

Sunday June 19th

10.00am - 5.30pm	Registration - Aotea Centre		
Session Chair	David Lambert		
1.00pm - 3.30pm	Free Lecture Series to the Public and Delegates - Aotea Auditorium	Axel Meyer, Chance and necessity in Evolution	Jim Watson, The Evolution of Sustainability
4.30pm - 6.30pm	Welcome and Maori Greeting - Aotea Auditorium Oxford University Press Welcoming Reception		

Monday, June 20th

Registration and Information - Aotea Centre				
Setup Posters				
Internet Room				
8.30am - 10.30am	Molecular Ecology	Genes and Gene Expression	Origin and Evolution of Photosynthetic Life	Evolution in the Pacific
8.30am	Bill Amos; Department of Genetics, Cambridge University; Genetic archaeology: new approaches to find out who was where and when	Craig P. Hunter; Molecular and Cellular Biology, Harvard University; The Molecular Genetics of Intercellular RNA Transport in Nematodes	Robert E. Blankenship, Sumeel 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	Rebecca Cann & 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	Franziska Nittinger, 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?	Graham Thompson, Jürgen Paar, Robert Kucharski, Ryszard Maleszka, Ben Oldroyd; University of Sydney; Molecular basis of worker sterility in the honey bee, <i>Apis mellifera</i>	William F. Martin; The Institute of Botany III, Heinrich-Heine-Universität Düsseldorf, Germany; Endosymbiotic gene transfer: A mechanism of genetic innovation unique to the eukaryotic lineage.	Mark Stevens, 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	B.E. Deagle, D.J. Tollit, S.N. Jarman, M.A. Hindle, 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	David M. Irwin, Shijun Yue, and Brian Tsai; Banting and Best Diabetes Centre, University of Toronto, Canada; Evolution of the Proglucagon Gene Promoter		GSA Frank E. Rheindt, 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 honeyeaters</i>
9.30am	Oscar E. Gagliotti; Laboratoire d'Ecologie Alpine, Université Joseph Fourier, France; Identifying the factors that influence dispersal processes and species distributions	Satoko Kaneko, Kaoru Tsuda, Kazuyuki Mekata, Kazuo Moriwaiki, Naoyuki Takahata, and Yoko Satta; Department of Biosystems Science, The Graduate University for Advanced Studies (Sokendai); Rapid turnover of regulatory processed pseudogenes of Makorin1 in rodents and primates	Hwan Su Yoon, Jeremiah Hackett, and Debashish Bhattacharya; Department of Biological Sciences and Roy J. Carver Center for Comparative Genomics, University of Iowa, USA; Eukaryotic Plastid Endosymbiosis	Tristan Armstrong & Ross Beever; Landcare Research, New Zealand; Phylogeography of an iconic endemic: the New Zealand cabbage tree, <i>Cordyline australis</i>
9.45am	Neil Gemmell, Victoria Metcalf, Katherine Gomas, Patrice Irvine, and Fred Allendorf; School of Biological Sciences, University of Canterbury, New Zealand; Do Mitochondrial Mutations Affect Population Viability?	Andrew Whitehead and Douglas L. Crawford; Department of Marine Biology and Fisheries, University of Miami; Neutral and Adaptive Variation in Gene Expression		David Blair, 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 Kardalisky, 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 Aotea Centre Foyer			
11.00am - 1.00pm	Molecular Ecology	Genes and Gene Expression	Species and Speciation	Evolution in the Pacific
11.00am	B. Smetanka, T. Kijewski, A. Burzyński, H. Hummel, B. Więcas; 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 Institutes 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 frutescens</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. Eytan, 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	Kazuwa 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>Tripterygiidae</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, Maharatunkamsi, Richard A How; School of Anatomy & Human Biology, The University of Western Australia; Geography and population structure in the bats of Wallacea	R. Haywood, J. P. Bollhoff, 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>Zyzyomys woodwardi</i>	GSA Karin S. Kassah, M. Julian Caley, Alistair 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 Raimcrow, 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 Stockler, David Havill, 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 Swadlow, Andrew McMillan 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. Mayle and Elaine B. Graham; Center for Population Biology, University of California, U.S.A.; Comparative genomics of hybrid incompatibility among <i>Lycopersicon (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, Sevkı Erdogan; University of Hawai'i, USA; GIS and Gene Flow	Mark M Tanaka, Roland R. Reago, 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 Hsieh, 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>	Cassir Ollivier, 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 - 2pm Session Chair & Location

