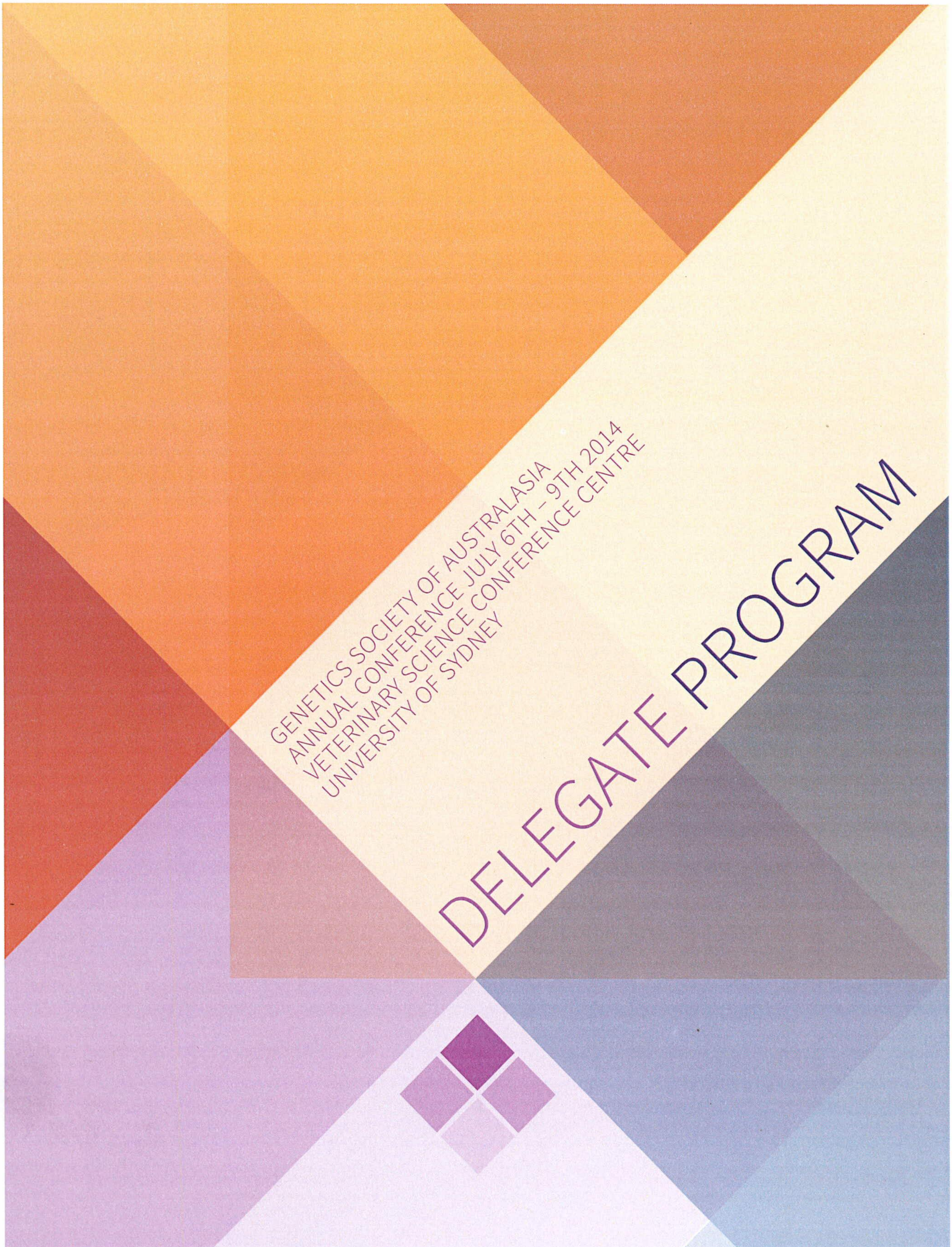

GENETICS SOCIETY OF AUSTRALASIA
ANNUAL CONFERENCE JULY 6TH – 9TH 2014
VETERINARY SCIENCE CONFERENCE CENTRE
UNIVERSITY OF SYDNEY

DELEGATE PROGRAM

In SWED

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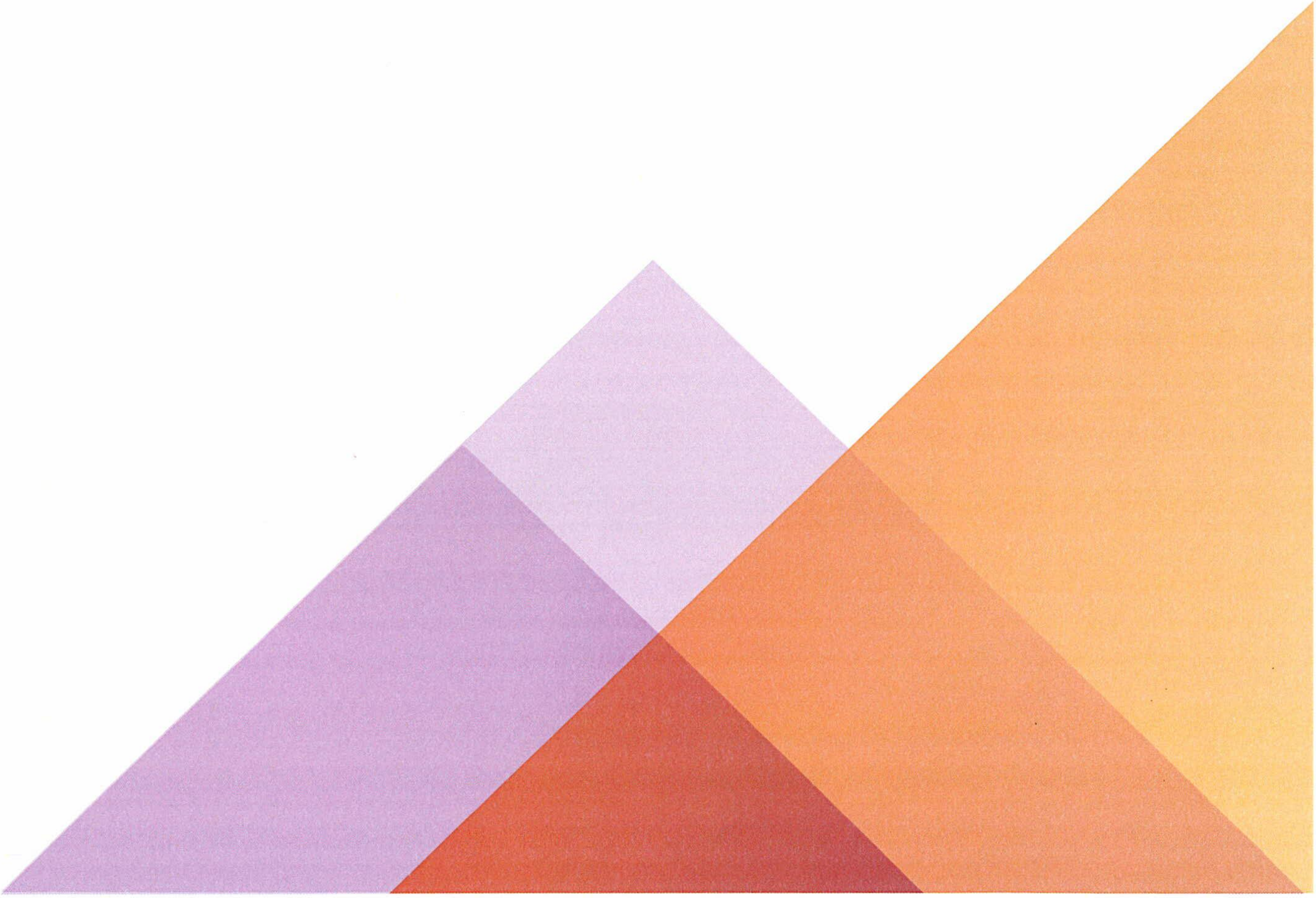

