

The *E. coli* Game of Clones

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Escherichia coli is the bacterial model organism and a near universal coloniser of the mammalian and bird gut, but also the most common cause of urinary tract and bloodstream infections globally. Classical approaches in population genetics revealed decades ago that the effective population size (N_e) of *E. coli* was much larger than that estimated for any animal and plant species. Today, *E. coli* is the second most commonly whole-genome sequenced bacterial species, with nearly 400,000 published genomes available. Recent longitudinal genomic surveys of *E. coli* combined with phylogenetic and epidemiological modelling have revealed evidence of negative frequency-dependent selection acting to maintain lineages in the population, and uneven expansion rates driven by differences in the gene content. Such genetic diversity is consistent with an evolutionary game-theoretic scenario where accessory genes largely determine the reproductive success of genotypes by traits that are subject to frequency-dependent selection. In this talk we review recent progress in understanding the drivers of *E. coli* population evolution using large-scale population genomics and experiments.