TITLE: Use of metagenomic data for bioprospecting and monitoring of resistance genes in the aquatic environment in Pereru.

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ABSTRACT:

With the progressive advances in sequencing technologies called New Generation Sequencing Technologies (NGS), they promoted DNA sequencing on platforms capable of generating information from millions of base pairs in a single race. Because these new techniques depend on independent culture approaches, they can access genomic information from the vast majority of bacteria that are not cultivable. Therefore, this study aimed to perform searches of various genes in the microbiome of Pereru, based on the comparison of sequences of the aquatic ecosystem against reference genomic libraries. In this sense, for the monitoring of resistance genes in the aquatic environment in Pereru, first, we obtained the raw data of the environment, therefore they went through a first filtration to determine the quality of the readings, thread 20. The average and standard deviation of the readings is then checked with a script in house and withdrawal of the readings larger and smaller than twice the standard deviation, from this data is made the conversion from FASTQ to Fasta. Finally, the alignment of these sequences is performed using the Blast + for an e-value less than 0.01, previously treated, with the databases of Archaeas, bacteria, integrases, plasmids, resistance which were obtained at various sites and was also Analysis of the phylogenetic diversity of diversity from the MG-RAST server was performed. As a final result of the blast + alignment were found from the plasmid database, resistance and integrase the most relevant genes for the study that are, pKpn70742 2 and pB11911 which correspond to the microorganisms Klebsiella pneumoniae and Acinetobacter Baumanni, besides the YP_002382193 and YP_002029849 of the genera Escherichia fergusonii and Stenotrophomonas Maltophilia, as well as idbc4776 and idbc3936 represented by Vibrio cholerae and Salmonella enterica these genes confer resistance to a Broad spectrum of antibiotics and are related to various pathogenicities in humans. The analyses of the MG-RAST showed the domain of bacteria with 99.96% followed by eukaryotes with 0.02% and viruses with 0.01%, in the genome studied, therefore, at the gender level, Shewanella represents 89.02% and Vibrio 3.05% are found in environments and are related to pathogens. Considering the approach, it could be concluded that the sampling of the microbiome of Pereru has a range of microorganisms that are related to strong environmental impacts by genes resistant to antibiotics and risk to human health.

Keywords: Metagenoma, resistance genes, sequence alignment.

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