Organizing Committee

Dr Rebecca Johnson, Australian Museum
Professor Kathy Belov, University of Sydney
Assoc. Professor Nathan Lo, University of Sydney
Dr Beata Ujvari, University of Sydney
Isobel Ronai, University of Sydney
Dr Emily Remnant, University of Sydney
Dr Camilla Whittington, University of Sydney
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THE UNIVERSITY OF
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Program Design: Holly Philip holly.philip.com

Welcome

Dear Geneticists,

Welcome to the annual conference of the Genetics Society of Australasia, which is dedicated to promoting genetics in our region. Unfortunately I am unable to attend this year's meeting but I am sure you will enjoy the scientific and social aspects of this year's meeting. The society is indebted to this year's local organising committee headed by Rebecca Johnson and Kathy Belov and consisting of Nathan Lo, Beata Ujvari, Emily Remnant, Isobel Ronai, Camilla Whittington, Yuanyuan Chen, Greta Frankham, Shafagh Waters, Bianca Haase, Claire Wade, Catherine Grueber, Mette Lillie, Amanda Lane, Belinda Wright, Katrina Morris, Georgina Cooke, Jian Cui, Emma Peel, Elizabeth Jones, Rebecca Gooley, Jenny Donald and Frank Grutzner.

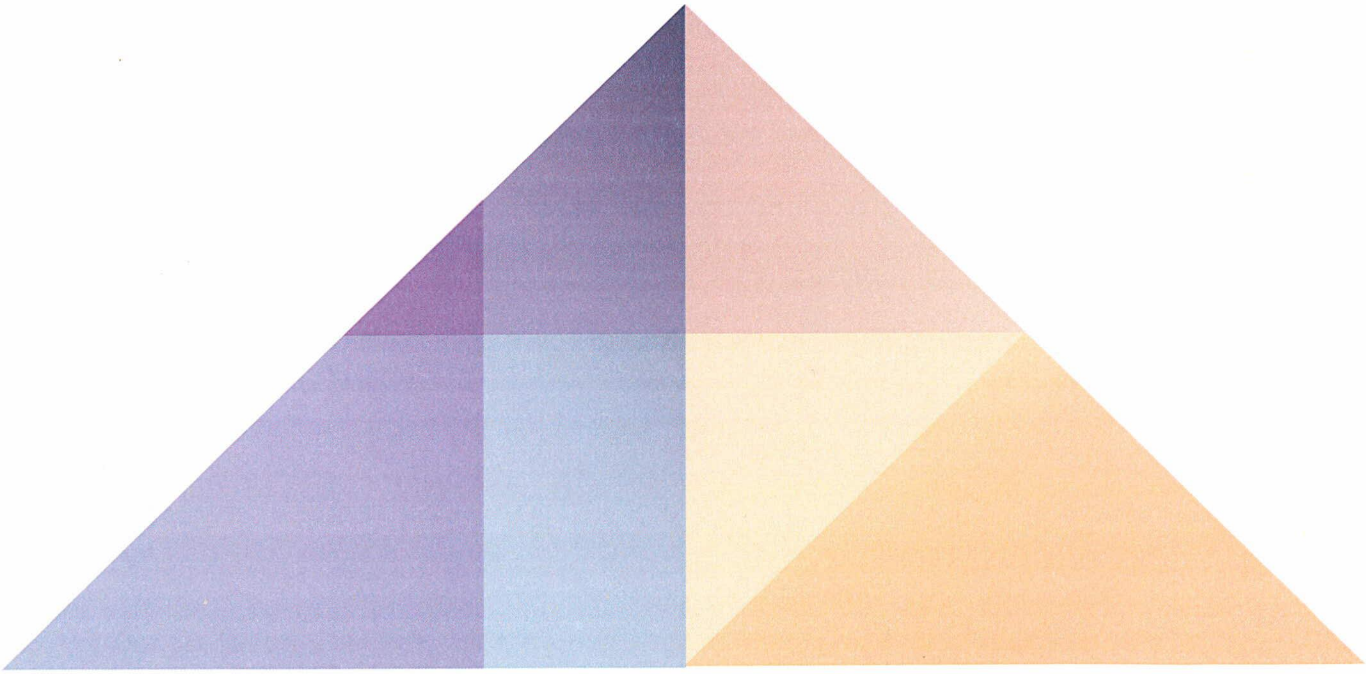
Genetics as a discipline is pervasive in biological research, as it should be. However that does not mean we can rest on our laurels. We need to continually draw people's attention to this fact. One way this can be achieved is by participating in our Twitter feeds for the conference (Genetics Australasia, @GeneticsAus) or by following us on our Facebook page (www.facebook.com/geneticsaus).

Sincerely,

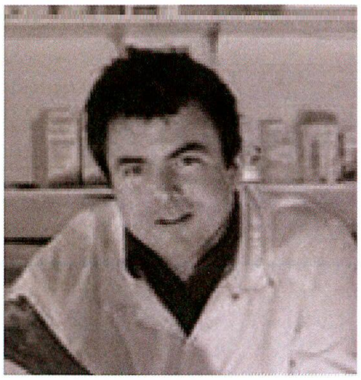
Alex Andrianopoulos

President, GSA.

