

Microsoc Seminar Series 2018-09-04:

# Soil-persistent *E. coli* and Mobile elements

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## Background

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# Sources



- o <https://www.nature.com/scitable/topicpage/transposons-the-jumping-genes-518>
- o <https://www.nature.com/scitable/topicpage/transposons-the-jumping-genes-518>
- o [https://www.researchgate.net/publication/283707425\\_The\\_Phage-Inducible\\_Chromosomal\\_Islands\\_A\\_Family\\_of\\_Highly\\_Evolved\\_Molecular\\_Parasites](https://www.researchgate.net/publication/283707425_The_Phage-Inducible_Chromosomal_Islands_A_Family_of_Highly_Evolved_Molecular_Parasites)
- o <https://www.sciencedirect.com/science/article/pii/S0043135416302226>
- o [http://www.bx.psu.edu/~ross/workmg/TranspositionCh9\\_files/](http://www.bx.psu.edu/~ross/workmg/TranspositionCh9_files/)
- o <https://www.frontiersin.org/articles/10.3389/fmicb.2018.00762>

# Acknowledgments



## NUIG Microbiology

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- ☐ Soil and Environmental Microbiology Research Group
- ☐ Functional Environmental Microbiology Group



## James Hutton Institute, Dundee

- ☐ Dr. Leighton Pritchard
- ☐ Dr. Ashleigh Holmes



- *E. coli* has been found to persist stably in the soil
- Isolates were cultured from lysimeter leachate
- Strains were sequenced, resulting in 149 soil-persistent *E. coli* genome



- What types of *E. coli* are able to persist in soil?



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- What virulence factors are harboured by these strains?
- What can we infer about adaptation?
- Can we differentiate soil-persistent *E. coli* from recent contamination?

## *E. coli* Pangenome

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Assembly  $\Rightarrow$  Annotation  $\Rightarrow$  presense/absence matrix



Assembly  $\Rightarrow$  Annotation  $\Rightarrow$  presense/absence matrix  
riboSeed  $\Rightarrow$  Prokka  $\Rightarrow$  Roary



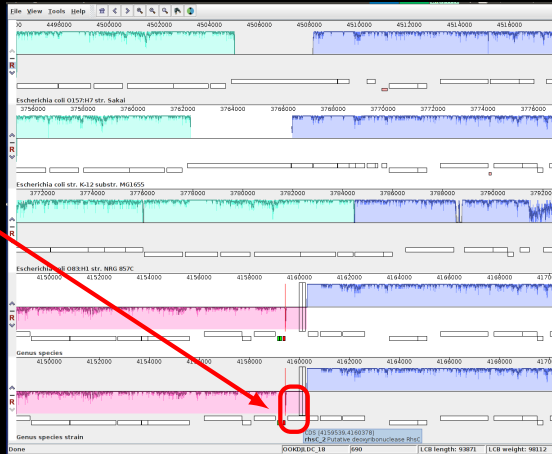
Assembly  $\Rightarrow$  Annotation  $\Rightarrow$  presense/absence matrix  
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	N	Core	total
Soil	149	2662	21,662
Enterobase	1193	1822	79,288
All	1342	1806	83,868

# Annotation



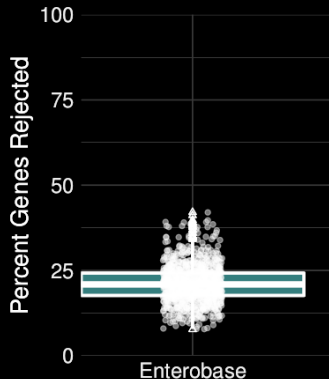
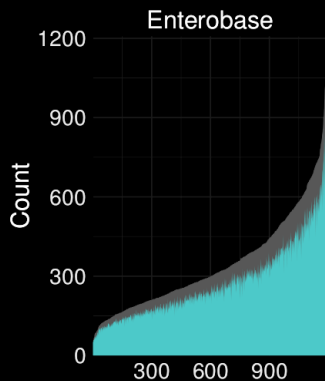
Partial



# Annotation Correction with annofilt performance



<https://nickp60.github.io/annofilt/>



# Detecting differential presence/absence



- o No statistically significant gene associations with source
- o *E coli* diversity add complexity



What does 10 years look like to *E. coli* ?

