Molecular Characterization of Fecal Escherichia coli isolates from Households (HH) of Veterans, Focusing on Sequence Type 131 and Other Fluoroquinolone-resistant E. coli (FQREC)

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Results

- Of the 627 unique fecal E. coli isolate, 66 (11%) were FQREC (of which 33 [50%] were ST131) and 49 (8%) were ST131 (of which 33 [67%] were FQREC).
- 215 total isolates were from the 86 HHs with at least one ST131 and/or FQREC-colonized member ("strain of interest" HHs).
- The 215 E. coli isolates (149 FQ-S, 66 FQREC) from the 86 "strain of interest" HHs included 7 of the 8 E. coli phylogroups, with group B2 highly predominant (42% of isolates) (Fig. 2).
- Among FQREC isolates, the 33 ST131 isolates had significantly higher VG scores than the 33 other FQREC isolates (median [range], 9 [4-12] vs. 4 [1-10]; P = 0.001) (Fig. 3).
- Colonizing isolates from "strain of interest" HHs exhibited a similar prevalence distribution of ST131 (22%), followed distantly by ST73 (15%).
- The 215 isolates from "strain of interest" HHs represented 173 unique pulsotypes. The most prevalent of these, 968 (47%) and 800 (19%) are also the leading pulsotypes among clinical FQREC ST131 isolates (Fig. 4). Here, they accounted for 23% and 12% of FQREC ST131 isolates, respectively.
- Fecal FQREC ST131 isolates closely resembled reference clinical ST131 isolates according to PFGE profile (Fig. 5).

Introduction

- A single E. coli strain, designated sequence type 131 (ST131) based on multi-locus sequence typing (MLST), has emerged globally over the past decade as a leading cause of antimicrobial-resistant E. coli infections in humans.
- Among veterans, FQREC infections are a significant problem and are caused mainly by E. coli ST131 strains which could emerge from the host’s gut reservoir.

Methods

- Fecal surveillance of 279 randomly selected veterans and their 309 HH members (including 142 pets) yielded 723 unique (by clone and subject) fecal E. coli isolate.
- Fecal E. coli from households with at least one strain of interest (FO-susceptible FO-S) ST131, FQREC ST131, other FQREC colonized member were characterized molecularly.
- Ten E. coli colonies per sample (as available) underwent PCR-based clonal screening.
- One isolate per clone was tested for 53 VGs using established multiplex PCR-based assays.
- Phylogenetic backgrounds for 8 groups (A, B1, B2, D, C, E, and F, and Escherichia cryptic clade I) were determined by multiplex PCR using the Clermont system. The ST was determined using ST-specific PCR assays.
- Xbat pulsed-field gel electrophoresis (PFGE) analysis was used to assign isolates to pulsotypes based on 94% profile similarity to reference strains.

Results

- Among veterans and their HH contacts ST131 is the single most common cause of FQREC colonization.
- Colonizing FQREC ST131 strains likely contributes to the high burden of ST131 disease among veterans.
- Development of interventions to decrease colonization of veterans and their household members with ST131 E. coli may help to halt on the current pandemic.

References


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