Genetics Society of AustralAsia



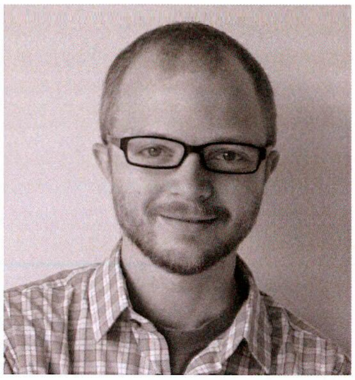
Plenary Speakers



Michael Bunce

Curtin University

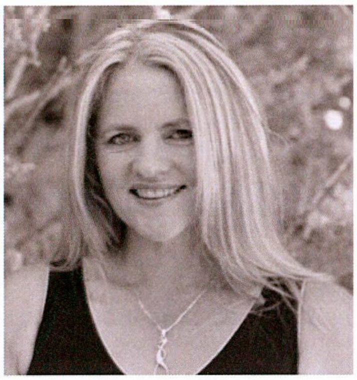
Professor Michael Bunce is an ARC Future Fellow at Curtin University where he runs the Trace and Environmental DNA (TrEnD) Laboratory. The TrEnD lab specialises in using next generation DNA sequencing to characterise degraded DNA samples for use in a wide variety of biological applications including paleontology, archaeology, paleoclimate, forensics and conservation. Mike did his PhD at the Australian National University and post-docs at Oxford (UK) and McMaster (Canada) Universities before moving to Western Australia in 2006. Mike is an internationally recognised researcher in the field of ancient and degraded DNA, with 7 co-authored publications in Nature and Science.



Aaron Darling

University of Technology, Sydney

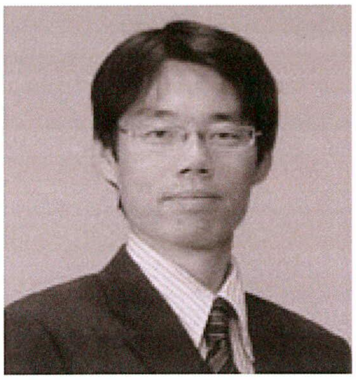
Microbes inhabit every surface of the planet and even within the human body they outnumber human cells by a factor of 10. New high throughput measurement technologies including DNA sequencing, metabolomics, and proteomics allow us to digitize information on the state of these biological systems. The Darling lab focuses on translating this wealth of information into knowledge about biological systems. We apply and design computational and statistical algorithms to automate data analysis methods.



Dianne Gleeson

University of Canberra

Dianne obtained her PhD from ANU in 1996 on the colonisation genetics of the Australian Sheep Blowfly. She then established the Ecological Genetics group at Landcare Research NZ and the DNA diagnostic service, EcoGene for which she was awarded the inaugural Woman in Science Entrepreneur Award (2011). Since 2013 she has been based at the Institute for Applied Ecology at the University of Canberra, where she leads a CRC funded project on eDNA technologies for invasive species detection. Her research interests are in the application of DNA technologies for biodiversity conservation outcomes. Specifically this has been applied to population genetics of threatened and invasive species as well as the developing field of wildlife forensics. A particular focus has been facilitating the translation of fundamental research into accessible services for end-users such as conservation management agencies, and environmental regulatory authorities.



Kenji Matsuura

Kyoto University

Professor Matsuura's research focuses on the social system and evolution of termites. He is primarily interested in understanding the reproductive mechanism and evolution of chemical communication and defensive strategies against various parasites and predators. He has been characterizing the molecular, genetic, physiological, behavioral, and ecological factors that regulate these processes. On the basis of these findings his lab is developing a novel technology to control termites most effectively by using their social behaviour.

Catherine Suter

Victor Chang Caridac Research Institute

Associate Professor Cath Suter is an ARC Future Fellow and head of the Epigenetics Laboratory at the Victor Chang Cardiac Research Institute in Sydney. She was the first to describe germline epigenetic defects in humans, and her major interest continues to be mammalian germline epigenetic phenomena and their inheritance. Her group focuses on the epigenetic contribution to phenotypic variation and disease risk, with a particular interest in the influence of early environmental factors on epigenetic inheritance.

Program Overview

Monday July 7th

9.00-10.00	**Opening Address and Plenary 1 (Webster Lecture Theatre)** Aaron Darling *Toward population genetics of dark matter in the microbial universe*		
10.00-10.30	Morning Tea		
10.30-12.30	**Concurrent Symposia: Session 1**		
	Symposium 1a Bioinformatics and Genomics (Carne Lecture Theatre) Chairs: Aaron Darling, Claire Wade	**Symposium 1b Adaptation** (Clunies Ross Lecture Theatre) Chairs: Ary Hoffmann, Beata Ujvari	**Symposium 1c Host-Parasite/ Symbiont interaction** (Gunn Teaching Room) Chairs: Mark Tanaka, Victoria Morin-Adeline
10.30	Ashley Farlow *The 10 megabases of Arabidopsis centromeric sequence behave as a single locus over evolutionary time*	Ary Hoffmann *Climate change and evolutionary adaptation: where are we?*	Mark Tanaka *Timing of antimicrobial use influences the evolution of antimicrobial resistance during disease epidemics*
11.00	Asa Perez-Bercoff *Genome sequencing, assembly and annotation of S. aurantiacum*	Kathryn Hodgins *The genomic basis of local adaptation to climate in conifers*	Victoria Morin-Adeline *One parasite and two unexpected hosts: Using transcriptomics to understand host-parasite adaptations of two strains of Tritrichomonas foetus*
11.15	Mani Grover *Novel therapeutics for complex diseases from genome-wide association data*	Paul Rymer *Effective population size and migration along a steep environmental gradient: Insights from niche models and population genomics*	Timothy L Sutton *Contrasting dispersal and inbreeding in a fig-pollinating wasp and its parasitoid*
11.30	Bianca Haase *Scottish Fold cats: an animal model for human digital arthropathy*	Hernan Morales *Exploring full mitochondrial genomes in search of signatures of positive and purifying selection*	Aidan Hall *Coevolution between bacterial endosymbionts and their psyllid hosts of the Cardiaspina genus (Hemiptera: Psyllidae)*
11.45	Hardip Patel *RNAnexus: A framework for RNA data mining and visualization*	Simon Baxter *Evolution of a butterfly mimicry locus through modular regulation of an input-output gene*	Michaela DJ Blyton *Functional genotypes are associated with commensal Escherichia coli strain abundance within host individuals and populations*
12.00	Tony Papenfuss *De novo assembly of the scabies mite mitochondrial genome from metagenomic sequencing reveals haplotype structuring and relationship between scabies varieties*	Andrew Young *Incest vs. abstinence: reproductive tradeoffs between mate limitation and progeny fitness in a self-incompatible invasive plant.*	Peter Kern *A new molecular sexing technique for butterflies – does Wolbachia really feminise genetic males in Eurema?*
12.15	Sham Nair *The dynamic genome: allelic variations in the genomes of single cells from an invertebrate metazoan*	Michael Whitehead *Sexual mimicry in sympatric orchid species promotes outcrossing, multiple paternity and reproductive isolation.*	Joshua Christie *Sex, slime and mitochondria*
12.30-1.30	Lunch		

Colin Why apomyxis is detrimental!

