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A highly conserved complete accessory type-III E. coli secretion system 2 (ETT2) is present in bloodstream isolates of the ST69 lineage

Stephen Fox*[1], Cosmika Goswami[2], James Connolly[3], Andrew Roe[3], Alistair Leanord[4], Thomas Evans[3]

[1]*University of Glasgow; Ri Infection Immunity & Inflammation*

[2]*University of Glasgow; Institute of Infection, Immunity and Inflammation*

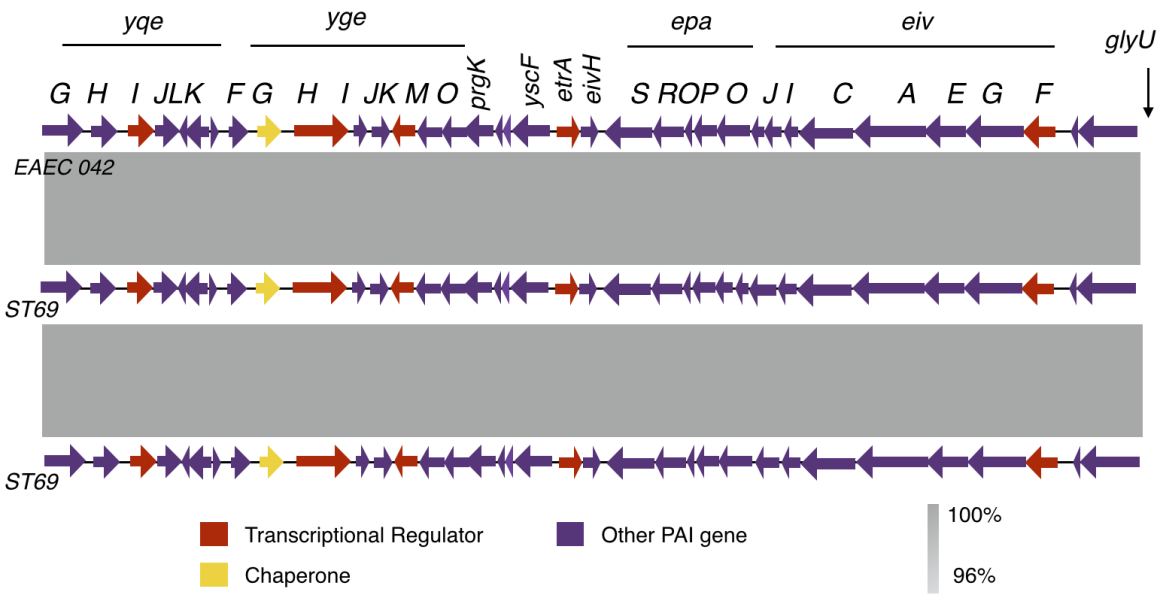
[3]*University of Glasgow*

[4]*Southern General Hospital; Southern General Hospital*

Background: An accessory type III secretion system termed *E. coli* type III secretion system 2 (ETT2) has been identified as a potential virulence determinant. In most strains the gene locus is highly degenerate, with mutational attrition rendering it non-functional. However, a potentially functional ETT2 has been identified in a strain of enteroaggregative *E. coli* (EAEC 042). We have sequenced 182 bloodstream isolates of *E. coli* to identify novel pathogenic mechanisms. We report the identification of an intact ETT2 locus and associated regulator and putative effector genes in blood stream isolates of the ST69 *E. coli* lineage, which made up 13.5% of our sequenced cohort.

Material/methods: 182 bloodstream *E. coli* isolates were selected from two Health boards in Scotland; Greater Glasgow and Clyde, and Dumfries and Galloway. Whole genome sequencing was performed using the Illumina HiSeq platform at Sanger Institute, Cambridge.

Results: Genome analysis showed that all of the 26 ST69 *E. coli* isolates contained a highly conserved complete ETT2 locus spanning a region of ~30kb. Comparison of two of the ST69 strains with the ETT2 locus in the EAEC strain 042 is shown below:



In addition, the sequenced ST69 strains contained the *SelC* locus that encodes *eilA* the global transcriptional regulator of the ETT2, as well as a number of putative effectors of the type III system and *EaeX*, a homologue of the outer-membrane invasion of *Yersinia* spp. and intimin of enteroinvasive *E.coli. EaeX* contains a number of bacterial immunoglobulin domain repeats; the sequenced ST69 strains had fewer repeats compared to the EAEC 042 type strain. ST69 strains belong to the ECOR phylogroup D, similar to EAEC 042 and other strains with an intact ETT2 which are in group D. In addition, origin of infection in the patients from whom these isolates were obtained was in most cases the urinary tract, not an intestinal infection. Functional studies to define the role of the ETT2 locus in these strains are ongoing.

Conclusions: This is the first description of an apparently functionally intact ETT2 locus with associated *SelC* genes encoding effectors and regulators. The functional significance of the ETT2 remains unclear, but the presence of this locus in a group of blood stream isolates of *E. coli* of mostly urinary origin suggests it may be of importance in infection.