Session Ecology and Management of Foodborne Agents

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065 - MEGaRES and AmrPlusPlus - A comprehensive database of antimicrobial resistance genes and user-friendly pipeline for analysis of high-throughput sequencing data

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Abstract

Antimicrobial resistance has become an imminent concern for public health. As methods for detection and characterization of antimicrobial resistance move from targeted culture and polymerase chain reaction to high throughput metagenomic sequencing, appropriate resources for the analysis of large-scale data are required. Currently, no database of antimicrobial resistance gene sequences meets these requirements, and no database-integrated tools are scaleable to allow analysis of large metagenomic datasets. Therefore, we have developed MEGaRES (https://megares.meglab.org), a hand-curated antimicrobial resistance database accompanied by an annotation structure designed for the development of high throughput classifiers and statistical analysis of big data. MEGaRES can be browsed as a stand-alone resource through the website or be easily integrated into sequence analysis pipelines through download. AmrPlusPlus is a user-friendly Galaxy pipeline of six interconnected analyses developed specifically for analyzing metagenomic sequence data (http://megares.meglab.org/amrplusplus) and can be easily installed and run on a small platform (i.e., notebook). This pipeline trims and filters raw reads in the FASTQ file, removes host DNA contamination, classifies reads through alignment to MEGaRES, calculates gene fraction and generates rarefaction curves, identifies single nucleotide polymorphisms (SNPs) and gene haplotypes, and performs microbiome classification of shotgun in metagenomic data.