Faculty of Science and Health

FACULTY RESEARCH COMMITTEE

Undergraduate Summer Research Internship Scheme 2017

Project Title: *Do harmless gut bacteria aid the transfer of drug resistance genes between infectious bacterial species?*

Principal Investigator: *Dr. Tim Downing, Infection Genomics*

School/Research Centre: *Biotechnology*

Project Description

Project Aims

The rate of infectious disease outbreaks globally is increasing and is driven by drug resistance in bacteria. Public health labs routinely screen thousands of cases annually, with a rising rate of positive tests. Treatment regimes are extending bacterial resistance to antimicrobials as a result of high levels of environmental, clinical and agricultural exposure. We hypothesise that harmless gut bacteria act like a portable mobile phone “app store” containing a spectrum of drug resistance genes (“apps”) that pathogenic bacteria install into their genomes and use to promote new functions and to resist treatment in patients. This project will examine the overlap of these microbiome (gut bacteria) genes with those driving drug-resistance in pathogenic bacteria. We will determine the effect of recent gene exchange events on antimicrobial resistance using human microbiome data and bacterial species. This will start with known cases of gene transfer, including ones conferring resistance to last-resort drugs like colistin, and then move on to testing for more novel connections based on shared environmental niches like the intestine and bloodstream. This will provide new ideas on how antimicrobial resistance genes get passed on among the diverse commensal and pathogenic bacteria lurking in our bodies.

Potential Candidates

This project would suit a motivated student interested in molecular and computational biology. The project involves skills such as DNA sequence comparison, visualising genomic data and computer programming: training will be provided. At the end of the project, you will be able to perform sequence alignments and interpret the effects on chromosome and plasmid structure. You will: (i) develop understanding of the scientific process; (ii) improve your skills in genome-based experiments; and (iii) learn how evolutionary model assumptions can affect results. Learning about these techniques is valuable for those interested in bioinformatics and biomedical research on genomic data.

Key steps

1. Select published data from the Human Microbiome Project and antimicrobial resistance genes
2. Infer antimicrobial resistance genes’ origins using sequence comparison
3. Add gene and functional annotation using gene annotation
4. Concatenate resistome segments and visualise them
5. Construct phylogenies and assess gene presence and absence

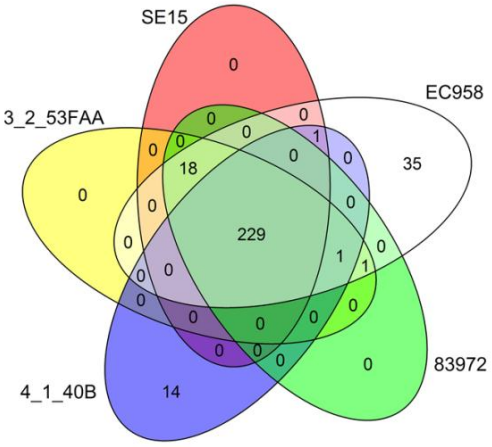

Figure: Drug-resistance genes shared by different bacterial samples taken from patients - 229 genes are shared by all five samples shown here.

References:

1. Downing T. Tackling drug resistant infection outbreaks of global pandemic *Escherichia coli* ST131 using evolutionary and epidemiological genomics. Microorganisms (2015) 3(2):236-267.
2. Raymond et al. "The initial state of the human gut microbiome determines its reshaping by antibiotics". The ISME Journal (2016) 10:707–720.
3. Brito et al. "Mobile genes in the human microbiome are structured from global to individual scales". Nature (2016) 535:435-439.