

Tuesday 20th

09:30 – 10:00 **Registration**

10:00 – 10:30 **Welcome & Housekeeping (Phil Wilcox & Matt Bixley)**

Primary sector: genotyping (chair: Andrew Hess)

10:30 – 11:00	Nahla Bassil	Invited talk: Black Spot Resistance Gene Characterization and Mapping in Polyploid Roses
11:00 – 11:15	Susan Thomson	Clever culling for better breeding strategies
11:15 – 11:30	Melanie Hess	High-throughput sequencing pipeline for metagenome profiling
11:30 – 11:45	David Chagné	Genome analysis for differentiating mānuka provenances
11:45 – 12:00	John McCallum	Development of a 10k Exome Capture Array and Application for Linkage Mapping and Disequilibrium Studies in <i>Actinidia</i> Breeding Populations
12:00 – 12:20	Aisling Rayne Kathryn McRae Natalie Graham Marissa Le Lec	Lightning talks

12:20 – 13:20 **Lunch**

Methodology advances in statistical genetics (chair: Phil Wilcox)

13:20 – 13:50	Benoit Auvray	Comparing estimates of inbreeding and breed composition using genomic relationship matrices and machine learning methods for a range of SNP densities in a simulated sheep population
13:50 – 14:05	Ken Dodds	A depth-adjusted F_{ST} calculation for low-depth sequencing data
14:05 – 14:20	Rachel Ashby	GBSathon: Evaluating GBS analysis workflows by comparison with SNP chip and pedigree data
14:20 – 14:35	Timothy Bilton	Constructing genomic relationship matrices for autopolyploid species using sequencing data
14:35 – 14:50	Chandan Pal	Discovery of new viruses from complex sequence datasets

14:50 – 15:20 **Afternoon tea**

Ecosystem genomics (chair: Jeanne Jacobs)

15:20 – 15:50	Anna Santure	Substantial sex-differences in recombination in hihi (<i>Notiomystis cincta</i>), a threatened New Zealand passerine with high levels of sexual conflict
15:50 – 16:05	Levi Collier-Robinson	Critical first steps towards building resilience in a critically endangered New Zealand freshwater endemic
16:05 – 16:35	Roger Moraga	Assembling the Kekewai (<i>Paranephrops zealandicus</i>) Genome Using Cloud Compute Infrastructure
16:35 – 16:50	Alana Alexander	Differential movement of song, morphology, and genes across the black-capped/Carolina chickadee hybrid zone in Missouri
16:50 – 17:05	Nick Sumpter	Hybrid Assembly of the Chytrid Genome – Insights into the Evolution and Outbreak of a Major Amphibian Pathogen
17:05 – 17:15	Jana Wold	Lightning talks

18:30 **Dinner** Harbourside Grill, 18 Fryatt St, Dunedin

Wednesday 21st

Keynote (chair: Shannon Clarke)

09:30 – 10:30	Steve Horvath	Epigenetic aging clocks for mammals
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10:30 – 11:00 **Morning tea**

Epigenetics and functional genomics (chair: Shannon Clarke)

11:00 – 11:15	John Mackay	Sampling and testing for American Foulbrood in bees using novel eDNA and multi-target qPCR methods
11:15 – 11:30	Alex Noble	Genomic effects of cannabis use: validating a high throughput methylation array
11:30 – 11:45	Andrew Cridge	Using environmental DNA to identify and monitor new plant incursions into New Zealand
11:45 – 12:00	Margaret Carpenter	Transcriptomic and metabolomic profiling of the potato plant response to zebra chip disease
12:00 – 12:15	Mary Hawkes Alex Caulton	Lightning talks

12:15 – 13:30 **Lunch**

Primary sector: breeding (chair: Melanie Hess)

13:30 – 14:00	Chad Harland	<u>Invited talk</u> : Rate of de novo mutation in dairy cattle and potential impact
14:00 – 14:15	Jaroslav Klápště	Multi-environment single-step evaluation of radiata pine progeny test using exome capture - GBS genotyping platform
14:15 – 14:30	Ahmed Ismael	Genetic variation of water use efficiency of radiata pine under drought stress
14:30 – 14:45	Lucy Egan	The identification of population-specific patterns in breeding programmes of <i>Trifolium repens</i> and <i>Trifolium pratense</i>
14:45 – 15:00	Michael Lee	National Evaluations of multiple breeds in NZ using single step GBLUP

15:00 – 15:30 **Afternoon tea**

15:30 – 16:00 **Mihi Whakatau**

Indigenous Health Genomics (chair: Phil Wilcox)

16:00 – 17:40	Speakers: Joe Yracheta, Irene Kereama-Royal, Karyn Paringatai, Phillip Wilcox and Stephen Robertson. See dedicated handout for schedule	
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