Flo Camus
Mito genome effects ♂ not ♀
13 mitolines

1.30-3.30	**Concurrent Symposia: Session 2**	
	Symposium 2a **Population genetics** (Carne Lecture Theatre) Chairs: John Sved, Belinda Wright	**Symposium 2b** **Immunogenetics** (Clunies Ross Lecture Theatre) Chairs: Catherine Grueber, Janine Deakin
1.30	John Sved *Queensland fruit fly and the Lewontin-Birch introgression hypothesis*	Rehana Hewavisenti *The Identification and Characterisation of Immune Genes in the Milk Transcriptome of the Tasmanian devil (Sarcophilus harrisii)*
1.45	Michaela Blyton *Maternal lineages best explain the associations of a semi-social marsupial in the presence of fine-scale genetic structure*	Catherine Grueber *Studying immunogenetic diversity to aid the conservation of threatened species.*
2.00	Collin Ahrens *Population stucture of the rare clonal Senecio macrocarpus in the grasslands of Victoria*	Jian Cui *Characterisation of Toll-like receptors in two bottlenecked species, Tasmanian devil and Koala*
2.15	Belinda Wright *A SNP-based approach to determining pedigrees and assessing genetic diversity in the Tasmanian devil insurance population.*	Jolene Sutton *Variation at innate immunity genes in Hawaiian honeycreepers*
2.30	Mark Richardson *Population genetics of the invasive northern Pacific seastar*	Hamutal Mazrier *Expression of the microRNA, mir-31, is reduced in leukocytes of dogs with atopic dermatitis*
2.45	Bill Sherwin *Population viability and major histocompatibility complex (MHC) genetic diversity of two dolphin populations in Western Australia*	Katrina M Morris *Characterisation of the Tasmanian devil immunome and identification of SNPs within devil immune genes*
3.00	Lee A Rollins *Selective replication of mitochondria at the edge of an expanding invasion*	Emma Peel *Cathelicidins in the Tasmanian devil (Sarcophilus harrisii)*
3.15	Florencia Camus *Sequence variation within the mitochondrial DNA affects patterns of gene expression in the mitochondrial transcriptome*	Elizabeth Jones *Novel Defensin Peptides of the Tasmanian Devil (Sarcophilus harrisii)*
3.30-4.00	Afternoon Tea	
4.00-5.00	**Plenary 2 (Webster Lecture Theatre)** Kenji Matsuura *Asexual queen succession system in termites: evolution and mechanism*	
5.00-7.00	Poster Session	
7.00-10.00	ECR Dinner	

Program Overview

Tuesday July 8th

9.00-10.00	**Plenary 3 (Webster Lecture Theatre)** Dianne Gleeson *How Robust is Species Detection using Environmental DNA?*	
10.00-10.30	Morning Tea	
10.30-12.30	**Concurrent Symposia: Session 3**	
	Symposium 3a **Reptile and Amphibian genetics** (Carne Lecture Theatre) Chairs: Jenny Graves, Camilla Whittington	**Symposium 3b** **Developmental and Cellular genetics** (Clunies Ross Lecture Theatre) Chairs: Richard Burke, Bianca Haase
10.30	Jenny Graves *Sex, Genomics and Epigenetics*	Adrian Moore *Genetic controls over neuron dendrite arvor shape: convergence on microtubules*
11.00	Matthew Brandley *Gene expression associated with the recent evolution of viviparity*	Richard Burke *Genetic Control of Cellular Zinc Distribution*
11.15	Chris Friesen *Persistent use of sperm stored over winter in multiply-mated female garter snakes*	Graham Thompson *Gene co-citation networks associated with worker sterility in honey bees*
11.30	Camilla M Whittington *Angiogenic genes in the skink uterus and the evolution of live birth*	Yee Lian Chew *Protein with tau-like repeats regulates neuronal aging and lifespan in C. elegans*
11.45	Sam Ryan *The evolution and conservation of the Major Histocompatibility Complex Class III region in Pogona vitticeps.*	Sebastian Judd-Mole *Functional Characterisation of Voltage Gated Chloride Channel Proteins in Drosophila*
12.00	Clare E Holleley *Sex chromosome markers reveal a rapid transition from genotypic to temperature dependent sex determination in the bearded dragon*	Waqar Ahmad *Dihydrolipoamide dehydrogenase (DLD) as a potential therapeutic target for Alzheimer's disease*
12.15	Mette Lillie *Diversifying selection at the Major Histocompatibility Complex class II beta in the New Zealand endemic Hochstetter's frog, Leiopelma hochstetteri*	Joseph Nguyen *Examining the genetic and environmental influences on nicotinic acetylcholine receptor trafficking*
12.30-1.30	Lunch (GSA executive committee meeting)	

