MICROBIAL GENOMICS

The research interests of my group are focused on applying high throughput genomic approaches to understand bacteria. Potential projects include:

USING PSEU D O M O N A S BACTERIA TO PROTECT PLANTS FROM DISEASE

Australia is home to a number of serious plant diseases, which, if left unchecked, could devastate our multibillion dollar agricultural industry. In modern agriculture diseases are typically controlled mainly through the use of agrochemicals, which are expensive and environmentally damaging. We are currently investigating a group of natural plant-associated bacteria that are able to act as biocontrol organisms suppressing infections from a range of important fungal, bacterial, viral and insect pests. This well-funded project will apply a combination of next-generation transcriptomic and proteomic technologies, as well as innovative genome-wide transposon mutagenesis methods to identify the key genes and gene clusters involved in biocontrol mediated by Pseudomonas bacteria.

FACTORS INFLUENCING THE SUCCESS OF THE PATHOGEN ACINETOBACTER BAUMANNII

The hospital intensive care unit should be a place of healing and care for the most vulnerable. Nonetheless, several microbial pathogens continue to plague this environment, causing serious infections in the immunocompromised patients that pose ever more challenging problems for clinicians. Acinetobacter baumannii has recently emerged as one of the most problematic hospital acquired pathogens worldwide due to its highly drug resistant nature. This project aims to define the key mechanisms of drug resistance operating in clinical A. baumannii isolates using a combination of cutting-edge next-generation transcriptomics and proteomics, and essential resistance genes identified by saturation mutagenesis methods. An alternative project in collaboration with A/Prof. Bridget Mabbutt uses structural and functional genomics to characterize laterally-acquired genes in A. baumannii that might help it flourish in clinical settings.

Molecular ecology of an ancient symbiosis between sponges and bacteria Marine sponges are crucial members of marine ecosystems that are often overlooked despite being a dominant and ubiquitous component of the sea bed. Research involving sponges is linked to various scientific aspects from environmental and evolutionary studies to biotechnological and medical applications, with anti-cancer drugs and anti-HIV products derived from sponges. A large proportion of species contains sponge-specific photosynthetic symbionts related to free-living cyanobacteria, which are abundant and key primary producers of marine environments. This projects aims to elucidate the molecular basis of the stable symbiosis of these two modern day "fossils", using a combination of traditional and next-generation genomics and transcriptomics.

GENOMICS AND ECOLOGY OF MARINE CYANOBACTERIA IN AUSTRALIAN WATERS

Tiny single-celled marine cyanobacteria constitute up to two thirds of all marine productivity. As the base of the marine food-web, the activity of these organisms impacts on all marine life. Using a rapid molecular diagnostic we will perform the first survey of the environmental distribution of marine Synechococcus cyanobacteria along ecosystem gradients of the Australian Coast. Representative isolates will be selected for further study to identify key genes and proteins involved in adaptation to tropical and temperate habitats.

This is a multidisciplinary project that will combine elements of fieldwork with the latest generation molecular techniques to understand the spatial and seasonal distribution of locally adapted 'ecotypes'. Understanding the environmental factors that affect the abundance and activity of these organisms is fundamental to predicting the impacts of climate change on our local marine resources.
COAL: PROKARYOTIC PIONEERS (with CSIRO)

Using natural gas, rather than coal for electricity generation provides a means of reducing CO2 emissions and combating climate change. In coal seams where moisture and sufficient nutrition is available, natural gas is produced from microbial activity. To date, we have identified the types of microbes that inhabit coal, but have not identified those microbial pioneers whose metabolic degradation of the coal, not only underpins the microbial community but also facilitates the production of natural gas. Using culturing, sequencing and bioinformatics techniques and an established coal-degrading microbial consortia, the project aims to identify these early pioneers and how they degrade coal.

LIFE IN A GLUEY STICKY MESS (with Packer, Super Science team)

The thick mucus that forms in the lungs of cystic fibrosis (CF) patients provides a breeding ground for chronic bacterial infection. *Pseudomonas aeruginosa*, an opportunistic human pathogen is one of the main and most successful colonisers in CF lungs. As a part of the multidisciplinary ARC Super Science project, this study will be aimed at identifying specific adaptations developed by *P. aeruginosa* during chronic CF infections, including its ability to form biofilms. Whole genome transcriptomic analysis using RNA-Seq to sequence the entire bacterial transcriptome will be applied to identify genes important for adaptation and virulence in CF lung mucus.

Selected publications


chem.mq.edu.au/academics/ipaulsen.html