Lunch provided in Aotea Centre Foyer

2pm - 4.00pm

	Molecular Ecology	Genes and Gene Expression	Species and Speciation	Rates and Dates
2.00pm	Colm Carragher, 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 B. Bailles, 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
2.15pm	Luciano B. Beheregaray, Ning L. Chao, Adalgisa Caccone, Shannon Carrigan, 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. Sgró; 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. Hart; 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; Bio21 Molecular Science and Biotechnology Institute, University of Melbourne, Australia; Expression and Sequence Analyses of Lepidopteran Linase 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 Ford 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 Sivadasan 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 Hsiuan 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 Marine Science, University of California, USA; Microarray analysis of vegetative incompatibility in <i>Neurospora crassa</i>	Laura A. Katz, Oona L.O. Snoeybos-West, Autumn Griffin, Kate Pirog, Wilhelm Folschner, Barbara Costas, George B. McManus; Department of Marine Science, 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 Onychophora from the Gourcock 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 Sawaj, 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, Kerr-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, Fabricio R. Santos, Miriam Marmonteil, 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 Treweek; Allan Wilson Centre, Massey University, Palmerston North, New Zealand; Hybrid origins of a parthenogenetic genus?	Jerel C. Davis, Onn Brandman, Penka V. Markova, Dmitri A. Petrov; 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: Hexatheledae) 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

4.00-6.00pm Refreshments provided during POSTER SESSION in Limelight Room

Tuesday June 21st

Registration and Information
Internet Ready Room

8.30am - 5.30pm Session Chair & Location

	Molecular Ecology	Bioinformatics and Phylogenetic Methods	Genome Evolution	Genetics of Diseases and Human Evolution
8.30am	AK Prashanth; UC Davis Genome Centre; Socio-Behavioral variation and rapid evolution: DNA duplex destabilization at regulatory DNA microsatellites as an underlying mechanism	Axel Meyer; Department of Biology, University of Konstanz, Germany; The evolution of cichlids and their genomes: from trees to comparative genomics	Jenny Marshall Graves; Comparative Genomics Research Group, The Australian National University; Exploring the genomes of weird mammals	Hamish Spencer; Allan Wilson Centre for Molecular Ecology and Evolution, University of Otago, New Zealand; Polymorphism of Imprinting Status: What Does it Mean?
9.00am	GSA Gabriela de Tezanos Pinto, K. Russell, A. Hutt, G. Stone, M. Oremus, C. Garrigue, C. Olavarria, D. Steel and C. S. Baker; The University of Auckland, New Zealand; Population structure and genetic diversity of coastal bottlenose dolphins (<i>Tursiops truncatus</i>) in New Zealand: a world-wide perspective	Thomas M. Keane, Thomas J. Naughton, James O. McInerney; Bioinformatics and Pharmacogenomics Laboratory, National University of Ireland; DPRml-II: A High-throughput Phylogenetics Platform	Kate Johnston, Patrick Dicker, Richard Edwards & Denis Shields; Bioinformatics Core Group, Department of Clinical Pharmacology, Royal College of Surgeons in Ireland; The Evolution of Specificity	Sara L. Sawyer, Lily I. Wu, Michael Emerman, Harmit S. Malik; Fred Hutchinson Cancer Research Center, USA; Positive selection of the primate TRMSa gene tailors its antiviral efficiency

