

## Day 2: Thursday 9 September

Chair	Presenter	Title	Start Time		
			AEST	ACST	AWST
	Jen Wood	Welcome to Day 2 of Microseq 2021	12:00	11:30	10:00
Jen Wood	<b>P</b> Benjamin Schwessinger	Genome structure and evolution in binucleated rust fungi	12:10	11:40	10:10
	<b>M</b> Claire Gorrie	Key parameters for genomics-based real-time detection and tracking of multidrug-resistant bacteria	12:40	12:10	10:40
	<b>M</b> Zulqarnain Fida	The role of microbial community in reduction of excess sludge during wastewater treatment by a membrane bioreactor (MBR) integrated with side-stream anoxic reactors	12:55	12:25	10:55
Rhys White & Lucie Semenech	<b>L</b> Ashleigh Porter	Metagenomic identification of viral and protozoan sequences in laboratory reagents			
	<b>L</b> Lijuan Luo	Elucidation of global and national genomic epidemiology of <i>Salmonella enterica</i> serovar Enteritidis through multilevel genome typing			
	<b>L</b> Kinza Asif	Characterisation of the whole genome sequence of an Avian Hepatitis E virus directly from clinical specimens reveals possible recombination events between European and USA strains	13:10	12:40	11:10
	<b>L</b> Mona Taouk	Sub-epidemics of <i>Treponema pallidum</i> infection characterise the contemporary syphilis outbreak in Australia			
	<b>L</b> Muhamad Fachrul	Assessing and removing the effect of unwanted technical variations in microbiome data			
		Lightning Talk Chats			
		<b>Break</b>	13:35	13:05	11:35
Tania de Silva Duarte & Ashley Dungan	<b>M</b> Brady Welsh	Vines, Wines and Microbiomes: How Fungicides Shape the Grapevine Microbiome	13:50	13:20	11:50
	<b>M</b> Yvonne Ogaji	De novo whole-genome assembly using long-read sequencing of <i>Ascochyta</i> Blight pathogens of field pea ( <i>P. pinodes</i> , <i>P. pinodella</i> and <i>P. koolunga</i> )	14:05	13:35	12:05
	<b>M</b> Ben Vezina	Transmission of <i>Klebsiella</i> strains and plasmids within and between grey-headed flying fox colonies	14:20	13:50	12:20
		<b>Gather Town Social Event</b>	14:35	14:05	12:35
Claire Gorrie & Rachael Lappan	<b>M</b> Jake Lacey	What can we learn from 13,000 Strep A genomes?	15:20	14:50	13:20
	<b>M</b> An Nguyen	The evolution of antibiotic resistance through horizontal gene transfer in <i>Helicobacter pylori</i>	15:35	15:05	13:35
	<b>M</b> Vasilli Kasimov	Fishing for chlamydia: Using RNA baits for the direct sequencing of <i>Chlamydia</i> from clinical samples	15:50	15:20	13:50
	<b>M</b> Ankita George	A novel and highly divergent Canine Distemper Virus lineage causing distemper in ferrets in Australia	16:05	15:35	14:05
	<b>L</b> Cassandra Stanton	Characterisation of three novel <i>Bacillus anthracis</i> phages using whole genome sequencing reveals two modes of infection			
	<b>L</b> Winton Wu	Uncovering the role of the functional small RNA interactome in antibiotic tolerance in <i>Staphylococcus aureus</i>			
	<b>L</b> Cheryl Sia	Population genomics of emerging resistance in <i>Salmonella</i> Dublin	16:20	15:50	14:20
	<b>L</b> Isabella Anna Joubert	Optimizing a dual RNA-sequencing protocol for the analysis of host-pathogen interactions during neonatal sepsis			
	<b>L</b> Wei-Shan Chang	Meta-transcriptomic virome analysis of invasive myna birds ( <i>Acridotheres tristis</i> ) in Australia			
		Lightning Talk Chats			
		<b>Break</b>	16:45	16:15	14:45
Mohammad Hamidian	<b>P</b> Martina Jelocnik	Molecular characterisation of veterinary <i>Chlamydia</i> : I will find it and I will type it	17:00	16:30	15:00
		<b>Awards</b>	17:30	17:00	15:30

Plenary talk (P), Medium Talk (M) and Lightning Talk (L)