

TITLE: GENOTYPIC CHARACTERIZATION OF *PROTEUS MIRABILIS* VIRULENCE FACTORS ISOLATED FROM SEVERAL SOURCES OF INFECTION

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ABSTRACT:

The genus *Proteus* is responsible for several hospital infections, such as: respiratory tract infections, wounds, eyes, nose, throat, skin and gastroenteritis. They can be found in soil, water and urinary tract of different mammals. Among the species of this genus the most prevalent in infections in humans is *Proteus mirabilis*. *P. mirabilis* presents as main virulence factors adhesins, hemolysins, toxins, capsule, siderophores, urease and proteases. This work aimed to investigate the presence of these virulence factors in 68 isolates of *P. mirabilis*. These isolates were collected from patients from the University Hospital of Londrina (HU-UDEL) during the period from January 2015 to March 2017 and identified through the VITEK® 2 automated system (bioMérieux Brazil). The virulence genes *hpmA*, *hlyA*, *zapA*, *mrpA*, *fimH*, *pmfA*, *ucaA*, *ireA*, *atfA* and *ureA* were searched by the Polymerase Chain Reaction (PCR) technique and the amplification products were subjected to agarose gel electrophoresis, stained with SYBR® Safe and visualized using UV light. As a result, it was possible to detect the presence of *hpmA* in 94.11% of isolates of urinary origin and in 100% of isolates from other sources of infection, *pmfA* in 97.05% of urinary isolates and 100% of other sources of infections, *ucaA* in 76.47% of urinary isolates and in 88.23% of isolates from other sources of infections, the *zapA* was present in 94.11% of urinary isolates and in 100% of isolates from other sources of infections, *mrpA* present in 88.23% of the urinary isolates and in 88.23% of the isolates from other sources of infection, it is present in 100% of the urinary isolates and in 97.05% of the isolates of other sources of infection. However, the *hlyA* and *fimH* genes were not found in any of the isolates, either urinary or other sources of infection. And the *atfA* and *ureA* genes were present in 100% of the isolates (urinary and other sources of infection). In this way, we can conclude that *P. mirabilis* isolates from other sources presented a higher percentage of virulence genes than urinary isolates. And that the enterobacterial genes *hlyA* and *fimH* are not present in *P. mirabilis*.

Keywords: *Proteus mirabilis*; PCR; Virulence factors.

Development Agency: Medical Microbiology - Bacteriology