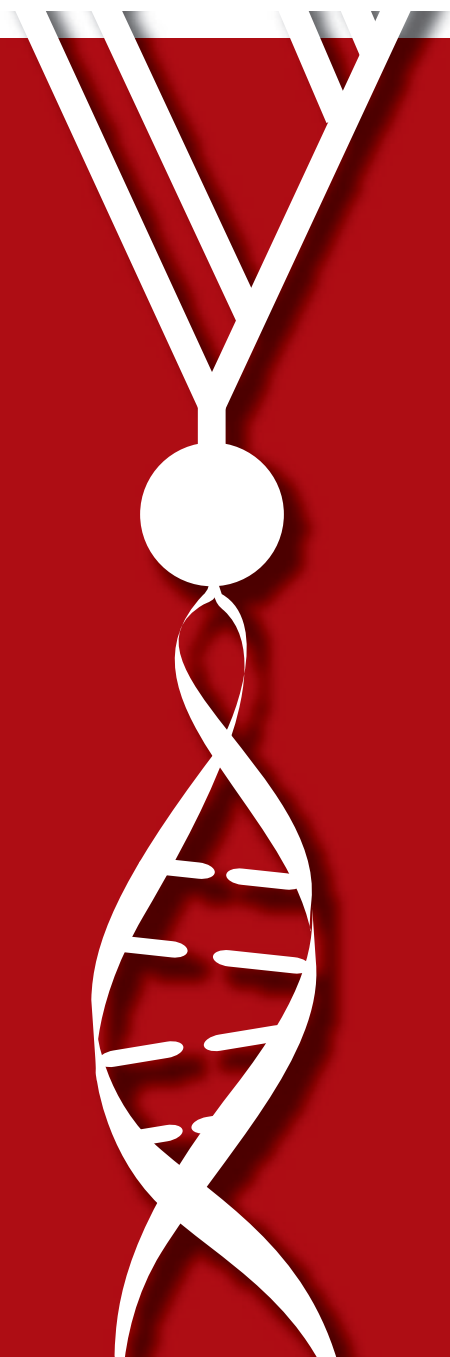


Molecular Biology & Evolution 2005

**in conjunction with the Genetics
Society of AustralAsia**

19 - 23 June, Auckland, New Zealand



Call for papers

Evolutionary Bioinformatics Online

Official journal of New Zealand's *Bioinformatics Institute*



Specific areas of interest include:

- Evolutionary genetics, with emphasis on computational solutions, and methods;
- Phylogenetic reconstruction;
- Computational models of evolution, and disease;
- Use of evolutionary methods to infer structure and function;
- Biodiversity informatics;
- Evolutionary modeling;
- Genome evolution; and
- Experimental evolution, particularly with the application or validation of computational methods.

Author instructions

Available online at www.libertasacademica.com/Instructions.htm

Availability

EBO will be published quarterly online, from June 2005.

MedLine/Index Medicus

The journal is designed to comply with the requirements of the National Library of Medicine for inclusion in MedLine.

EVOLUTIONARY BIOINFORMATICS

ONLINE

Published by
Libertas Academica Ltd
PO Box 302-624, North
Harbour
Auckland 1330, NEW
ZEALAND

Phone + 64 9 415-7704 ■
Fax + 64 9 448-5034 ■
editorial@la-press.com

Journal home page

www.la-press.com/ebo.htm

Journal Table of Contents

www.la-press.com/evolbio.htm



Welcome to the Molecular Biology and Evolution Meeting 2005 co-hosted with the Genetics Society of AustralAsia

Kia ora – Welcome to New Zealand, Aotearoa. We are very pleased that so many of you have been able to join us for what we hope will be an interesting and stimulating meeting. The meeting has attracted approximately 500 visitors, the majority from overseas, some having traveled very great distances. We hope that you will have an enjoyable and productive time here in Auckland, the City of Sails.

Like all such conferences, there has been a great deal of work in putting this meeting together. The Organising Committee comprised the following people: David Lambert, Craig Millar, Lisa Matisoo-Smith, Richard Newcomb, Mike Hendy and Lesley Collins. The Conference Secretary, Monique van Rensburg, has worked tirelessly to correspond with many of you regarding your talks, posters and general issues regarding your attendance. We thank her for her efforts. Susan Wright, Joy Wood and Karen Sinclair organised travel and accommodation for invited speakers, together with all registrations. We thank them also.

Vivian Ward from the School of Biological Sciences at the University of Auckland created the logo and website graphics. Vivian was also responsible for the layout and graphics in this Conference Booklet and for the design of the conference poster and advertising for our Public Lecture Series. We are especially grateful to Vivian for taking on tasks at short notice. Photographs for the posters and the website were kindly provided by Michael Hurst. Jevon Wright was responsible for the conference homepage design and for the regular updates that were required. We thank him for his efforts. Richard Newcomb, the Genetics Society of AustralAsia representative on the Organising Committee, helped us to communicate with GSA members. We are also grateful to Richard and Susan Wright for arranging sponsorship.

We thank the session chairs for their help. Generally, we have requested New Zealand researchers to chair sessions so as to extend local hospitality to our overseas guests.

In relation to our Public Lecture Series, we thank Axel Meyer, Jim Watson and Jennifer Graves for kindly agreeing to help us extend the impact of the conference to the public of Auckland. We would also like to extend our thanks to the distinguished visitors who agreed to introduce these speakers.

Massey University's printery provided all the copies of posters and other material. We thank them for their help.

This conference would not have been possible without the support of the New Zealand Government's Centres of Research Excellence Fund, via its support for the Allan Wilson Centre for Molecular Ecology and Evolution. Finally, we thank the Society for Molecular Biology and Evolution and the Genetics Society of AustralAsia for the opportunity to host this important conference.

David Lambert
Craig Millar
June 19th, Auckland, New Zealand

Table of Contents

General Conference Information	1
Genetics Society of AustralAsia and Australian Conservation Society Prizes	3
Program at a Glance	4
Free Public Lecture Series and Conference Opening	6
Information for Session Chairs, Speakers and Poster Presenters	10
Special Meetings - SMBE Young Investigators' Workshop 2005	11
Concurrent Sessions	
Monday June 20 th	12
Tuesday June 21 st	16
Wednesday 22 nd	20
Thursday 23 rd	23
Map of Venue	26
Poster Session	28
Acknowledgement of Sponsorship and Support	35
Auckland - Popular Attractions	39
Map of the central Auckland	42
Author Index	46



INFORMATION

Registration Desk

The conference registration desk is located in the Upper NZI foyer of the Aotea Centre and will be staffed during the following periods:

Sunday June 19th	10.00am - 5.30pm
Monday June 20th	8.30am - 5.30pm
Tuesday June 21st	8.30am - 5.30pm
Wednesday June 22nd	8.30am - 5.30pm
Thursday June 23rd	8.30am - 1.00pm

Day Fees are NZ \$150 per day and we will accept credit card, cheques and cash payments

Oxford University Press, Welcoming Reception

There will be a Maori Welcome at 4.30pm on Sunday 19th June in the ASB Auditorium. After this, there will be a reception for all those attending the conference, in the Air NZ foyer directly outside the auditorium.

Morning Tea

Refreshments will be provided each day of the Conference in the Upper and Lower NZI foyers between 10.30am and 11.00am, except on the opening day Sunday the 19th.

Lunch

Lunch will be provided for three days of the Conference (Monday, Tuesday and Wednesday) in the Upper and Lower NZI foyers between 1.00pm and 2.00pm.

Conference Banquet

This is being held on Wednesday evening from 7.30pm to 10.30pm. The costs of this was included in your registration fee. The dinner will be held on the Lower level of the NZI wing at the Aotea Centre.

Message Board

A message board is located near the conference registration desk on the Upper NZI level. Messages can be left by phoning the registration desk. In case of emergency registrants can phone +64 (0)21 376 427 and leave a message.

Taxis and Shuttle Bus Services

Taxis and shuttle buses are available for all arriving and departing flights from both the international and domestic terminals of Auckland Airport. Taxis and shuttle bus ranks are situated outside the international terminal and in front of the domestic terminals.

The airport to central city taxi fare is approximately NZ\$60.00. Shared shuttle buses are significantly cheaper.

Shuttle buses offer economical transportation between the central city, suburbs and the airport on a 'shared ride' basis. Passengers are advised to book shuttle trips to the airport in advance.

Airport Shuttle Bus - (09) 300 1111

Air Bus - 0508 247 287 or www.airbus.co.nz

Auckland Co-op Shuttles - (09) 300 3000 or www.cooptaxi.co.nz

Those of you staying at the Carlton Hotel should be aware that a courtesy van is available from the airport and, if you arrange with them, they will collect you on arrival. Other hotels are likely to have a similar arrangement.

Telephone

There will be a phone at the registration desk which can be use by conference participants for local calls. Overseas calls are possible, by arrangement.

Smoking Policy

All our venues are all completely smokefree.

Medical and Health

Aotea Center staff are trained in Basic First Aid, the nearest medical centre is City Med Medical Centre on the corner of Albert St & Mills Lane in Auckland Central.

Safety and Security

Security personnel will be on duty throughout the conference but participants are warned not to leave their belongings unattended. The Aotea Center has a security team on site that monitor CCTV. All venues are locked at night and will only be accessible once exhibitors and conference organisers are on site each day.

ATM and Banking

There closest ATM machine to the Aotea Center is a National Bank Cashpoint opposite the Aotea Centre on Queen St.

Parking

Ample parking, on an hourly or daily basis, is available under the Aotea Centre in the Civic Carpark.

Internet Room

This is located on the Upper NZI level. There will be internet ready PCs and Macintosh computers for those attending the meeting.

GSA and the Australian Conservation Society Student Prizes

Genetics Society of AustralAsia student prizes

Mayo Prize

Valued at \$500 this prize is awarded for the best talk given by a PhD student at the GSA annual conference. The prize honours the contribution to GSA and, more generally, to Genetics made by Drs Jean and George Mayo.

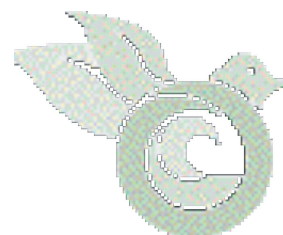
Sidney James Prize

Valued at \$500 this prize is awarded for the best poster presentation by a Ph.D. student. The prize honours the contribution to GSA and, more generally, to genetics made by the late Dr Sid James.



Australian Section of the Conservation Society Prize

Awarded for the best presentation by a graduate student in conservation biology, this prize is a two year subscription to the Society for Conservation Biology, including a choice of journal subscription to either "Conservation Biology", "Conservation in Practice", or "Pacific Conservation Biology".



Further student prizes will be announced at the meeting

PROGRAM AT A GLANCE

	Sunday, June 19th			
10.00am - 5.30pm	Registration - Aotea Centre			
1.00pm - 3.30pm	Free Lecture Series - ASB Auditorium	Axel Meyer Chance & Necessity in Evolution	Jim Watson The Evolution of Sustainability	Jennifer Marshall Graves Sex Chromosomes & the Future of Men
4.30pm - 6.30pm	Welcome and Maori Greeting, ASB Auditorium Oxford University Press Welcoming Reception, Air NZ Foyer			
	Monday, June 20th			
8.30am - 5.30pm	Registration and Information - NZI Upper Foyer			
8.30am - 4.00pm	Poster Setup			
8.30am - 5.30pm	Internet Room			
8.30am - 10.30am	Molecular Ecology	Genes & Gene Expression	Origin & Evolution of Photosynthetic Life	Evolution in the Pacific
10.30am - 11.00am	Morning Tea Provided in NZI Foyers			
11.00am - 1.00pm	Molecular Ecology	Genes & Gene Expression	Species and Speciation	Evolution in the Pacific
1.00pm - 2.00pm	Lunch Provided in NZI Foyers			
2.00pm - 4.00pm	Molecular Ecology	Genes & Gene Expression	Species and Speciation	Rates & Dates
4.00pm - 6.00pm	Refreshments and Poster Session in the Limelight Room			
	Tuesday, June 21st			
8.30am - 5.30pm	Registration and Information - NZI Foyer			
8.30am - 5.30pm	Internet Room			
8.30am - 10.30am	Molecular Ecology	Bioinformatics & Phylogenetic Methods	Genome Evolution	Genetics of Diseases & Human Evolution
10.30am - 11.00am	Morning Tea Provided in NZI Foyers			
11.00am - 1.00pm	Agricultural Genomics	Bioinformatics & Phylogenetic Methods	Genome Evolution	Genetics of Diseases & Human Evolution
1.00pm - 2.00pm	Lunch Provided in NZI Foyer			
2.00pm - 4.00pm	Walter Fitch Symposium	Bioinformatics & Phylogenetic Methods	Genome Evolution	Primate & Human Evolution
		Genetics of Diseases & Human Evolution		
4.00pm - 5.00pm	GSA Annual General Meeting and MBE Business Meeting			
7.30pm - 10.30pm	Conference Banquet in the Aotea Centre NZI Lower Level			

	Wednesday, June 22nd			
8.30am - 5.30pm	Registration and Information - NZI Upper Foyer			
8.30am - 5.30pm	Internet Room			
10.30am - 11.00am	Evolution & Development	Species & Speciation	Genome Evolution	Conservation Genetics
10.30am - 11.00am	Morning tea provided in NZI Foyers			
11.00am - 1.00pm	Ancient Biomolecules	Origin & Evolution of Photosynthetic Life	Phylogenetics	Conservation Genetics
		Rates & Dates		
1.00pm - 2.00pm	Lunch provided in NZI Foyers			
2.00pm - 3.00pm	GSA - MJD White Lecture			
3.00pm - 4.00pm	MBE - Nei Lecture			
6.30pm - onwards	Optional Waiheke Island Dinner			
	Thursday, June 23rd			
8.30am - 1.00pm	Registration and Information - NZI Upper Foyer			
8.30am - 1.00pm	Internet Room			
8.30am - 10.30am	Microbial Evolution	Conservation Genetics	Genome Evolution	RNA World
10.30am - 11.00am	Morning tea provided in NZI Foyers			
11.00am - 1.00pm	Protein Evolution	Conservation Genetics	DNA Barcoding & Biodiversity	RNA World
1.00pm - 1.30pm	Conference Closing and Prize Giving - Lower Level NZI Foyer			

Key to Rooms

NZI 4/5	
NZI 1	
NZI 2	
NZI 3	

Genes, Evolution & Biotechnology

Date: Sunday 19th June, Time: 1.00 - 3.30pm

Molecular Biology & Evolution 2005 in conjunction with the Genetics Society of AustralAsia Annual meeting



Speaker: Axel Meyer

Lecture title: Chance and Necessity in Evolution.

Abstract: What is the role of chance and are there rules or even laws that dictate a necessary, deterministic outcome of evolution? What are species, how different are they from each other, and do new ones originate through necessity or by chance alone? Are all types of organisms equally affected by the seemingly random doom of mass extinctions? These are old questions that continue to be debated vigorously even until today, 150 years after Darwin. In the last decade increasingly genetic information based on DNA-sequences of genes and entire genomes are used to tackle questions about the evolutionary

past of life on this planet. Seemingly random mutations afflict genes, yet, the comparative analyses of gene networks and entire genomes recently demonstrated an unexpected degree of genetic conservation even between morphologically highly divergent organisms that are separated by hundreds of millions of years of evolution. For example, "eye genes" were found to be surprisingly exchangeable between flies and mice whose eyes differ markedly, and humans and our closest relatives the chimpanzees differ by only about 1% in our genetic makeup. This raises the question of how the paradox between astonishing genomic conservation and rampant biological diversity can be solved.

Biographical information Professor Dr. Axel Meyer holds the chair for Zoology and Evolutionary Biology at the University of Konstanz in Germany. He studied biology, chemistry and physics at the Universities of Marburg and Kiel in Germany and moved 1982 to the USA where he studied biology at the University of Miami, the University of California at Berkeley (Ph.D. 1988 in Zoology) and Harvard University. From 1988 to 1990 he held a Sloan-Foundation Postdoctoral Fellowship with professor Allan C. Wilson at the Biochemistry Department in Berkeley. From 1990 to 1997 he was a professor at the Department of Ecology and Evolution at the State University of New York before he returned to Germany for his present post.

Prof Meyer is the recipient of several fellowships and prizes including a Guggenheim Fellowship, a Miller-Research Professorship at Berkeley, and the Science Prize of the Berlin Academy of Sciences.

His main research interests are the study of the origins of biological and genetic diversity, and the comparative analyses of genomes.



Speaker: Jim Watson

Lecture title: The Evolution of Sustainability

Abstract: For centuries economic development has been driven by land, climate, geography, and an ingenuity often borne out of scarce resources. The evolution of society has closely followed plant and livestock breeding, increasing agricultural intensity, and, colonisation of new territories to provide new resources for wealth creation. For the past century oil has been the dominant resource of economic growth.

Agriculture today is being shaped today by the application of the tools of modern molecular biology to use processes from living systems to increase crop diversity and yield – biotechnology - and the growing need to adopt new and sustainable farming practices. The current practice of high fertiliser use, herbicide and pesticide application and irrigation employed to maintain high crop yields is unlikely to be sustainable without increasing damage to soils and the environment generally. And we can't ignore our oil economy and the cost of energy for the agricultural industry.

"The Stone Age did not end for lack of stone, and the Oil Age will end long before the world runs out of oil." The quotation is from Sheikh Zaki Yamani, a Saudi Arabian who served as his country's oil minister three decades ago. Sheikh Yamani first came to the world's attention during the Arab oil embargo of the United States, which began three decades ago and whose effects altered the course of modern economic and political history.

A generation after the embargo began, the facts seem plain: the world remains addicted to Middle Eastern oil. So why is Sheikh Yamani predicting the end of the Oil Age? Because he believes that something fundamental has shifted since that first oil shock. Advances in technology are beginning to offer a way for economies, especially those of the developed world, to diversify their supplies of energy and reduce their demand for petroleum, thus loosening the grip of oil and the countries that produce it.

It's biotechnology that has the potential to provide energy security and sustainability in the near future. Woody crops are a source of energy through the extraction of cellulose and lignin from woody biomass and the fermentation of cellulose to ethanol, for use as a transport fuel to replace petrol, and the use of lignin to produce chemicals and biomaterials to replace petrochemical products. They are serious challenges to the oil industry. The industry needs new woody crops and new biotechnologies to make a serious dent in the oil economy.

This talk will explore the evolution of biotechnology, energy resources and the environmental sustainability issues the next generation faces unless science provides smart solutions to economic growth and social well-being.

Biographical information: Dr James Watson founded Genesis Research & Development Corporation Limited, a biotechnology company 1994. He was Chief Executive until December, 2004 when he moved to the position of Chief Scientist.

He received his PhD from the University of Auckland in 1967 then worked as a postdoctoral

fellow worked at Syntex Corporation in Palo Alto, California (1967-69) and the Salk Institute (1969-75). He has held Professorships at the University of California, Irvine (1976-81) and the University of Auckland (1981-93) serving as Head of the Department of Molecular Medicine (1983-93).

His field of endeavour has been immunology.

He was a Director of the Foundation for Research, Science and Technology (1999-2002) and President of the Australasian Society of Immunology (2001). He is currently President of the Royal Society of New Zealand, a Member of the Government's Growth and Innovation Advisory Board from 2001 to 2005, and a Trustee of the Malaghan Institute of Medical Research.



Speaker: Jennifer Marshall Graves

Lecture title: Sex chromosomes and the future of men

Abstract: In humans and other mammals, females have two X chromosomes, and males a single X and a Y. The Y chromosome is male determining because it bears a gene (SRY) that switches on the development of testis, which pumps out male hormones. The X is a decent, ordinary chromosome, though it has more than its fair share of genes involved in male sex and reproduction – and maybe sexual behaviour and intelligence. But the Y is a genetic wasteland – small and full of genetic junk, bearing only 45 genes, mostly active only in testis.

The X and Y evolved from an ordinary chromosome pair as the Y degraded progressively. Comparing Y chromosomes between distantly related mammals, as well as their antecedents in birds and reptiles, reveals links to ancient bird/reptile sex chromosomes. The Y chromosome looks like a degraded relic of the X because most of its genes – even those with important male-specific functions – have partners on the X from which they evolved.

The human Y chromosome is running out of time. At the rate it is degrading, it will lose its last 45 genes in just 10 million years. What happens when SRY goes? Since imprinting means we can't go in for a female-only lifestyle, would this be the end of the line for our species? The good news is that SRY has been lost in at least two groups of rodents. Somewhere else in the genome, a new sex determining gene must have taken over the function of SRY. So as the human Y runs out of options, new sex determining genes may evolve, maybe leading to different hominid species.

