

Título: Evaluation of virulence factors and antimicrobial susceptibility of *Aeromonas hydrophila* and *Aeromonas caviae* from different sources in Brazil

Autores: Roges, E. M.¹; Siciliano, S.²; Rocha, E. L.³; Alves, C. F. M.⁴; Droppa, E.⁵; Magalhães, L. F. C.⁶; Tristão, E. B.⁷; Cosmo, L. M. S. S.⁸; Cavalcanti, V. O.⁹; Rodrigues, D. P.¹

Instituição:¹FIOCRUZ – Fundação Oswaldo Cruz (Av. Brasil, 4365 - Manguinhos, Pavilhão Rocha Lima 3º andar, sala 320, Rio de Janeiro / RJ - CEP: 21040-900), ²FIOCRUZ – Fundação Oswaldo Cruz (R. Leopoldo Bulhões 1.480 – Manguinhos, Rio de Janeiro / RJ - CEP: 21040-360), ³LACEN DF - Laboratório Central do Distrito Federal (Lotes O e P - Sgan 601 - Asa Norte, Brasília / DF, 70830-010), ⁴FUNED – Fundação Ezequiel Dias (Rua Conde Pereira Carneiro, 80 – Gameleira - Belo Horizonte / MG - CEP 30.510-010), ⁵LACEN PR - Laboratório Central do Estado do Paraná (R. Ubaldino do Amaral 545 - Alto da XV - Curitiba / PR – CEP: 80060-190), ⁶LACEN RR - Laboratório Central de Saúde Pública de Roraima (Av. Rio Branco, 152 Fundos – Centro - Boa Vista / RR – CEP: 88015201); ⁷LACEN ES - Laboratório Central de Saúde Pública do Espírito Santo (Av. Marechal Mascarenhas de Moraes, 2025 - Bento Ferreira - Vitória - ES - CEP: 29050-625); ⁸LACEN MA - Laboratório Central de Saúde Pública do Maranhão (R. Afonso Pena, Centro - São Luiz / MA - CEP: 65010030); ⁹LACEN PE - Laboratório Central de Saúde Pública de Pernambuco (R. João Fernandes Vieira s/n – Recife / PE – CEP: 50050-215)

Resumo:

Aeromonas spp. are natural inhabitants of aquatic environments and may be associated with numerous infections in humans and animals. Its pathogenesis is multifactorial, associated with a wide variety of virulence factors. The present study selected 120 strains being 56 *A. caviae* and 64 *A. hydrophila* isolated between 2008 and 2012. In phenotypic analysis the enzymes collagenase, elastase, hemolysin and DNase were identified. The antimicrobial susceptibility testing was performed by disk diffusion method according to CLSI guidelines. The PCR was performed to detect hemolysin (*hlyA* / *aerA*), enterotoxin (*act* / *alt*) lipase (*lip* / *gcat*) and *dnase*. The *dnase* was observed in 97.5% strains, hemolysis on 62,5% and the enterotoxins *act* and *alt* in 20% and 17,5% strains, respectively. Genes *lip* (36%) and *gcat* (38%) and enzymes collagenase (13%) and elastase (11%) are produced by *Aeromonas* able to degrade physiological proteins present in the serum and tissues as fibrinogen, albumin, elastin and collagen. We observed hemolytic capacity in most isolates. Collagenase activity was identified in skin *Aeromonas hydrophila* in agreement with the role assigned to this enzyme in the infection of wounds. The distribution of different virulence profiles showed prevalence of the following profiles: *hlyA-dnase-gcat-hem* in 14 strains; *aerA-dnase-lip-act-hem* in 9 strains and *aerA-hlyA-dnase-lip-act-hem* in 8 strains, all of animal origin. Particularly among those of human origin, diverse profiles were observed. All the strains showed sensitivity to nitrofurantoin, and distribution of resistance to other drugs was AMK 11.67%, NAL 12.5%, GEN 3.34%, SXT 7.5%, TCY 7.5%, CHL 1%, CAZ 2.5%, CIP 3.34 %, CTX 2.5% and IPM 13.35%. Two *A. hydrophila* strains isolated from feces were multi-resistant AMK-GEN-NAL-TCY-CTX and AMK-NAL-SXT-GEN-TCY-CIP-CTX. The presence of extracellular enzymes, virulence genes and increasing antimicrobial resistance in *Aeromonas* are pointing their importance and possibility of environmental gene exchanges, showing their ability of gene transfer and relevance for public health.

Palavras chave: *Aeromonas*, Virulence, Antimicrobial resistance.