9.15am	GSA Danielle A. Hannan, Anthony J. R. Hickey, Kendall D. Clements; School of Biological Sciences, University of Auckland; Hybridisation between New Zealand triplefin fishes (Family Tripterygiidae)	Tae-Kun Seo, Hirohisa Kishino and Jeffrey L. Thorne; Professional Programme for Agricultural Bioinformatics, University of Tokyo, Japan; Incorporating gene-specific variation when inferring and evaluating optimal evolutionary tree topologies from multilocus sequence data	Matthew W. Hahn; Center for Population Biology, University of California, Davis, USA; Estimating the Tempo and Mode of Gene Family Evolution from Comparative Genomic Data	William Klitz, Martin Maier and Loren Grager; National Marrow Donor Program, University of California, USA; A Global Assessment of Population Level Selection in the MHC: Evidence for Strong and Pervasive Effects.
9.30am	GSA Vimoksalehi Lukoschek; School of Tropical Environment Studies and Geography, James Cook University, Australia; Phylogeographic structure of the olive seahorse, <i>Alipysurus laevis</i> (Hydrophiidae) indicates recent expansion event from Pleistocene refugia	Thomas R. Buckley, Jim Willgenbusch, Mark Holder, and David Swofford; Landcare Research, Auckland, New Zealand; Measures of Phylogenetic Support on Large Data Sets	Shintaro Iwashita, Sadao Ueno, Hiroshi Yasue, Naoki Osada, and Katsuhiko Fukuta; Mitsubishi Kagaku Institute of Life Sciences, National Institute of Agrobiological Sciences, Nagoya University, and National Institute of Infectious Diseases, Japan; The time frame of creation of the ruminant-specific paralogueous bucentaur (p97bcnt) gene: gene duplication and RTE-1 radiation	LL Feng, J Liu, N Bains, KK Lau, RJ Bryson-Richardson, D Fatkin, MA Wouters; The Victor Chang Cardiac Research Institute, Australia; A Computational Pipeline for the Rapid Identification of Candidate Disease Genes
9.45am	GSA Simon D. Song, Richard Drew, Jane Hughes; Australian School of Environmental Studies, Griffith University, Australia; A population analysis of the wild tobacco fly, <i>Bactrocera cacuminata</i> (Diptera: Tephritidae: Dacinae), using microsatellite markers	Barbara R. Holland, Vincent Mouton; Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Palmerston North, New Zealand; Weighted Consensus networks: Combining information from many gene loci	B.G. Fry, S.F.R. Ramjan, J. Norman; Australian Venom Research Unit, University of Melbourne, Australia; From genome to 'venome': The molecular origin and evolution of the snake venom proteome.	Rod A Lea; The Institute of Environmental Science and Research Ltd, Wellington, New Zealand; Genetic Structure of the Maori Population: Prospects for Disease Gene Mapping
10.00am	Angela McLaughran, 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.	Matthew Goodie, Stéphane Guindon, Allen Rodrigo; Bioinformatics Institute, University of Auckland, New Zealand; Modeling Time-Dependent Changes in Codon Selection Pressure using Serially Sampled Sequence Data	Naoko Takezaki, Shin-ichi Nakamura, Akinobu Okabe, and Osamu Matsushita; Information Technology Center, Kagawa University, Japan; Frequent domain organization changes in the evolution of clostridial collagenases	Sistonen Johanna, Fuselli Silvia, 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
10.15am	F.D. Frenstju, 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	Ingo Ebersberger, Petra Galgoczy, Stefan Taudien, Simone Taenzler, Rüdiger Lehmann, Matthias Platzer and Arndt von Haeseler; WE Informatik, Heinrich-Heine-Universität Düsseldorf Germany; Towards a map of our genetic ancestry	Katherine Below, Hannah Siddle, Janine Deakin; Centre for Advanced Technologies in Animal Genetics and Reproduction, University of Sydney, Australia; Unraveling the MHC of marsupials	Andrew Laurie and Peter George; Molecular Pathology, Canterbury Health Laboratories, New Zealand; High frequency of disease-causing mutations in the LDL-receptor gene
10.30am - 11.00am	Morning Tea provided in Aotea Centre Foyer			
11.00am - 1.00pm	Session Chair & Location			
	Agricultural Genomics	Bioinformatics and Phylogenetic Methods	Genome Evolution	Genetics of Diseases and Human Evolution