Biographical information: Professor Jenny Graves' work on Australian mammals provides a unique view on the way that the human genome evolved and how it works. Geneticists use variation to test the influence of genes on characteristics – she has capitalized on the very distant relationship between humans, kangaroos and platypus to provide enough variation to study even very fundamental genetic processes, like sex and embryonic development.

One of her group's big successes was in her research on sex and sex chromosomes. It was their work on kangaroos that first showed that the prevailing hot favourite candidate for the sex determining factor was the wrong gene, and it was her PhD graduate who then went on to clone the right gene (SRY) in London. SRY is on the Y chromosome, which is present only in males. The Y is a very odd chromosome – it is small, and largely made of junk. Professor Graves' group discovered from comparisons across species that the Y is just a broken down X chromosome. It has lost most of its original 1000-odd genes at such a rate that Jenny Graves predicts that the Y will disappear in another 10 million years or so, as has already happened in some weird rodents.

Most recently, Jenny Graves has lead the effort to see that the genomes of the kangaroo and the platypus are sequenced, marshalling resources in Australia and overseas and building Australian teams and international collaborations. The genomes of these unique animals are treasure troves full of unknown genes, and information on how they work. Being able to compare sequences in and around the same genes in humans and kangaroos can identify new human genes and the signals that switch them on and off, and can also lead to the discovery of genes that control marsupial-specific characteristics that might be handy for agriculture and medicine.

Information for Session Chairs, Speakers and Poster Presenters

Session Chairs

If you are moderating a session, please arrive 30 minutes early to ensure that audio-visual equipment is in place and functional and that all presenters are accounted for. You need also to check that their presentations have been loaded on to the resident computer. At each session, a technician will be on hand to load the speaker's files onto the resident computer and to help with any audio-visual problems. Each room will be equipped with a PC with CD drive, a USB flash drive port, a laser-pointer and a timer. Zip drives will not be available. Invited speakers have been allotted 30 minutes and contributed papers have been given 15 minutes, including time for questions. The moderator should alert speakers when 3 minutes remain (by standing) and again (verbally) when 1 minute remains. After the allocated time, speakers will have to be asked to immediately leave the podium without taking questions. Please announce this format at the beginning of the session, and please stick to the schedule. If a speaker ends early or there is a cancellation, do not introduce the next speaker until their designated time to speak.

Speakers

Oral presentations are limited to 30 minutes for invited speakers, and 15 minutes for other speakers. We suggest that invited speakers talk for 25 minutes, with 5 minutes for questions. All other presentations should be 12 minutes, with 3 minutes for questions (15 minutes, total). Please consult the program ahead of time to confirm the time and location of your talk. Only PCs with data projectors will be available for presentations in each room, with CD drives and USB flash drive ports.

Speakers in morning sessions will need to load their talk the day before, since the meeting starts at 8.30am with no prior time to do this. Speakers at the midday and afternoon sessions must check in 30 minutes before the start of your session in order to load your presentation and meet the session chair. The Internet room will be available from 8.30am-5.30pm throughout the conference, for presenters to check software compatibility. Please be sure to do this the day before your presentation. Apple (Macintosh) users should verify that their files are compatible with PowerPoint or Adobe Acrobat for Windows. Both PCs and Macs will be available in the Internet room, but only PCs will be available in each room.

Poster Presenters

The poster session is from 4pm - 6pm on Monday June 20th and will be held in the Limelight Room (see map in your Conference Program). Please note your poster number in the Conference Program starting on page 28. On the day of the poster session you will need to pin up your poster on a display board featuring this number. You can do this from 8.30am on Monday, onwards. During the poster session, the presenting author should be standing by his/her poster. The space available for a poster is limited to 900mm wide x 1200mm high. We will supply Velcro and pins for attaching your posters to the boards.

Special Meetings - SMBE Young Investigators' Workshop 2005

The Society for Molecular Biology and Evolution announces the third Tri-National Young Investigators' Workshop, 24 - 26 June 2005, to be held in conjunction with our annual meeting in New Zealand (19 - 23 June). Senior graduate students and postdoctoral researchers from the US, Japan, and New Zealand will be participants in the workshop. Participants will be awarded travel funds for the workshop. While the workshop is open to all fields of molecular evolution, the workshop will focus on the five following subject areas:

1. Epigenetics and adaptive evolution – transcriptomes and proteomes
2. Connections between phenotype and genotype
3. Phylogeny, phylogeography, and geology
4. Hominid evolution
5. Genome evolution and complexity

SMBE is committed to international intellectual partnerships, and to diversity as a component of excellence in science.

Partial funding provided by SMBE, NSF, the Graduate University for Advanced Studies, and the Allan Wilson Centre.

Workshop Organizers:

Marta L. Wayne and Laura Katz, US

Yoko Satta and Naoyuki Takahata, Japan

Mike Hendy and David Penny, New Zealand

Monday, June 20th

8.30am - 5.30pm Registration and Information, Upper NZI Foyer - Aotea Centre

8.30am - 4.00pm Setup Posters- Limelight Room

8.30am - 5.30pm Internet Room

Session Chair & Location	Karen Armstrong (Lincoln University) Room NZI 4/5	Richard Newcomb (HortResearch) Room NZI 1	John Archibald (Dalhousie University) Room NZI 2	Lisa Matisoo-Smith (AWC, Auckland University) Room NZI 3
	Molecular Ecology	Genes and Gene Expression	Origin and Evolution of Photosynthetic Life	Evolution in the Pacific
8.30am	<u>Bill Amos</u> ; Department of Genetics, Cambridge University; Genetic archaeology: new approaches to find out who was where and when	<u>Craig P. Hunter</u> ; Molecular and Cellular Biology, Harvard University; The Molecular Genetics of Intercellular RNA Transport in Nematodes	<u>Robert E. Blankenship</u> , Sumedha Gholba and Jason Raymond; Department of Chemistry and Biochemistry, Arizona State University, USA; The Evolutionary Transition from Anoxygenic to Oxygenic Photosynthesis and How it Changed the Earth	<u>Rebecca Cann</u> & Karl Diller; Dept of cell and molecular biology, University of hawaii (Manoa); Why molecular evolutionists need to reassert their independence: eurocentrism hijacks the human MSY and FoxP2
9.00am	<u>Franziska Nittinger</u> , Elisabeth Haring, Wilhelm Pinsker and Anita Gamauf; Museum of Natural History, Vienna, Austria; Genetic variation within the Hierofalcon complex – shared ancestral polymorphism or gene flow?	<u>Graham Thompson</u> , Jürgen Paar, Robert Kucharski, Ryszard Maleszka, Ben Oldroyd; University of Sydney; Molecular basis of worker sterility in the honey bee, <i>Apis mellifera</i>	<u>William F. Martin</u> ; The Institute of Botany III, Heinrich-Heine-Universität Düsseldorf, Germany; Endosymbiotic gene transfer: A mechanism of genetic innovation unique to the eukaryotic lineage.	<u>Mark Stevens</u> , Paul Sunnucks, Penny Greenslade; Allan Wilson Centre for Molecular Ecology & Evolution; Massey University, Palmerston North, New Zealand; Living fossils or island hoppers: molecular studies of the origins and dispersal of <i>Cryptopygus antarcticus</i> in the Southern Hemisphere
9.15am	<u>B.E. Deagle</u> , D.J. Tollit, S.N. Jarman, M.A. Hindell, A.W. Trites and N.J. Gales; Zoology Department, University of Tasmania; Molecular scatology as a tool to study diet: analysis of prey DNA in scats from captive Steller sea lions	<u>David M. Irwin</u> , Shijun Yue, and Brian Tsai; Banting and Best Diabetes Centre, University of Toronto, Canada; Evolution of the Proglucagon Gene Promoter		<u>GSA Frank E. Rheindt</u> , Janette A. Norman, Diane L. Rowe and Les Christidis; Department of Genetics, University of Melbourne, Australia; Speciation dynamics in the Australo-Papuan region: The case of <i>Meliphaga</i> honeyeaters
9.30am	<u>Oscar E. Gaggiotti</u> ; Laboratoire d'Ecologie Alpine, Université Joseph Fourier, France; Identifying the factors that influence dispersal processes and species distributions	<u>Satoko Kaneko</u> , Kaoru Tsuda, Kazuyuki Mekata, Kazuo Moriwaki, Naoyuki Takahata, and Yoko Satta; Department of Biosystems Science, The Graduate University for Advanced Studies (Sokendai); Rapid turnover of regulatory processed pseudogenes of <i>Makorin1</i> in rodents and primates	<u>Hwan Su Yoon</u> , Jeremiah Hackett, and Debashish Bhattacharya; Department of Biological Sciences and Roy J. Carver Center for Comparative Genomics, University of Iowa, USA; Eukaryotic Plastid Endosymbiosis	<u>Tristan Armstrong</u> & Ross Beever; Landcare Research, New Zealand; Phylogeography of an iconic endemic: the New Zealand cabbage tree, <i>Cordyline</i> <i>australis</i>
9.45am	<u>Neil Gemmell</u> , Victoria Metcalf, Katherine Gomas, Patrice Irvine, and Fred Allendorf; School of Biological Sciences, University of Canterbury, New Zealand; Do Mitochondrial Mutations Affect Population Viability?	<u>Andrew Whitehead</u> and Douglas L. Crawford; Department of Marine Biology and Fisheries, University of Miami; Neutral and Adaptive Variation in Gene Expression		<u>David Blair</u> , Kim Sewell, Lester Cannon, Keith Crandall, Tim Littlewood and Susan Lawler; School of Tropical Biology, James Cook University, Australia; History of an Association: Temnocephalan Flatworms and Freshwater Crayfish in Australia and New Zealand

10.00am	Damien Broderick, Jenny Ovenden and Rik Buckworth; Department of Primary Industries and Fisheries, Queensland, Australia; Estimating harvest rates in a Spanish mackerel (<i>Scomberomorus commerson</i>) fishery using genetic mark-recapture	Kasper Munch, Paul Gardner, Anders Krogh; University of Copenhagen, Denmark; A probabilistic method for determining transcripts from genomic tiling microarrays	Nicola Patron, Ross Waller, John Archibald, Patrick Keeling; Canadian Institute for Advanced Research, University of British Columbia, Canada; Targeting to secondary red plastids	K McBreen, D Huson, M Lysak, O Kardailsky, PA McLenachan, PB Heenan and PJ Lockhart; Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, New Zealand; Using a Super Network to define the phylogenetic neighborhood of <i>Arabidopsis thaliana</i>
10.15am	Ian M. Ehrenreich, Michael D. Purugganan; Department of Genetics, North Carolina State University, U.S.A.; The Molecular Population Genetics of the More Axillary Growth (MAX) Pathway in <i>Arabidopsis thaliana</i>	Wen-Hui Lee, Yan Li, Ren Lai, Sha Li, Yun Zhang, and Wen Wang; Kunming Institute of Zoology, The Chinese Academy of Sciences (CAS), Kunming, China; Variety of Antimicrobial Peptides in the <i>Bombina maxima</i> Toad and Evidence of their Rapid Diversification		Andrew C. Clarke, Michael K. Burtenshaw, Patricia A. McLenachan, David L. Erickson, Bruce D. Smith, and David Penny; Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, New Zealand; Prehistoric human contact between Polynesia and South America? DNA analysis of the bottle gourd
10.30am - 11.00am	Morning Tea Provided in NZI Foyers			
Session Chair & Location	Dianne Gleeson (Landcare Research) Room NZI 4/5	Mark Stevens (AWC, Massey University) Room NZI 1	Mike Hendy (AWC, Massey University) Room NZI 2	David Penny (AWC, Massey University) Room NZI 3
	Molecular Ecology	Genes and Gene Expression	Species and Speciation	Evolution in the Pacific
11.00am	B. Smietanka, T. Kijewski, A. Burzynski, H. Hummel, R. Wenne; Institute of Oceanology, Poland; Genetic differentiation of the European populations of marine mussels <i>Mytilus</i> (Bivalvia)	Nobuhiko Tanaka, Shozo Yokoyama, Kazuho Ikeo, Takashi Gojobori; National Institute of Genetics, Japan; Various adaptations for the perpetual darkness in the diversification process from an eyed surface-dwelling form to an eyeless cave-dwelling form of Mexican tetra, <i>Astyanax mexicanus</i>, by cDNA microarrays	GSA Pia Langhoff, Allen Rodrigo, Astrid Authier, Thomas Buckley, John Dugdale, Richard Newcomb; Molecular Olfaction Group, HortResearch, New Zealand; Speciation genes and barcoding in native NZ leafroller moths	Anya E. Hinkle; Department of Integrative Biology, University and Jepson Herbaria, USA; Population structure and reproductive biology of the ti plant (<i>Cordyline fruticosa</i>) with implications for Polynesian prehistory
11.15am	Margaret Byrne, Carole Elliott, Colin Yates, David Coates; Department of Conservation and Land Management, Australia; Impact of Fragmentation on Patterns of Gene Flow in <i>Eucalyptus Wandoo</i> and <i>Calothamnus quadrifidus</i> in Western Australia	Marta L. Wayne, Sergey V. Nuzhdin, and Lauren McIntyre; Department of Zoology, University of Florida, USA; Section of Ecology; Additivity and trans-acting effects on gene expression	Kendall D. Clements, Sarah L. Eyton, C. Scott Baker, Danielle A. Hannan and Tony J.R. Hickey; School of Biological Sciences, University of Auckland, New Zealand; Radiation and speciation in the New Zealand triplefin fishes	Melanie Pierson, Neil Gemmell, Matthew Hurles, Barbara Holland; Allan Wilson Centre for Molecular Ecology and Evolution, University of Canterbury, New Zealand; MtDNA genomes and the peopling of the Pacific
11.30am	Stephen F. Chenoweth; School of Integrative Biology, University of Queensland, Australia; Using QST-FST comparisons to detect divergent natural selection on quantitative traits: an evaluation in a system of natural populations	Kazuya Yuge, Kazuho Ikeo and Takashi Gojobori; National Institutes of Genetics, Japan; Analysis of sexual dimorphism of gene expression in mouse brain	Anthony Hickey; School of Biological Sciences, University of Auckland; Allopatric speciation in the marine realm: an explanation of New Zealand's triplefin fish (Family <i>Tripterygiida</i>) diversity?	Dan Schmidt, Roger Grund, Jane Hughes; Centre for Riverine Landscapes, Faculty of Environmental Sciences, Griffith University, Australia; East-west relationships in Australia revisited: genealogical concordance among three threatened <i>Ogyris</i> butterflies restricted to southeastern and southwestern Australia.
11.45am	Lincoln H Schmitt, Christopher N Newbound, Susan Hisheh, Maharadatunkamsi, Richard A How; School of Anatomy & Human Biology, The University of Western Australia; Geography and population structure in the bats of Wallacea	R. Haygood, J. P. Balhoff, W. J. Nielsen, and G. A. Wray; Biology Department, Duke University, USA; Polymorphism and divergence in regulatory regions of sea urchin genes	Kirsten M. Donald, Martyn Kennedy and Hamish G. Spencer; Allan Wilson Centre for Molecular Ecology and Evolution, University of Otago, New Zealand; Topshells and Trematodes in Tandem: Evolution of Intertidal Molluscs and their Parasitic Digeneans	GSA Mark de Bruyn, John C. Wilson and Peter B. Mather; School of Natural Resource Sciences, Queensland University of Technology, Australia; Molecular phylogeography of <i>Macrobrachium rosenbergii</i>: diversification mediated by climate change or plate tectonics?

12.00pm	Susan Hisheh, Greg Cozens, Richard A How and Lincoln H. Schmitt; School of Anatomy & Human Biology, The University of Western Australia; Rats on the rocks: Decline in diversity in Kimberley island populations of <i>Zyomys woodwardi</i>	GSA Karin S. Kassahn, M. Julian Caley, Alister Ward, Ross H. Crozier; School of Tropical Biology, James Cook University, Australia; Thermal stress in reef fish: insights from a microarray study	Yong-Jin Won, Yong Wang, Arun Sivasundar, Jeremy Raincrow, Jody Hey; Department of Genetics, Rutgers the State University of New Jersey, U.S.A.; Persistence of ancestral polymorphisms in the cichlid species flock of Lake Malawi	GSA Michael Knapp, Karen Stöckler, David Havell, Frédéric Delsuc, Federico Sebastiani and Peter J. Lockhart; Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Palmerston North, New Zealand; Of ancient relics and travellers across the oceans
12.15pm	Abraham Passmore, Simon Jarman, Kerrie Swadling, Andrew McMinn and So Kawaguchi; Institute of Antarctic and Southern Ocean Studies, University of Tasmania; DNA as a dietary biomarker: Lessons from Antarctic krill?	GSA A.R. Anderson and S.W. McKechnie; Centre for Environmental Stress and Adaptation Research (CESAR) Monash University, Australia; Microarray and QTL analysis of Chill Coma recovery selection in <i>Drosophila melanogaster</i>	Leonie C. Moyle and Elaine B. Graham; Center for Population Biology, University of California, U.S.A.; Comparative genomics of hybrid incompatibility among <i>Lycopersicon</i> (<i>Solanum</i>) species	Abby Harrison; University Of Oxford, England; Hepatitis B virus in the Pacific: Coevolution, Codivergence, or Coincidence
12.30pm	Tammy Steeves, David Anderson and Vicki Friesen; School of Biological Sciences, University of Canterbury, New Zealand; A role for non-physical barriers to gene flow in the diversification of a highly vagile pantropical seabird, the masked booby (<i>Sula dactylatra</i>)	Jean-Vincent Chamary and Laurence D. Hurst; Department of Biology and Biochemistry, University of Bath, United Kingdom; Selection at silent sites in mammalian genes	Luisa Orsini, Helena Koivulehto and Ilkka Hanski; Department of Biological and Environmental Sciences, University of Helsinki, Finland; A multi-gene approach to resolve molecular phylogeny of Malagasy dung beetles	Hong Shi, Yong-li Dong, Bo Wen, Chun-Jie Xiao, Peter A. Underhill, Pei-dong Shen, Ranajit Chakraborty, Li Jin and Bing Su; Kunming Institute of Zoology, Chinese Academy of Sciences, China; Y Chromosome Evidence of Southern Origin of the East Asian Specific Haplogroup O3-M122
12.45pm	C. Cam Mui, Sevki Erdogan; University of Hawai'i, USA; GIS and Gene Flow	Mark M Tanaka, Roland R Regoes, Shane Crotty, Rustom Antia; School of Biotechnology and Biomolecular Sciences, University of New South Wales, Australia; Optimal replication of positive-strand RNA viruses within cells: a life-history theory point of view	GSA Christopher N. Newbound, Susan Hisheh, Maharadatunkamsia, Richard A. Howa, Lincoln H. Schmitt; School of Anatomy and Human Biology, University of Western Australia; Phylogeny of the Dog-faced fruit bats of the genus <i>Cynopterus</i>	Cassar Olivier, Capuano Corinne, Meertens Laurent, Chungue Eliane, Martin Paul, Gessain Antoine; Laboratoire de Microbiologie et Environnement de l'Institut Pasteur de Nouvelle-Calédonie Human T-cell Leukemia Virus type 1 (HTLV-1) distribution in Vanuatu Archipelago, Melanesia
1.00pm - 2.00pm	Lunch Provided in NZI Foyers			
Session Chair & Location	Peter Ritchie (Victoria University) Room NZI 4/5	Kathyn Stowell (Massey University) Room NZI 1	Kendell Clements (Auckland University) Room NZI 2	Howard Ross (Auckland University) Room NZI 3
2.00pm	Molecular Ecology	Genes and Gene Expression	Species and Speciation	Rates and Dates
2.15pm	Colm Carraher, Franz Pichler, C Scott Baker; School of Biological Sciences, Auckland University, Auckland, New Zealand; Mitogenomics of coastal and oceanic dolphins in the Southern Hemisphere	GSA Helena J. Bailes, A.E.O. Trezise, W.L. Davies and S.P. Collin; School of Biomedical Sciences, The University of Queensland, Australia; The molecular basis of spectral tuning in visual pigments of the Australian lungfish (<i>Neoceratodus forsteri</i>)	Thomas L. Turner, Matthew W. Hahn, & Sergey V. Nuzhdin; Center for Population Biology, University of California; Genomic Islands of Speciation in <i>Anopheles gambiae</i>	Michael D Hendy; Allan Wilson centre for Molecular Ecology and Evolution Massey University, Palmerston North, New Zealand; Rates and Dates
	Luciano B. Beheregaray, Ning L. Chao, Adalgisa Caccone, Shannon Corrigan, Luciana M. Möller, Joanna Wiszniewski; Department of Biological Sciences, Macquarie University, Australia; Comparative Phylogeography and Patterns of Diversification in Amazonian Flooded Forest Fishes	GSA Vanessa Kellermann, Ary A. Hoffmann and Carla M. Sgrò; Centre for Environmental Stress and Adaptation Research, University of Melbourne, Australia; Breaking evolutionary limits: The role of Hsp90 in adaptive evolution	Atsushi Ogura, Daniel L. Hartl; Department of Organismic and Evolutionary Biology, Harvard University; Genomic diversity and speciation of <i>Drosophila</i> Species	