1.30-3.30	**Concurrent Symposia: Session 4**	
	Symposium 4a **Landscape and Conservation genetics** (Carne Lecture Theatre) Chairs Dianne Gleeson, Craig Sherman	**Symposium 4b** **Gene expression and function** (Clunies Ross Lecture Theatre) Chairs: Emily Remnant, Isobel Ronai
1.30	Bernd Gruber *LandGenReport - a landscape genetic tool to analyse the effect of landscape features on population structure using genetic data*	Simon M. Tierney *Eye gene transcriptomes of diving water beetles: a contrast of surface and subterranean photic niches*
1.45	Jackie Chan *Genetic management of harvest and restocking in Australian eastern king prawns*	Isobel Ronai *A role for apoptosis in worker sterility: gene expression in the plastic ovaries of the honey bee*
2.00	Adam P Cardilini *Understanding genetic variation across a heterogeneous landscape in an invasive species*	Tristan Stevens *Expressing the diamondback moth ABC transporter C2 in transgenic Drosophila causes susceptibility to Bt insecticidal toxin*
2.15	Floyd Reed *Genetically Engineering Underdominace for Species Conservation Applications in Hawai'i*	Llewellyn Green *Characterizing resistance and the potential for adaptation to a new diamide insecticide in D. melanogaster*
2.30	Anna J MacDonald *Species from faeces: predator scat metabarcoding in Tasmania*	Kathryn A Raphael *Comparative, quantitative transcriptomes in sympatric fruit fly species reproductively isolated by time of mating*
2.45	Craig Sherman *The South American seagrass Zostera chiliensis, endangered or invasive?*	Jennifer Morrow *Expression patterns and transcriptome analysis of sex determination genes in Bactrocera fruit flies*
3.00	Carolyn J Hogg *Blending molecular genetics with pedigree data to breed endangered species*	Michelle W Pearce *The Drosophila melanogaster phospholipid flippase dATP8B is required for odorant receptor function*
3.15		Lalith K Dammannagoda *Expression patterns of selected digestive enzyme genes in the hepatopancreas of redclaw (Cherax quadricarinatus) fed two different carbohydrate sources*
3.30-4.00	Afternoon Tea	
4.00-5.00	**Plenary 4 (Webster Lecture Theatre)** **Cath Suter** *Epigenetic inheritance and the legacy of parental obesity*	
5.00-5.30	Jaime Vandenberg - Science and Technology Australia	
7.00-10.00	Conference Dinner	

Program Overview

Wednesday July 9th

9.00-10.00	**Plenary 5 (Webster Lecture Theatre)** **Mike Bunce** *The (genetic) book of dead; why deep-sequencing trace, degraded & ancient DNA is both interesting and useful*	
10.00-10.30	Morning Tea	
10.30-12.30	**Concurrent Symposia: Session 5**	
	Symposium 5a **Phylogenetics I** (Carne Lecture Theatre) Chairs: Simon Ho, Nathan Lo	**Symposium 5b** **Cancer and Human Genetics** (Clunies Ross Lecture Theatre) Chairs: Tony Papenfuss, Jenny Donald
10.30	Rob Lanfear *Improving phylogenetic analyses of large and small datasets*	Janine Deakin *Evolution of devil facial tumor disease chromosomes*
11.00	Sebastian Duchene *Comparing pacemaker models of genome evolution in mammals*	Anneke C Blackburn *Polymorphisms in Cyp2r1 and disruption of the vitamin D pathway associate with the SuprMam1 breast cancer susceptibility locus in mice*
11.15	Steve Donnellan *Invasion history of Black rats (Rattus rattus) in Australia - insights from mitochondrial and nuclear phylogeography*	Zhibo Gao *Identification of genomic alterations in oesophageal squamous cell cancer*
11.30	Fangzhi Jia *Testing methods for inferring population history from individual genome-scale sequences*	Robert Richards *WWOX, Chromosomal Fragile Site FRA16D Spanning Gene: its role in metabolism and contribution to cancer*
11.45	Carlos E. Gonzalez-Orozco *Phylogenetic regionalization: a new framework to support conservation biogeography*	Beata Ujvari *Anthropogenic selection enhances cancer evolution in Tasmanian devil tumours*
12.00	Charles Foster *Estimating the evolutionary timescale of flowering plants using complete chloroplast genome sequences*	Nicholas S Archer *Sweet Taste Gene Expression And Obesity: Is There A Link?*
12.15	Daej Arab *Phylogenetics and evolution of Australian Nasutitermitinae*	Robert Richards *RNA pathogenesis via Toll-like receptor-activated inflammation in expanded repeat neurodegenerative diseases*
12.30-1.30	Lunch (GSA 2014 AGM, Carne Lecture Theatre)	

1.30-3.30	**Concurrent Symposia: Session 6**	
	Symposium 6a **Phylogenetics II** (Carne Lecture Theatre) Chairs: Rob Lanfear, Nathan Lo	**Symposium 6b** **Gene Regulation and Epigenetics** (Clunies Ross Lecture Theatre) Chairs: Cath Suter, Hannah Nicholas
1.30	Simon Ho *Estimating evolutionary timescales using genomic data*	Alyson Ashe *Can immunity against viral infection be inherited epigenetically in Caenorhabditis elegans?*
1.45	Georgina M Cooke *A fish out of water: understanding the evolution of land-dwelling fish using contemporary analogues of a critical step in vertebrate evolution*	
2.00	Jun Tong *Estimating the evolutionary timescale for Dictyoptera*	Justin Bloomfield *Assembling the methylome of an oilseed Brassica*
2.15	Peter Unmack *Origins of Australian freshwater fishes*	Shafagh A Waters *DNA methylation: silencing sex chromosomes in amniote vertebrates*
2.30	Andrew Richie *Evaluation of the Generalised Mixed Yule-Coalescent method for species delimitation across multiple mitochondrial genes*	Emily Remnant *The dynamic DNA methylation cycle in honey bee development and reproduction*
2.45	Lars Jermiin *Mixture models of nucleotide sequence evolution, and the evolution of yeast genomes*	Matthew Hoe *SUMV-1 antagonizes the activity of synthetic Multivulva genes in Caenorhabditis elegans*
3.00	Slavica Berber *Homeodomain interacting protein kinase (HPK-1) is required in the soma for robust germline proliferation in C. elegans*	Anna Reid *The transcriptional repressor CTBP-1 functions in the nervous system of Caenorhabditis elegans to regulate lifespan*
3.15-4.00	Afternoon Tea	
4.00-5.00	**Awards** Chair: Kathy Belov	
4.00	Dong Wang (Catcheside Prize)	
4.20	Katie Ayers (Alan Wilton Award) *RNA sequencing reveals novel candidate sex determination genes in chicken embryonic gonads*	
4.50	Peter Dearden (Crozier Medal; Video) MJDWhite prize Best poster prize, Highly commended prize, Peoples Choice poster prize	