11.00am	Theresa Wilson; AgResearch MBU, University of Otago, Dunedin New Zealand; Genomics of Livestock: the New Century	Murray R. Grigori; Bioinformatics Institute, University of Auckland, New Zealand; Evolution of lipocalin genes: Accelerated gene evolution at evolutionarily fragile genomic regions	Uwe Maier; Philipps-University Marburg, Germany; Primary, secondary and tertiary endosymbiosis	Hong-liang Liu, Yin-gui 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 TRIM5 _L a Gene Restricting HIV-1 Infection
11.15am	To be advised			
11.30am	Adam Williams; Genetics Department, University of Melbourne, Australia; Gene manipulation in <i>Helicoverpa armigera</i>	Martin Kennedy, 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	Andreas Fehrer, Ingo Paulsen, Arndt von Haeseler; Department of Bioinformatics, University of Duesseldorf, Germany; Maximum Likelihood Estimation of Gene Duplication- and Deletion-Rates	Brett Easton; Mathematical Sciences Institute Australian National University, Australia; Identifying compensatory substitutions for pathogenic mutations via a non-reversible model
11.45am	GSA Emilie Cameron, Stuart Gilchrist and John Svod; Fruit Fly Research Centre, University of Sydney, Australia; Queensland Fruit Fly in Northwestern Australia: Determining outbreak parameters	James O. McInerney 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	Frank Grützner, 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 <i>platypus</i> a ten membered meiotic chain links mammal and bird sex chromosomes	Davies R., Conroy, S.-J., Davies, W.L., I.C. Potter and Ann E.O. Trezise; School of Biomedical Science, University of Queensland, Australia; Evolution and Regulation of the Cystic Fibrosis Gene
12.00am	GSA Sean MacEachern, 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>	Von Bing Yap; Department of Statistics and Applied Probability, National University of Singapore, Singapore; The Most General Markov Substitution Model on an Unrooted Tree	Huifeng Jiang, 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	Brian C. Verrelli, 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	Yael Salzman; Stanford University, USA; Gene truncation by a transposable element leads to pesticide resistance in <i>D.melanogaster</i>	Tim White, Ravikumar Gaddam, Simon Hills and David Penny; Allan Wilson Centre for Molecular Ecology and Evolution; Finding the Tree: Best Explanation for Molecular Sequence Data	Edda Kölna, Cristina L. Walcher, Christine M. Distèche, Jennifer Marshall Graves; ARC Centre for Kangaroo Genomics, The Australian National University, Australia; Characterization of the Marsupial MECP2 Gene	Eric T. Wang, Greg Kodama, Pierre Baldi, & Robert K. Moyzis; Department of Biological Chemistry, University of California, USA; Global Landscape of Recent Inferred Darwinian Selection for Homo sapiens
12.30pm	Amanda Chamberlain, Theo Meuwissen, Michael Goddard; Primary Industries Research Victoria, Australia; Estimation of the distribution of QTL effects	William B. Atchley; Department of Genetics and Center for Computational Biology, North Carolina State University, USA; Solving the protein sequence metric problem	Mike Macpherson, 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	Teruaki Watabe, 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 Om P. Rajora; Forest Genetics and Biotechnology Group, Dalhousie University, Canada; Comparative Functional Genetic Analysis of Black Spruce (<i>Picea mariana</i>) Expressed Genes	Michael Charleston, Russell Gray and Mahé Ben Hamed; Department of Psychology, University of Auckland; Pareto Parsimony and Historical Linguistics	William J. Murphy, 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 Jess Hayward, 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 - 2pm	Lunch provided in Aotea Centre Foyer			
2pm - 4.15pm	Session Chair & Location			
	Walter Fitch Symposium	Bioinformatics and Phylogenetic Methods	Genome Evolution	Primate and Human Evolution
2.00pm	Bejon Kumar Bhowmick, Naoyuki Takahata and Yoko Saitta; Department of Biosystems Science, The Graduate University for Advanced Studies (Sokendai), Japan; Evolution of human male-specific Y-linked (MSY) genes	David Welch, Geoff Nicholls, Allen Rodrigo, Wiremu Solomon; University of Auckland, New Zealand; Building and fitting models of coupled host-virus genealogies	Masafumi Nozawa, 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	O. Thalmann, A. Fischer, S. Paäbo and L. Vigilant; Max Planck Institute for Evolutionary Anthropology, Germany; Gorilla population genetics - The nuclear perspective

