynamics lab

- Identify and detect plasmid material from whole genome sequences.
- Detect specific point mutations related to AMR genes.
- Use pangenome GWAS to measure the association between gene presence and phenotypic traits of interest.

What is a plasmid

- Is a small circular DNA molecule found in bacteria and some other microscopic organisms.
- Plasmids are physically separate from chromosomal DNA and replicate independently.
- They typically have a small number of genes.
- They are highly associated with the transmission of AMR, virulence, and stress genes.



- Plasmids carrying **AMR** genes can confer resistance to antibiotics.
- Plasmids carrying **virulence and stress** genes can enhance the pathogenicity and survival of bacteria.
- The transfer of plasmids between bacteria can occur **within the same species or across different species**.
- Plasmids can also serve as **reservoirs** of genetic diversity within bacterial communities, allowing bacteria to adapt to changing environments.

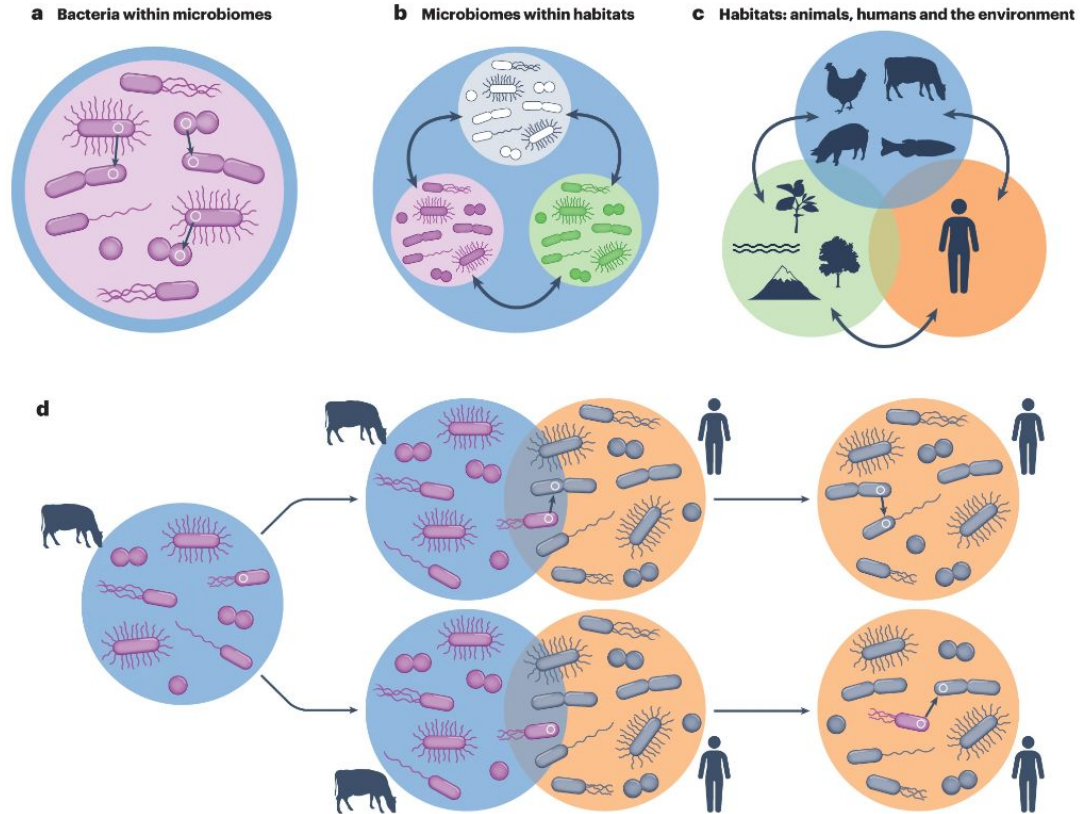


Figure from: Castañeda-Barba, S., Top, E. M., & Stalder, T. (2024). Plasmids, a molecular cornerstone of antimicrobial resistance in the One Health era. *Nature Reviews Microbiology*, 22(1), 18-32.