Poster Presentations

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13127	Woo-Jin Kim	Genome-wide BAC-end sequencing of olive flounder (Paralichtys olivaceus) using two BAC libraries
14060	Peter Unmack	Comparative phylogeography of four aquatic species from the Murray-Darling Basin
14063	jung soo Seo	Phosphoinositide-specific phospholipase C (PLC) functions as an effector molecule in the signal transduction process.
14093	Mallory Wood	Investigating the Role of Homeodomain-Interacting Protein Kinase in Caenorhabditis elegans
14098	Jonas Bylemans	Monitoring freshwater fish communities using eDNA metabarcoding.
14104	Rheyda Hinlo	Parameterisation of eDNA Detection Probabilities for the Identification of Rare Aquatic Species
14112	Sally Mortlock	Early T-cell gene response to activation in Bullmastiffs
14121	Xiuwen zhang	Expansion of olfactory receptor gene family in Australia lizard Pogona vitticeps
14155	Kianoush Nikoumanesh	T-DNA Insertion Lines with Altered Root System Architecture in Arabidopsis thaliana
14163	Cali Willet	ArrayMaker: effortless genotyping-by-sequencing from whole genome sequence alignments
14391	Shea Andrews	Further evidence of a lack of interaction between APOE and late-life blood pressure in predicting cognitive decline: The PATH Through Life Study
14432	Emory Ingles	Epigenetic analysis of devil facial tumour chromosomes
14446	Niklas Mather	Varroa, viral vectors and virulence: the evolution of honeybee diseases.
14472	Jessica Gurr	The cross-species use of high-density SNP genotyping arrays for kinship analysis in threatened equid species.
14491	Tracy Chew	Detection of de novo mutations in parent to offspring trios in whole genome sequences of the domestic dog
14497	Annie Ying-Hui Pan	Detection of cerebellar abiotrophy mutations in Australian Working Kelpie dogs using whole genome sequencing
14610	Denise Alves	Sneaky queen bees selectively detect and infiltrate queenless colonies
14838	Kyle Ewart	DNA Identification of Rhinoceros Horn
15012	Jennifer Sinclair	Unexpected gene-flow patterns highlight importance of peripheral populations of the world's smallest penguin
15054	Lotte van Boheemen	Genomic architecture and repeatability of rapid local adaptation
15076	Perran Ross	Effects of Larval Competition on the Fitness of Wolbachia-Infected Aedes aegypti (Diptera : Culicidae)
15450	Denis O'Meally	Bioinformatics Resource Australia – EMBL: Data Integration
16192	Jessica Hacking	Factors shaping disease-resistance-gene diversity in an Australian reptile
16397	Jaime Gongora	Comparative analyses of Complement genes in Crocodilians
16398	Hilary Miller	Geneious R7: A bioinformatics platform for biologists

ID	Presenter	Title
16399	Hilary Miller	De novo assembly of circular genomes using Geneious R7.
16402	Jaime Gongora	Characterisation and comparative analyses of the saltwater crocodile MHC
16403	Akira Gokoolparsadh	Functional Role of IMMP2L in Astrocytes and its Implication in Tourette Syndrome
16468	Jaime Gongora	Genome-wide SNP and population genetics of platypuses from across Australia
16488	Jaime Gongora	European and Asian contribution to the genetic diversity of South American chickens
17563	Grace Campbell	Ribosomal Protein Mutants Affect Female Fertility in Arabidopsis thaliana
18309	Caitlin Hennessey	Identification of polycomb group genes and Phosphoinositide-3-Kinase as new regulators of wing disc eversion in Drosophila
18317	Bill Sherwin	Population viability and major histocompatibility complex (MHC) genetic diversity of two dolphin populations in Western Australia
18331	Mark Crowe	Bioinformatics Infrastructure and Training Resources in Australia
18332	Charles Foster	Gone with the wind? A systematic revision and biogeographic treatment of Logania R.Br. (Loganiaceae)
18333	Sebastian Duchene	Improving estimation of evolutionary timescales from multi-gene data sets using ClockstaR

Workshops

Thursday July 10th

Accessing EBI resources through the Bioinformatics Resource Australia EMBL

Organizer	Dr Mark Crowe
Time	9am – 12:30pm
Location	Loxton Flexible Teaching Lab (Lvl 2), JD Stewart building (B01), The University of Sydnety

An Introduction to Galaxy with the Genomics Virtual Lab

Organizer	Dr Mark Crowe
Time	1:30pm – 5pm
Location	Loxton Flexible Teaching Lab (Lvl 2), JD Stewart building (B01), The University of Sydney

Introduction to GenAlEx

Organizer	Prof. Rod Peakall
Time	9am -5pm
Location	Room 223 Small Group teaching space (Lvl2), RMC Gunn building (B19), The University of Sydney

Introduction to Phylogenetic Analysis

Organizer	A/Prof. Simon Ho
Time	9am -5pm
Location	Charles Perkins Centre, Room TBC

Friday July 11th

Introduction to R

Organizer	Sebastián Duchêne
Time	9am -5pm
Location	Charles Perkins Centre, Room TBC

1 JD Steward Building
2 Gunn Building
3 Charles Perkins Centre (CPC)

General Conference Information

Conference Venue

Veterinary Science
Conference Centre (VSCC)
University of Sydney

Internet access

WiFi available, see registration desk for details

GSA Conference App

http://gsa2014.m.asnevents.com.au/

Conference Dinner Venue

The Grandstand Restaurant
(Bruce Williams Pavilion)
University of Sydney

Early Career Research Event

Forest Lodge Hotel, 117 Arundel St,
Forest Lodge NSW 2037
(about 5 min. walk from Veterinary Science Conference Centre)

Transport Information

Travelling from Sydney Airport

Taxis from the airport to the vicinity of the University of Sydney are about $40 depending on traffic. Please see www.sydneyairport.com.au/go/by-taxi for further information.

Trains run regularly between the airport and the city. Fares to the city from the domestic terminal are $15.90 (full) or $11.40 (concession) one way. Please see www.sydneyairport.com.au/go/by-train.for more information.

