TITLE: VIRULENCE GENES AND BIOFILM FORMATION IN *Klebsiella Pneumoniae* PRODUCING KPC ISOLATED IN A TERTIARY HOSPITAL OF SÃO JOSÉ DO RIO PRETO-SP

AUTHORS: TOMAZ, F. M. M. B.; ANDRADE, B. S.; ANDRADE, L. K.; GOZI, K. S.; MADELA, N. K.; MARTINS, E. R.; PRADELA, L. K.;CASELLA, T.; NOGUEIRA, M. C. L.

INSTITUTION: FACULDADE DE MEDICINA DE SÃO JOSÉ DO RIO PRETO, SÃO JOSÉ DO RIO PRETO, SÃO PAULO (AVENIDA BRIGADEIRO FARIA LIMA, 5416, CEP: 15090-000 SÃO JOSÉ DO RIO PRETO-SP, BRASIL)

ABSTRACT:

Klebsiella pneumoniae is an important opportunistic pathogen, causing nosocomial infections such as pneumonia, urinary tract infections, invasive infections and surgical site infections. In the last decades, acquisition of resistance to several antimicrobials made these infections difficult to treat, resulting in high rates of morbidity and mortality. Several virulence genes have been identified in *K. pneumoniae*, genes that encode the capsule (*magA*, *k2A*, *wcaG*), hypermucoviscosity (*magA*, *rpmA*), fimbrial adhesins (*fimH*, *kpn, mrkD, ycfM*), cell wall lipopolysaccharides (*wabG*, *uge*), iron acquisition system (*entB, iroN, iutA*) and toxins (*hly*, *cnf-1)*. Important virulence factors that contribute to biofilm formation in *K. pneumoniae* are the capsular polysaccharides, type 1 and type 3 fimbriae. In this study, 91 strains of KPC-producing *K. pneumoniae* isolated in 2015 and 2016 from patients with urinary tract infections (UTI) admitted to a tertiary hospital in São José do Rio Preto – SP, Brazil, were evaluated. These bacteria were identified and evaluated for the antimicrobial susceptibility profile by the Vitek®2 Compact System (Biomerieux, France). Molecular typing was performed by PFGE, and the BioNumerics software was used for dendrogram construction and determination of the similarity among strains. Specific primers were used to detect the virulence genes *rmpA*, *magA*, *k2A*, *wcaG*, *fimH*, *mrkD*, *kpn*, *wabG*, *uge*, *ycfM*, *iutA*, *iroN*, *entB*, *allS*, *hly*, *cnf-1*. Biofilm formation was evaluated as described by Wakimoto et al. 2004. The biofilm was quantified using an automated plate reader (Synergy ™ HT, Bio-Tek, Winooski, VT, USA). EAEC strain O42 and E. coli DH5α were used as controls. The results showed the presence of *ycfM* (n = 91), *entB* (n = 90), *wabG* (n = 90), *fimH* (n = 87), mrkD (n = 87), *kpn* (n = 84), *uge* (n = 74) and *all* (n = 1). Molecular typing showed a wide diversity of PFGE patterns. In relation to biofilm formation, sixty one were identified as strong biofilm forming strains, twenty as weak forming and ten were non-biofilm forming strains.These preliminary results show that several clones of KPC-producing *K. pneumoniae* are associated with UTI in the studied institution, and also that many virulence factors perform a role on the colonization and maintenance of these infections. Our results also suggest that *fimH* and *mrkD* genes that codify type 1 and type 3 fimbriae, respectively, may an important role in urinary tract infections and promote biofilm development.

Keywords: Virulence, *Klebsiella pneumoniae*, KPC, Urinary tract infections, Biofilm

Development Agency: FAPESP and CAPES