2.30pm	GSA Line Kolind Bay, Ross H Crozier and M Julian Caley; School of Marine Biology and Aquaculture, James Cook University, Australia; Genetic structure and demographic bottlenecks in a metapopulation of coral reef fishes	GSA Ariadne Tan-Kristanto, David Heckel and Phil Batterham; Bio Molecular Science and Biotechnology Institute, University of Melbourne, Australia; Expression and Sequence Analyses of Lepidopteran Lipase Genes	Belinda Appleton, Les Christidis and Jakob Fahr; Department of Genetics, University of Melbourne, Australia; Cryptic diversity of the African bent-wing bats	David P. Mindell, Joseph W. Brown, and Joshua S. Rest; Dept. of Ecology & Evolutionary Biology and Museum of Zoology, University of Michigan, USA; Dates and changing rates of sequence evolution among avian orders
2.45pm	GSA Amy Gilchrist; School of Biological Sciences, University of Sydney, Australia; What makes a honey bee scout?	GSA John Humphries, Sharon Orford and Jeremy Timmis; School of Molecular and Biomedical Sciences, The University of Adelaide, Australia; Analysis of genes involved in cotton fibre initiation	Jody Hey, Yong-Jin Won, Arjun Sivasundar and Yong Wang; Department of Genetics, Rutgers University, On the Origin of Lake Malawi Cichlid Species : a Population Genetic Analysis of Divergence	Anne C. Stone, Laura A. Salter, George H. Perry Jr. Evan Trudeau and Hsiuman Lin; Department of Anthropology, Arizona State University; Analysis of complete mtDNA sequences in Pan
3.00pm	GSA Melanie Lancaster, Paul Sunnucks and Simon Goldsworthy; La Trobe University, Australia; Temporal changes in species composition and hybridisation in a fur seal population on Macquarie Island	GSA Sarah C. Brown and N. Louise Glass; Department of Plant and Microbiology, University of California, USA; Microarray analysis of vegetative incompatibility in <i>Neurospora crassa</i>	Laura A. Katz, Oona L.O. Snoeyenbos-West, Autumn Griffin, Kate Pirog, Wilhelm Foissner, Barbara Costas, George B. McManus; Department of Marine Sciences, University of Connecticut, USA; Reframing the microbial "Everything is Everywhere" debate: Evidence for high gene flow and diversity in ciliate morphospecies	Emma C. Teeling, Mark S. Springer, Ole Madsen, Paul J. J. Bates, Stephen J. O'Brien, William J. Murphy; Department of Zoology, University College Ireland; A molecular time scale for bats investigates the missing fossil record and illuminates the evolution of echolocation in bats
3.15pm	GSA Chester Sands, Ryan Garrick, Mark Blacket, David Rowell and Paul Sunnucks; Department of Genetics, La Trobe University, Australia; Comparative phylogeography of <i>Onychophora</i> from the Gourrock Range, NSW	Douglas L. Crawford; Rosenstiel School of Marine Sciences, University of Miami, USA; Functional Genomic: microarrays and physiological performance in <i>Fundulus</i>	Hiromi Sawai, Yoko Satta and Naoyuki Takahata; Department of Biosystems Science, The Graduate University for Advanced Studies, Japan; The origin of high polymorphism in domestic chickens	Russell D. Gray, Adrian M. Paterson, Kerri-Anne Edge and Allan J. Baker; Department of Psychology, University of Auckland, New Zealand; Origin and Expansion of Penguins Out of Antarctica
3.30pm	GSA Susana Caballero, Fernando Trujillo, Juliana A. Vianna, Héctor Barrios, Sandra Beltrán, María Gabriela Montiel, Fabrício R. Santos, Miriam Marmontel6, Marcos Cesar de Oliveira -Santos, Marcos Rossi-Santos, and C. Scott Baker; School of Biological Sciences, University of Auckland, New Zealand; Phylogeography of the South American Coastal and River Dolphin <i>Sotalia</i> sp.: Diving into the Amazonian Biodiversity	Issa Medraj, Frank Smith, Jane Hughes and Zhihong Xu; AES Griffith University, Australia; Isolation of phosphate transporters from Hoop Pine (<i>Araucaria cunninghamii</i> Aiton ex D. Don) trees	Mary Morgan-Richards and Steve Trewick; Allan Wilson Centre, Massey University, Palmerston North, New Zealand; Hybrid origins of a parthenogenetic genus?	Jerel Davis; Department of Biological Sciences, Stanford University, USA; Protein Evolution in the Context of <i>Drosophila</i> Development
3.45pm	GSA Amber Beavis and Dave Rowell; Division of Botany & Zoology, Australian National University, Australia; A phylogeographic study of two undescribed species of funnel web spider (Araneae: Mygalomorphae: Hexathelidae) from alternative habitat niches in the Tallaganda region (New South Wales, Australia)	Xue-bin Qi, Su Yang, Hong-kun Zheng, Yin-qiu Wang, Cheng-hong Liao, Ying Liu; Kunming Institute of Zoology, the Chinese Academy of Sciences, China; Detecting Darwinian Positive Selection in Brain-expressed Genes during Human Evolution	GSA Jane Hughes, Giovanna Carini, Joel Huey, Mia Hillyer, Andrew Baker and Mark Ponniah; Centre for Riverine Landscapes, Griffith University, Australia; Estimates of the timing of separation of two major drainages in central Australia inferred from mitochondrial DNA sequence data from six obligate freshwater species	Sheila van Holst Pellekaan, June Roberts-Thomson and Rosalind Harding; School of Biotechnology and Biomolecular Sciences, University of New South Wales, Australia; Mitochondrial haplogroups in aboriginal Australians
4.00pm - 6.00pm	Refreshments Provided During POSTER SESSION In Limelight Room			

Tuesday June 21st

8.30am -
5.30pm
8.30am -
5.30pm

Session
Chair &
Location

Registration and Information

Internet Room

	Jenny Hay (AWC, Massey University) Room NZI 4/5	Tim White (AWC, Massey University) Room NZI 1	Murray Grigor (Auckland University) Room NZI 2	Don Love (Auckland University) Room NZI 3
	Molecular Ecology	Bioinformatics and Phylogenetic Methods	Genome Evolution	Genetics of Diseases and Human Evolution
8.30am	<u>Ak Prashanth</u> ; UC Davis Genome Centre; Socio-Behavioral variation and rapid evolution: DNA duplex destabilization at regulatory DNA microsatellites as an underlying mechanism	<u>Axel Meyer</u> ; Department of Biology, University of Konstanz, Germany; The evolution cichlids and their genomes: from trees to comparative genomics	<u>Jennifer Marshall Graves</u> ; Comparative Genomics Research Group, The Australian National University; Exploring the genomes of weird mammals	<u>Hamish Spencer</u> ; Allan Wilson Centre for Molecular Ecology and Evolution, University of Otago, New Zealand; Polymorphism of Imprinting Status: What does it mean?
9.00am	GSA <u>Gabriela de Tezanos Pinto, K. Russell, A. Hutt, G. Stone, M. Oremus, C. Garrigue, C. Olavarria, D. Steel and C. S. Baker</u> ; <u>The University of Auckland, New Zealand</u> ; Population structure and genetic diversity of coastal bottlenose dolphins (<i>Tursiops truncatus</i>) in New Zealand: a world-wide perspective	<u>Thomas M. Keane, Thomas J. Naughton, James O. McInerney</u> ; <u>Bioinformatics and Pharmacogenomics Laboratory, National University of Ireland</u> ; DPRml-II: A High-throughput Phylogenetics Platform	<u>Kate Johnston, Patrick Dicker, Richard Edwards & Denis Shields</u> ; Bioinformatics Core Group, Department of Clinical Pharmacology, Royal College of Surgeons in Ireland; The Evolution of Specificity	<u>Sara L. Sawyer, Lily I. Wu, Michael Emerman, Harmit S. Malik</u> ; <u>Fred Hutchinson Cancer Research Center, USA</u> ; Positive selection of the primate TRIM5a gene tailors its antiviral efficiency
9.15am	GSA <u>Danielle A. Hannan</u> , Anthony J. R. Hickey, Kendall D. Clements; <u>School of Biological Sciences, University of Auckland</u> ; Hybridisation between New Zealand triplefin fishes (family Tripterygiidae)	<u>Tae-Kun Seo, Hirohisa Kishino and Jeffrey L. Thorne</u> ; <u>Professional Programme for Agricultural Bioinformatics, University of Tokyo, Japan</u> ; Incorporating gene-specific variation when inferring and evaluating optimal evolutionary tree topologies from multilocus sequence data	<u>Matthew W. Hahn</u> ; <u>Center for Population Biology, University of California, Davis, USA</u> ; Estimating the Tempo and Mode of Gene Family Evolution from Comparative Genomic Data	<u>William Klitz, Martin Maiers and Loren Gragert</u> ; <u>National Marrow Donor Program, University of California, USA</u> ; A Global Assessment of Population Level Selection in the MHC: Evidence for Strong and Pervasive Effects
9.30am	GSA <u>Vimoksalehi Lukoschek</u> ; <u>School of Tropical Environment Studies and Geography, James Cook University, Australia</u> ; Phylogeographic structure of the olive seasnake, <i>Aipysurus laevis</i> (Hydrophiidae) indicates recent expansion event from Pleistocene refugia	<u>Thomas R. Buckley, Jim Wilgenbusch, Mark Holder, and David Swofford</u> ; <u>Landcare Research, Auckland, New Zealand</u> ; Measures of Phylogenetic Support on Large Data Sets	<u>Shintaro Iwashita, Sadao Ueno, Hiroshi Yasue, Naoki Osada, and Katsuhiro Fukuta</u> ; <u>Mitsubishi Kagaku Institute of Life Sciences, National Institute of Agrobiological Sciences, Nagoya University, and National Institute of Infectious Diseases, Japan</u> The time frame of creation of the ruminant-specific paralogous bucentaur (p97bcnt) gene: gene duplication and RTE-1 radiation	<u>L.L. Feng, J. Liu, N Bains, K.K. Lau, R.J. Bryson- Richardson, D. Fatkin, M.A. Wouters</u> ; <u>The Victor Chang Cardiac Research Institute, Australia</u> ; A Computational Pipeline for the Rapid Identification of Candidate Disease Genes
9.45am	GSA <u>Simon D. Song, Richard Drew, Jane Hughes</u> ; <u>Australian School of Environmental Studies, Griffith University, Australia</u> ; A population analysis of the wild tobacco fly, <i>Bactrocera cacuminata</i> (Diptera: Tephritidae: Dacinae), using microsatellite markers	<u>Barbara R. Holland, Vincent Moulton</u> ; <u>Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Palmerston North, New Zealand</u> ; Weighted Consensus networks : Combining information from many gene loci	<u>B.G. Fry, S.F.R. Ramjan, J. Norman</u> ; <u>Australian Venom Research Unit, University of Melbourne, Australia</u> ; From genome to 'venome': The molecular origin and evolution of the snake venom proteome.	<u>Rod A Lea</u> ; <u>The Institute of Environmental Science and Research Ltd. Wellington, New Zealand</u> ; Genetic Structure of the Maori Population: Prospects for Disease Gene Mapping

10.00am	<p><u>Angela McGaughan</u>, Ian Hogg, Mark Stevens; Allan Wilson Centre, Massey University, Palmerston North, New Zealand; Phylogeographic patterns for springtails and mites throughout southern Victoria Land, Antarctica: a Pleistocene and Holocene legacy of repeated cycles of glacial refugia and range expansion</p>	<p><u>Matthew Goode</u>, Stéphane Guindon, Allen Rodrigo; Bioinformatics Institute, University of Auckland, New Zealand; Modeling Time-Dependent Changes in Codon Selection Pressure using Serially Sampled Sequence Data</p>	<p><u>Naoko Takezaki</u>, Shin-ichi Nakamura, Akinobu Okabe, and Osamu Matsushita; Information Technology Center, Kagawa University, Japan; Frequent domain organization changes in the evolution of clostridial collagenases</p>	<p>Sistonen Johanna, <u>Fuselli Silvia</u>, Barbujani Guido and Sajantila Antti; Department of Forensic Medicine, University of Helsinki, Finland; Molecular variation and genetic structure of variable drug response in a worldwide population sample</p>
10.15am	<p><u>F.D. Frentiu</u>, S. M. Clegg, M. W. Blows, I. P. F. Owens and T. A. Burke; Ecology and Evolutionary Biology, University of California, USA; Molecular-marker assisted estimates of quantitative inheritance: a test case in a wild bird population</p>	<p><u>Ingo Ebersberger</u>, Petra Galgoczy, Stefan Taudien, Simone Taenzer, Rüdiger Lehmann, Matthias Platzer and Arndt von Haeseler; WE Informatik, Heinrich-Heine-Universität Düsseldorf Germany; Towards a map of our genetic ancestry</p>	<p><u>Katherine Belov</u>, Hannah Siddle, Janine Deakin; Centre for Advanced Technologies in Animal Genetics and Reproduction, University of Sydney, Australia; Unraveling the MHC of marsupials</p>	<p><u>Andrew Laurie</u> and Peter George; Molecular Pathology, Canterbury Health Laboratories, New Zealand; High frequency of disease-causing mutations in the LDL-receptor gene</p>
10.30am - 11.00am	Morning Tea provided in NZI Foyers			
Session Chair & Location	<p>Richard Newcomb (HortResearch) Room NZI 4/5</p>	<p>David Green (Otago University) Room NZI 1</p>	<p>Russell Snell (ViaLactia Biosciences) Room NZI 2</p>	<p>Hamish Spencer (AWC, Otago University) Room NZI 3</p>
	Agricultural Genomics	Bioinformatics and Phylogenetic Methods	Genome Evolution	Genetics of Diseases and Human Evolution
11.00am	<p><u>Theresa Wilson</u>; AgResearch MBU, University of Otago, Dunedin New Zealand; Genomics of Livestock: the New Century</p>	<p><u>Murray R. Grigor</u>; Bioinformatics Institute, University of Auckland, New Zealand; Evolution of lipocalin genes: Accelerated gene evolution at evolutionarily fragile genomic regions</p>	<p><u>Uwe Maier</u>; Philipps-University Marburg, Germany; Primary, secondary and tertiary endosymbiosis</p>	<p><u>Hong-liang Liu</u>, Yin-qiu Wang, Cheng-hong Liao, Yi-qun Kuang, Yong-tang Zheng and Bing Su; Kunming Primate Research Center, Chinese Academy of Sciences, Kunming, Yunnan, China; Adaptive Evolution of Primate TRIM5a Gene Restricting HIV-1 Infection</p>
11.15am		<p><u>Éena Jakó</u>; Hungarian Academy of Sciences and Eötvös Loránd University, Hungary; Relatedness of tRNAs to class I/II aminoacyl-tRNA synthetase families, detected by using a discrete mathematical approach</p>		<p><u>Brett Easton</u>; Mathematical Sciences Institute Australian National University, Australia; Identifying compensatory substitutions for pathogenic mutations via a non-reversible model</p>
11.30am	<p><u>Adam Williams</u>; Genetics Department, University of Melbourne, Australia; Gene manipulation in <i>Helicoverpa armigera</i></p>	<p><u>Martyn Kennedy</u>, Barbara R. Holland Russell D. Gray and Hamish G. Spencer; Allan Wilson Centre for Molecular Ecology and Evolution, University of Otago, New Zealand; Untangling Long Branches: Identifying Conflicting Phylogenetic Signals using Spectral Analysis, Neighbor-Net, and Consensus Networks</p>	<p><u>Andrea Fuehrer</u>, Ingo Paulsen, Arndt von Haeseler; Department of Bioinformatics, University of Dueseldorf, Germany; Maximum-Likelihood Estimation of Gene Duplication- and Deletion-Rates</p>	<p><u>Sean Myles</u>, Kun Tang, Mark Stoneking; Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Germany; Detecting the signature of local positive selection using genome-wide SNP data from 3 human populations</p>
11.45am	<p>GSA <u>Emilie Cameron</u>, Stuart Gilchrist and John Sved; Fruit Fly Research Centre, University of Sydney, Australia; Queensland Fruit Fly in Northwestern Australia: Determining outbreak parameters</p>	<p><u>James O. McInerney</u> and Christopher J. Creevey; Bioinformatics Laboratory, National University of Ireland; Performance of Maximum Likelihood analysis of concatenated data and Supertree methods when horizontal gene transfer is present</p>	<p><u>Frank Grützner</u>, Willem Rens, Enkhjargal Tsend-Ayush, Nisrine El-Mogharbel, Patricia C.M. O'Brien, Russell C. Jones, Malcolm A. Ferguson-Smith and Jennifer A. Marshall Graves; Research School of Biological Sciences, Australian National University; In platypus a ten membered meiotic chain links mammal and bird sex chromosomes</p>	<p>R. Davies, S.-J. Conroy, W.L. Davies, I.C. Potter and <u>Ann E. O. Trezise</u>; School of Biomedical Science, University of Queensland, Australia; Evolution and Regulation of the Cystic Fibrosis Gene</p>

12.00am	GSA <u>Sean MacEachern</u> , John McEwan, Andrew Mather, Alan McCulloch, Paul Sunnucks and Mike Goddard; Department of Genetics, La Trobe University, Australia; Within and between species DNA sequence variation: Testing the neutral theory of evolution with genomic data from <i>Bos taurus</i> and <i>Homo sapiens</i>	<u>Von Bing Yap</u> ; Department of Statistics and Applied Probability, National University of Singapore, Singapore; The Most General Markov Substitution Model on an Unrooted Tree	<u>Huifeng Jiang</u> , Zhenglong Gu, Dongyuan Liu and Wen Wang; Kunming Institute of Zoology, Chinese Academy of Sciences, China; Rapid Evolution in a Pair of Recently Duplicated Segments of Rice	<u>Brian C. Verrelli</u> , Cecil M. Lewis, Sarah A. Tishkoff, and Anne C. Stone; Center for Evolutionary Functional Genomics, The Biodesign Institute and School of Life Sciences, Arizona State University, USA; Contrasting evolutionary histories at human and chimpanzee G6PD and OPN1LW genes
12.15pm	<u>Yael Salzman</u> ; Stanford University, USA; Gene truncation by a transposable element leads to pesticide resistance in <i>D. melanogaster</i>	<u>Tim White</u> , Ravikumar Gaddam, Simon Hills and David Penny; Allan Wilson Centre for Molecular Ecology and Evolution; Finding the Tree-est Explanation for Molecular Sequence Data	<u>Edda Koina</u> , Cristina L. Walcher, Christine M. Distech, Jennifer Marshall Graves; ARC Centre for Kangaroo Genomics, The Australian National University, Australia; Characterization of the Marsupial MEC2 Gene	Eric T. Wang, Greg Kodama, Pierre Baldi, & <u>Robert K. Moyzis</u> ; Department of Biological Chemistry, University of California, USA; Global Landscape of Recent Inferred Darwinian Selection for <i>Homo sapiens</i>
12.30pm	<u>Amanda Chamberlain</u> , Theo Meuwissen, Michael Goddard; Primary Industries Research Victoria, Australia; Estimation of the distribution of QTL effects	<u>William R. Atchley</u> ; Department of Genetics and Center for Computational Biology, North Carolina State University, USA; Solving the protein sequence metric problem	<u>Mike Macpherson</u> , Daniela Witten, Aaron Hirsh and Marcus Feldman; Department of Biological Sciences, Stanford University, USA; The Power of Neutrality Tests To Detect a Partial Selective Sweep from Polymorphism Data	<u>Teruaki Watabe</u> , Hirohisa Kishino, and Yasuhiro Kitazoe; Center of Medical Information Science, Kochi University, Japan; Dissecting evolution of influenza HA + Fab binding ability
12.45pm	Ishminder K. Mann, Joy K. Roy and <u>Om P. Rajora</u> ; Forest Genetics and Biotechnology Group, Dalhousie University, Canada; Faculty of Forestry and Environmental Management, University of New Brunswick, Canada; Comparative Functional Genomic Analysis of Black Spruce (<i>Picea mariana</i>) Expressed Genes	<u>Michael Charleston</u> , Russell Gray and Mahé Ben Hamed; Department of Psychology, University of Auckland; Pareto-Parsimony and Historical Linguistics	<u>William J. Murphy</u> , Denis M. Larkin, Annelie Everts-van der Wind; Department of Veterinary Integrative Biosciences, Texas A&M University, USA; Dynamics of Mammalian Chromosome Evolution Inferred From Multispecies Comparative Maps	GSA <u>Jess Hayward</u> , Allen Rodrigo, John Taylor; School of Biological Sciences, University of Auckland, New Zealand; The Molecular Epidemiology of Feline Immunodeficiency Virus in New Zealand's Domestic Cats
1.00pm - 2.00pm	Lunch provided in NZI Foyers			
Session Chair & Location	Montserrat Aguade (Universitat de Barcelona) Room NZI 4/5	Jo Stanton (Otago University) Room NZI 1	Neil Gemmell (Canterbury University) Room NZI 2	Russell Gray (Auckland University) Room NZI 3
2.00pm	Walter Fitch Symposium	Bioinformatics and Phylogenetic Methods	Genome Evolution	Primate and Human Evolution
	<u>Bejon Kumar Bhowmick</u> , Naoyuki Takahata and Yoko Satta; Department of Biosystems Science, The Graduate University for Advance Studies (Sokendai), Japan; Evolution of human male-specific Y-linked (MSY) genes	<u>David Welch</u> , Geoff Nicholls, Allen Rodrigo, Wiremu Solomon; University of Auckland, New Zealand; Building and fitting models of coupled host-virus genealogies	<u>Masafumi Nozawa</u> , Masahiko Kumagai, Tadashi Aotsuka, and Koichiro Tamura; Department of Biological Sciences, Tokyo Metropolitan University, Japan; Genome-wide explosion of a repeat sequence during the evolution of the <i>Drosophila ananassae</i> subgroup	<u>O. Thalmann</u> , A. Fischer, S. Pääbo and L. Vigilant; Max Planck Institute for Evolutionary Anthropology, Germany; Gorilla population genetics – The nuclear perspective
2.15pm	<u>Tamara Sirey</u> ; University of Auckland/ The Horticulture and Food Research Institute of NZ, Auckland, New Zealand; Effects of differential gene regulation on mate recognition and speciation in a species complex of New Zealand native leafroller moths	Scotland C. Leman, Yuguo Chen, Jason E. Stajich, Mohamed A. F. Noor, and <u>Marcy K. Uyenoyama</u> ; Duke University, USA; A likelihood-based approach to inferring population parameters from multiple summary statistics	<u>Phillip Smith</u> ; Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Albany, New Zealand; Conditional Neutrality as a Potential Cancer Therapy	<u>Susan E. Ptak</u> , David A. Hinds, Kathrin Koehler, Birgit Nickel, Nila Patil, Dennis G. Ballinger, Molly Przeworski, Kelly A. Frazer, Svante Pääbo; Max Planck Institute for Evolutionary Anthropology, Germany; Fine-scale recombination patterns differ between chimpanzees and humans

