Microsoc Seminar Series 2018-09-04:

Soil-persistent *E. coli* and Mobile elements

Nicholas Waters

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National University of Ireland, Galway, Ireland
The James Hutton Institute, Dundee, Scotland

Outline

Background

Project Overview

- *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

Research Questions

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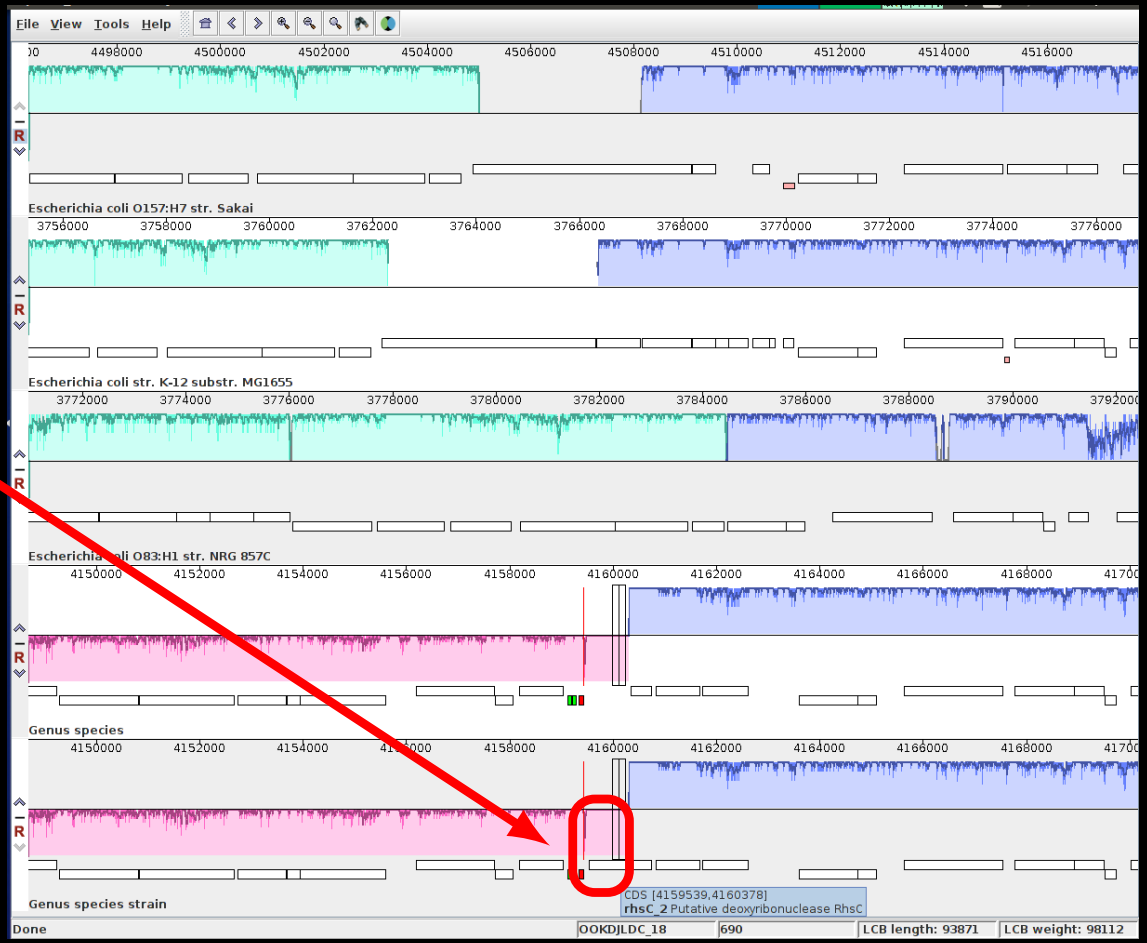
- What virulence factors are harboured by these strains?
- What can we infer about adaptation?
- Can we differentiate soil-persistent *E. coli* from recent contamination?