Getting to the University of Sydney

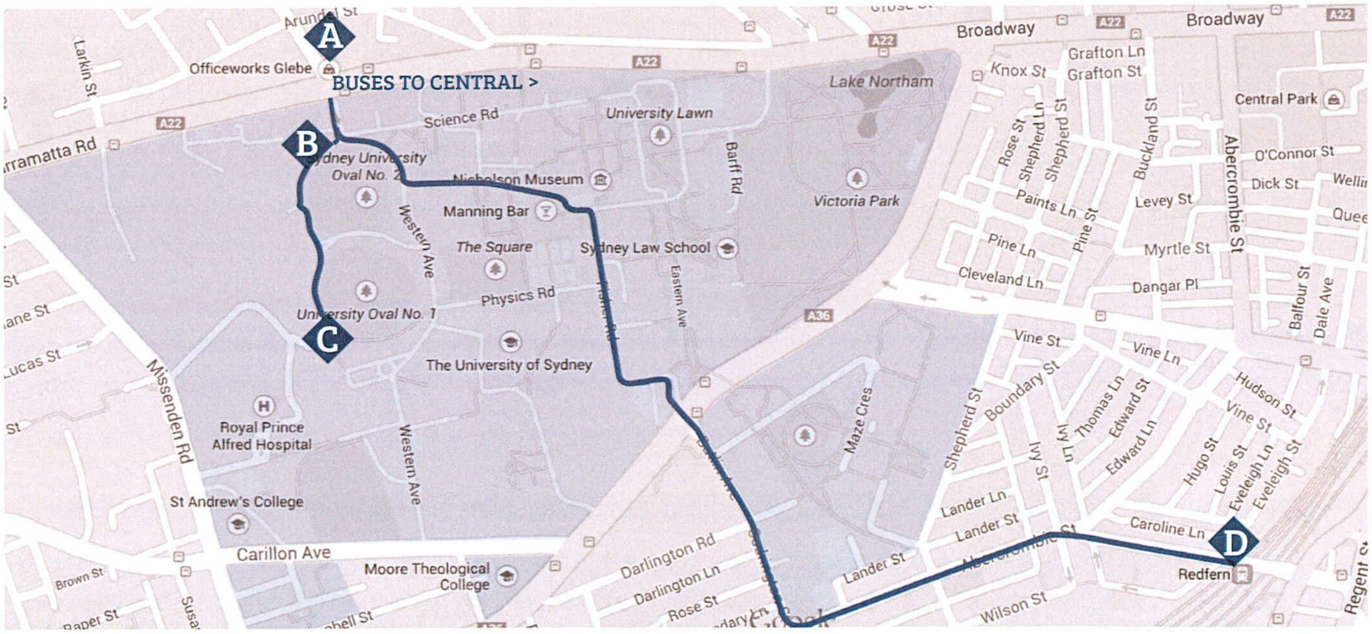
The conference venue is the Veterinary Science Conference Centre at the University of Sydney (closest entrance at Ross Street).

From Central station, it is a 2 km walk or a 10 minute bus ride to the University of Sydney. From Stand D at Railway Square (on the western side of Central Station), routes M10, 412, 413, 436, 438, 439, 440, 461, 480, and 483 will drop you at Ross Street, which is 50m from the conference venue. From Stand C at Railway Square, routes 422, 423, 426, 428 and M30 will drop you in Newtown (closest stop King Street opposite Carillon Avenue), which is a 10 minute walk to the conference venue. These buses depart from Railway square every few minutes.

Please note that these buses are pre-pay only between 7am and 7pm on weekdays; tickets can be purchased from most convenience stores as well as a ticket office at railway square, and the multi-use tickets are fairly economical.

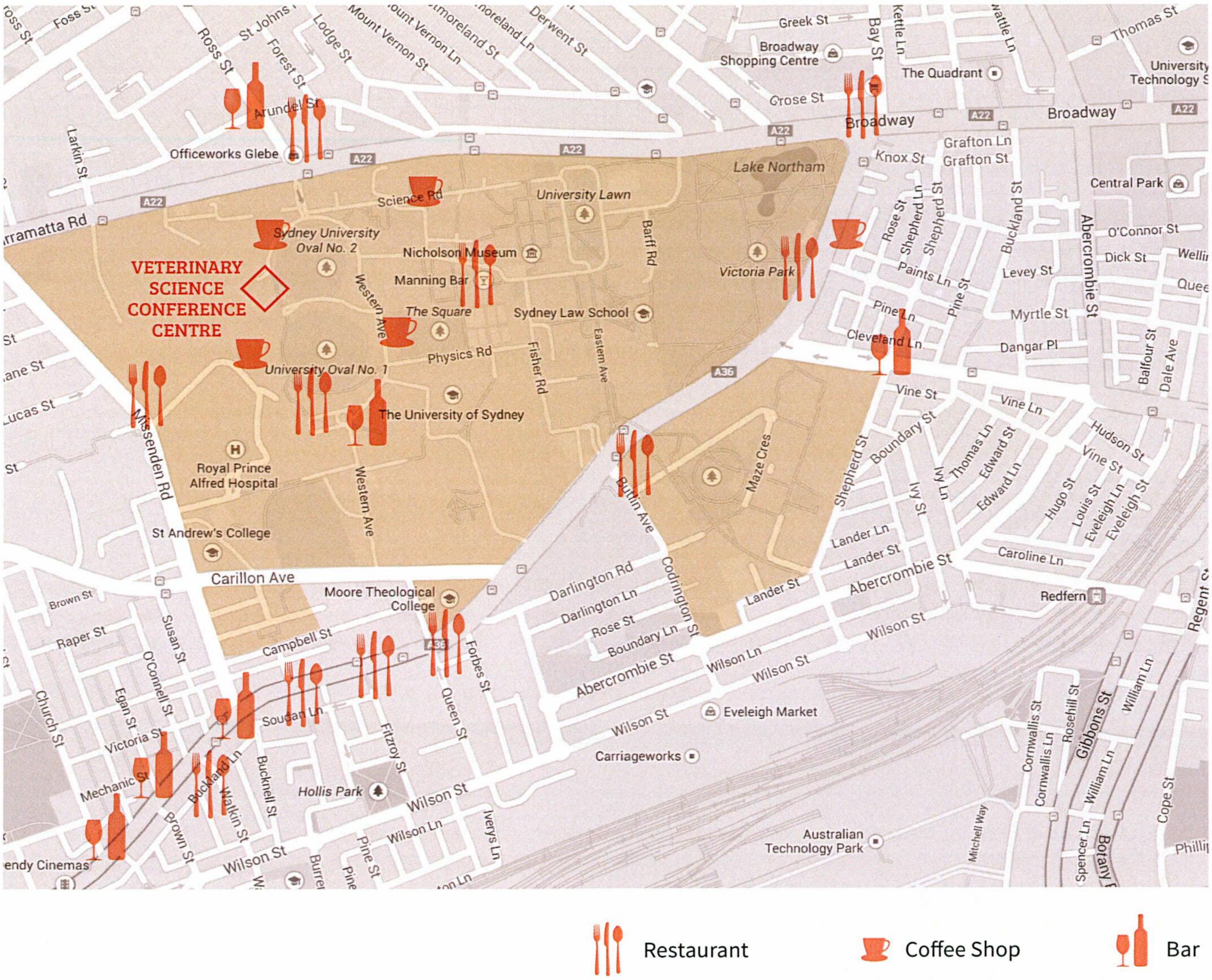
From Redfern station, it is a 2km walk to the University of Sydney.

A Forest Lodge Hotel
B Veterinary Science Conference Centre
C The Grandstand Restaurant (Bruce Williams Pavilion)
D Redfern Train Station



General Conference Information

Gastronomic Services



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Notes

Aaron Darling ~~Mau~~ MAUVE

in E.coli ≈ Eukaryote recomb. - Ave size = 540bp INTEGRONS?
Problem with breaking up samples - single cell sequencing?
Human microbiome project
Kai Darling - poop family science project
1 week on formula - diversity increased - then returned
2 months - stable config
Variants 0 → 100%
Hi-C - Glue two DNA molecules together ~~PeerJ~~ PeerJ 2014?