2.15pm	Tamara Sirey ; 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 Marcy K. Uyenoyama; Duke University, USA; A likelihood-based approach to inferring population parameters from multiple summary statistics	Phillip Smith ; Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Albany, New Zealand; Conditional Neutrality as a Potential Cancer Therapy	Susan E. Ptak, David A. Hinds2, Kathrin Koehler1, Birgit Nickel1, Nila Patil2, Dennis G. Ballinger2, Moly Przeworski3*, Kelly A. Frazer2*, Svante Pääbo1; Max Planck Institute for Evolutionary Anthropology, Germany; Fine-scale recombination patterns differ between chimpanzees and humans
2.30pm	Slim Sassi ; 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	James Cotton and Mark Wilkinson; The Natural History Museum, London, UK; Inferring Trees from Trees : Investigating properties of Supertree Methods	Andrew M. Schurko , 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	Quentin D. Atkinson , 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	Bryan Kolaczkowski ; University of Oregon, USA; Phylogenetic mixed-models for incorporating evolutionary heterogeneity	Greg Ewing , 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	Sasha Tetu , Neil Wilson, Nick Coleman and Andrew Holmes; School of Molecular and Microbial Biosciences, University of Sydney, Australia; Gene Cassettes as an evolutionary resource for Pseudomonas	Ines Hellmann ; Max-Planck-Institute of Evolutionary Anthropology, Germany; Evolutionary constraint on silent sites within the hominoid lineage
3.00pm	Simon Ho ; Evolutionary Biology Group, Dept of Zoology, University of Oxford; Phylogenetic inference in a relaxed clock framework	To be advised	Jeremy N. Timmis ; 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	David Allen Hughes and Mark Stoneking; Max Planck Institute for Evolutionary Anthropology, Germany; Genomic Investigations of Local Selection in Humans
3.15pm	Kelly Dyer ; 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 A.P.Kozlova, L.Krukovskaja, D.Poleva, I.Duhovinova, Y.Nosova, Y.Galachyantsa, N. Samusika, T.Tyazelovab, A.Baranovaa; The Biomedical Center, St.Petersburg, Russia; Expression of Evolutionary New Sequences in Human Tumors	Fumi Tsujino and Etsuko T. Matsuura; Department of Biosystems Science, the Graduate University for Advanced Studies (Sokendai), Japan; Evolution of BCL-2 homologs in insects	Ana Rebelo Marques , 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	Stefanie De Bodt ; 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	Mineyo Iwase 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	Austen R.D. Ganley 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	Sarah A. Tishkoff , 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	Lesley Collins ; 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.	Jack da Silva ; 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	Karen D. Crow-Sanchez ; Department of Ecology and Evolutionary Biology, Yale University; The "fish specific" Hox cluster duplication is coincident with the origin of teleosts	Floyd A. Reed , 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 AGM		MBE Business Meeting	
7.30pm - 10.30pm	Conference Banquet			

