Investigating the genomics of soil-persistent Escherichia coli

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Introduction

E. coli is a common bacteria originally isolated as from the gut in 1886. While the majority of strains are commensal, several lineages of *E. coli* are capable of causing disease in humans (primarily in the gastrointestinal and urinary tract, but occasionally more systemic infections). The primary route of transmission is through ingestion of water or crops exposed to faecal contamination. The WHO estimates that *E. coli* accounts for about 5 million disability adjusted life years lost annually, making it the second most problematic food-borne pathogen in the world (Kirk 2015).

Because of its ubiquity in faecal material and it's perceive inability to survive for extended periods in the environment, *E. coli* is widely used as an indicator of faecal contamination. However, a growing body of work now supports the idea that while *E. coli* is often indicative of faecal contamination, stable populations may persist in the soil for long periods of time. This compromises *E. coli's* effectiveness as an indicator species.

Our aim is to use advances in DNA sequencing technology to study the genomes of these soil-persistent *E. coli*. By looking at the genomic differences exhibited by these bacteria compared to their gut-associated relatives, we hope to discover what allows them to adapt to an alternative lifestyle from the gut, and to assess whether soil-persistent strains pose a threat to human health.

Objectives

1. Determine the basis for the remarkable long-term survival of E. coli in maritime temperate soil

2. Determine if environmentally persistent soil E. coli populations constitute a health risk to human populations

3. Determine if enteric E. coli-specific genomic markers exist

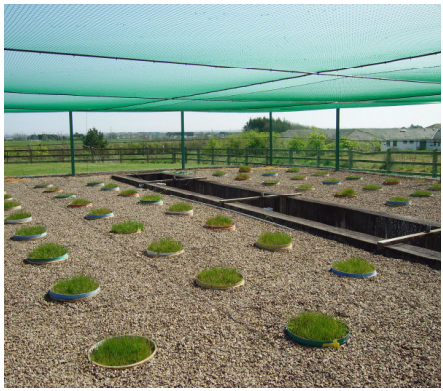

Figure 1: Lysimeter unit, Johnstown Castle

Materials and Methods

To isolate soil-persistent strains, *E. coli* were enriched from leachate from soil lysimeters housed at Teagasc, Johnstown Castle. These soil columns were originally set up by Ryan and Fanning (1996) to study effects of

fertiliser on various soil types, and later used by Brennan, et al. (2010) to study the transport of pathogens from slurry through soil columns.

The control columns from the latter experiment were last exposed to slurry in 1998. Thus, at least 9 years passed between the last contamination event and the isolation, and any isolates obtained from these lysimeters represent strains exhibiting soil-persistence for at least 9-13 years. Leachate from these control columns was collected, and *E. coli* was enriched from the liquid. After the resulting colonies were purified, DNA was extracted and sent for Illumina sequencing.

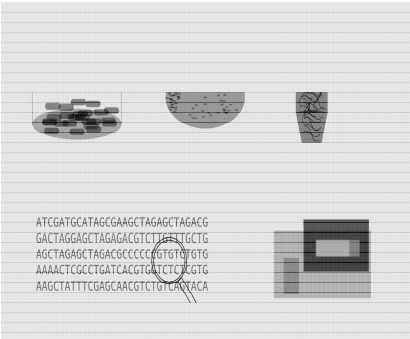

Figure 2: Summary of workflow

Overview of the collection

153 soil-persistent *E. coli* were successfully isolated and sequenced. The isolates exhibited a large degree of phylogenetic diversity, with representative members from each of the phylogroups of *E. coli*.

This suggests that soil-persistent *E. coli* are not a succinct clade, but that a diverse subgroup is capable of becoming naturalised in soils.

Next Steps

This collection offers a unique look into the genomics of soil-persistent *E. coli*. While the genomes of thousands of *E. coli* have been sequenced, these genomes are dominated by clinical isolates and environmentally derived strains are poorly represented. To our knowledge this is the only collection of soil-persistent strains currently in existence, made possible by the long-term curation of the lysimeters. Current work is underway to characterize the virulence and antimicrobial resistance capacities of the strains, to determine metabolic adaptations involved with soil-persistence, and to identify markers that could potentially be used to differentiate between enteric and environmental strains.

Acknowledgements

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References

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