2.30pm	<u>Slim Sassi</u> ; University of Florida USA; The past as a key to unlock the future: The resurrection of ancestral proteins to elucidate the function of Seminal Ribonuclease	<u>James Cotton</u> and Mark Wilkinson; The Natural History Museum, London, UK; Inferring Trees from Trees : Investigating properties of Supertree Methods	<u>Andrew M. Schurko</u> , KariAn Lee and John M. Logsdon, Jr.; Roy J. Carver Center for Comparative Genomics, University of Iowa, USA; Meiotic genes in bdelloid rotifers provide evidence for sex	<u>Quentin D. Atkinson</u> , Simon J. Greenhill and Russell D. Gray; Department of Psychology, University of Auckland, New Zealand; If Our Genes Could Talk: Reconstructing human population history with genetic and linguistic data
2.45pm	<u>Bryan Kolaczkowski</u> ; University of Oregon, USA; Phylogenetic mixed-models for incorporating evolutionary heterogeneity	<u>Greg Ewing</u> , Geoff Nicholls and Allen Rodrigo; Bioinformatics Institute, University of Auckland, New Zealand; Coalescent-based estimation of population parameters when the number of demes change over time	<u>Sasha Tetu</u> , Neil Wilson, Nick Coleman and Andrew Holmes; School of Molecular and Microbial Biosciences, University of Sydney, Australia; Gene Cassettes as an evolutionary resource for <i>Pseudomonas</i>	<u>Ines Hellmann</u> ; Max-Planck-Institute of Evolutionary Anthropology, Germany; Evolutionary constraint on silent sites within the hominoid lineage
3.00pm	<u>Simon Ho</u> ; Evolutionary Biology Group, Dept of Zoology, University of Oxford; Phylogenetic inference in a relaxed clock framework	To be advised	<u>Jeremy N. Timmis</u> ; Department of Molecular Biosciences, The University of Adelaide, Australia; Cytoplasmic organellar DNA has contributed massively to the genetic complexity of the nucleus during endosymbiotic evolution	<u>David Allen Hughes</u> and Mark Stoneking; Max Plank Institute for Evolutionary Anthropology, Germany; Genomic Investigations of Local Selection in Humans
3.15pm	<u>Kelly Dyer</u> ; Dept of Biology, University of Rochester, USA; Molecular evolution of an intra-genomic arms race: X-chromosome meiotic drive in <i>Drosophila recens</i>	Genetics of Diseases and Human Evolution <u>A.P. Kozlova</u> , L. Krukovskajaa, D. Poleva, I. Duhovlinova, Y. Nosovaa, Y. Galachyantsa, N. Samusika, T. Tyezelovab, A. Baranovaa; The Biomedical Center, St.Petersburg, Russia; Expression of Evolutionary New Sequences in Human Tumors	<u>Fumi Tsujino</u> and Etsuko T. Matsuura; Department of Biosystems Science, the Graduate University for Advanced Studies (Sokendai), Japan; Evolution of BCL-2 homologs in insects	<u>Ana Rebelo Marques</u> , Isabelle Dupanloup, Nicolas Vinckenbosch, Alexandre Reymond, and Henrik Kaessmann; Center for Integrative genomics, University of Lausanne, Switzerland; Emergence of young human genes after primate burst of retroposition
3.30pm	<u>Stefanie De Bodt</u> ; Dept of Plant Systems Biology, University of Ghent, Belgium; Modeling the birth and death of genes in <i>Arabidopsis thaliana</i> to explain plant evolution and complexity	<u>Mineyo Iwase</u> , Yoko Satta and Naoyuki Takahata; Department of Biosystems Science, The Graduate University for Advanced Studies (Sokendai) The evolutionary dissection of the Kallmann syndrome 1 gene	<u>Austen R.D. Ganley</u> and Takehiko Kobayashi; National Institute for Basic Biology, Japan; Identification of gene-independent non-coding elements in the ribosomal RNA repeats by phylogenetic footprinting: Implications for concerted evolution	<u>Sarah A. Tishkoff</u> , M. Katherine Gonder, Floyd A. Reed, Holly Mortensen, Jibril Hirbo, Brenna M. Henn, Uma Ramakrishnan, R. Alec Knight, Peter A. Underhill, Joanna L. Mountain; Department of Biology, University of Maryland, USA; Origins of click-speaking populations in Africa inferred from mtDNA and Y chromosome data
3.45pm	<u>Lesley Collins</u> ; Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Palmerston North, New Zealand; Cutting it in the RNA world: The Spliceosome and Splicing in Ancestral Eukaryotes	<u>Jack da Silva</u> ; School of Molecular and Biomedical Science, The University of Adelaide, Australia; Simulating Realistic Selection at the Molecular Level: A Method and its Implementation with HIV-1	<u>Karen D. Crow-Sanchez</u> ; Department of Ecology and Evolutionary Biology, Yale University; The "fish specific" Hox cluster duplication is coincident with the origin of teleosts	<u>Floyd A. Reed</u> , James L. Weber, and Sarah A. Tishkoff; Department of Biology, University of Maryland, USA; The demographic pattern of human populations in Africa inferred from genome-wide genetic markers
4.00pm	GSA Annual General Meeting		MBE Business Meeting	

7.30pm -
10.30pm

Conference Banquet Lower NZI Level

Wednesday June 22nd

8.30am -
5.30pm
8.30am -
5.30pm

Session
Chair &
Location

Registration and Information

Internet Room

	Clive Evans (Auckland University) Room NZI 4/5	Jonathan Waters (University of Otago) Room NZI 1	Leon Huynen (AWC, Massey University) Room NZI 2	Mark Hauber (Auckland University) Room NZI 3
	Evolution and Development	Species and Speciation	Genome Evolution	Conservation Genetics
8.30am	Peter Dearden; Biochemistry Department, Otago University; Segmentation in the Honeybee; not just another fly!	GSA Gaynor Dolman and Craig Moritz; School of Integrative Biology, University of Queensland, Australia; Demographic history and divergence among a trichotomy of Australian rainforest endemic skinks	Paul Datson and Brian Murray; Horticulture and Food Research Institute of New Zealand; Variable substitution rates of nrDNA in relation to locus number in Nemesia	Richard Frankham; Department of Biological Sciences, Macquarie University; Genetics and Extinction
8.45am		GSA Siu-Fai Lee, Matthew Morgan, Choon-Wei Wee, Philip Batterham and David Heckel; Centre for Environmental Stress and Adaptation Research (CESAR), The University of Melbourne, Australia; Comparative linkage mapping in Lepidoptera	Jerel C. Davis, Onn Brandman, Penka V. Markova, Dmitri A. Petrov; Departments of Biological Sciences, Stanford University, USA; Do Disparate Mechanisms of Duplication Contribute Similar Types of Genes to the Genome?	
9.00am	Yasuhiro Go, Yoko Satta, Kaori Kuno, and Naoyuki Takahata; Department of Biosystems Science, The Graduate University for Advanced Studies (Sokendai), Japan; Reduced repertoires of olfactory receptor genes in water-life mammals, Cetacea	GSA Cara Francis; School of Animal Biology, University of Western Australia, 35 Stirling Hwy, Crawley, Western Australia; Population structure of stygobitic isopods in the Pilbara, Western Australia	GSA Rami Stiglec, Matthias Kohn, Horst Hameister, Jennifer A. Marshall Graves; Research School of Biological Sciences, The Australian National University; Testing the hypothesis that bird sex chromosomes are depleted of cancer genes	GSA Tom Kashiwagi & Jenny Ovenden; School of Integrative Biology, University of Queensland, Australia; Genetic population structure in tropical sharks between Indonesia and northern Australia
9.15am	Steven F. Field, Maria Y. Bulina, Ilya V. Kelmanson, Joseph P. Bielawski and Mikhail V. Matz; Whitney Laboratory for Marine Bioscience, University of Florida, USA; Molecular paleontology suggests adaptive evolution of color diversity in corals	Mark Ponniah and Jane M. Hughes; Australian School of Environmental Studies, Griffith University, Australia; Exploring the biogeographic factors responsible for the diversification of freshwater crayfish in eastern Australian uplands	GSA James Fong, Janine Deakin, Margaret Delbridge and Jennifer A. Marshall Graves; Research School of Biological Sciences, The Australian National University; Finding functional elements with the kangaroo genome	GSA Dominique P. Sigg, Anne W. Goldizen, and Andrew J. Lowe; School of Integrative Biology and The Ecology Centre, University of Queensland, Australia; Strong evidence of fine-scale spatial genetic structure and male-biased dispersal within the only known remnant population of an endangered macropod
9.30am	Philipp Khaitovich, Ines Hellmann, Wolfgang Enard, Katja Nowick, Marcus Leinweber, Henriette Franz, Gunter Weiss, Michael Lachmann and Svante Pääbo; Max Planck Institute for Evolutionary Anthropology, Germany; Parallel Patterns of Evolution in the Genomes and Transcriptomes of Humans and Chimpanzees	Linda Neaves, Kyall Zenger, Ern Snaith and Des Cooper; Department of Biological Sciences, Macquarie University, Australia; Evidence of putative hybrid grey kangaroos in the wild	GSA Anna MacDonald, Stephen Sarre & Nancy FitzSimmons; Applied Ecology Research Group, University of Canberra, Australia; The evolution of microsatellite DNA: Testing models of mutation in an Australian marsupial	GSA Kym Ottewell, Steve Donnellan, David Paton; University of Adelaide; Pollen-mediated gene flow amongst scattered Eucalyptus camaldulensis trees in an agricultural landscape

9.45am	<p><u>Billie J. Swalla</u>; Biology Department, University of Washington, USA; Man is but a worm..... Evolution of the Chordates</p>	<p><u>Hayley Sharp and Dave Rowell</u>; School of Botany and Zoology, Australian National University, Australia; Unprecedented chromosomal diversity and meiotic behaviour in an Australian huntsman spider</p>	<p><u>Andrew Kern</u>; University of California, USA; Recurrent deletion and gene presence/absence polymorphism: telomere dynamics dominate DNA evolution at the tip of 3L in <i>Drosophila melanogaster</i> and <i>D. simulans</i></p>	<p>GSA <u>Sean Byars</u>; Melbourne University; Plant trait variability and gene flow along altitudinal gradients as a measure of stress, adaptation and response of alpine plants to climate change</p>
10.00am	<p><u>Ann E. O. Trezise, M.A. Knight, W.L. Davies, H.J. Bailes, T.J. Lisney, I.C. Potter, D.M. Hunt & S.P. Collin</u>; School of Biomedical Sciences, The University of Queensland, Australia; Molecular Evolution of the Vertebrate Visual System: Colour vision came first!</p>	<p><u>Anthony J. Greenberg, Sarah Moorhead and Chung-I Wu</u>; Department of Ecology and Evolution and Committee on Genetics, The University of Chicago, USA; Molecular population genetics of racial differentiation in <i>D. melanogaster</i></p>	<p><u>Misha Lipatov, Peter F. Arndt, Terence Hwa and Dmitri A Petrov</u>; Department of Biological Sciences, Stanford University, USA; A novel analysis of single-nucleotide substitutions in the human genome</p>	<p>GSA <u>R. C. Garrick, C. J. Sands, D. M. Rowell, P. Greenslade P. Sunnucks</u>; Department of Genetics, La Trobe University, Australia; Phylogeography of a log-dependent endemic Australian springtail (<i>Collembola</i>) – a multigene approach</p>
10.15am	<p><u>Kimberley C. Snowden, Bart J. Janssen, Kerry R. Templeton, Joanne L. Simons, Revel S.M. Drummond, Toshi Foster, Cyril Brendolise</u>; HortResearch, Auckland, New Zealand; Control of axillary branching in <i>Petunia</i></p>	<p><u>Julia J. Day</u>; Department of Biological Sciences, Imperial College London, United Kingdom; Speciation and diversification in the Lake Tanganyika cichlid tribe, Lamprologini</p>	<p><u>Ondrej Podlaha</u>; Ecology and Evolutionary Biology, University of Michigan, USA; In search of functional “pseudogenes”</p>	<p><u>Hilary C. Miller, Katherine Belov, Scott V. Edwards, Charles H. Daugherty</u>; Allan Wilson Centre for Molecular Ecology and Evolution, Victoria University, New Zealand; Evolution of MHC genes in an ancient reptilian order, <i>Sphenodontia</i> (tuatara)</p>
10.30am - 11.00am	Morning Tea Provided in NZI Foyers			
Session Chair & Location	<p>Craig Millar (AWC, Auckland University) Room NZI 4/5</p>	<p>Peter Lockhart (AWC, Massey University) Room NZI 1</p>	<p>Kirsten Donald (AWC, Otago University) Room NZI 2</p>	<p>Shane Lavery (Auckland University) Room NZI 3</p>
	Ancient Biomolecules	Origin and Evolution of Photosynthetic Life	Phylogenetics	Conservation Genetics
11.00am	<p><u>Johannes Krause, Paul H. Dear, Joshua Pollack, Monty Slatkin, Ian Barnes, Adrian Lister, Svante Pääbo and Michael Hofreiter</u>; Max Planck Institute for Evolutionary Anthropology, Germany; Multiplex amplification of the complete mitochondrial genome of <i>Mammuthus primigenius</i> and the evolutionary relationship of mammoths, African and Asian elephants</p>	<p><u>Paul R. Gilson, Vanessa Mollard, Claudio Slamovits, Michael Reith, Patrick Keeling and Geoffrey I. McFadden</u>; The Walter and Eliza Hall Institute of Medical Research, Australia; Complete nucleotide sequence of the chlorarachniophyte nucleomorph: Nature's smallest nucleus.</p>	<p><u>Angie Shuetrim, Simon Robson, Ross Crozier</u>; James Cook University, School of Tropical Biology, Australia; Molecular evolution of transferrin in Polyrhachis (<i>Formicidae</i>) with varying life history attributes</p>	<p><u>Megan J. Osborne and Thomas F. Turner</u>; Department of Biology and Museum of Southwestern Biology, University of New Mexico, USA; Major histocompatibility complex (class II beta) polymorphism in an endangered freshwater cyprinid, the Rio Grande silvery minnow (<i>Hybognathus amarus</i>).</p>
11.15am			<p>GSA <u>L.R. Castro and M. Dowton</u>; Institutes for Biomolecular Sciences, and Conservation Biology, Wollongong University, Australia; A Bayesian Analysis of Apocritan (<i>Insecta: Hymenoptera</i>) Superfamily Relationships - Impact of a Conserved Gene</p>	<p><u>Erika Alacs</u>; Applied Ecology Research Group, University of Canberra, Australia; Wildlife Forensics and Trade Monitoring using Phylogenetic Approaches</p>

11.30am	<u>Christina M. Nielsen-Marsh</u> ; Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, Germany ; The use of proteomics in the analysis of surviving proteins in fossil bone	Christopher E. Lane, Melissa MacKinnon, Hameed Khan, Anna Fong, and <u>John M. Archibald</u> ; Department of Biochemistry and Molecular Biology, Dalhousie University, Canada ; The nucleus and nucleomorph of cryptomonad algae—two extremes of a genomic continuum	<u>M. S. Bulmer</u> and R. H. Crozier; School of Tropical Biology, James Cook University, Australia ; Positive selection in termite relish	<u>Lara Shepherd</u> & David Lambert; Allan Wilson Centre for Molecular Ecology and Evolution, Albany, Massey University ; Ancient DNA reveals contrasting past levels and patterns of genetic diversity in New Zealand kiwi species
11.45am	Carol Hartley, Robyn Russell, Allan Devonshire, David Yeates, John La Salle, <u>Richard Newcomb</u> , John Oakeshott; HortResearch, Auckland, New Zealand ; Reconstructing the evolutionary history of insecticide resistance		<u>Heidi M. Meudt</u> , Peter J. Lockhart, and Phil Garnock-Jones; Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Palmerston North, New Zealand ; Rapid speciation in the New Zealand alpine flora: Phylogeography of the genus <i>Ourisia</i> (Plantaginaceae)	<u>Dianne M. Gleeson</u> , Robyn Howitt, Andrea Byrom; Ecological Genetics Laboratory, Landcare Research, Auckland, New Zealand ; Improving the accuracy of DNA-based methods for estimating population parameters of vertebrate pests
12.00am	<u>Alan Cooper</u> , Mike Bunce, Simon Ho, Beth Shapiro; Earth and Environmental Sciences, University of Adelaide, Australia ; Using ancient DNA to analyse macro and micro-evolutionary processes	<u>Min Chen</u> , Roger Hiller, and Anthony Larkum; School of Biological Sciences, The University of Sydney, Australia ; Evolution of chlorophyll antenna complexes in oxyphotobacteria	<u>Von Bing Yap</u> and Terry Speed; Department of Statistics and Applied Probability, National University of Singapore ; Rooting Phylogenetic Trees with Nonreversible Substitution Models	<u>Olivia Holland</u> , Phil Cowan, Larry Chamley & Dianne Gleeson; Landcare Research Auckland, New Zealand ; Possums on the pill: Immun contraception and MHC variation in New Zealand possums
12.15pm	<u>Frantz Depaulis</u> , L. Orlando, V. Ung and C. Hänni; Fonctionnement et Evolution des Systèmes Ecologiques, France ; Population genetics of temporally interspaced data: an application on cave bear ancient DNA		<u>N. Murphy</u> , V.W. Framenau, S. Donellan, M.S. Harvey, A.D. Austin; Centre for Evolutionary Biology & Biodiversity, The University of Adelaide, Australia ; How many times did the wolves lose their web? A molecular phylogeny of the <i>Lycosidae</i> (Araneae)	<u>Marc Oremus</u> , Helen Kettles, Dorothea Heimeier, Debbie Steel and C. Scott Baker; Population Genetics and Evolution Research Group, University of Auckland, New Zealand ; Death on the Beach: Genetic Investigation into Mass Strandings of Long-finned Pilot Whales
12.30pm	<u>David Lambert</u> , Craig Millar, Lara Shepherd, Leon Hynen; Allan Wilson Centre, Massey University, Albany, New Zealand ; Ancient ecology of the extinct huia	Rates and Dates <u>Jonathan Waters</u> , Chris Burridge, Graham Wallis, Richard Norris, and Dave Crow; Department of Zoology, University of Otago, Dunedin, New Zealand ; Geological Dates and Evolutionary Rates: Using River Vicariance to Pinpoint the Pace of Molecular Change	<u>Dorothy Steane</u> , Susan Foster, René Vaillancourt and Brad Potts; Cooperative Research Centre for Sustainable Production Forestry, and School of Plant Science, University of Tasmania ; Genotypes and phenotypes: reconstructing the phylogeographic evolution of the Tasmanian blue gum, <i>Eucalyptus globulus</i> (Myrtaceae).	<u>Jenny Ovenden</u> , Raewyn Street, David Peel, Samantha Peel, Tony Courtney, Heather Podlich, Kaye Basford and Simon Hoyle; School of Land and Food Sciences, The University of Queensland and CSIRO Marine Science, Australia ; Genetic Estimates of the Effective Population Size: A New Data Source For Fisheries Resource Assessment?
12.45pm		<u>Chris Burridge</u> & <u>Jonathan Waters</u> ; Department of Zoology, University of Otago, Dunedin, New Zealand ; River capture, range expansion, and cladogenesis: a multispecies approach to freshwater phylogeography	<u>Rob Smissen</u> and Ilse Breitwieser; Manaaki Whenua Landcare Research, New Zealand ; Chloroplast and nuclear rDNA reticulation among species of the Asteraceae genera <i>Leucogenes</i> (New Zealand edelweiss) and <i>Raoulia</i>	<u>Anne Fischer</u> , Joshua Pollack and Svante Paabo; Max-Planck Institut for Evolutionary Anthropology, Germany ; Population history of chimpanzees and bonobos
1.00pm - 2.00pm	Lunch Provided in NZI Foyers			
2.00pm	GSA - MJD White Lecture Ary Hoffman; Using DNA markers for environmental monitoring: from <i>Drosophila</i> genes monitoring climate change to chironomid species monitoring aquatic pollutants			
Session Chairs & Location	Introduction from MBE President, John Avise			
3.00pm	MBE - Nei Lecture Jeffrey Powell; Silent mutations speak to the neutral theory of molecular evolution			
6.30pm	Optional Waiheke Dinner			

