

TITLE: GENOMIC CHARACTERIZATION OF TWO *AEROMONAS* STRAINS THAT PRODUCE ANTIMICROBIAL SUBSTANCES

AUTHORS: SILVA, S.; GUEDES, F. A. F.; RIBEIRO, J. R.; DINIZ, F. S.; AMARAL, J. R. V.; PINHEIRO, Y.; THOMPSON, F.; MACRAE, A.; OLIVEIRA, S. S.

INSTITUTION: DEPARTAMENTO DE MICROBIOLOGIA GERAL, INSTITUTO DE MICROBIOLOGIA PAULO DE GÓES, CCS, UNIVERSIDADE FEDERAL DO RIO DE JANEIRO. (AVENIDA PROF. RODOLPHO PAULO ROCCO, S/N - PRÉDIO DO CCS - BLOCO I, 1º ANDAR - SALA 047, RIO DE JANEIRO, RJ, CEP-21941-902, RIO DE JANEIRO - RJ, BRASIL).

ABSTRACT: Microorganisms are a source of compounds with biotechnological potential, the genus *Aeromonas* is composed of Gram-negative bacilli, facultative anaerobes and it is known for producing antimicrobial substances. Studying these substances is relevant for their use in the food and pharmaceutical industry as preservatives and new antibiotics, respectively. The aims of this work are to detect bacteria producing these substances and to make a genomic characterization of two strains. Deferred plate assays were made with 57 strains of the genus *Aeromonas* isolated from fish: *Mugil brasiliensis* and *Carangilidae* using the agar well diffusion assay method and the indicator strains: *Escherichia coli* ESBL; *Klebsiella pneumoniae* KPC; *Pseudomonas aeruginosa* SPM; *Salmonella typhimurium* ATCC 14028. Following the assays, strains were selected for DNA extraction. Genome sequencing was performed by the Miseq illumina platform; The quality cut was made using the Trimmomatic tool. *De novo* assembly was performed with SPAdes, followed by mapping assembly with MeDuSa. The annotation method was classic RAST v. 2.0 and bacteriocins were searched with AntiSMASH v. 3.0 and BAGEL v 4.0. As a result 38 strains producing antimicrobial substances were obtained. The AE59 and AE38 strains were sequenced due to their spectrum of action. Sequencing generated 532,201 raw reads for strain AE59 and 1,661,394 for AE38. After the quality cut, were obtained 365,719 quality reads for AE59 and 1,174,934 for AE38; AE59 strain assembly generated a 4,519,057 bp Scaffold, whereas the AE38 strain generated a 4,669,369 bp Scaffold. RAST scored 4050 coding sequences for the AE59 strain and 4225 for the AE38 strain. RAST found a 489 bp production gene for a putative Colicin-V for AE38 and a 1520 bp production gene for a putative Colicin-V for AE59. The AntiSMASH tool found no sequence for bacteriocin in *Aeromonas allosaccharophila* AE59 strain but found one Bacteriocin gene cluster for *Aeromonas salmonicida* AE38 strain, which contains a biosynthetic and a regulatory gene. The Bagel tool did not localize any bacteriocin-related gene. The results suggest that

both strains produce a Colicin V-like bacteriocin. The next steps are to characterize these bacteriocins and to deepen the analysis of these sequences.

Keywords: *Aeromonas allosaccharophila* AE59; *Aeromonas salmonicida* AE38; bacteriocin; Colicin V; antimicrobial substance; Illumina MiSeq; Genome Assembly.

Development Agency: Conselho Nacional de Desenvolvimento Científico e Tecnológico.