Wednesday June 22nd

Registration and Information
Internet ready room

8.30am - 5.30pm 8.30am - 5.30pm Session Chair & Location				
8.30am - 10.30am	Evolution and Development	Species and Speciation	Genome Evolution	Conservation Genetics
8.30am		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	Peter Dearden ; Biochemistry Department, Otago University; Segmentation in the Honeybee; not just another fly!	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 , Dmitri A. Petrov; Department 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 Hamelster, 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 Owendy ; School of Integrative Biology, University of Queensland, Australia; Genetic population structure in tropical sharks between Indonesia and northern Australia
9.15am	Steven E. 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 Pennell 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 Ottewill , Steve Donnellan, David Paton; University of Adelaide; Pollen-mediated gene flow amongst scattered Eucalyptus camaldulensis trees in an agricultural landscape
9.45am	Billie J. Swalla ; Biology Department, University of Washington, USA; Man is but a worm...Evolution of the Chordates	Hayley Sharp and Dave Rowell ; School of Botany and Zoology, Australian National University, Australia; Unprecedented chromosomal diversity and meiotic behaviour in an Australian huntsman spider	Andrew Kern ; University of California, USA; Recurrent deletion and gene presence/absence polymorphism: telomere dynamics dominate DNA evolution at the tip of 3L in Drosophila melanogaster and D. simulans	GSA Sean Byars ; 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
10.00am	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; School of Biomedical Sciences, The University of Queensland, Australia; Molecular Evolution of the Vertebrate Visual System: Colour vision came first!	Anthony J. Greenberg , Sarah Moorhead and Chung-I Wu; Department of Ecology and Evolution and Committee on Genetics, The University of Chicago, USA; Molecular population genetics of racial differentiation in D. melanogaster	Misha Lipatov , Peter F Arndt, Terence Hwa and Dmitri A Petrov; Department of Biological Sciences, Stanford University, USA; A novel analysis of single nucleotide substitutions in the human genome	GSA B. C. Garrick , C. J. Sands, D. M. Rowell, P. Greenslade & P. Sunnucks; Department of Genetics, La Trobe University, Australia; Phylogeography of a log-dependent endemic Australian springtail (Collembola) – a multigene approach
10.15am	Kimberley C. Snowden , Bart J. Janssen, Kerry R. Templeton, Joanne L. Simons, Revel S.M. Drummond, Toshi Foster, Cyril Brendolise; HortResearch, Auckland, New Zealand; Control of axillary branching in Petunia	Julia J. Day ; Department of Biological Sciences, Imperial College London, United Kingdom; Speciation and diversification in the Lake Tanganyika cichlid tribe, Lamprologini	Ondrej Podlaha ; Ecology and Evolutionary Biology, University of Michigan, USA; In search of functional "pseudogenes"	Hilary C. Miller , Katherine Belov, Scott V. Edwards, Charles H. Daugherty; Allan Wilson Centre for Molecular Ecology and Evolution, Victoria University, New Zealand; Evolution of MHC genes in an ancient reptilian order, Sphenodontia (tuatara)
10.30am - 11.00am	Morning Tea provided in Aotea Centre Foyer			
11.00am - 1.00pm Session Chair & Location	Ancient Biomolecules	Origin and Evolution of Photosynthetic Life	Phylogenetics	Conservation Genetics
11.00am	Johannes Krause , Paul H. Dear, Joshua Pollack, Monty Slatkin, Ian Barnes, Adrian Lister, Svante Pääbo and Michael Hofreiter; Max Planck Institute for Evolutionary Anthropology, Germany; Multiplex amplification of the complete mitochondrial genome of Mammuthus primigenius and the evolutionary relationship of mammoths, African and Asian elephants	Paul R. Gilson , Vanessa Mollard, Claudio Siamovits, Michael Reith, Patrick Keeling and Geoffrey I. McFadden; The Walter and Eliza Hall Institute of Medical Research, Australia; Complete nucleotide sequence of the chlorarachniophyte nucleomorph: Nature's smallest nucleus.	Anjie Shuetrim , Simon Robson, Ross Crozier; James Cook University, School of Tropical Biology, Australia; Molecular evolution of transferrin in Polyrhachis (Formicidae) with varying life history attributes	Megan J. Osborne and Thomas F. Turner; 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 (Hybognathus amarus).
11.15am			GSA L.R. Castro and M. Dowton; Institutes for Biomolecular Sciences, and Conservation Biology, Wollongong University, Australia; A Bayesian Analysis of Aporina (Insecta: Hymenoptera) Superfamily Relationships - Impact of a Conserved Gene	Erika Alacs ; Applied Ecology Research Group, University of Canberra, Australia; Wildlife Forensics and Trade Monitoring using Phylogenetic Approaches.
11.30am	Christina M. Nielsen-Marsh ; 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 John M. Archibald ; Department of Biochemistry and Molecular Biology, Dalhousie University, Canada; The nucleus and nucleomorph of cryptomonad algae—two extremes of a genomic continuum	M. S. Bulmer and R. H. Crozier; School of Tropical Biology, James Cook University, Australia; Positive selection in termite relish	Lara Shepherd & 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, Richard Newcomb, John Oakeshott; HortResearch, Auckland, New Zealand; Reconstructing the evolutionary history of insecticide resistance		Hsidi M. Meudt ; 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>Orisia</i> (Plantaginaceae)	Dianne M. Gleeson , 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	Alan Cooper ; Mike Bunce, Simon Ho, Beth Shapiro; Earth and Environmental Sciences, University of Adelaide, Australia; Using ancient DNA to analyse macro and micro-evolutionary processes	Min Chen , Roger Hiller, and Anthony Larkum; School of Biological Sciences, The University of Sydney, Australia; Evolution of chlorophyll antenna complexes in oxyphotobacteria	Von Bing Yap and Terry Speed; Department of Statistics and Applied Probability, National University of Singapore; Rooting Phylogenetic Trees with Nonreversible Substitution Models	Possums on the pill: Immunoprotection and MHC variation in New Zealand possums
12.15pm	Franz Depaulis , L. Orlando, V. Ung and C. Hänni; Fonctionnement et Evolution des Systemes Ecologiques, France; Population genetics of temporally interspersed data: an application on cave bear ancient DNA		N. Murphy , V.W. Framenau, S. Donnellan, 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 Lycosidae (Araneae)	Marc Oremus , 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
		Rates and Dates		