Thursday June 23rd

8.30am -
1.00pm
8.30am -
1.00pm

Registration and Information

Internet Room

Session
Chair &
Location

	Craig Millar (AWC, Auckland University) Room NZI 4/5	Shelly Ball (Lincoln University) Room NZI 1	Leon Huynen (AWC, Massey University) Room NZI 2	David Lambert (AWC, Massey University) Room NZI 3
	Microbial Evolution	Conservation Genetics	Genome Evolution	RNA World
8.30am	<u>Paul Rainey</u> ; School of Biological Sciences, University of Auckland, New Zealand; Extensive pleiotropy underlies the evolutionary transition from single cells to simple undifferentiated groups	<u>Om P. Rajora</u> ; Faculty of Forestry and Environmental Management, University of New Brunswick, Canada; Genetic Impacts of Forest Harvesting and Renewal Practices and Forest Fires in Canadian Forest Trees: Implications for Conservation and Sustainable Management of Forest Genetic Resources	<u>Martin A. Lysak</u> ; Jodrell Laboratory, Royal Botanic Gardens, UK; Genome evolution in crucifers (Brassicaceae)	<u>John Mattick</u> ; University of Queensland; The hidden layer of noncoding RNA in the evolution and development of complex organisms
8.45am		<u>Meaghan Rourke</u> , Jennifer Lade, Andrea Taylor, Brett Ingram; School of Biological Sciences, Monash University; Conservation and management of genetic diversity in Murray cod (<i>Maccullochella peelii peelii</i>).		
9.00am	<u>GSA Luke G. Barrett</u> , Peter H. Thrall, Jeremy J. Burdon & Marlien van der Merwe; Centre for Plant Biodiversity Research, CSIRO – Plant Industry, Australia; A comparison of pancontinental patterns of virulence in the rust fungus <i>Melampsora lini</i> with genetic variation as assessed by AFLP and SSR markers	<u>Oliver Berry & Dianne M. Gleeson</u> ; Institute of Molecular BioSciences, Massey University, Palmerston North, New Zealand; Distinguishing historical fragmentation from a recent population decline in skinks from New Zealand	<u>Janine E. Deakin</u> , Robert Mason and Jennifer A. Marshall Graves; ARC Centre for Kangaroo Genomics, The Australian National University; The Marsupial Dystrophin Gene	<u>David Penny</u> ; Allan Wilson Center for Molecular Ecology and Evolution, Massey University, Palmerston North, New Zealand; RNA-world and deep eukaryote evolution – the role of theory
9.15am	<u>Vickery L. Arcus</u> , Paul B. Rainey and Susan J. Turner; AgResearch Structural Biology Laboratory, University of Auckland, New Zealand; The PIN-domain toxin- antitoxin array in Mycobacteria	<u>GSA Eleanor O'Brien</u> ; School of Animal Biology, University of Western Australia; Strategies to conserve adaptive genetic variation within restored populations of plant species	<u>M. Pilar Francino</u> ; Lawrence Berkeley National Laboratory, USA; An adaptive radiation model for the origin of new gene functions	
9.30am	<u>T.H. Bowers</u> , N.M. Reid, S.M. Foote and T.R. Stuthridge; Eco-Smart Technologies Scion, Rotorua, New Zealand; 16S rDNA and nifH gene Clone Library Analysis of a Nitrogen Fixing Pulp and Paper Waste Water Treatment System	<u>GSA Melinda Pickup</u> , Andrew Young and Dave Rowell, School of Botany and Zoology, Australian National University; Testing the home-site advantage: Local adaptation and success of transplanted populations of <i>Rutidosia leptorrhynchoidea</i> (Asteraceae)	<u>Nadia D. Singh</u> , Jerel C. Davis and Dmitri A. Petrov; Stanford University, USA; X-linked genes evolve higher codon bias in <i>Drosophila</i> and <i>Caenorhabditis</i>	<u>Christina L. Burch</u> ; Department of Biology, University of North Carolina, USA; Is Eigen's 'Error Threshold' relevant for RNA virus populations?
9.45am	<u>Tal Dagan</u> , Ran Blekhan, and Dan Graur; Department of Zoology, Tel Aviv University, Israel; The "Domino Effect" of Gene Death in Bacterial Genomes	<u>GSA Clare E. Holleley</u> , William B. Sherwin, Richard A. Nichols; School of Biological, Earth and Environmental Sciences, University of New South Wales, Australia; Rapid origin of heterosis in recently isolated laboratory populations of <i>Drosophila melanogaster</i>	<u>Dusan Kordis</u> , Nika Lovsin, and Franc Gubensek; Department of Biochemistry and Molecular Biology, Josef Stefan Institute, Slovenia; Phylogenomic analysis of the L1 retrotransposons in vertebrates	

10.00am	<p>Hsiao Nai-hua, Cammy M. Kao, David W. Weaver and Ralph Kirby; Department of Life Science, National Yang-Ming University, Taiwan; Analysis of Actinomycetales evolution by microarray genotyping</p>	<p>GSA Linda Broadhurst, Andrew Young, Peter Thrall and Brian Murray; CSIRO Plant Industry, Centre for Plant Biodiversity Research, Australia; All that glitters is not Gold Dust Wattle</p>	<p>Simon A. Travers and Mario A. Fares; Molecular Evolution and Bioinformatics Laboratory, National University of Ireland, Ireland; Uncovering new cofactor-interacting regions in Heat-shock proteins (Hsps) using inter-molecular coevolutionary analyses</p>	<p>Anthony Poole & Derek Logan; Department of Molecular Biology & Functional Genomics, Stockholm University, Sweden; Modern mRNA proofreading & repair: clues that the Last Universal Common Ancestor (LUCA) possessed an RNA genome?</p>
10.15am	<p>Molecular Ecology</p> <p>GSA Karen Sommerville, Maurizio Rossetto and Alex Pulkownik; Department of Environmental Sciences, University of Technology Sydney, Australia; Genetic structure and diversity in populations of the vulnerable saltmarsh plant, <i>Wilsonia backhousei</i> – implications for habitat restoration efforts</p>	<p>GSA Dorothea Heimeier, Kirsty Russell, Padraig Duignan, Greg Stone, Alistair Hutt, C. Scott Baker; School of Biological Sciences, University of Auckland, New Zealand; Diversity of expressed MHC class I and class II genes in the New Zealand endemic Hector's dolphin</p>	<p>Dee R. Denver and Michael Lynch; Department of Biology, Indiana University, USA; Evolution of Eukaryotic Mismatch Repair Systems</p>	
10.30am - 11.00am	Morning Tea Provided in NZI Foyers			
Session Chair & Location	<p>Paul Rainey (Auckland University) Room NZI 4/5</p>	<p>Chrissen Gemmill (Waikato University) Room NZI 1</p>	<p>Ian Hogg (Waikato University) Room NZI 2</p>	<p>Lesley Collins (AWC, Massey University) Room NZI 3</p>
	Protein Evolution	Conservation Genetics	DNA Barcoding and Biodiversity	RNA World
11.00am	<p>Jeffrey Mower; Department of Biology and School of Informatics Indiana University, USA; Quick and Accurate Prediction of RNA Editing Sites in Plant Mitochondrial Genes</p>	<p>GSA Steve Smith and Jane Hughes; Centre for Riverine Landscapes, Griffith University, Australian; Genetic basis of the population recovery plan for the western barred bandicoot (<i>Perameles bougainville</i>): low variation reinforces the need for population augmentation and management</p>	<p>Paul Herbert; Department of Integrative Biology & Biodiversity Institute of Ontario, University of Guelph; DNA Barcodes and Biodiversity</p>	<p>Rob Knight; Department of Chemistry and Biochemistry, University of Colorado, USA; How abundant are functional RNAs in random-sequence pools?</p>
11.15am		<p>GSA Stephanie L. Hazlitt, Anne W. Goldizen and Mark D.B. Eldridge; School of Integrative Biology, University of Queensland, Australia; Spatial genetic structure analyses provide the first evidence for matrilineal structuring in a macropod marsupial</p>		
11.30am	<p>Irene Horne and Victoria S. Haritos; Commonwealth Scientific and Industrial Research Organization (CSIRO), Australia; Evolution of a lipase gene cluster in <i>Drosophila</i></p>	<p>GSA Hannah Siddle, Janine Deakin, Katherine Below; Centre for Advanced Technologies in Animal Genetics and Reproduction, University of Sydney, Australia; Characterization of class I MHC genes from the tammar wallaby (<i>Macropus eugenii</i>)</p>	<p>Christopher Lane; Centre for Evolutionary Marine Algal Research, University of New Brunswick, Canada; When to Check Your Barcode: An Example From the Kelp Genus <i>Alaria</i> (Laminariales, Phaeophyceae)</p>	<p>Mike Yarus; Cellular and Developmental Biology, University of Colorado Boulder, USA; Evolution of the translation apparatus</p>

11.45am	<p><u>Takashi Makino</u> and Takashi Gojobori; Center for Information Biology and DNA Data Bank of Japan, National Institute of Genetics, Japan; The evolutionary rate of a protein influenced by features of the interacting partners</p>	<p>GSA <u>David Field</u>, Andrew Young, Rob Whelan, David Ayre; Centre for Plant Biodiversity Research, CSIRO Plant Industry, Australia; Hybrid Happy or Hardly Hybridising?</p>	<p><u>Judith H. Robins</u>, Howard A. Ross and Elizabeth Matisoo-Smith; Department of Anthropology and Allan Wilson Centre for Molecular Ecology and Evolution, The University of Auckland; Identifying <i>Rattus</i> species using small fragments of mitochondrial DNA</p>	
12.00pm	<p>David A. McClellan; Department of Integrative Biology, Brigham Young University, USA; Physicochemical Evolution and Molecular Adaptation of the Cetacean and Artiodactyl Cytochrome <i>b</i> Proteins</p>	<p><u>David Coates</u>, Colin Yates, Carole Elliott, Margaret Byrne and Jane Sampson; Department of Conservation and land management, Australia; Population size and isolation are key factors influencing mating systems, reproductive output and persistence in fragmented populations of the bird pollinated <i>Calothamnus quadrifidus</i> and generalist pollinated <i>Eucalyptus wandoo</i></p>	<p>Simon Jarman Australian Antarctic Division, Department of the Environment and Heritage, Australia; Estimating confidence in biological identifications made by comparing DNA sequences</p>	<p>Roger P. Hellens, Cas Simons, Betty Chung and Chris Brown; HortResearch, Auckland, New Zealand; Exploring the value of introns that reside within non-coding sequence</p>
12.15pm	<p><u>Kazuharu Misawa</u> and Reiko F. Kikuno; Chiba Industry Advancement Center, Japan; A Diagonal Method for Estimating the Rates of Codon Substitutions</p>	<p>HC Hauffe, C Vernesi, E Pecchioli, B Crestanello, F Davoli, D Caramelli, G Bertorelle; Centre for Alpine Ecology, Trento, Italy; High genetic structure and hybridization on a micro-geographic scale in five game species of the Italian Alps</p>	<p><u>Shane Lavery</u>, Howard Ross, Mary Sewell, Allen Rodrigo, C. Scott Baker; School of Biological Sciences, University of Auckland, New Zealand; DNA is not a barcode: molecular taxonomy and the importance of phylogenetic relationships</p>	
12.30pm	<p><u>Tsuyoshi Tanaka</u>, Yoshio Tateno and Takashi Gojobori; Genome Research Department, National Institute of Agrobiological Science (NAIS), Japan; Number of protein-protein interaction but not protein-low-weight molecule interaction affects evolutionary rates of proteins involved in a metabolic network</p>	<p><u>Jennifer M Hay</u> & David Lambert; Allan Wilson Centre, Massey University, Albany, New Zealand; Phylogeography of extinct and extant populations of <i>Sphenodon</i> reptiles in New Zealand</p>	<p><u>Yvonne Parsons</u> and Jon Martin; Centre for Environmental Stress and Adaptation Research & Department of Genetics, La Trobe University, Australia; High-throughput species identification for effective biomonitoring</p>	<p><u>Scott William Roy</u>; Department of Organismic and Evolutionary Biology, Harvard University, USA; Intron loss and gain in <i>Drosophila</i></p>
12.45pm	<p><u>Adriana Maria Montaño</u>, Naoyuki Takahata and Yoko Satta; Department of Biosystems Science, The Graduate University for Advanced Studies, Japan; Origin of peptidoglycan recognition proteins in vertebrates</p>	<p><u>Jawahar G Patil</u>, Rasanthi M Gunasekera, Felicity McEnnulty and Nicholas J Bax; CSIRO Marine Research Laboratories, Tasmania; Development of genetic probes for rapid assessment of the impacts of marine invasive species on native biodiversity – <i>Maoricolpus roseus</i></p>	<p><u>Shelley Ball</u> and Karen Armstrong; National Centre for Advanced Bio-Protection Technologies, Lincoln University, New Zealand; Biotype biodiversity supported and revealed by DNA barcoding</p>	
1.00pm	Conference Closing and Prize Giving - Lower NZI Foyer			