- Point mutations are single nucleotide changes in the DNA sequence of an organism's genome.
- They involve the substitution, insertion, or deletion of a single nucleotide base pair.
- These mutations can lead to changes in the amino acid sequence of proteins encoded by the affected gene.
- Point mutations in genes encoding antimicrobial targets or resistance mechanisms can confer resistance to antibiotics.
- For example, point mutations in the *gyrA* gene can confer resistance to fluoroquinolone antibiotics, such as ciprofloxacin and levofloxacin.

RefSeq/ <i>gyrA</i> /P0AES4.1	77	Y	H	P	H	G	D	S	A	V	D	T	I	V	R	M	A	Q	P	F	S	L	R	Y	M	L	V	D	G	G	N	F	G	S	I	D	G	S		
Mf66/ <i>gyrA</i>	1	V	H
Mf67/ <i>gyrA</i>	3	N	
Mf68/ <i>gyrA</i>	3	N	
Mf69/ <i>gyrA</i>	3	N	
Mf70/ <i>gyrA</i>	3	N	
Mf71/ <i>gyrA</i>	3	N	
Mf72/ <i>gyrA</i>	3	N	
Mf73/ <i>gyrA</i>	3	N	
Mf74/ <i>gyrA</i>	3	N	
Mf75/ <i>gyrA</i>	3	N	
Mf76/ <i>gyrA</i>	3	H	
Mf77/ <i>gyrA</i>	3	N	
Mf78/ <i>gyrA</i>	3	N	
Mf79/ <i>gyrA</i>	3	N	
Mf80/ <i>gyrA</i>	3	N	
Mf81/ <i>gyrA</i>	3	N	
Mf82/ <i>gyrA</i>	3	N	
Mf83/ <i>gyrA</i>	3	N	
Mf84/ <i>gyrA</i>	3	N	
Mf85/ <i>gyrA</i>	3	N	
Mf86/ <i>gyrA</i>	1	N	
Mf87/ <i>gyrA</i>	3	N	
Mf88/ <i>gyrA</i>	3	N	
Mf89/ <i>gyrA</i>	3	N	
Mf90/ <i>gyrA</i>	3	N	
Mf91/ <i>gyrA</i>	3	N	
Mf92/ <i>gyrA</i>	3	N	
Mf93/ <i>gyrA</i>	3	N	

To identify the presence of plasmids in bacterial genome contigs, we recommend using **Staramr**.

It is linked to the following databases:

- PlasmidFinder
- ResFinder
- PointFinder (Point mutations)

Correlation between Phenotypic and In Silico Detection of Antimicrobial Resistance in *Salmonella enterica* in Canada Using Staramr

by  Amrita Bharat 1,2,*  Aaron Petkau 1  Brent P. Avery 3  Jessica C. Chen 4  Jason P. Folster 4  Carolee A. Carson 3  Ashley Kearney 1  Celine Nadon 1,2  Philip Mabon 1  Jeffrey Thiesen 1  David C. Alexander 5  Vanessa Allen 6  Sameh El Bailey 7  Sadjia Bekal 8  Greg J. German 9  David Haldane 10  Linda Hoang 11  Linda Chui 12,13  Jessica Minion 14  George Zahariadis 15  + Show full

More information

<https://github.com/phac-nml/staramr>

 | Research Article | 12 June 2014



In Silico Detection and Typing of Plasmids using PlasmidFinder and Plasmid Multilocus Sequence Typing

Authors: Alessandra Carattoli, Ea Zankari, Aurora García-Fernández, Mette Voldby Larsen, Ole Lund, Laura Villa, Frank Møller Aarestrup, Henrik Hasman | [AUTHORS INFO & AFFILIATIONS](#)

DOI: <https://doi.org/10.1128/aac.02412-14> • 

[Microb Genom.](#) 2022; 8(1): 000748.