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# BoE Calculations for Doubling Time



High estimate:

$$0.013865 * 60 * 24 * 365 * 10 \approx 72\text{k generations}$$

# BoE Calculations for Doubling Time



Medium estimate:

$$(5.9^* / 2) * 365 * 10 \approx 10\text{k generations}$$

\*(assuming generation time roughly equals half of turnover rate)

# Other estimates



No remaining bacteria after:

- 22 days
- 32 days
- 114 days
- 8 weeks



*E. coli* approximately .092% prevalence in soil metagenomes

# Hypothesis



Stressed and outnumbered?

# Hypothesis



Stressed and outnumbered?

rapid > incremental

# Hypothesis



Stressed and outnumbered?

rapid > incremental

. . . adaptation via mobile elements



# Mobile Genetic Elements

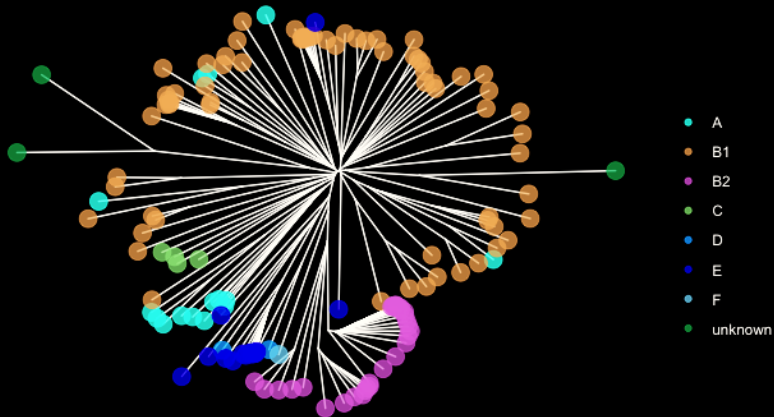
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# Overview

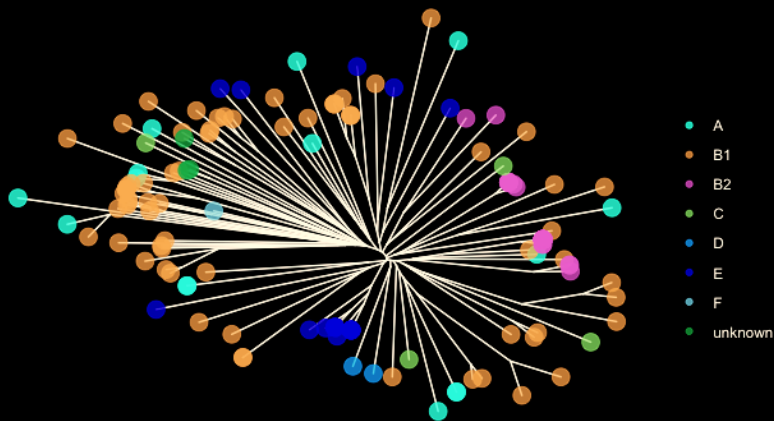


	Kb	Mobility	Detection
IS	.75-1.5	transposase	ITR and transposase
Non-composite Tn	<3	IS	IS with bonus genes
Composite Tn	<5kb	double IS	flanking ISs
Integron	<10	integrase*	<i>attI</i> site, AMR genes
Genetic Island	>10	phage	GC Skew, ORF phylogeny
Phage Inducible CI	5-15	phage	phage inhibitors
Prophage	≈50	lysogeny	integrase, tail, capsule
Plasmid	1-1Mb	various	run a gel, <i>oriT</i>

# Genomic NJ on Pangenome



## Horizontally Acquired Partial Pangenome of Inserted Elements



In Closing

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## What we know:

- soil *E. coli* is very diverse
- wide range of estimates exist for doubling time in soil
- diversity prevents robust statistical trait association
- MGE phylogeny does not reflect genome phylogeny

## What we want to know:

- how the mobile pangenomes of soil vs enteric *E. coli* compare
- which *types* of phages, etc, are correlated by source
- whether genomic islands reflect phylogeny
- which regions are interrupted by IS, Tns, etc