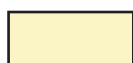
Key to Rooms

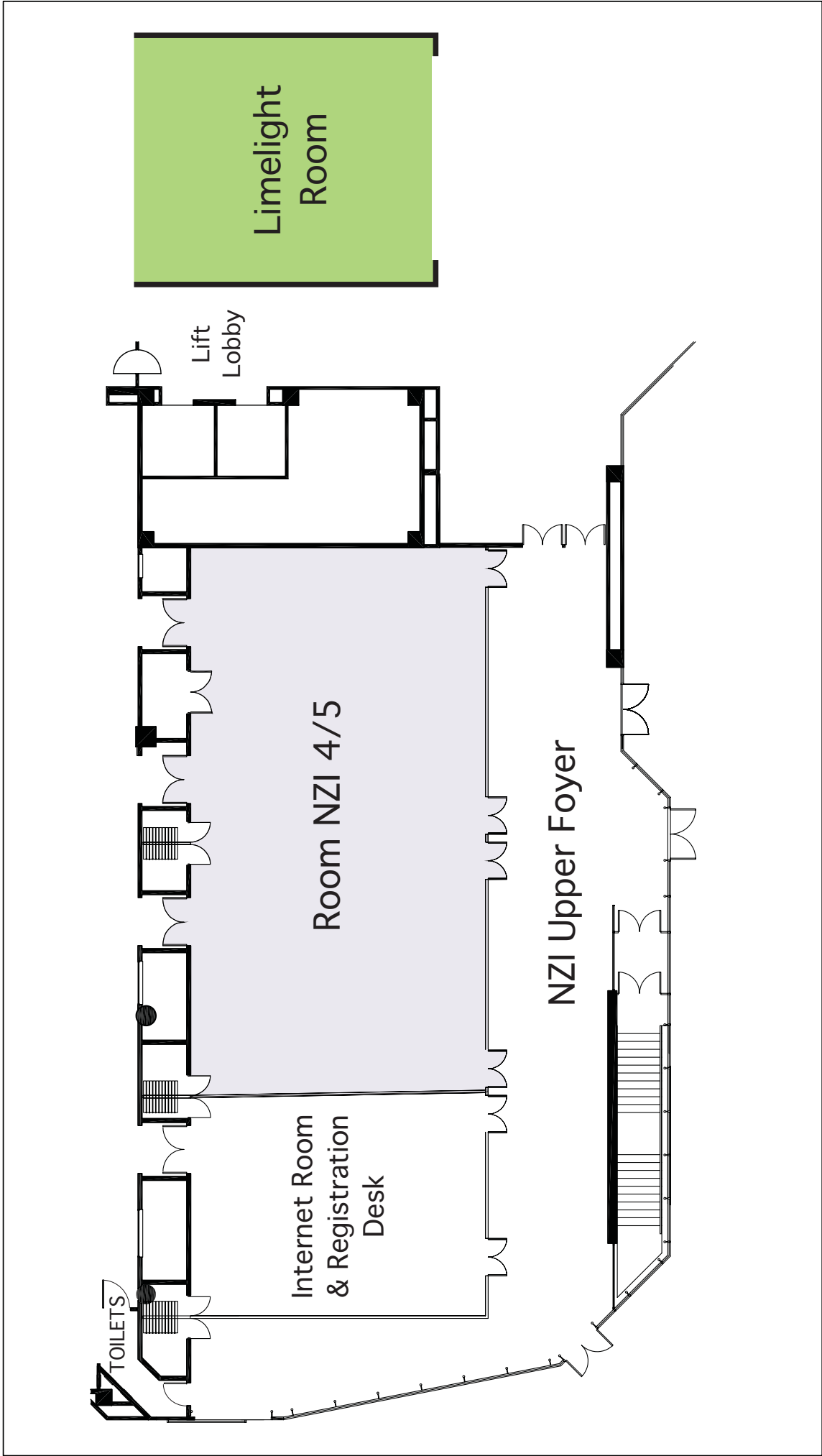
NZI 4/5

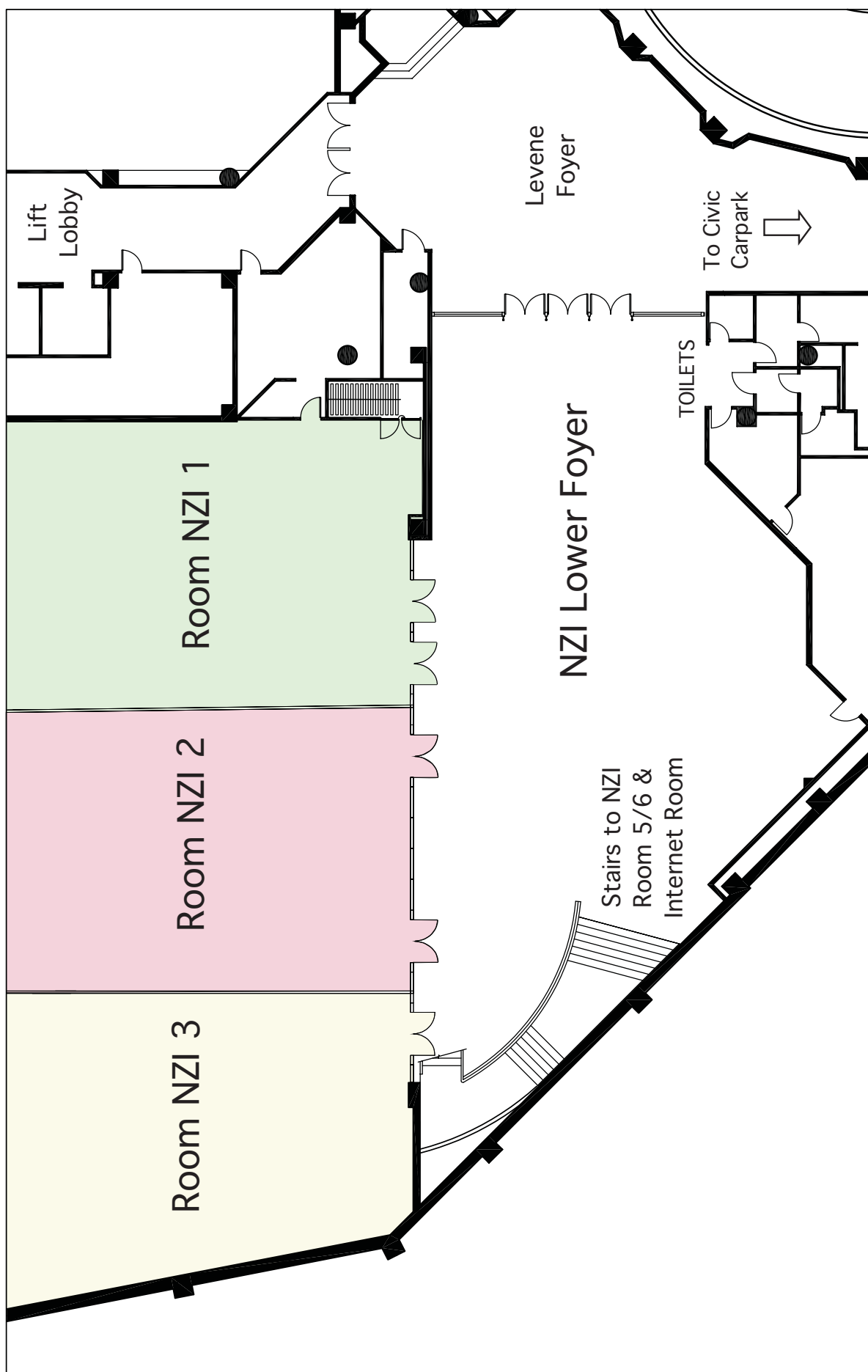
NZI 1

NZI2

NZI 3







Poster Session - Limelight Room

No.	Presenter	Authors	Poster Title
1	Alansari	Aliya Alansari, Aisha Al-Khayat, Andrew Spalton, Khamis Al-Dafry & Shoaib AL-Zadjali.	The molecular genetics of the Arabian leopard: preliminary study.
2	Alsop	A. Alsop, M. Wakefield, K-J. Wei, J. Deakin, E. Koina, K.R. Zenger, C. Wang, D.W. Cooper & J. Graves.	An integrated cytogenetic map of the tammar wallaby.
3	Baldo	Laura Baldo, Nathan Lo & John H. Werren.	The mosaic nature of the Wolbachia surface protein.
4	Beiko	Robert G. Beiko, Timothy J. Harlow & Mark A. Ragan.	Genome partners at the prokaryotic dance.
5	Bilgmann	Kerstin Bilgmann, Luciana M. Möller, Robert G. Harcourt, Catherine M. Kemper, Susan E. Gibbs & Luciano B. Beheregaray.	Comparative population genetic structure of bottlenose and common dolphins in South Australian waters.
6	Blair	David Blair, Kim Sewell, Lester Cannon, Keith Crandall, Tim Littlewood & Susan Lawler.	Mitochondrial DNA diversity in the invasive tropical marine mussel, <i>Perna viridis</i> and differentiation from other <i>Perna</i> species.
7	Brown*	Sarah C. Brown & N. Louise Glass - GSA.	Microarray analysis of vegetative incompatibility in <i>Neurospora crassa</i> .
8	Cai	James Jing Cai, David K. Smith, Xuhua Xia & Kwok-Yung Yuen.	MBEToolbox: a matlab toolbox for sequence data analysis in molecular biology and evolution.
9	Caramelli	David Caramelli, Albano Beja Pereira, Martina Lari, Cristiano Vernesi, Guido Barbujani, Carles Lalueza Fox, Gordon Luikart & Giorgio Bertorelle.	Italian aurochs in the Palaeolithic had cattle-like mtDNA.
10	Carlsson	Britt-Louise Carlsson, Alan N Wilton & David Jenkins.	The imminent extinction of the Australian dingo.
11	Chan	Zeke S. H. Chan, Lesley Collins and N. Kasabov	An efficient Greedy EM Algorithm for Global Gene Trajectory Clustering.
12	Chen	Zhenzhong Chen, Ayscha Hill-Williams, John A. McKenzie & Philip Batterham.	Overexpression of cytochrome P450 genes and insecticide resistance in the sheep blowfly, <i>Lucilia cuprina</i> .
13	Chen	Min Chen, Roger Hiller & Anthony Larkum.	Evolution of chlorophyll antenna complexes in oxyphotobacteria.
14	Chen	Sylvia (Xiaowei) Chen.	Evolution of eukaryotic non-coding RNA: insights from the RNA library of early eukaryote <i>Giardia intestinalis</i> .

No.	Presenter	Authors	Poster Title
15	Collinge	Derek Collinge, Karl Gordon, Carolyn Behm & Steve Whyard.	Delivering a silent punch: stable transformation and RNAi in <i>Helicoverpa armigera</i> .
16	Cook	Catherine A. Cook, Xin An & Kathryn A. Raphael.	The role of cryptochrome in mating time difference in tephritid fruit flies.
17	Corrigan	Shannon Corrigan, Tonia S. Schwartz, Charlie Huveneers & Luciano B. Beheregaray.	Conservation genetics of Wobbeong Sharks (<i>Orectolobus</i>) in Australian waters.
18	Coucheron	Dag H. Coucheron, Kari Haugli, & Steinar D. Johansen.	Phylogeny of the <i>Physaridae</i> slime molds (and other <i>Myxomycota</i>) based on a combined data-set of nuclear small subunit and large subunit ribosomal DNA sequences.
19	Damiano	John Damiano, Trent Perry & Philip Batterham.	Resistance: to be or not to be-screening the genome for mutants.
20	de Salas	M.F. de Salas, A. Koutoulis, L.L. Rhodes, & G.M. Hallegraeff.	Genetic diversity in unarmoured dinoflagellates: design of molecular probes.
21	Docking	T. Roderick Docking & Daniel J. Schoen	Retrotransposon sequence variation in four asexual plant species.
22	Druzhinina	Irina S. Druzhinina, Alexei G. Kopchinski, Monika Komon, & Christian P. Kubicek.	An oligonucleotide barcode for species identification in <i>Trichoderma</i> and <i>Hypocrea</i> .
23	Duffy*	Angela Duffy & Peter B. Mather - GSA	Isolation by distance at small spatial scales in lacustrine populations of freshwater turtles.
24	Duffy*	Angela Duffy, Satya Nandlal & Peter B. Mather - GSA	Phylogeography of a pan tropical freshwater prawn with extensive marine larval dispersal potential.
25	Ezawa	Kiyoshi Ezawa, Satoshi Oota, & Naruya Saitou.	An extensive search for gene conversion events in mouse and rat genomes.
26	Fang	Shu Fang, Yen-Po Lin, Yu-Po Chen & Shun-Chern Tsaur.	Evolution of Acp26Aa, the male accessory gland protein gene, in <i>Drosophila mauritiana</i> .
27	Feng	L.L. Feng, J. Liu, N. Bains, K.K. Lau, R.J. Bryson-Richardson, D. Fatkin & M.A. Wouters.	A computational pipeline for the rapid identification of candidate disease genes.
28	Froula	Jeff Froula, Araceli M. Huerta & Pilar Francino.	Testing for over/under-representation of sigma 70 promoter-like signals in different genomic regions.
29	Gaddam	Ravikumar Gaddam, Tim White, Simon Hills, Barbara Holland & David Penny.	Deep divergence in green plant phylogeny.
30	Garrick	R. C. Garrick, C. J. Sands, D. M. Rowell, P. Greenslade & P. Sunnucks - GSA	High local endemism of a saproxylic 'giant' springtail (Collembola) from south-east Australia

No.	Presenter	Authors	Poster Title
31	Gibb	Gillian C. Gibb, Olga Kardailsky, Edward Braun & David Penny	Avian evolution using complete mitochondrial genome sequences.
32	Gleave	Andrew Gleave, Charles Dwamena, Bhawana Nain, Ross Crowhurst, Annette Richardson, Daya Dayatilake, Philip Martin, Michael Clearwater, Bart Janssen, Robert Schaffer, Kate Thodey, Rebecca Bishop & Robin MacDiarmid.	Identification of small RNAs in fruit crops.
33	Goldberg	Julia Goldberg & Steve Trewick	Rates of speciation – patterns of diversification among New Zealand insects.
34	Goode	Matthew Goode, Howard Ross, Helen Sherman, C. Scott Baker, Shane Lavery & Allen Rodrigo.	DNA - Surveillance – creating curated databases for molecular taxonomy using phylogenetic identification.
35	Grady	Deborah L. Grady, Maria M. Corrada, Valentina Ciobanu, Claudia Kawas, James Swanson & Robert K. Moyzis.	A recently selected human dopamine receptor variant (DRD4 7R) is at higher frequency in individuals over 90 years old.
36	Grams	Raymond W. Grams & David A. McClellan.	Adaptation of physicochemical properties of competing proteins TNF- α and LTA.
37	Guzik	Michelle T. Guzik, Steven J.B. Cooper, William F. Humphreys, Chris H.S. Watts & Andrew D. Austin.	Identifying mechanisms of speciation in subterranean cave organisms.
38	Hara	Yuichiro Hara, Kanako O. Koyanagi & Hidemi Watanabe.	Significant contribution of gene conversion to the evolution of tandemly duplicated genes.
39	Haynes	Gwilym D. Haynes, Peter Grewe, Dean Gilligan & Frank W. Nicholas	Population genetics of common carp in the Murray-Darling Basin.
40	Hedges	S. Blair Hedges, Joel Dudley, Davide Pisani, Vinod Swarna, Graziela Valente & Sudhir Kumar.	TimeTree: a database of species divergence times.
41	Horn	Thorsten Horn, Christopher Robert Bridges & Neil Gemmell.	Telomere length change in vertebrates - a new aging-tool for field studies.
42	Huerta	Araceli M. Huerta & Pilar Francino	Comparing the fine structure of promoter regions across bacterial species.
43	Janssen	Bart Janssen, Robert Schaffer, Kate Thodey, Shavindra Bajaj, Lena Balakrishnan, Ross Crowhurst, Judith Bowen, Susan Ledger, Yar-Khing Yauk, Shayna Ward, Steve McCartney & Jens Wunsche.	Microarray analysis of fruit development in apple.
44	Johansen	Steinar D. Johansen, Ragna Breines, Anita Ursvik & Dag H. Coucheron.	Mitochondrial genomics of <i>Gadidae</i> fishes: molecular phylogeny and evolution based on complete mtDNA sequences.

No.	Presenter	Authors	Poster Title
45	Johnston	Kate Johnston, Patrick Dicker, Richard Edwards & Denis Shields.	The evolution of specificity.
46	Jones*	Julia C. Jones, Benjamin P. Oldroyd & Ryszard Maleszka - GSA .	The genetics of thermoregulation in honey bee colonies.
47	Kopchinskiy	Alexey Kopchinskiy, Monika Komo, Christian P. Kubicek & Irina S. Druzhinina.	TrichoBLAST: a multiloci database of phylogenetic markers for <i>Trichoderma</i> and <i>Hypocrea</i> powered by sequence diagnosis and similarity search tools.
48	Kumar	S. Kumar, K. Tamura & M. Nei.	MEGA3: an integrated software for molecular evolutionary genetics analysis and sequence alignment.
49	Kumar	S. Kumar.	Launch of the FlyExpress resource: the <i>Drosophila</i> in situ gene expression pattern database and search tool.
50	Kuraku	Shigehiro Kuraku, Junko Ishijima, Shigeru Kuratani & Yoichi Matsuda.	Chromosome size-dependent GC-compartmentalization in sauropsids estimated by cDNA sequencing and gene mapping in Chinese soft-shelled turtle <i>Pelodiscus sinensis</i>
51	Lasser	Elyse Lasser, Frances Terry, Jessica Grant and Laura A. Katz.	Diversity of amoebae among eukaryotes: insights from multigene analyses.
52	Laukien	Frank Laukien.	Postulate of an externally-driven irreversible transferable adaptation (EDITA) mechanism as a second generator of evolutionary change.
53	Lawrence	Hayley Lawrence, Graeme Taylor, Craig Millar & David Lambert	Conservation genetics of New Zealand's rarest seabird; Whakapapa o te Taiko (<i>Pterodroma magentae</i>)
54	Lea	Rod A. Lea.	Tracking the evolutionary history of the warrior gene across the South Pacific.
55	Lee	Clare Lee.	The three-dimensional structure of anthranilate phosphoribosyl transferase, TrpD, from <i>Mycobacterium tuberculosis</i> .
56	Lightfoot*	Damien Lightfoot, Sharon Orford & Jeremy Timmis - GSA .	Development of cotton boll wall-specific promoters.
57	Maxwell	Peter Maxwell, Matthew Wakefield, Brett Easton & Gavin Huttley.	PyEvolve: a toolkit for statistical molecular evolutionary analysis of genomes
58	Meneses	Isabel Meneses, Rodrigo Vidal & Macarena Smith.	Phylogeography of the spongiates genus (<i>Corallinales</i> , <i>Rhodophyta</i>): how many populations and how many species exist in the coasts of Chile?
59	Möller	Luciana Möller, Jennifer Kingston, Shannon Corrigan, Joe Waas, Mark Hindell, Luciano Beheregaray & Robert Harcourt.	Are there genetic benefits from mate choice in marine mammals?

No.	Presenter	Authors	Poster Title
60	Muirhead*	K. A. Muirhead, A. D. Austin, M. N. Sallam & S. C. Donnellan - GSA .	Genetic variation in the <i>Cotesia flavipes</i> complex of parasitic wasps: towards the effective biological control of stemborer pests in Australia.
61	Muller	Chris Muller, Lesley Hughes & Luciano B. Beheregaray.	The phylogeny of the butterfly genus <i>Delias</i> (Lepidoptera): a biogeographical perspective.
62	Murray	Brent W. Murray, John Wang, John Stevens, Ross Daley, Jim Reist, Aaron Fish & Bill Bechtol.	Mitochondrial cytochrome <i>b</i> variation in sleeper sharks (<i>Somniosus</i>), subgenus <i>Somniosus</i> .
63	Nielsen	Rasmus Nielsen & Mikhail Matz.	Statistical approaches for DNA barcoding.
64	Noda-Ogura	Akiko Noda-Ogura, Kazuho Ikeo, Etsuko Matsuura & Takashi Gojobori.	Comparative genome analyses of nervous system-specific genes.
65	Nowick	Katja Nowick, Joshua Pollack, Florian Heissig, Hilliary Creely, Philipp Khaitovich, Birgit Nickel & Svante Pääbo.	Identification of genes regulated by FOXP2.
66	Ottewell*	Kym Ottewell, David Ayre & Rob Whelan - GSA .	The genetic composition of a canopy stored seed bank: variation across years and with plant reproductive effort.
67	Oxley*	Peter Oxley, Ben Oldroyd & Jürgen Paar - GSA .	The genetics of hygienic behaviour of honey bees (<i>Apis mellifera</i>).
68	Pingault	N.M. Pingault , D. Lehmann, J. Bowman & T.V. Riley.	Comparison of molecular typing methods for <i>Moraxella catarrhalis</i> .
69	Pocwierz-Kotus	A. Pocwierz-Kotus, A. Burzynski, W. Makalowski R. Wenne.	Occurrence of Tc1 transposons in commercial fish species from the Baltic Sea.
70	Pratt	Renae Pratt, Mary Morgan-Richards & Steve Trewick.	Weta worldwide - sytematics and biogeography of the Anostomatids.
71	Qin	Jinyi Qin, Chee Yang Lee, John Wetherall & David Groth.	Identification of clones spanning the sheep MHC gene region.
72	Raterman	Raterman Denise & M. S. Springer.	A comparative genomics approach to elucidating acrosin's role in mammalian fertilization.
73	Roach	Jennifer L. Roach & Douglas L. Crawford.	Phylogenomics: isolation and evolutionary analysis of random EST sequences.
74	Robbens	Steven Robbens, Stephane Rombauts, Pierre Rouzé, Jan Wuyts, Sven Degroeve, Hervé Moreau & Yves Van de Peer.	Genome analysis of the world's smallest free-living eukaryote <i>Ostrecococcus tauri</i> unveils unique genome heterogeneity.
75	Rogers	Stephanie A. Rogers, Sudhir Kumar & Jeffrey W. Touchman.	Primate lineage sequence conservation in promoter regions.

No.	Presenter	Authors	Poster Title
76	Roy	Scott William Roy.	Low level of polymorphism in the untranslated regions of three highly polymorphic genes of the human malaria parasite, <i>Plasmodium falciparum</i> .
77	Roy	Scott William Roy.	Parallel gain can not explain the level of intron conservation between eukaryotic orthologs.
78	Salaün	Laurence Salaün, Fabrice Mérien, Guy Baranton & Mathieu Picardeau.	Genotyping of pathogenic <i>Leptospira</i> based on tandem repeat polymorphism.
79	Santure	Anna Santure.	Influence of mum and dad: imprinting and maternal effects.
80	Schliep	Klaus Schliep, Barbara Holland, Mike Hendy & David Penny.	Some connects between Hadamard conjugation and regression models.
81	Shaw	Matthew Shaw, Robert Cruickshank & Adrian Paterson.	Multiple episodes of reversibility of parasitism in dermanyssoid mites (<i>Acari: Mesostigmata</i>)?
82	Simons	Jo Simons, Kerry Templeton, Kim Plummer, Christine Beveridge & Kimberley Snowden.	Characterisation of the genetic and hormonal controls of plant branching.
83	Steeves	Tammy Steeves, Richard Maloney, Glenda Singleton, Maureen Waite & Neil Gemmell.	Conservation genetics of a critically endangered New Zealand endemic, the black stilt (<i>Himantopus novaezelandiae</i>).
84	Stiglec	Rami Stiglec, Shargal Tsend-Ayush, Frank Grützner, Tariq Ezaz, Anne Gaeth, Steve Sarre, Arthur George & Jennifer Marshall Graves.	DMRT1 in the tiger snake.
85	Tay	Gajanan Behere, Wee Tek Tay, Sandhya Kranthi, Phil Batterham & Derek Russell.	Mitochondrial DNA analyses of <i>Helicoverpa armigera</i> populations from Australia, India and China.
86	Tay	W. T. Tay, E. M. O'Mahony, J. Klee, S. Walker & R. J. Paxton.	Single spore DNA analyses indicate that the multiple copies of rRNA genes in <i>Nosema bombi</i> (<i>Microsporidia: Nosematidae</i>) have different sequences.
87	Travers	Simon A. A. Travers & Mario A. Fares.	Uncovering new cofactor-interacting regions in heat-shock proteins (Hsps) using inter-molecular coevolutionary analyses.
88	VanWye	Jeffrey D. VanWye, M. Danielle McDonald, Patrick J. Walsh & Douglas L. Crawford.	Biological variation in gene expression.
89	Vargas	Iris M. Vargas Jentzsch, Angelika Merkel, Emmanuel Buschiazzi & Neil J. Gemmell	Do simple sequences evolve simply?
90	Vaughan	Meredith Vaughan & Douglas Crawford	A nuclear gene phylogeny for fundulus.

