

ABSTRACT

E. cloacae and *E. aerogenes* are important agents of opportunistic infections in hospitalized patients that became a target of increasing interest, due to dissemination of multidrug-resistant (MDR) strains, especially those producing ESBL and KPC. The identification of mechanisms of virulence is important for understanding the pathogenesis of these MDR pathogens. Several factors can contribute to the virulence of *E. cloacae* and *E. aerogenes*, including fimbrial adhesins, capsules, lipopolysaccharides (LPS) and iron acquisition systems. The aim of this study was identify virulence genes in MDR *E. cloacae* and *E. aerogenes* and the clonal relationship among isolates. Twenty nine *E. cloacae* and 6 *E. aerogenes* isolated from clinical specimens of 35 patients admitted to a tertiary hospital in the São José do Rio Preto/SP, between the years of 2013 to 2017 were included in this study. Species identification and antimicrobial susceptibility tests were performed by an automated system. The presence of virulence genotypes and genes codifying carbapenemases, ESBL, AMEs and PMQR were evaluated by PCR. For confirmation of variant *aac(6')Ib-cr*, the restriction enzyme BseGI was used. Molecular typing was done by PFGE. Among the 35 isolates, 30% originated from urine, 26% tracheal aspirate, 14% blood, 8% catheter tip, 8% sterile biological fluids, and 14% other biological samples. The majority of patients (46%) were admitted to Intensive Care Units. The *entB* gene was detected in 97% of isolates. With respect to *E. aerogenes* the *bla_{KPC}+entB+iroN+wabG* association was the found in 4 of the isolates. The *bla_{SHV}* gene was detected in 1 isolate, and *ant(2'')-Ia* was detected associated with *bla_{KPC}+entB+iroN* genes. PFGE typing generated one cluster with 2 strains presenting 100% similarity. Regarding *E. cloacae*, *bla_{CTX-M-15}* was detected in 34%, *ant(2'')-Ia* in 28%, and *aac(6')-Ib-cr* in 21% of strains. Among the virulence genes found in *E. cloacae*, the results showed 52% *entB+iroN*, 24% *uge*, and 14% *mrkD* genes. One *E. cloacae* harboured *bla_{KPC}+bla_{CTX-M-15}+aac(3)IIa+aph(3)Ia+aac(6')-Ib+ant(2'')Ia+uge+mrkD+iroN* genes. No relationship between *E. cloacae* from different inpatient units was detected. The accumulation of virulence genes responsible for the biosynthesis of fimbriae, LPS, capsule and siderophores together with antimicrobial multiresistance strains may result in poor patient prognosis due to the potential for promoting serious infectious and therapeutic limitations.

Keywords: *E. cloacae*; *E. aerogenes*; Resistance; Virulence Factors.