

Day 2 Program

Thursday 8th September

| Chair | Presenter | Title | Start Time | | | Session |
|---------------------------------------|---|---|------------|-------|-------|---------|
| | | | AEST | ACST | AWST | |
| | Lucie Semeneć | Welcome to Day 2 MicroSeq2022 | 10:30 | 10:00 | 8:30 | |
| Jackie Mahar | P Barbara Brito Rodriguez @BarbaraBrito16 | Challenges in interpreting the metatranscriptome in cattle health and disease | 10:35 | 10:05 | 8:35 | 2.1 |
| Lucie Semeneć | M Gus McFarlane @gusmcfarlane | Multiplexed pathogen detection using Cas9-enriched nanopore sequencing | 11:05 | 10:35 | 9:05 | |
| Break | | | 11:20 | 10:50 | 9:20 | |
| | M Jacqueline Morris @jacmmorris | Hidden resistances: How routine whole genome sequencing uncovered an otherwise undetected blaNDM-1 gene in <i>Vibrio alginolyticus</i> isolated from imported seafood | 11:30 | 11:00 | 9:30 | |
| | M Sabrina Sadiq @RoyalFizzbin | Resolving deep evolutionary relationships within the RNA virus phylum Lenarviricota | 11:45 | 11:15 | 9:45 | |
| Zahra Islam & Ellen de Vries | L Kanishka Kamathewatta Walawwe | Transcriptomic analysis of the effects of tylosin on the protective immunity provided by the <i>Mycoplasma gallisepticum</i> vaccine MG ts-304 | | | | 2.2 |
| | L Remy Young @Remy_Young | Characterising the functional response of the gastrointestinal microbiota to dietary compounds | 12:00 | 11:30 | 10:00 | |
| | L Laurence Luu @laurenceluu | Genomic dissection of the microevolution of Australian epidemic <i>Bordetella pertussis</i> | | | | |
| Lightning Chats | | | 12:20 | 11:50 | 10:20 | |
| Lunch | | | 12:30 | 12:00 | 10:30 | |
| | M Chris Connor | Impact of hospital multi-drug resistance organism screening strategies on genomics informed transmission identification | 13:30 | 13:00 | 11:30 | |
| Rhys Parry & Johanna Wong-Bajracharya | M Paul Worden | The use of next generation sequencing and phylogenomics in tracking <i>Paenibacillus</i> larvae, the etiological agent of American Foulbrood in honeybees | 13:45 | 13:15 | 11:45 | 2.3 |
| | L Samridhi Thakur | Exploring the genomic epidemiology of invasive non-typhoidal <i>Salmonella Virchow</i> and <i>Salmonella Panama</i> | | | | |
| | L Ajani Athukorala @AjaniAthukorala | The recent advent of sequencing data shed new light on avian Adenovirus evolution | 14:00 | 13:30 | 12:00 | |
| | L Helena Cooper @helena_bethany | Genomics and metabolic modelling of Klebsiella, a priority drug resistant pathogen | | | | |
| Lightning Chats | | | 14:20 | 13:50 | 12:20 | |
| Break | | | 14:30 | 14:00 | 12:30 | |
| | M Veronica Jarocki @VMJarocki | Genomic analysis of Australian wastewater <i>Escherichia coli</i> | 14:45 | 14:15 | 12:45 | |
| Ben Vezina & Binod Rayamajhee | M Rhys Parry @RhysHParry | Metagenomics of <i>Ixodes</i> ticks sampled from Australian wildlife reveal diverse vertebrate viruses and <i>Rickettsia tasmanensis</i> in New South Wales. | 15:00 | 14:30 | 13:00 | 2.4 |
| | L Natalie Hejl @natalie_hejl1 | Characterising swamp biodiversity and community structure with eDNA | | | | |
| | L Elizabeth Mullens | The saliva and faecal microbiome of horses with Pituitary pars intermedia dysfunction: the search for better diagnosis and treatment of the disease. | 15:15 | 14:45 | 13:15 | |
| | L Kate Van Brussel | Faecal virome of the Australian grey-headed flying fox from urban/suburban environments contains novel coronaviruses, retroviruses and sapoviruses | | | | |
| Lightning Chats | | | 15:35 | 15:05 | 13:35 | |
| Break | | | 15:45 | 15:15 | 13:30 | |
| Danielle Ingle | P Guillaume Meric @phyloge | Exploring links between the gut microbiota and health using large multi-omics population cohort datasets | 16:00 | 15:30 | 14:00 | 2.5 |
| | Danielle Ingle | Awards | 16:30 | 16:00 | 14:30 | |
| End | | | 16:45 | 16:15 | 14:45 | |

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