DrZ "climate genes" - why tied up? gene duplications?
AdapTree Lodgepole pine transcriptomes (~~[illegible]~~ Canada)
Identify ~~[illegible]~~ genotypes for new introductions.

Paul Rymer Waratah - Telopea -
(?) germination ≈ survival 90% ≈ 100% ? Tissues!
Morales - Sunnucks Eastern Robin - mitochondrial proteins - adap?
Direc. selec ≠ Purifying
Simon Baxter Heliconius - Mullerian mimicry - 3 loci ≠ optix in red locus
Andrew Young Wild radish incompatibility
Dominance of S alleles - selection for dominance
Michael Whitehead - Peakall - sex pheromone evolution in plants

Kenji
1♀, 1♂ → colony → secondary queens (64), itting
K > Q1 ⇛ K > q larger · parthenogenesis)
micropyles - variation in number
Competition between secondary queens ?!

Dendrite shape (arbor) class I . II III IV Cn + Kn TFs (~~Ab~~ robust is opposite)
microtubules - Cnn centrosomin -end → +end "
myosin VI goes + → -
Richard Burke ZIP brings Zn in, ZnT efflux - WC & eye phenotype
(10 of these in Dm) (7 in Dm)
Thornton - worker sterility in honeybee
co-citation of genes !!? Ben's gene?
C.elegans Tau homologue PTL-1 - regulates neuronal aging (touch neurons)
RNAi feeding - bacteria?
Burke Lab Voltage gated chloride channels CLC - Single Dm analogue
for each of 3 classes CLCa, b, c - P element excision
Mosaic analysis - twin spot
Alzheimer Amyloid Beta AB - impaired mitochondria

Notes

rs, Aβ in C.elegans

Human Aβ → C.elegans !!?

Nicotinic acetylcholine receptors (Botterham lab)

Nicotine = chemical chaperone

Dα6 - spinosad resistance

Receptors move from ?

Spinosad ≥ Nicotine (?)

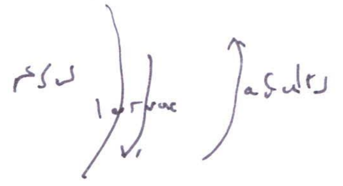
Berndt Gruber

Geog distance matrix - Genetic D.M. Friction D.M. (cost)

(2) (1) (3) ?

Landgen Report - unused in Aust.

Jackie Chan EKP



96 stocks

mt haps - each indiv unique

Equal contribution expectation (?)

Starlings - Invasive species 6 GBS plates from Cornell

Missing SNPs

Kathie Lack of [illegible] in interaction (?)

Jen Timing Bt slower than Bj

Michelle Pearce

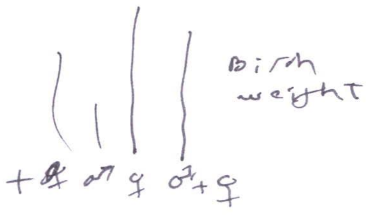
Antennae receptors

Found dATP8B

Clawfish

Cath Suter

MLH1 (2004?)



~~epi~~ methylation

IAP ⇒ Agouti

→

A^{vy}/a

Feed ⇒ F1 + germ-line cells

6 gens of feeding

Notes

Variably methylated regions VMR

Epigenetics → more evolution

Supplement + selection

Remove supplement — selection reversed

Stabilised germline ???

Diabetes –

♀ × a/a . obese – a/a

↓

a/a ~~x~~. a/a

Normal unless fed on western diet

Many genes involved

Adaptive response ?

Caterpillars Steve Simpson ?

More important in ♂ offspring

♂ overweight igf2bp2

microRNAs ~~xx~~ in liver down-regulated

small RNA in sperm tRNA ⇒ tRFs *

Catriona Jackson CEO of STA

Bunce COI ?

Bulk bone - 7 samples - devil, potoroo, tree kangaroo!?

Striated pardalote

Test - penguin poo

Herbal medicines - eg Asarum

MP

Rob Lanfear Felsenstein model - 1 model 1904909384
→ n models

Partitions! - 0 AIC - PF (partition finder)

BIC score ? , Effective Sample Size)

(Bayesian ESS ? >200 ?

Higher partition ←

Duchene

Gene effects Lineage effects multiple pacemakers !?

Gene + Lineage "

Steve Donnellan

Black rats - worst pests of humans

Christmas Island -

10 mt lineages - admixed

55 karyotypes - Jon Martin "Ship rats"

Fan Zia

Bayesian skyline plot

Li + Durbin 2011 TMRCA PSMC

Relationship between BSP + LD ???

Single genome !?

Carlos Different groups, different hotspots (Murray-Darling basin)

Nicholas Archer

Umami taste Fat ??

(5)

Bariatric patients - gain sweet taste

TAS1R3 expression

Reduced receptors - preference ??

CAG CAG
GUC

ATATAT
TATA

Rob Richards Loss ≠ gain Polyglutamine

ds RNA ?? Dicer - Toll receptors required

Directed to 7-mer

CAGCAGCAGCAGCAG

A B C D
A

Simon Ho Relaxed molec clocks (lineage effects)

Bird phylogeny

Potato blight fungus

Jun Tong Dictyoptera (mantids cockroaches + termites)

Nuclear genes, rDNA + Bacterial symbionts

Justin Bloomfield

m_C reset in meiosis !   Brassica rapa

Leaf → bisulph → illumina   CG CHG? ~~CHH~~

CG low or high ???   86%   ~20%

$\mathrm{C}\begin{smallmatrix}A\\T\\C\\G\end{smallmatrix}\mathrm{G}$ middle

Shafagh Waters

15% X-chr inactivation

genome-wide methylation

Histone modif. vs. methylation

Emily Remnant

<1% of CG   75% in genes

Not promoter silencing !! ⊛

DNMT3 + RNAi ⇒ worker - queen

Unfertilized eggs (1)   Drones (2) → sperm (3)

Core set of meth.

eggs overmeth.   sperm undermeth

Stoned-B

POP SIZE EST.

Li + Durbin 2011

Dong Wang

From Timmins lab - select resistant

DS break ?

Katie Dyers

~~[illegible]~~ Sex development

~~[illegible] 2 genes~~ DMRT, ~~[illegible]~~ W ~~[illegible]~~ Z? one gene ?

Lost W genes