E. coli Pangenome

Collection overview

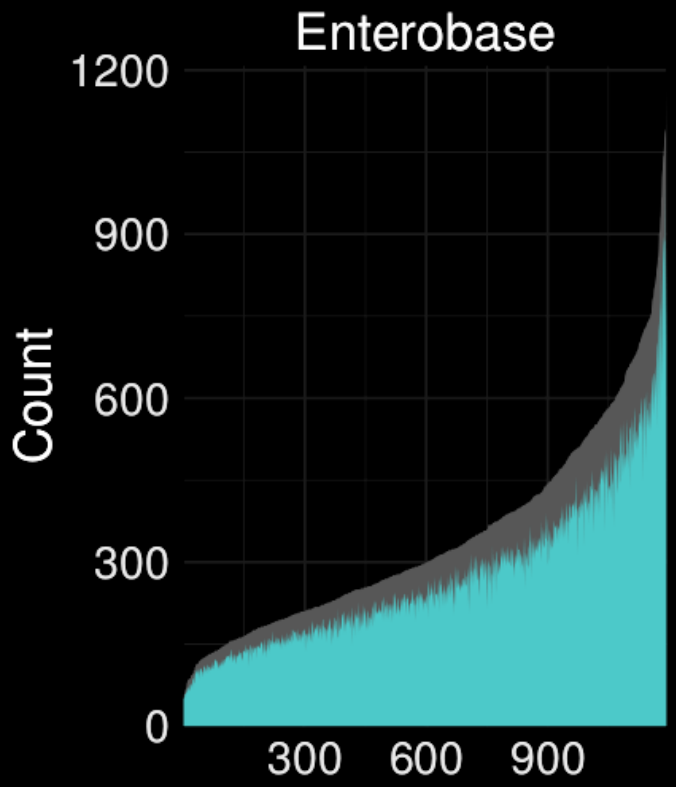
Annotation

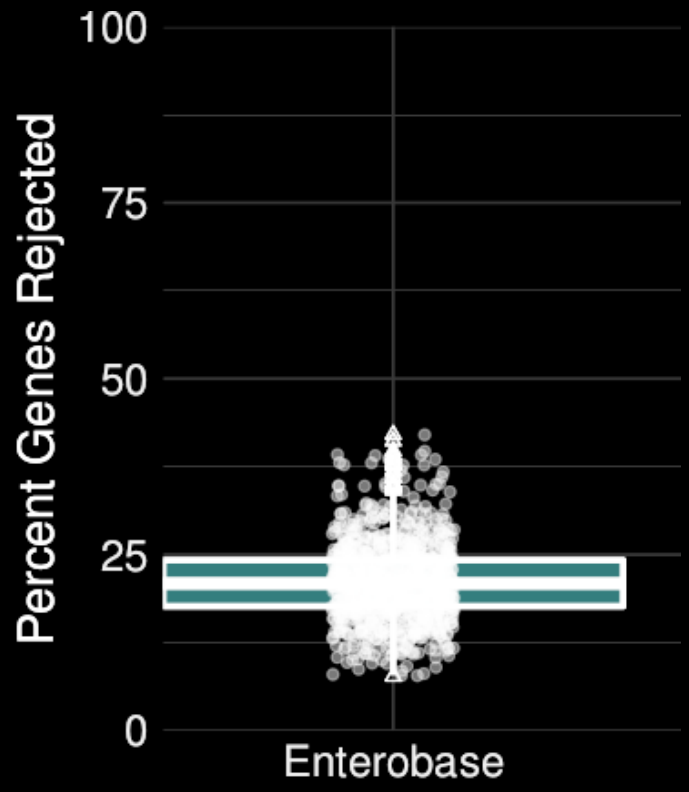
Partial



Annotation Correction with annofilt performance

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





Detecting differential presence/absence

- Statistically compare traits to a pangenome

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

BoE Calculations for Doubling Time

High estimate:

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

BoE Calculations for Doubling Time

Medium estimate: (5.9 / 2) * 365 * 10

$\approx$ 10k generations

Bååth 1998

(assuming generation time roughly equals half of turnover rate)

Other estimates

No remaining bacteria after:

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

Detection of Escherichia coli in sequenced soil

E. coli approximately .092% prevelence in soil metagenomes

Hypotheses

Stressed and outnumbered?

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rapid > incremental

Hypotheses

Stressed and outnumbered?

