XIII JORNADAS DE GENÉTICA
E BIOTECNOLOGIA
III JORNADAS IBÉRICAS
DE GENÉTICA Y BIOTECNOLOGÍA

14 - 16 April 2021

Book of Abstracts

Título: Livro de Resumos das XIII Jornadas de Genética e Biotecnologia / III Jornadas Ibéricas de Genética y Biotecnología

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Editor: UTAD - Universidade de Trás-os-Montes e Alto Douro

Editor Gráfico: Beatriz Bettencourt

ISBN: 978-989-704-430-4

ISBN: 978-989-704-431-1 (versão eletrónica)

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Diversity of Aeromonas species isolated from surface waters: Occurrence of antibiotic resistance to β-lactamase.

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Keywords: *Aeromonas spp.*; Antimicrobial resistance; Anthropogenic pressures; One health concept.

The extensive use of water and anthropogenic activities associated with the inappropriate use of antibiotics and their overuse throughout history are one of the causes for the high incidence of antimicrobial-resistant genes (ARGs) and bacteria (ARBs) isolated from aquatic ecosystems. According to the World Health Organization (WHO) ARGs and ARBs is considered as a major public health concern. *Aeromonas* spp. are ubiquitous bacteria, primarily recovered from aquatic ecosystems. They have been isolated from wastewater, natural water such as rivers, lakes and estuaries, aquacultures, urban drinking water, and in association with numerous autochthonous aquatic organisms in these environments. This study aimed to evaluate antimicrobial resistance among riverine *Aeromonas* spp., taken as representative of the autochthonous microbiota, to assess the level of antibacterial resistance in water, and the potential risk that it represents. Water samples were collected from the hydrographic basins of Tua river, Portugal. Samples were filtered through a cellulose nitrate pore membrane filter. The filters were incubated at 37°C for 24 h in Glutamate Starch Phenol red (GSP) agar. *Aeromonas* isolates were identified by API 20 NE. Antimicrobial susceptibility testing was performed by the Kirby-Bauer disk diffusion method. A broad range of antibiotics covering the β-lactams family were used to determine the resistance of isolates. The results indicate a greater incidence of multiple antibiotic resistance *Aeromonas* isolates, as follows: AML-amoxicillin (93.33%); AMC-amoxicillin/clavulanic acid (73.33%); TIC-ticarcillin (83.33%); TIM-ticarcillin/clavulanic acid (56.67%); PRL-piperacillin (40.00%); TZP-piperacillin/tazobactam (40.00%); ATM-aztreonam (33.33%); IPM-imipenem (43.33%); KF-cephalothin (70.00%); CTX-cefotaxime (40.00%). The high aeromonads β-lactamases resistance suggest that this species can be used as bioindicator organisms for monitoring ARGs in rivers, and should be considered in a “One Health—One World” concept.

Acknowledgments: This work is supported by National Funds by FCT - Portuguese Foundation for Science and Technology, under the project UIDB/04033/2020