



## Fluoroquinolone-Resistant Sequence Type 131 Subgroups O25b and O16 Among Extraintestinal *Escherichia coli* Isolates from Community-Acquired Urinary Tract Infections

### Abstract

**Aim of the work:** We aimed to evaluate the commonality of clones ST131-O25b and ST131-O16 among fluoroquinolone-resistant *E. coli* isolates causing community-acquired urinary tract infections in the Fayoum University Hospital, in Egypt. **Materials and Methods:** Ninety-two fluoroquinolone-resistant *E. coli* isolates were subjected to multiplex PCR for detection of ST131 of either O25b or O16 subgroups. Positive isolates were then assessed for antimicrobial susceptibility and virulence genotyping. **Results:** Out of 92 fluoroquinolone-resistant *E. coli* isolates, 56 (60.9 %) isolates were O25b/O16 subgroups of ST131, including 44 (78.6%) ST131-O25b and 12 (21.4%) ST131-O16 subgroups. All the O25b/O16 ST131 isolates were sensitive to meropenem, where ST131-O25b isolates were significantly more resistant to extended spectrum cephalosporins compared to ST131-O16 strains. All the O25b/O16 ST131 isolates harbored three or more of the virulence factors associated with extra-intestinal pathogenic *E. coli* (ExPEC) status. ST131-O16 showed a significantly higher virulence score than ST131-O25b isolates. **Conclusion:** Our results bring to highlights the emergence of O25b/O16 ST131 isolates between community acquired urinary tract infections among Egyptian patients. This is the first report for the presence of O16 isolates in Egypt, showing a lower predominance than the O25b subgroup