

TITLE: IDENTIFICATION OF GENES ASSOCIATED WITH VIRULENCE IN *MORGANELLA MORGANII* IN CLINICAL NON-URINARY HOSPITAL ISOLATES IN LONDRINA, PARANÁ.

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ABSTRACT:

Morganella morganii is part of the Enterobacteriaceae family, belonging to the *Proteeae* tribe that groups two other genera: *Proteus sp* and *Providencia sp*. It is considered an opportunistic pathogen, causing urinary tract infections and postoperative wounds. It is described as a Gram-negative rod that has several virulence factors that contribute to the colonization of the pathogen causing nosocomial infections, so understanding the virulence mechanisms is essential to prevent serious infections. Then the objective of this work was verifies the presence of 9 genes (*zapA*, *mrpA*, *fimH*, *iutA*, *ireA*, *hlyA*, *shIA*, *tibA* e *invA*) in strains of *M. morganii*. Thus, 22 non-urinary isolates from the hospital environment from tissue, bone fragment, eye swab, tracheal secretion, blood and bronchial aspirate were collected between 2015 and 2019 and analyzed through this study. The virulence genes were identified by the Polymerase Chain Reaction (PCR) the prevalence of virulence genes in hospital clinical isolates refer to 1 strain cepa (4.54%) *invA* (adhesina), 2 (9.09%) *hlyA* (hemolysin), 4 (18.18%) *tibA* (adhesin), 9 (40.90%) *shIA* (hemolysin), 20 (90.90%) *mrpA* (fimbriae), 20 (90.90%) *ireA* (siderophore), 21 (95.45%) *zapA* (protease), 22 (100%) *iutA* (siderophore) and finally 22 (100%) *fimH* (fimbriae). Considering the results found, the pathogenicity of the studied strains of *M. morganii* can be associated with the presence of virulence factor genes favoring clinical infections. The genes of interest were obtained through the genotypic test whose virulence of *M. morganii* represents a great risk and should not be neglected, especially in the hospital environment.

Keywords: pathogenicity , virulence, Gram-negative, hospital, *Morganella morganii*

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