No.	Presenter	Authors	Poster Title
91	Whittall	Justen B. Whittall, Claudia Voelckel & Scott Hodges.	The molecular basis of convergent evolution: loss of floral anthocyanins in <i>Aquilegia</i> .
92	Wikmark	Odd-Gunnar Wikmark, Peik Haugen, Anna Vader, Dag H. Coucheron, Eva Sjøttem & Steinar Johansen.	The recent transfer of a homing endonuclease gene between distantly related group I introns.
93	Wilson	Neil Wilson, Sasha Tetu, Nick Coleman, Michael Gillings & Andrew Holmes.	The significance of integrons outside the clinical environment.
94	Winder	Louise Winder, Frances Wall, Craig Phillips, Stuart Young & Stephen Goldson.	Nuclear and mitochondrial DNA sequence and ISSR variation in the Argentine Stem Weevil (<i>Listronotus bonariensis</i>) from South America and New Zealand.
95	Wolff	Jonci Wolff.	When good molecules go bad: how common are paternal inheritance of mitochondria and mitochondrial recombination?
96	Woods*	Ryan Woods, Mark Ponniah & Jane M Hughes - GSA .	Fine scale population structure in the widely distributed freshwater fish: Australian smelt (<i>Retropinna semoni</i>).
97	Yockey*	Heather Yockey, Graham Thompson & Ben Oldroyd - GSA	Control of worker sterility in honey bees (<i>Apis mellifera</i>): differential gene expression in queens and workers.
98	Zamora	Alejandro Zamora, Qi Sun, Charlotte Acharya, Martha Hamblin, Rebecca Nelson, Sharon Mitchell & Stephen Kresovich.	A comparative evolutionary genomic approach identifies rapidly evolving genes in the genome of <i>Sorghum bicolor</i> (L.) Moench, involved in biotic and abiotic stresses.
99	Zenger	K.R. Zenger, C. Wang, K-J. Wei, M. Wakefield, J. Deakin, E. Koina, A. Alsop, D.W. Cooper & J. Graves.	An integrated genetic linkage map of the tammar wallaby.
100	Zufall	Rebecca A. Zufall, Casey McGrath & Laura Katz.	Exploring genome landscapes: evolution of proteins and processing in extensively fragmenting ciliates.

* indicates a GSA student poster

Acknowledgement of Sponsorship & Support

Company Name. Allan Wilson Centre for Molecular Ecology and Evolution.

Type of Sponsorship. Conference pads and pens.

Representative at MBE/GSA05. David Lambert, Principal Investigator, David Penny
Director - Research, Mike Hend, Director - Executive.

Contact Details. Massey University, Private Bag 11-222, Palmerston North, New Zealand,
Phone: 06 350 5448, Fax: 06 350 5626, Email: d.penny@massey.ac.nz, Website: <http://awcmee.massey.ac.nz>

Description of the Organisation. The overarching science goal of our Centre is to give an unprecedented understanding of New Zealand's biota, its past and its future. The Centre has been established as part of the government's Centres of Research Excellence initiative and brings together senior researchers from five universities. The Centre comprises world-class evolutionary biologists, mathematicians, and ecologists working together to unlock secrets of our plants, animals, and microbes. How did they get here? How fast does evolution happen? What underlying genetic and ecological processes explain the evolution of our biota? How might these processes affect us in the future?

Company Name. Alphatech Systems Ltd

Type of Sponsorship. Trade Booth 13

Representative at MBE/GSA05. Trish Fenton, Product Manager; Sylvia Victor, Technical sales Rep

Contact Details. 630A Great South Road, Greenlane 1006, P O Box 62613, Ellerslie South, Auckland, Phone: 09 580 1959, Fax: 09 580 2044, Email: Trish.Sales@alphatech

Description of the Organisation. Alphatech is the exclusive distributor in New Zealand for a range of market leading brands of laboratory equipment and consumables, providing for a range of solutions across the life sciences, diagnostics, physics and medical physics fields.

Company Name. Applied Biosystems

Type of Sponsorship. Trade Booth 7

Representative at MBE/GSA05. Jacqui Kent, Sales Specialist; Nicole Kirkham, Sales Specialist.

Contact Details. 52 Rocco Drive, Scoresby Victoria 3179, Australia, Freecall 1 800 033 747 (Australia), 0 800 446 416 (New Zealand), Email: Jacqueline.kent@appliedbiosystems.com, Nicole.j.kirkham@appliedbiosystems.com, Website: www.appliedbiosystems.com.au

Description of the Organisation. Applied Biosystems provides new and innovative systems for the analysis of DNA, RNA, small molecules and proteins. Our objective is to provide fully integrated instrument-based systems, reagents, consumables, software and contract services to the life science industry and research community. Today we offer the most comprehensive line of products used in basic research, commercial research (pharmaceutical and biotechnology) and standardized testing, including forensic human identification, paternity testing and food testing. Applied Biosystems has demonstrated its position as a technology and industry leader in Sequencing, PCR, Real-Time PCR, Reagents and Consumables.

Company Name. Bioinformatics Institute

Type of Sponsorship. Internet Room

Representative at MBE/GSA05. Prof. Allen Rodrigo, Director

Contact Details. School of Biological Sciences, University of Auckland, Private Bag 92019, Auckland, New Zealand, Email: a.rodrigo@auckland.ac.nz, URL: www.bioinformatics.org.nz, Website <http://www.bioinformatics.org.nz/>

Description of the Organisation. New Zealand's Bioinformatics Institute was established with funding from AgResearch Ltd, the country's largest Crown Research Institute, and the University of Auckland, New Zealand's top-ranked and largest university. With ten full-time researchers and twenty-five affiliate investigators, the Bioinformatics Institute is a centre of research excellence in bioinformatics, with specialisations in evolutionary bioinformatics, genomics, microarray analysis, and population and conservation genetics. The Institute hosts several distinguished visitors a year, runs a series of one-day workshops in bioinformatics, and scientific workshops for postdoctoral fellows and graduate students. In addition, the Institute also provides facilities for graduate students at the University of Auckland.

Company Name. Biolab Ltd

Type of Sponsorship. Trade Booths 5 & 6

Representative at MBE/GSA05. Andy Palairat, BioScience, Sales Specialist, Andrew Scott, Sales Specialist; Dennis Wrobel, Sales/Marketing Manager – BioScience

Contact Details. 244 Bush Road, Albany, Auckland, Private Bag 102 922, North Shore Mail Centre, Auckland, Phone: 0800 933 966, 09 980 6700, Fax: 09 980 6788, Email: taral@nzl.biolabgroup.com, Website: www.biolabgroup.com

Description of the Organisation. Our bioscience team is committed to providing integrated solutions for the biosciences sector. If you are working in genomics, proteomics, cell biology, immunology and/or molecular biology, we have a broad range of products and solutions to meet your needs.

Company Name. Bio-Strategy – Kendro

Type of Sponsorship. Trade Booth 12

Representative at MBE/GSA05. Charles Lockie, General Manager

Contact Details. 22 William Pickering Drive, Albany, Auckland, Phone: 09 525 0333, Fax: 09 525 0337, Email: charles@kendro.co.nz, Website: www.kendro.co.nz

Description of the Organisation. Suppliers and service agents of recognised brands of scientific instrumentation including Heraeus, Sorvall, Revco, Biotec. Bio-Strategy/Kendro provides 'turnkey' solutions for practically all laboratory requirements.

Company Name. CSIRO Publishing

Type of Sponsorship. Satchel insert

Representative at MBE/GSA05. Melinda Chandler, Marketing Coordinator

Contact Details. P O Box 1139, Collingwood, Victoria 3006, Australia, Phone: +61 3 9662 7601, Fax: +61 3 9662 7600, Email: elinda.chandler.csiro.au

Company Name. GE Healthcare

Type of Sponsorship. Trade Booth 11

Representative at MBE/GSA05. Mani Narayanaswamy, National Sales Manager; Tracy Ross, Account Manager

Contact Details. P O Box 17122, Greenlane, New Zealand, Phone: 09 523 5890, Fax: 09 522 7342, Email: sales.nz@ge.com, Website: www.amershambiosciences.com

Description of the Organisation. GE Healthcare's portfolio now includes Amersham Biosciences' solutions for life science research and protein purification and production.

Company Name. Geneworks (NZ) Ltd

Type of Sponsorship. Trade Booth 10

Representative at MBE/GSA05. Helen Robinson, Territory Manager (NZ); Arran Greenhalgh, Territory Manager (Australia)

Contact Details. P O Box 107 012, Airport Oaks, Auckland, Phone: 09 275 6465, Email: helenr@geneworks.co.nz, Website: www.geneworks.co.nz; www.geneworks.com.au

Description of the Organisation. Geneworks is a South Australian Company specialising in the manufacture and distribution of quality products for molecular biology and genomics research. Our core business is the synthesis and supply of custom oligonucleotides. We also offer a comprehensive and complementary range of leading-edge products from around the world.

Company Name. HortResearch

Type of Sponsorship. Invited speakers, travel & advertising

Representative at MBE/GSA05. Richard Newcomb, Science Leader; Kim Snowden, Science Leader; Roger Hellen, Science Leader; Robin MacDairmid, Scientist

Contact Details. Private Bag 92169, Auckland, 120 Mt Albert Road, Mt Albert, Auckland, Phone (09) 8154200, Fax (09) 8154201, Email: rnewcomb@hortresearch.co.nz, Website: www.hortresearch.co.nz

Description of the Organisation. HortResearch is a world-class fruit science company. We use our unique resources in fruit, plants and environmentally sustainable production systems to produce innovative fruit and food products. We assist industry by developing innovative solutions and future plans.

Company Name. Libertas Academica Ltd

Type of Sponsorship. Advertising inside front cover.

Contact Details. 2 Rimu Rise, Bushlands Park, P O Box 300-008, Albany, Auckland, Phone: 09 415 7704, Fax: 09 448 5032, Email: ebo@libertasacademica.com, Website: www.libertasacademica.com

Description of the Organisation. Libertas Academica was established in 2004 to promote and expand Open Access to scientific, technical and medical information. Our mission is to implement Open Access journals whilst preserving the very high editorial standard that have characterized conventional subscription-based publishing in the past.

Company Name. Logical Freight Solutions NZ Ltd

Type of Sponsorship. Trade Booth 8

Representative at MBE/GSA05. Philip Robinson, Managing Director; Neal Robinson, General Manager

Contact Details. PO Box 107012, Airport Oaks, Auckland, 2C Rennie Drive, Airport Oaks, Auckland, Phone: 09 275 9995, Fax: 09 275 9929, Email: philr@lfsnz.co.nz

Description of the Organisation. Logical Freight Solutions NZ Ltd specialise in national and worldwide freight logistics for the Life Science industry, including temperature sensitive shipments and dangerous goods. Our warehouse and distribution section offers a range of temperature controlled environments from ambient to -80C. With branches world wide Logical Freight Solutions can provide freight logistics to or from anywhere in the world, at any temperature.

Company Name. NZ Scientific Ltd

Type of Sponsorship. Trade Booth 9

Representative at MBE/GSA05. Laurence Van Dam, Director

Contact Details. P O Box 301-256, Albany, Auckland, Tel: 0800 776 767, Fax 0800 776 000, Email: Info@NZScientific.co.nz

Description of the Organisation. NZ Scientific is the supplier of Perkin Elmer Life and Analytical Science and complementary products into New Zealand.

Company Name. National Evolutionary Synthesis Center (NESCent)

Type of Sponsorship. Trade Booth 1

Representative at MBE/GSA05. Jory P. Weintraub, Science Outreach Manager

Contact Details. 605 Broad Street, Durham, NC 27705, Phone: +1 919 270-7429, Email: jory@unc.edu, Website: <http://www.nescent.org>

Description of the Organisation. The Center for Synthesis in Biological Evolution has as its goal the cross-disciplinary synthesis of evolutionary databases.

Company Name. Oxford University Press

Type of Sponsorship. Trade Booth 2, opening reception Sponsor, advertising inside rear cover.

Representative at MBE/GSA05. Cathy Kennedy, Senior editor- Journals Division

Contact Details. Oxford University Press, Great Clarendon Street, Oxford, OX2 6DP, United Kingdom, Phone: +44 1865 353907, Fax: +44 1865 353835, Email: jnls.cust.serv@oupjournals.org, Website: www.oupjournals.org

Description of the Organisation. Oxford Journals, a division of Oxford University Press, is proud to publish Molecular Biology and Evolution on behalf of the Society for Molecular Biology and Evolution. Other Oxford journals include Behavioural Ecology, Nucleic Acids Research, Human Molecular Genetics, Journal of Heredity, and PEDS: Protein Engineering, Design, and Selection. For more information please visit our website.

Company Name. Roche Applied Science

Type of Sponsorship. Trade Booth 3, advertisement in programme

Representative at MBE/GSA05. John Mackay, Product Manager; Sharon Bradley, Account Manager

Contact Details. 15 Rakino Way, P O Box 62-089, Mt Wellington, Auckland, Tel: 09 536 4664, Fax: 09 276 8917, Email: john-f.mackay.jm1@roche.com, Website: www.roche-applied-science.co.nz

Description of the Organisation. Roche Applied Science is a provider of bioanalytical solutions for life science researchers. Rapid real-time PCR, automated DNA/RNA preparation, and gene detection are just a few of the integrated solutions we offer.

Company Name. Total Lab Systems Ltd

Type of Sponsorship. Trade Booth 4

Representative at MBE/GSA05. Trevor Lowe, Director; Barry Cowen, Territory Manager; Colin Denver, Bioline

Contact Details. P O Box 29071, Greenwoods Corner, Auckland, Phone: 09 629 6660, Fax: 09 629 6661, Email: t.lowe@totallab.co.nz, Website: www.totallab.co.nz

Description of the Organisation. Total Lab Systems is fast becoming a major supplier of high quality laboratory instrumentation and some speciality consumables.

Auckland - Popular Attractions

Kelly Tarlton's Antarctic Encounter & Underwater World

Kelly Tarlton's offers a fascinating discovery of underwater life, journeying beneath the sea to come face to face with sharks, stingrays, moray eels and more.

The Antarctic Centre awaits with a snow cat ride through a landscape of snow, ice and subzero temperatures to see real King and Gentoo penguins.

New Zealand National Maritime Museum

Located on the waterfront, the New Zealand National Maritime Museum tells the story of 1000 years of New Zealand's seafaring history. The museum features include an America's Cup display, restored sailing boats and displays giving a fascinating account of New Zealand's maritime heritage.

Auckland War Memorial Museum

Located in the middle of Auckland Domain, with sweeping views over the harbour and Hauraki Gulf, the museum is a fantastic place for a visit.

Enjoy a glimpse into New Zealand history and the opportunity to see New Zealand's largest collection of Polynesian artefacts. Two new Pacific galleries, Masterpieces and Lifeways, house the museum's world famous collection.

A Maori cultural performance is held three times daily introducing the legends, songs and dances of New Zealand's indigenous Maori people.

Golf

Auckland has more than 40 golf courses all within one hour's drive of the city. Golf packages can be arranged which include hotel transfer, green fees, golf equipment, and coaching from a golf professional.

Auckland Bridge Climb

A guided two and a half hour adventure packed with amazing discoveries! The Auckland Bridge Climb is hosted by professional climb leaders and takes adrenalin lovers along specially-designed walkways, to experience thrilling heights, unique engineering features and great views.

Sky City Auckland

Sky City is New Zealand's largest casino and entertainment complex situated in the heart of Auckland city. It is also home to Sky Jump, a 192m (630ft) base jump by wire from Auckland's Sky Tower, while Vertigo is a climb inside the Sky Tower mast to the open air crow's nest 300m above sea level.

Auckland City Sights

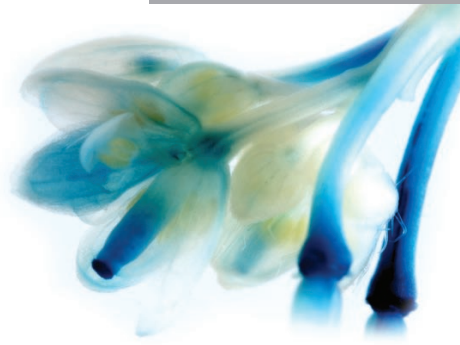
Sightseeing tours around the city offer a great overview of Auckland's highlights with informative commentaries on history and points of interest

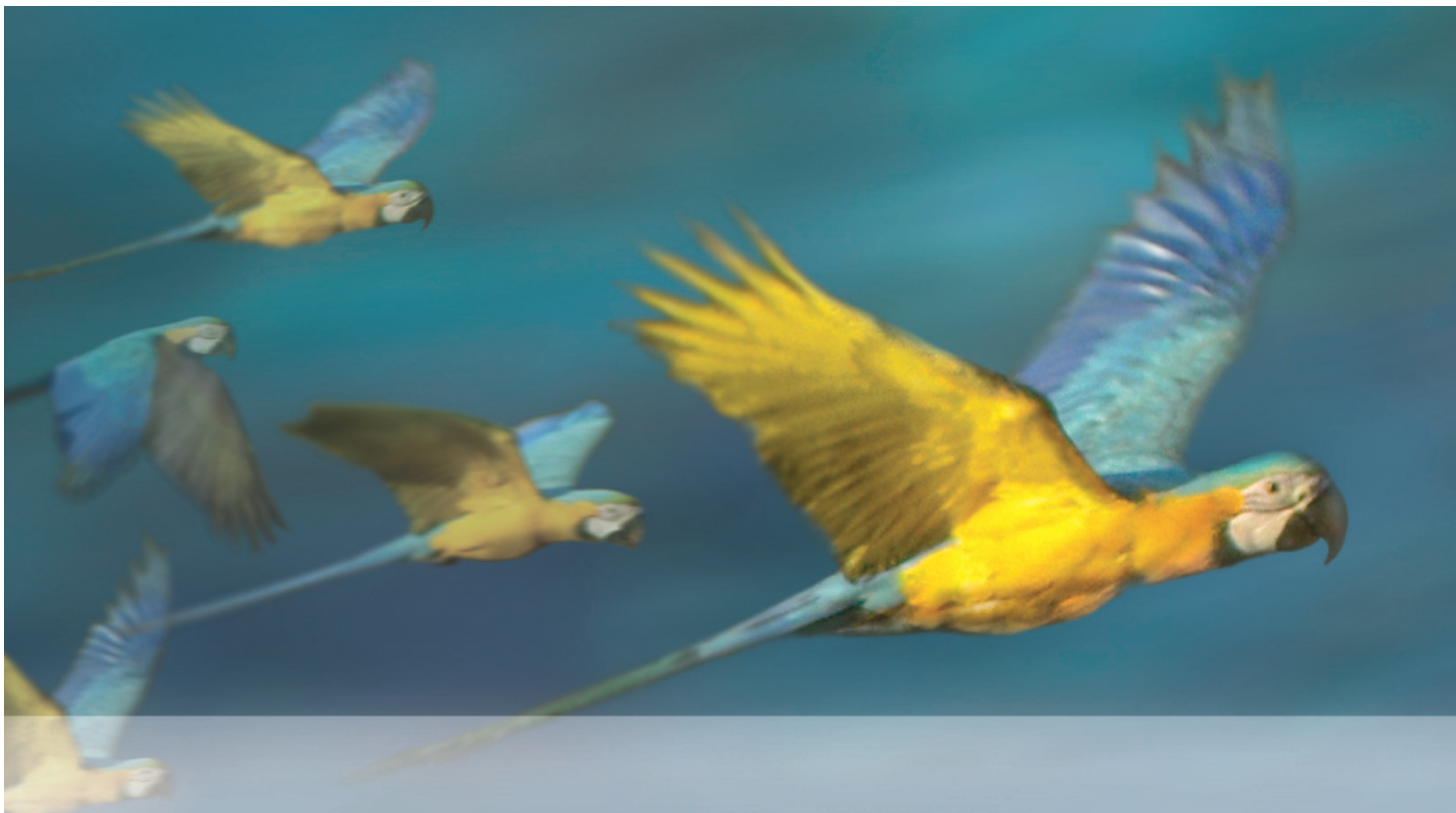


ADVANCED RESEARCH, MEANINGFUL APPLICATIONS →
Global leader in fruit and food science → Researchers with
skills in bioinformatics to plant breeding → World-class
facilities → Over 200 PhD qualified staff → Opportunities for
graduate training and post-doctoral study.

 **HortResearch**

**FOR CAREER OPPORTUNITIES // CONTACT NADINE ANDREWS
NANDREWS@HORTRESEARCH.CO.NZ
HORTRESEARCH, NEW ZEALAND // WWW.HORTRESEARCH.CO.NZ**





Roche Applied Science
LightCycler® Real-Time PCR System

Insist on More Accurate Quantification of Gene Expression

	Without efficiency correction	Efficiency correction with linear fit function	Efficiency correction with non-linear fit function
Calibrator-normalized target/housekeeping ratios			
40 ng	1.03	1.18	1.41
8 ng	2.21	1.79	1.01
1.6 ng	6.00	4.17	1.17
Mean	3.08	2.38	1.21
S.D.	2.60	1.58	0.22
C.V.	84.3%	66.4%	18.0%

Figure 1: Impact of different PCR efficiency adjustments on accuracy of relative quantification. Total RNA was used for quantitative RT-PCR on the LightCycler® System. Sample data were evaluated with the LightCycler® Relative Quantification Software, using the efficiency correction functions described above, to generate calibrator-normalized target/housekeeping ratios. The significantly lower Coefficient of Variation (C.V.) demonstrates the greater accuracy made possible by the LightCycler® Software's use of efficiency corrections and a non-linear fit function.

