High-risk lineages among extended-spectrum β-lactamase-producing Escherichia coli from extraintestinal infections in Maputo Central Hospital, Mozambique

Abstract

Extended-spectrum β-lactamase (ESBL)-producing extraintestinal pathogenic Escherichia coli (ExPEC), particularly high-risk lineages, are responsible for severe infections and increased mortality and hospital costs worldwide, with a major burden in low-income countries. Here we determined the antimicrobial susceptibility and performed whole-genome sequencing of E. coli isolates from extraintestinal infections of patients during 2017-2018 at Maputo Central Hospital (Mozambique). Multidrug resistance was displayed by 71% of isolates (17/24). All isolates resistant to cefotaxime and ceftazidime were positive for ESBL genes (16/24; 67%) and were co-resistant to amoxicillin/clavulanate (14/16; 88%), piperacillin/tazobactam (8/16; 50%), gentamicin (12/16; 75%), trimethoprim/sulfamethoxazole (15/16; 94%) and ciprofloxacin (11/16; 69%). Several major high-risk ExPEC lineages were identified, such as H30Rx-ST131, fimH41-ST131, H24Rx-ST410, ST617, ST361 and ST69 harbouring blaCTX-M-15, and H30R-ST131, ST38 and ST457 carrying blaCTX-M-27. Dissemination of CTX-M transposition units (ISEcp1-blaCTX-M-15-orf477 and ISEcp1-blaCTX-M-27-IS903B) among different sequence types could be occurring through the mobility of IncF plasmids. Additionally, all H24Rx-ST410 isolates carried ISEcp1-mediated blaCMY-2 AmpC and specific mutations in PBP3/OmpC proteins, potentially contributing to carbapenem resistance even in the absence of carbapenemase genes. Genome analysis highlighted a high assortment of ExPEC/UPEC virulence-associated genes mainly involved in adhesion, invasion, iron uptake and secretory systems among isolates, and an ExPEC/EAEC hybrid pathotype (fimH27-ST131\_O18-ac:H4) showing the highest virulence gene content. cgMLST showed clonality and closely related isolates, particularly among ST131 and ST410, suggesting hospital-acquired infections and long-term ward persistence. Our study provides new insights into ExPEC clones, urging measures to prevent and contain their diffusion in this hospital and Mozambique.

Keywords: AmpC; ESBL; Escherichia coli; ExPEC; Virulence determinant; Whole-genome sequencing.

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