INTRODUCTION

• ESBL-producing organisms have evolved over the past two decades to become a phenomenon of paramount medical importance.

• At the American University of Beirut Medical Center (AUBMC), the proportion of ESBL E. coli (ESBL-EC) and Klebsiella spp. (ESBL-KP) has risen between 1999 and 2008 from 2.5% and 9.8% to 22% and 27%, respectively.

• Few reports exist of ESBL-producing organisms that have been isolated from rectal, axillary and upper respiratory tract samples during investigations of outbreaks, raising concern for colonization of patients at sites other than those of the primary infection.

• Colonization in the absence of outbreaks has so far not been looked at systematically, especially in a high-endemicity area such as Lebanon.

• Our principal question is two-fold: what other colonization sites exist, and are the organisms at colonization sites identical by molecular methods to those at the primary site of infection.

MATERIALS AND METHODS

• Prospective cohort study

• Adult patients hospitalized July 2011-February 2014 and diagnosed with an infection due to ESBL-EC or ESBL-KP were included.

• Patients were excluded if they had infection with the same organism within the preceding year and if they had been on effective antibiotic therapy for longer than 48 hours at the time of enrollment.

• Study intervention: screening cultures for potential sites of colonization were obtained from the skin (axillary, umbilical, and inguinal areas), nasopharynx, urine, rectum, and wounds (if applicable).

• Molecular analysis: DNA extraction was performed and PCR for CTX-M-15 and TEM-1 were performed. Pulsed-field gel electrophoresis (PFGE) was carried to determine genomic relatedness of isolates using standard operating procedure for PulseNet PFGE.

RESULTS

• 22/100 patients (22%) had positive cultures at sites other than the original source of infection.

• 54 isolates recovered from various screening sites in these 22 patients were subjected to molecular analysis.

• 80% of the isolates tested were positive for CTX-M-15, while 39% were positive for TEM-1.

• While in 11 patients the same genes were detected from the different isolates collected from various sites, in 10 other patients, there were minor variations in the genetic distribution in the isolates recovered from different sites.

• PFGE analysis indicates that isolates collected from the same patient were 100% genomically related in 11 of the 22 patients, while in the rest of the patients genomic relatedness varied between 42.9% and 97.1% (Figures A and B).

CONCLUSIONS

• A minority of patients with ESBL-EC and ESBL-KP infections are colonized at body sites other than primary site of infection.

• CTX-M-15 is the predominant ESBL gene.

• Multiple bacterial clones are circulating at our institution.

• No evidence to justify routine active surveillance.

FIGURE A

FIGURE B