12.30pm	David Lambert, Craig Millar, Lara Shepherd, Leon Hymen; Allan Wilson Centre, Massey University, Albany, New Zealand; Ancient ecology of the extinct huia	Jonathan Waters, 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	Dorothy Steane, 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).	Jenny Ovenden, 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	Jennifer M Hay & David Lambert; Allan Wilson Centre, Massey University, Albany, New Zealand; Phylogeography of extinct and extant populations of <i>Sphenodon</i> reptiles in New Zealand	Chris Burridge & Jonathan Waters; Department of Zoology, University of Otago, Dunedin, New Zealand; River capture, range expansion, and cladogenesis: a multispecies approach to freshwater phylogeography	Rob Smissen 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 <i>edelweiss</i>) and <i>Raoulia</i>	Anne Fischer, 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 Aotea Centre Foyer			
2.00pm	GSA - Michael White Lecture Ary Hoffman; Using DNA markers for environmental monitoring: from <i>Drosophila</i> genes monitoring climate change to chironomid species monitoring aquatic pollutants			
3.00pm	MBE - Nei Lecture Jeffrey Powell - Silet Mutations Speak to the Neutral Theory of Molecular Evolution			
6.30pm	Pre-booked Waiheke Dinner			

Thursday June 23rd

Registration and Information
Internet ready room

8.30am - 1.00pm 8.30am - 1.00pm Session Chair & Location	Registration and Information Internet ready room			
8.30am - 10.30am	Microbial Evolution	Conservation Genetics	Genome Evolution	RNA World
8.30am	Paul Rainey; School of Biological Sciences, University of Auckland, New Zealand; Extensive pleiotropy underlies the evolutionary transition from single cells to simple undifferentiated groups	Om P. Rajora; Faculty of Forestry and Environmental Management, University of New Brunswick, Canada; Genetic Impacts of Forest Harvesting and Renewal Practices and Forest Fires - Canadian Forest Trees: Implications for Conservation and Sustainable Management of Forest Genetic Resources Meaghan Rourke, 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>).	Martin A. Lysak; Jodrell Laboratory, Royal Botanic Gardens, UK; Genome evolution in crucifers (Brassicaceae)	John Mattick; University of Queensland; The hidden layer of noncoding RNA in the evolution and development of complex organisms
8.45am				
9.00am	GSA Luke G. Barrett, 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	Oliver Berry & Dianne M. Gleeson; Institute of Molecular BioSciences, Massey University, Palmerston North, New Zealand; Distinguishing historical fragmentation from a recent population decline in skinks from New Zealand	Janine E. Deakin, Robert Mason and Jennifer A. Marshall Graves; ARC Centre for Kangaroo Genomics, The Australian National University; The Marsupial Dystrophin Gene	David Penny; 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	Vickery L. Arcus, Paul B. Rainey and Susan J. Turner; AgResearch Structural Biology Laboratory, University of Auckland, New Zealand; The PIN-domain toxin-antitoxin array in <i>Mycobacteria</i>	GSA Eleanor O'Brien; School of Animal Biology, University of Western Australia; Strategies to conserve adaptive genetic variation within restored populations of plant species	M. Pilar Francisco; Lawrence Berkeley National Laboratory, USA; An adaptive radiation model for the origin of new gene functions	
9.30am	Bowers III, Reid NM, Foote SM, Stuthridge TR; Eco-Smart Technologies, Forest Research, Rotorua, New Zealand; 16S rDNA and nifH gene Clone Library Analysis of a Nitrogen Fixing Pulp and Paper Waste Water Treatment System	GSA Melinda Pickup, 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>Rutidosis leptorhynchoides</i> (Asteraceae)	Nadia D. Singh, 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>	Christina L. Burch; Department of Biology, University of North Carolina, USA; Is Eigen's 'Error Threshold' relevant for RNA virus populations?