Quantify more accurately with the LightCycler® Instrument

- Cycle faster to minimize non-specific products that may overestimate copy numbers.
- Analyze all samples in the same thermal chamber to ensure temperature homogeneity and consistent PCR efficiencies.

Analyze data more accurately with LightCycler® Relative Quantification Software

- Use calibrator normalization to ensure consistency between PCR runs.
- Within runs, rely on an efficiency-correction feature that accounts for differences in PCR efficiencies between target and reference genes.
- Obtain sample concentrations from non-linear standard curves to more precisely quantify low-copy genes, which often suffer from non-linear PCR efficiencies (Figure 1).

Shouldn't accurate quantification be the primary goal of gene expression studies? Contact your Roche Applied Science representative and visit www.lightcycler-online.com today!

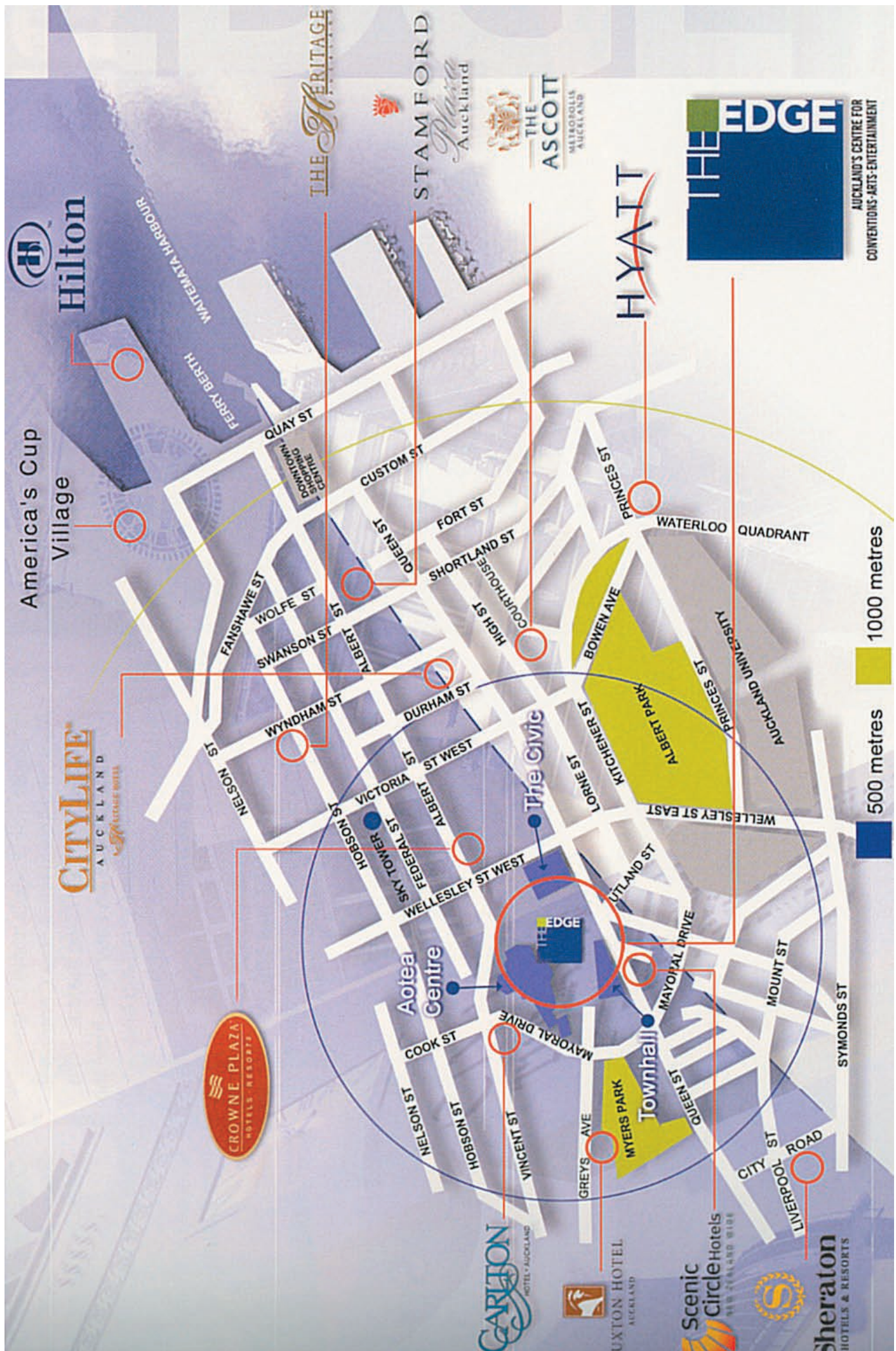


Diagnostics

LIGHTCYCLER is a trademark of Roche.
 The technology used for the LightCycler® System is licensed from Idaho Technology, Inc., Salt Lake City, UT, USA.
 © 2005 Roche Diagnostics. All rights reserved.



Roche Diagnostics N.Z. Ltd
 PO Box 62-089
 15 Rakino Way
 Mt. Wellington, Auckland
 New Zealand





EVOLUTION
2007

Evolution 2007

Auckland, New Zealand June 18th - 22nd

The Venue and Location

The conference venue for Evolution 2007 is the Aotea Centre in central Auckland, New Zealand. This is New Zealand's premier conference centre and is a modern state of the art facility.

Auckland offers a diverse range of hotels, attractions and touring options. Auckland is a city of more than one million people, with a beautiful harbour, beaches and hiking in lush bush in close proximity. Auckland International Airport is serviced by most major international airlines.

Travelling to New Zealand is more affordable than you may think!

Evolution 2007

The 2007 Evolution meeting will be jointly sponsored by the Society for the Study of Evolution, The Society of Systematic Biology and the American Society of Naturalists. Evolution 2007 will be held June 18th - 22nd in Auckland, New Zealand.

The conference will be hosted by the Allan Wilson Center for Molecular Ecology and Evolution ([www.http://awcmee.ac.nz](http://awcmee.ac.nz)).

For inquiries or further information please contact D.M.Lambert@massey.ac.nz

Dear Colleague,

On behalf of the organizing committee I would like to invite you to attend the next Evolution Conference in Auckland, New Zealand, 2007. This will be a broadly based conference of interest to those researching or teaching in evolution. Your participation will be greatly appreciated and I urge you to start planning for this event now. Look forward to seeing you at the meeting.

David Lambert
Chair of the Organising Committee





The Allan Wilson Centre Genome Service (AWCGS) is based within the Allan Wilson Centre of Research Excellence at Massey University.

The AWCGS consists of two services, one at Massey University, Palmerston North, and the other at Massey University, Albany, Auckland.

The AWCGS offers services to customers both within New Zealand and internationally.

The AWCGS provides for customers:

- **Long-length sequencing of plasmid clones, BAC DNA, Lambda clones, and bacterial genomic DNA, with reads of >1000bp**
- **Rapid throughput sequencing of short PCR products**
- **Genotyping analysis of microsatellites and AFLPs**
- **Sequencing of homopolymer and repeat regions**

Both sequencing and genotyping is carried out using new ABI 3730 DNA Analyzers, allowing a fast turn around time and lower costs to the customer.

The AWCGS provides an easy to operate web-based submission and data download system, for customers to submit sequencing and genotyping, and to retrieve their results once completed.



Ms Lorraine Berry
Allan Wilson Centre Genome Service
Massey University
Palmerston North
Ph: +64 6350 5378
Fax: +64 6350 5626
Email: L.Berry@massey.ac.nz

Mr Charlie Gao
Allan Wilson Centre Genome Service
Massey University
Albany, Auckland
Ph: +64 9414 0800 ext 41117
Fax: +64 9441 8142
Email: C.Y.Gao@massey.ac.nz

<http://awcmee.massey.ac.nz>

MOLECULAR BIOLOGY AND EVOLUTION

Published on behalf of the
Society for Molecular Biology and Evolution

VISIT THE OXFORD UNIVERSITY PRESS
STAND AT **SMBE 2005** AND
SUBSCRIBE AT A DISCOUNTED RATE



**All subscriptions include membership to the
Society for Molecular Biology and Evolution**

Online Features at
WWW.MBE.OUPJOURNALS.ORG:

- Full-Text online with advanced search facilities•
- Online submission and peer review•
- Customized alerts•
- Free 'hot' papers on the home page•
- Free online sample copy•

WWW.MBE.OUPJOURNALS.ORG



OXFORD JOURNALS
OXFORD UNIVERSITY PRESS

Index

A

Alacs, Erika 21
 Alansari, Aliya 28
 Alsop, A. 28
 Amos, Bill 12
 Anderson, A.R. 14
 Appleton, Belinda 15
 Archibald, John M. 22
 Arcus, Vickery L. 23
 Armstrong, Tristan 12
 Atchley, William R. 18
 Atkinson, Quentin D. 19

B

Bailes, Helena J. 14
 Baldo, Laura 28
 Ball, Shelley 25
 Barrett, Luke G. 23
 Bay, Line Kolind 15
 Beavis, Amber 15
 Beheregaray, Luciano B. 14
 Beiko, Robert G. 28
 Belov, Katherine 17
 Bhowmick, Bejon Kumar 18
 Bilgmann, Kerstin 28
 Blair, David 12, 28
 Blankenship, Robert E. 12
 Bodt, Stefanie De 19
 Bowers, T.H. 23
 Broadhurst, Linda 24
 Broderick, Damien 13
 Brown, Sarah C. 15, 28
 Bruyn, Mark de 13
 Buckley, Thomas R. 16
 Bulmer, M. S. 22
 Burch, Christina L. 23
 Burrige, Chris 22
 Byars, Sean 21
 Byrne, Margaret 13

C

Ca, James Jing 28
 Caballero, Susana 15
 Cameron, Emilie 17
 Cann, Rebecca 12
 Caramelli, David 28
 Carlsson, Britt-Louise 28
 Carraher, Colm 14
 Castro, L.R. 21
 Chamary, Jean-Vincent 14
 Chamberlain, Amanda 18
 Chan, Zeke S. H. 28
 Charleston, Michael 18
 Chen, Min 22, 28
 Chen, Sylvia (Xiaowei) 28
 Chen, Zhenzhong 28
 Chenoweth, Stephen F. 13
 Clarke, Andrew C. 13
 Clements, Kendall D. 13

Coates, David 25
 Collinge, Derek 29
 Collins, Lesley 19
 Cook, Catherine A. 29
 Cooper, Alan 22
 Corrigan, Shannon 29
 Cotton, James 19
 Coucheron, Dag H. 29
 Crawford, Douglas L. 15
 Crow-Sanchez, Karen D. 19

D

Dagan, Tal 23
 Damiano, John 29
 Datson, Paul 20
 Davis, Jerel 15
 Davis, Jerel C. 20
 Day, Julia J. 21
 Deagle, B.E. 12
 Deakin, Janine E. 23
 Dearden, Peter 20
 Denise, Raterman 32
 Denver, Dee R. 24
 Depaulis, Frantz 22
 Docking, T. Roderick 29
 Dolman, Gaynor 20
 Donald, Kirsten M. 13
 Druzhinina, Irina S. 29
 Duffy, Angela 29
 Dyer, Kelly 19

E

Easton, Brett 17
 Ebersberger, Ingo 17
 Ewing, Greg 19
 Ezawa, Kiyoshi 29

F

Fang, Shu 29
 Fares, Mario A. 24
 Feng, L.L. 16, 29
 Field, David 25
 Field, Steven F. 20
 Fischer, Anne 22
 Fong, James 20
 Francino, M. Pilar 23
 Francis, Cara 20
 Frankham, Richard 20
 Frentiu, F.D. 17
 Froula, Jeff 29
 Fry, B.G. 16
 Fuehrer, Andrea 17

G

Gaddam, Ravikumar 29
 Gaggiotti, Oscar E. 12
 Ganley, Austen R.D. 19
 Gardner, Paul 13
 Garrick, R. C. 21, 29

Gemmell, Neil 12
 Gibb, Gillian C. 30
 Gilchrist, Amy 15
 Gilson, Paul R. 21
 Gleave, Andrew 30
 Gleeson, Dianne M. 22, 23
 Go, Yasuhiro 20
 Goldberg, Julia 30
 Goode, Matthew 17, 30
 Grady, Deborah L. 30
 Grams, Raymond W. 30
 Graves, Jennifer Marshall 9, 16
 Gray, Russell D. 15
 Greenberg, Anthony J. 21
 Grigor, Murray R. 17
 Grützner, Frank 17
 Guzik, Michelle T. 30

H

Hahn, Matthew W. 16
 Hannan, Danielle A. 16
 Hara, Yuichiro 30
 Harrison, Abby 14
 Hay, Jennifer M. 25
 Haygood, R. 13
 Haynes, Gwilym D. 30
 Hayward, Jess 18
 Hazlitt, Stephanie L. 24
 Hedges, S. Blair 30
 Heimeier, Dorothea 24
 Hellens, Roger P. 25
 Hellmann, Ines 19
 Hendy, Michael D. 14
 Herbert, Paul 24
 Hey, Jody 15
 Hickey, Anthony 13
 Hinkle, Anya E. 13
 Hisheh, Susan 14
 Ho, Simon 19
 Hofreiter, Michael 21
 Holland, Barbara R. 16
 Holland, Olivia 22
 Holleley, Clare E. 23
 Horn, Thorsten 30
 Horne, Irene 24
 Huerta, Araceli M. 30
 Hughes, David Allen 19
 Hughes, Jane 15
 Humphries, John 15
 Hunter, Craig P. 12

I

Irwin, David M. 12
 Iwase, Mineyo 19
 Iwashita, Shintaro 16

J

Jakó, Éena 17
 Janssen, Bart 30

Jarman, Simon 25
 Jiang, Huifeng 18
 Johansen, Steinar D. 30
 Johnston, Kate 16, 31
 Jones, Julia C. 31

K

Kaneko, Satoko 12
 Kashiwagi, Tom 20
 Kassahn, Karin S. 14
 Katz, Laura A. 15
 Keane, Thomas M. 16
 Kellermann, Vanessa 14
 Kennedy, Martyn 17
 Kern, Andrew 21
 Kirby, Ralph 24
 Klitz, William 16
 Knapp, Michael 14
 Knight, Rob 24
 Koina, Edda 18
 Kolaczowski, Bryan 19
 Kopchinskiy, Alexey 31
 Kordis, Dusan 23
 Kozlova, A.P. 19
 Kumar, S. 31
 Kuraku, Shigehiro 31

L

Lachmann, Michael 20
 Lambert, David 22
 Lancaster, Melanie 15
 Lane, Christopher 24
 Langhoff, Pia 13
 Lasser, Elyse 31
 Laukien, Frank 31
 Laurie, Andrew 17
 Lavery, Shane 25
 Lawrence, Hayley 31
 Lea, Rod A. 16, 31
 Lee, Clare 31
 Lee, Siu-Fai 20
 Lightfoot, Damien 31
 Lipatov, Misha 21
 Liu, Hong-liang 17
 Lukoschek, Vimoksalehi 16
 Lysak, Martin A. 23

M

MacDonald, Anna 20
 MacEachern, Sean 18
 Macpherson, Mike 18
 Maier, Uwe 17
 Makino, Takashi 25
 Marques, Ana Rebelo 19
 Martin, William 12
 Mattick, John 23
 Maxwell, Peter 31
 McBreen, K. 13
 McClellan, David A. 25

McGaughran, Angela 17
 McInerney, James O. 17
 Medraj, Issa 15
 Meneses, Isabel 31
 Meudt, Heidi M. 22
 Meyer, Axel 6, 16
 Miller, Hilary C. 21
 Mindell, David P. 15
 Misawa, Kazuharu 25
 Möller, Luciana 31
 Montaña, Adriana Maria 25
 Morgan-Richards, Mary 15
 Mower, Jeffrey 24
 Moyle, Leonie C. 14
 Moyzis, Robert K. 18
 Mui, C. Cam 14
 Muirhead, K. A. 32
 Muller, Chris 32
 Murphy, N. 22
 Murphy, William J. 18
 Murray, Brent W. 32
 Myles, Sean 17

N

Neaves, Linda 20
 Newcomb, Richard 22
 Nielsen, Rasmus 32
 Nielsen-Marsh, Christina M. 22
 Nittinger, Franziska 12
 Noda-Ogura, Akiko 32
 Nowick, Katja 32
 Nozawa, Masafumi 18

O

O'Brien, Eleanor 23
 Ogura, Atsushi 14
 Olivier, Cassar 14
 Oremus, Marc 22
 Orsini, Luisa 14
 Osborne, Megan J. 21
 Ottewell, Kym 20, 32
 Ovenden, Jenny 22
 Oxley, Peter 32

P

Parsons, Yvonne 25
 Passmore, Abraham 14
 Patil, Jawahar G. 25
 Patron, Nicola 13
 Pellekaan, Sheila van Holst 15
 Penny, David 23
 Pickup, Melinda 23
 Pierson, Melanie 13
 Pingault, N.M. 32
 Pinto, Gabriela de Tezanos 16
 Pocwierz-Kotus, A. 32
 Podlaha, Ondrej 21
 Ponniah, Mark 20
 Poole, Anthony 24

Prashanth, Ak 16
 Pratt, Renae 32
 Ptak, Susan E. 18

Q

Qi, Xue-bin 15
 Qin, Jinyi 32

R

Rainey, Paul 23
 Rajora, Om P. 18, 23
 Reed, Floyd A. 19
 Rheindt, Frank E. 12
 Roach, Jennifer L. 32
 Robbins, Steven 32
 Robins, Judith H. 25
 Rogers, Stephanie A. 32
 Rowell, Dave 21
 Roy, Scott William 25, 33

S

Salas, M.F. de 29
 Salaün, Laurence 33
 Salzman, Yael 18
 Sands, Chester 15
 Santure, Anna 33
 Sassi, Slim 19
 Sawai, Hiromi 15
 Sawyer, Sara L. 16
 Schliep, Klaus 33
 Schmidt, Dan 13
 Schmitt, Lincoln H. 13
 Schurko, Andrew M. 19
 Seo, Tae-Kun 16
 Shaw, Matthew 33
 Shepherd, Lara 22
 Shi, Hong 14
 Shuetrim, Angie 21
 Siddle, Hannah 24
 Sigg, Dominique P. 20
 Silva, Jack da 19
 Silvia, Fuselli 17
 Simons, Jo 33
 Singh, Nadia D. 23
 Sirey, Tamara 18
 Smissen, Rob 22
 Smith, Phillip 18
 Smith, Steve 24
 Snowden, Kimberley C. 21
 Sommerville, Karen 24
 Song, Simon D. 16
 Spencer, Hamish 16
 Steane, Dorothy 22
 Steeves, Tammy 14, 33
 Stevens, Mark 12
 Stiglec, Rami 20, 33
 Stone, Anne C. 15
 Swalla, Billie J. 21

T

Takezaki, Naoko 17
 Tan-Kristanto, Ariadne 15
 Tanaka, Mark M 14
 Tanaka, Nobuhiko 13
 Tanaka, Tsuyoshi 25
 Tay, Wee Tek 33
 Teeling, Emma C. 15
 Tetu, Sasha 19
 Thalmann, O. 18
 Thompson, Graham 12
 Timmis, Jeremy N. 19
 Tishkoff, Sarah A. 19
 Travers, Simon A. A. 33
 Trezise, Ann E. O. 17, 21
 Tsujino, Fumi 19
 Turner, Thomas L. 14

U

Uyenoyama, Marcy K. 18

V

VanWye, Jeffrey D. 33
 Vargas, Iris M. 33
 Vaughan, Meredith 33
 Vernesi, C 25
 Verrelli, Brian C. 18

W

Watabe, Teruaki 18
 Waters, Jonathan 22
 Watson, Jim 7
 Wayne, Marta L. 13
 Welch, David 18
 Wenne, R. 13
 White, Tim 18
 Whitehead, Andrew 12
 Whittall, Justen B. 34
 Wikmark, Odd-Gunnar 34
 Williams, Adam 17
 Wilson, Neil 34
 Wilson, Theresa 17
 Winder, Louise 34
 Wolff, Jonci 34
 Won, Yong-Jin 14
 Woods, Ryan 34

Y

Yap, Von Bing 18, 22
 Yarus, Mike 24
 Yockey, Heather 34
 Yoon, Hwan Su 12
 Yuge, Kazuya 13

Z

Zamora, Alejandro 34
 Zenger, K.R. 34
 Zufall, Rebecca A. 34

