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Dissemination of IncF-type plasmids in multi-resistant CTX-M-15-producing *Enterobacteriaceae* isolates from surgical site infections in Bangui, Central African Republic (CAR)

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Introduction: Surgical-site infection is the most frequent health care-associated infection in the developing world with a strikingly higher prevalence than in developed countries. We studied the prevalence of resistance to antibiotics in *Enterobacteriaceae* isolates from surgical-site infections collected in three major tertiary care centers in Bangui, Central African Republic. We also studied the genetic basis for antibiotic.

Methods: Between April 2011 and April 2012, 195 patients with nosocomial surgical-site infections were consecutively recruited into the study at five surgical departments in three major tertiary care centers. The nosocomial bacterial strains were isolated by using conventional bacteriology and among them; the strains resistant to broad spectrum cephalosporins were screened for antibiotic resistance genes by direct sequencing. Resistance transfer was studied by bacterial conjugation in one representative strain of the resistance gene content in each repetitive extragenic palindromic and enterobacterial repetitive intergenic consensus sequence-PCR banding pattern. Plasmids were characterized by PCR-based replicon typing and subtyping schemes. Multi Locus Sequence Typing (MLST) was used to study the genetic background of *E. coli* strains.

Results: Of the 165 bacterial isolates collected, most were *Enterobacteriaceae* (102/165, 61.8%). Of these, 65/102 (63.7%) isolates were resistant to third generation cephalosporins. The blaCTX-M-15 and aac(6')-Ib-cr genes were detected in all strains usually associated with qnr genes (98.5%). *Escherichia coli*, the most commonly recovered species (33/65, 50.8%) occurred in six different sequence types including the pandemic B2-O25b-ST131 group (12/33, 36.4%). In most isolates (18/27, 66.7%), blaCTX-M-15 genes were found in incompatibility groups F/F31:A4:B1 and F/F36:A4:B1 conjugative plasmids.

Conclusion: This study is of particular importance because of the difficulty of carrying out such studies in hospitals in countries with inadequate health care systems. Horizontal transfer of both plasmids is probably an important mechanism for the spread of blaCTX-M-15 among *Enterobacteriaceae* species and hospitals. The presence of sets of antibiotic resistance genes in these two plasmids indicates their capacity for gene rearrangement and their evolution into new variants. All necessary measures should be taken in African hospitals to prevent nosocomial infections and the selection of resistant bacteria with efficient nosocomial infection surveillance programs.

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