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Sharing Raw Data from Bacterial Genomes for Collaborative Research on the AMPed Server at URI

Sponsor: Lenore Martin (Cell and Molecular Biology)

The AMPed (*AntiMicrobial Peptide Editable Database*), is a research server at URI that links researchers all over the world so that they can share their data and collaborate on developing new antimicrobial peptides. This server is being expanded to also provide users and collaborators with raw bacterial genomes sequencing data to yield better reproducibility in research. This research project marks the first steps taken to upload high-throughput genome sequencing data on this URI server. The human pathogens used in this research are *Staphylococcus aureus* (gram-positive and found on the skin), *Escherichia coli* (gram-negative and found in the gut microbiota), *Pseudomonas aeruginosa* (gram-negative, multidrug-resistant pathogen and found in the skin flora), and *Enterococcus faecalis* (gram-positive and found in the gastrointestinal tract of humans). These species underwent genomic DNA extraction, then isolated genomic DNA was evaluated as to yield and purity using analytical measurements on the Nanodrop Spectrophotometer and via DNA Gel Electrophoresis to evaluate the integrity of the samples prior to sequencing. The 4 bacterial genomes used for antimicrobial testing in the Martinlab are then sequenced using a single MiSeq NextGen sequencing run; the raw sequencing data that is acquired from the Illumina MiSeq Next Generation Sequencing provides sequences of gene fragments that are then assembled by aligning the raw data with the ATCC standard reference strains for these pathogens. Once the experimentally determined genomic sequences have been aligned with the reference genomes and assembled into a single contig, the sequences will be imported into the AMPed database, thereby facilitating the sharing of experimental data with other researchers around the world.