

POSTER - DNA AND GENOMICS

**METAGENOMIC SEQUENCING REVEALS THE DIVERSITY OF ANTIBIOTIC
RESISTANCE GENES IN BRAZILIAN SEWAGE SAMPLES**

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Antimicrobial resistance (AMR) is a global health threat that is increasing at an alarming rate. In order to better understand the prevalence of AMR genes in the environment, metagenomic sequencing of sewage samples has been employed as a non-invasive way to assess the dissemination and potential sources of resistance genes. In this study, whole genome sequencing (WGS) was performed on six sewage libraries from Brazil available in the NCBI Sequence Reads Archive (SRA) database. The raw data was imported into Galaxy Australia, a web-based platform for data analysis, where MEGAHIT was used for de novo assembly of contigs, and functional annotation of obtained sequences was performed by ABRicate using Card, NCBI, Arg-Annot, and Resfinder databases. The results of the study showed that the NCBI database

identified the highest number of annotations (289) and gene diversity (103) compared to other databases. However, the Card database had three classes of antibiotics not identified by any other database. Furthermore, the analysis showed that the macrolides (293) were the most abundant class of antibiotics detected in the samples, followed by beta-lactams (239). The study provides valuable information on the genes and antibiotic classes found in Brazilian sewage samples, which can contribute to the surveillance of resistance genes and possible hosts in Brazilian sewage. By identifying the sources and prevalence of AMR genes, decision-makers can take action to prevent the indiscriminate use of antibiotics, which is a major driver of the development and spread of AMR. In summary, this study demonstrates the importance of metagenomic sequencing of sewage samples for surveillance of AMR genes in the environment. The use of multiple databases for functional annotation of sequences provides a more comprehensive analysis of the genes and antibiotic classes present in the samples. The results of this study can inform public health policies on the prevention and control of AMR, as well as guide future research in the field of environmental AMR.