Commentary

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Archives of Clinical Microbiology
ISSN 1989-8436

2021
Vol. 12 No. S6: 004

A Short Note on Genomics of *Escherichia coli*

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Received: December 09, 2021; **Accepted:** December 23, 2021; **Published:** December 30, 2021

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Citation: Hassan A (2021) A Short Note on Genomics of *Escherichia Coli*. Arch Clin Microbiol Vol.12 No. S6: 004.

Description

Comparative genomics has proven useful in identifying putative virulence factors in bacterial pathogens. *Escherichia coli* is a major cause of sickness and mortality in humans around the world, yet it can also be found as a companion in the human gastrointestinal system. It has served as a model organism for comparative genomic studies to explore the link between genetic content and virulence potential, has many genomic sequences. However, no comprehensive investigation of its entire "virulome" has been conducted to far with the goal of identifying universal or pathotype-specific vaccine targets. The creation of a pathotype database comprising 107 well-characterized totally sequenced pathogenic and nonpathogenic *E. coli* strains, which we classified for main Virulence Factors, is described here (VFs).

The data was cross-referenced for patterns against pathotype, phylogroup, and sequence type, and the results were confirmed against the NCBI RefSeq database's 1,348 complete *E. coli* chromosomes. Many of the "pathotype-associated" VFs are driven by phylogenetic clade, and ExPEC-associated VFs are mostly found in the B2/D/F/G phylogenetic clade, implying that these phylogroups are better adapted to infect human hosts. Finally, we used this data to develop polyvalent vaccine targets with extraintestinal strain specificity, focusing on key invasive strategies such as immune evasion (group 2 capsule), iron acquisition (FyuA, IutA, and Sit), adherence (SinH, Afa, Pap, Sfa, and Iha), and toxins (SinH, Afa, Pap, Sfa, and Iha) (Usp, Sat, Vat, Cdt, Cnf1, and HlyA).

Escherichia coli has long been a major cause of sickness and mortality in humans. It is a common gastrointestinal tract inhabitant that readily transmits antibiotic resistance-associated elements and has an enormous pangenome of at least 13,000 genes (and perhaps over 100,000) that includes multiple Virulence Factors (VFs) that complicate illness aetiology. There is currently no vaccine available, and efforts to develop one have been hampered by the absence of universal protection against all invasive strains or forms of illness that this organism can cause.

Unlike diphtheria and pertussis, which are largely regarded as toxigenic diseases caused by secreted toxins from *Corynebacterium diphtheriae* and *Bordetella pertussis*, respectively, *E. coli* infections are multifactorial-a composite of virulence factors contributing to each step in the diverse range of diseases . This, combined with the fact that the organism is on the approach of becoming an opportunistic pathogen, with commensal strains expressing identical virulence characteristics, makes vaccine development complicated. Strains are classified into pathological categories, or "pathotypes," in this manner (also known as pathovars). Pathotypes are disease phenotypes shared by groupings of pathogenic strains.

In a general sense, they can be divided into two kinds based on whether the strain causes disease outside of the intestines (Extraintestinal Pathogenic *E. coli* [ExPEC]) or inside the intestines (Intestinal Pathogenic *E. coli* [InPEC]). These two pathotypes are further divided into subtypes based on the disease they cause. ExPECs comprise Entero Aggregative *E. coli* (EAEC) and Entero-Hemorrhagic *E. coli* (EHEC), while InPECs comprise Neonatal Meningitis *E. coli* (NMEC) and Uro-Pathogenic *E. coli* (UPEC).