Evaluation of the antibiotic resistance of enterobacteriaceae producing extended-spectrum beta-lactamases and carbapenemase isolated in Brazzaville (Congo)

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Abstract

Objective: To molecularly characterize the ESBL/AmpC/OXA-48 genes in clinical and environmental enterobacteriaceae.

Material and methods: The strains were identified by Api 20E and confirmed MALDI-TOF-MS. Sensitivity to antibiotics achieved by agar diffusion on HD, as well as the ESBL phenotype. Antibiotic resistance genes were characterized by PCR and sequencing. Sequences were assembled by Codon Code Aligner and compared by BlastX with Genbank, NCBI and ARGANNOT. Phylogenetic trees were constructed by MEGA7. The transfer of resistance genes carried out by conjugation using E. coli J53 as the recipient strain. The clonal relationship between the strains was made by MLST.

Results: 209 strains were isolated: 56 environmental and 153 clinical. 95 strains (45.45%) were ESBL. 43 E. coli, 35 *K. pneumoniae*, 7 *Ent. cloacae*, and 3 *C. freundii*. 3 *P. mirabilis*, 3 *S. marcescens* and 1 *Arizona spp*. Except for imipenem, total resistance to the majority of beta-lactams, as well as aminosides and fluoroquinolones. TEM-1 were predominant (42.10%), followed by CTX-M-15

(32.63%). ACT-1 was found in 6 strains and CMY-2 in 2 strains; OXA-48 in 5 strains. MLST showed that the 2 *K. pneumoniae* OXA-48 strains were genetically different ST15 and ST460. Conjugation and transformation showed that blaOXA-48 was not carried by a plasmid. **Conclusion:** Our study revealed the spread of ESBL type TEM-1, CTX-M15 and AmpC in our hospitals which exposes to a growing problem of therapeutic management.

Biography:

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