

Biochemical traits that *Escherichia coli* evolved during its adaption to the gastrointestinal tract of humans

Wenfa Ng

Unaffiliated researcher, Singapore, Email: ngwenfa771@hotmail.com

Abstract

What biochemical tricks did *Escherichia coli* obtained or evolved during its time as a commensal in the human gastrointestinal system? *E. coli* is a natural symbiont of the human gastrointestinal tract. Thus, through evolutionary timescales, the bacterium must have co-evolved with humans with conditions in the gastrointestinal tract serving as selection pressure for the evolution of a variety of biochemical and physiological adaptations. These adaptations came about through mutations that arise in the genome, and thus, could be retrospectively profiled to understand the differing evolutionary pressure that selected for specific traits in the bacterium useful for its survival in the changing conditions of the human gut. Using sequenced and annotated genome information of different strains of *E. coli* as a guide and starting point, possibility exists to use a combination of bioinformatics, biochemical, and genetic approaches to decipher the biochemical tricks that *E. coli* evolved or pick up during its time as a commensal in the human gastrointestinal tract. Specifically, sequenced genomes serve as a molecular fossil from which we could obtain imprints of the various evolutionary events that impact on the bacterium. Adaptations to changing conditions could also be deciphered through analysis of single nucleotide polymorphism (SNPs). Comparison of the profiled mutations and altered gene sequences between different *E. coli* strains with different co-evolutionary history with the human gut might help reveal the different length of time in which different *E. coli* strains have co-evolved with humans. More importantly, multiple sequence alignment and phylogenetic analysis could also reveal which genes first evolve due to selection pressure exerted on the bacterium by fluctuating environmental conditions in the human gut. Genetic knockdowns of the putative genes would help indicate the overall essentiality of the genes to the physiology and functioning of the modern *E. coli* bacterium. The approach outlined should help answer some of the most fundamental questions regarding the evolution of different *E. coli* strains as well as how natural selection exerts its influence on the physiology of a commensal organism with respect to host adaptation.

Keywords: *Escherichia coli*, gastrointestinal tract, humans, evolution, natural selection, genome sequencing, single nucleotide polymorphism, phylogenetic analysis, biochemical traits, metabolism,

Subject areas: microbiology, cell biology, bioinformatics, genomics, biochemistry,

Conflicts of interest

The author declares no conflicts of interest.

Funding

No funding was used in this work.