Non-coding RNAs in the genus *Aeromonas*

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The *Aeromonas* spp are Gram-negative bacteria that do not form spores, they are chemoorganotrophic and facultative anaerobes. The first genre description dates from the late nineteenth century, however the genre was only set after a phylogenetic analysis of 16S rRNA in 1992, establishing a new *Aeromonas* genus, which comprises the *Aeromonadaceae* family, *Aeromonadales* order, Proteobacteria class and subclass gama-Proteobacteria. This bacterium has a high degree of pathogenicity causing opportunistic infections. In Bacteria, non-coding RNAs with regulatory function (ncRNAs) can modulate physiological responses and act by different mechanisms such as RNA-RNA pairing bases and RNA-protein interactions. Technologies for non-coding RNA prediction analysis such as the Infernal program (Inference RNA Alignment), can predict different types of ncRNAs, indicating that the amount of regulatory ncRNAs can be higher than previously thought. Traditionally, these approaches along with the help of targeting programs as TargetRNA2 and more advanced technologies, such as RNA-Seq, allows to identify ncRNAs involved with the virulence process, biofilm formation, resistance to antibiotics and survival. The aim of this study is to identify ncRNAs present in the *Aeromonas* strains: *A. hydrophila, A. caviae, A. sóbria, A. trota* and *A. veronii*. The genomes deposited inside the NCBI database were used as input data for the Infernal 1.1 tool. The output data were separated into ribosomal RNAs, carrier RNAs and ncRNAs. The ncRNAs were classified as smallRNAs, regulatory ncRNAs and riboswitches. The identity of ncRNAs was determined on the Rfam database. The TargetRNA2 software was used for target prediction. A total of 237 ncRNAs were found. Fifty ncRNAs were assigned as regulatory, 6 as riboswitches, 6 as microRNAs and 175 as smallRNAs. We identified regulatory ncRNAs that acts in cis, ncRNAs that associates with Hfq, ncRNAs involved in virulence, pathogenicity, responsible for biofilm formation and cell survival. Regarding microRNAs found in this analysis in prokaryotes, we have the following hypothesis: the isolates came from clinical specimens, which strengthens a pathogen-host relationship and the predictor program identifies the sequence as microRNA since this sequence is in your database. They were compared with other enteropathogenic bacterium references (*E. coli* and *Salmonella spp*.), showing a great similarity between these species.