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Whole genome sequencing of *Aeromonas caviae* strain 429865 and preliminary comparative analysis of the A. caviae genome

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Aeromonas caviae is a rod-shaped, gram-negative, ubiquitous bacterium which has been identified to be implicated in a variety of intestinal and extra-intestinal illnesses, as well as soft-tissue infections in humans. It is also one of the bacteria in the genus *Aeromonas* responsible for the majority (>85%) of human infections and clinical isolates, and related to the most prevalent in pediatric patients. The genome of *Aeromonas caviae* strain 429865 isolated from an infected 2 years and 4 months old patient in Mexico was sequenced using the Illumina Miseq platform according to the standard operation based on a Pair-End library and a Mate-Pair library of 5Kb fragments. The genome was assembled *de novo* into 4 contigs using SPAdes v3.5.0 and Consed v29.0. The length of the assembled genome was 4,700,593 bp and has an overall G+C content of 61.0%. Annotation was performed using the NMPDR's RAST server, upon which 4,258 Coding Sequences (CDS) were identified, as well as 144 RNAs. BLAST-based Average Nucleotide Identity (ANIb) analysis confirmed that the sequenced genome belonged to the *Aeromonas caviae* species. OrthoMCL and Java Script Codes were utilized to determine the pan-genome (6,957 proteins) and core-genome (3,293 proteins) of 10 sequenced genomes of *A. caviae*. 114 unique CDS to *A. caviae* strain 429865's genome were found. Various genes that could be involved in infection were identified, including the genes encoding for toxins, antibiotic resistance and motility.

Biography

Juan Carlos A Padilla is a Graduate student currently on his final semester towards his Master of Science degree in Genomics and Biotechnology from the Instituto Politécnico Nacional.

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