PMCID: PMC8914360

Published online 2022 Jan 24. doi: [10.1099/mgen.0.000748](https://doi.org/10.1099/mgen.0.000748)

PMID: [35072601](https://pubmed.ncbi.nlm.nih.gov/35072601/)

ResFinder – an open online resource for identification of antimicrobial resistance genes in next-generation sequencing data and prediction of phenotypes from genotypes

[Alfred Ferrer Florensa](#), ¹[Rolf Sommer Kaas](#), ¹[Philip Thomas Lanken Conradsen Clausen](#), ¹[Derya Aytan-Aktug](#), ¹ and [Frank M. Aarestrup](#)[✉]

PointFinder: a novel web tool for WGS-based detection of antimicrobial resistance associated with chromosomal point mutations in bacterial pathogens

[Ea Zankari](#), [Rosa Allesøe](#), [Katrine G Joensen](#), [Lina M Cavaco](#), [Ole Lund](#), [Frank M Aarestrup](#) 

Journal of Antimicrobial Chemotherapy, Volume 72, Issue 10, October 2017, Pages 2764–

- Pangenome GWAS investigates the association between gene presence/absence patterns and phenotypic traits of interest across multiple strains.
- Use statistical methods to assess the significance of genetic associations.
- Methodologies for pangenome GWAS include gene-by-gene association tests.

Traditional GWAS approach

- Single nucleotide polymorphism (SNPs) variation
- Core genome level
- Population-specific genetic variations

Pan-GWAS approach

- Gene variations
- Pangenome level
- Comprehensive picture of the genetic landscape

To perform Pangenome-GWAS analysis, we use **Scoary**.

More information

<https://github.com/AdmiralenOla/Scoary>

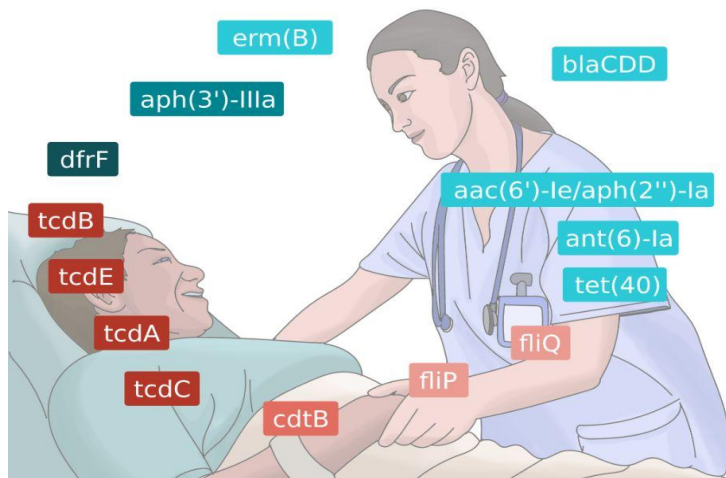
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Rapid scoring of genes in microbial pan-genome-wide association studies with Scoary

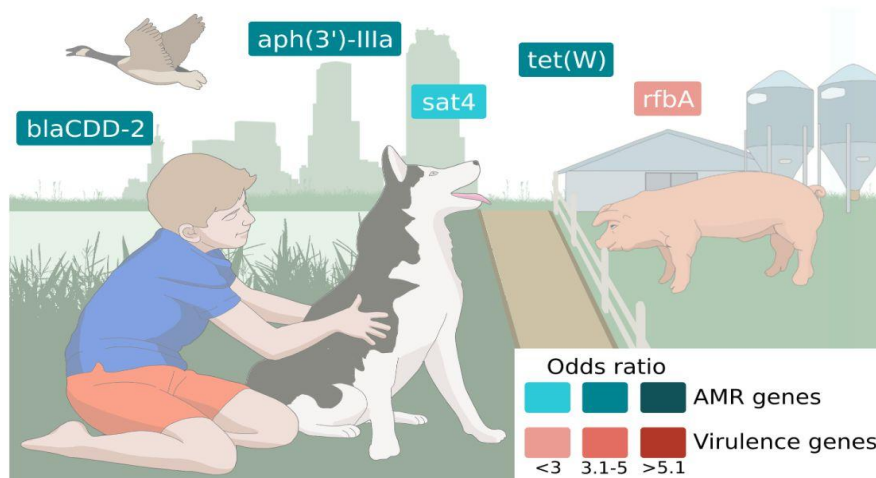
Software | [Open access](#) | Published: 25 November 2016

Volume 17, article number 238, (2016) | [Cite this article](#)

Healthcare



Non-healthcare



Questions

