

## **TITLE: Genotypic Characterization Of Virulence Factors In *Aeromonas* spp. From Brazilian Food Chain.**

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*Aeromonas* spp. are ubiquitous microorganisms, isolated from different environmental niches and capable of causing infectious intestinal and extraintestinal pictures in amphibians, birds, fish, mammals and reptiles. Over the last 30 years the knowledge about this microorganism has evolved greatly, as can the increase in its isolation. Mobile genetic elements recovered from *Aeromonas* strains have genes involved in virulence, stress response, resistance to heavy metals and / or antimicrobials, and toxic compounds. Among the most frequently isolated species are: *A. hydrophila*, *A. dhakensis* (considered the most virulent), *A. veronii* and *A. caviae*. The aim of this study was to evaluate the diversity of the virulence genes of the *A. hydrophila* and *A. dhakensis* species from environmental, food, animal and human sources isolated from 2016 to 2019 at the National Reference Laboratory for Bacterial Enteropathic Infections. Through the Polymerase Chain Reaction genes associated to hemolysins (aer A and hly A) and enterotoxins (act and alt) were investigated. Among the 118 *Aeromonas* isolates (31 *A. dhakensis* and 87 *A. hydrophila*) it was possible to identify 60% of positive strains for at least one of the genes studied. In *A. dhakensis*, 30.7% act, 15.3% alt, 23% aer A and 38.5% hly A, were identified in 5 virulence profiles, with emphasis on the act, aer A, hly A profile in strains of environmental origin. In *A. hydrophila*, 64.5% presented virulence genes: 25.8% act, 32.3% alt, 22.6% aer A and 32.3% hly A distributed in 8 profiles with emphasis to act, aer A, hly A and act, aer A, alt found in strains of human and environmental origin. Studies have reported *A. dhakensis* as having greater pathogenic potential between *Aeromonas* spp. and perhaps even more prevalent, being, however, a victim of incorrect identification during the diagnostic process. However during the period of this study greater isolation of *A. hydrophila* was observed. The presence of genes associated with hemolytic and enterotoxic activity in *Aeromonas* from different sources points out its diversity and pathogenicity. The continuity of the genotypic characterization of these microorganisms will allow us to obtain a profile about the characteristics that are present and prevalent in *A. dhakensis* and *A. hydrophila* strains circulating in our country.

**Key words:** *Aeromonas* spp., *A. hydrophila*, *A. dhakensis*, Virulência