rapid $>$ incremental

$\therefore$ adaptation via mobile elements

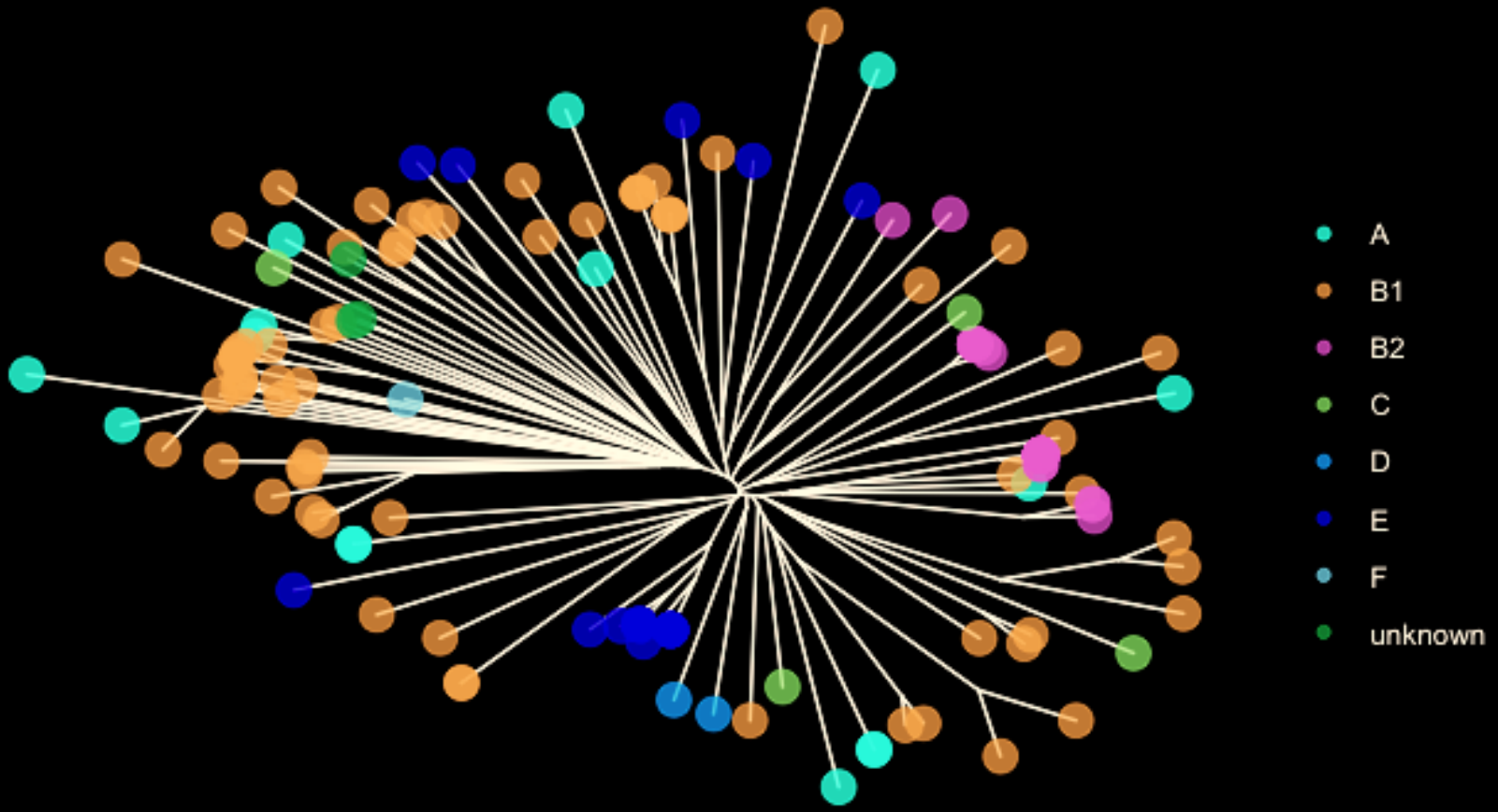
Mobile Genetic Elements

Overview

	Kb	Mobility	Detection
Insertion Seq	.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*	*attI* 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, *oriT*

https://github.com/nickp60/happpie/

Horizontally Aquired Partial Pangenome of Inserted Elements



In Closing

Summary

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

Future plans

- compare mobile pangenome of soil vs enteric *E. coli*
- source analysis: which *types* of phages, etc
- incorporate genomic islands into analysis
- include regions interupted by IS, Tns, etc

Sources

- https://www.nature.com/scitable/topicpage/transposons-the-jumping-genes-518
- https://www.nature.com/scitable/topicpage/transposons-the-jumping-genes-518
- https://www.researchgate.net/publication/283707425_The_Phage-Inducible_Chromosomal_Islands_A_Family_of_Highly_Evolved_Molecular_Parasites
- https://www.sciencedirect.com/science/article/pii/S0043135416302226
- http://www.bx.psu.edu/~ross/workmg/TranspositionCh9_files/
- https://www.frontiersin.org/articles/10.3389/fmicb.2018.00762/full

Acknowledgments

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Questions?