9.45am	Tal Dagan, Ran Blekhan, and Dan Graur; Department of Zoology, Tel Aviv University, Israel; The "Domino Effect" of Gene Death in Bacterial Genomes	GSA Clare E. Holleley, 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>	Dusan Kordis, 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	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	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	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	
10.15am	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</i> in backhouse - implications for habitat restoration efforts	GSA Dorothea Heimeier, Kirsty Russell, Patricia Dugan, 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	Dee R. Denver and Michael Lynch; Department of Biology, Indiana University, USA; Evolution of Eukaryotic Mismatch Repair Systems	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?
10.30am - 11.00am Session Chair & Location	Morning Tea provided in Aotea Centre Foyer			
11.00am - 1.00pm	Protein Evolution	Conservation Genetics	DNA Barcoding and Biodiversity	RNA World
11.00am	Jeffrey Mower; Department of Biology and School of Informatics Indiana University, USA; Quick and Accurate Prediction of RNA Editing Sites in Plant Mitochondrial Genes	GSA Steve Smith and Jane Hughes; Centre for Riverine Landscapes, Griffith University, Australia; 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	Paul Herbert; Department of Integrative Biology & Biodiversity Institute of Ontario, University of Guelph; DNA Barcodes and Biodiversity	Rob Knight; Department of Chemistry and Biochemistry, University of Colorado, USA; How abundant are functional RNAs in random-sequence pools?
11.15am		GSA Stephanie L. Hazlett, 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		
11.30am	Irene Horne and Victoria S. Haritos; Commonwealth Scientific and Industrial Research Organization (CSIRO), Australia; Evolution of a lipase gene cluster in <i>Drosophila</i>	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 tamar wallaby (<i>Macropus eugenii</i>)	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)	Mike Yarus; Cellular and Developmental Biology, University of Colorado Boulder, USA; Evolution of the translation apparatus
11.45am	Takashi Makino 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	GSA David Field, Andrew Young, Rob Whelan, David Ayre; Centre for Plant Biodiversity Research, CSIRO Plant Industry, Australia; Hybrid Happy or Hardly Hybridising?	Judith H. Robins, 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	
12.00pm	David A. McClellan; Department of Integrative Biology, Brigham Young University, USA; Physicochemical Evolution and Molecular Adaptation of the Cetacean and Artiodactyl Cytochrome b Proteins	David Coates, 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>	Simon Jarman; Australian Antarctic Division, Department of the Environment and Heritage, Australia; Estimating confidence in biological identifications made by comparing DNA sequences	Roger P. Hellens, Cas Simons, Betty Chung and Chris Brown; HortResearch, Auckland, New Zealand; Exploring the value of introns that reside within

12.15pm	Kazuhanu Misawa and Reiko F. Kikuno; Chiba Industry Advancement Center, Japan; A Diagonal Method for Estimating the Rates of Codon Substitutions	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.	Shane Lavery, 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	non-coding sequence
12.30pm	Tsuyoshi Tanaka, Yoshio Tateno and Takashi Gojobori; Genome Research Department, National Institute of Agribiological 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	To be advised	Yvonne Parsons and Jon Martin; Centre for Environmental Stress and Adaptation Research & Department of Genetics, La Trobe University, Australia; High-throughput species identification for effective biomonitoring	Scott William Roy; Department of Organismic and Evolutionary Biology, Harvard University, USA; When, how, and why of spliceosomal introns: what we know, and some guesses
12.45pm	Adriana Maria Montaña, Naoyuki Takahata and Yoko Satta; Department of Biosystems Science, The Graduate University for Advanced Studies, Japan; ORIGIN OF PEPTIDOGLYCAN RECOGNITION PROTEINS IN VERTEBRATES	Jawahar G Patil, Rasanthi M Gunasekera, Felicity McEnulty 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>	Shelley Ball and Karen Armstrong; National Centre for Advanced Bio-Protection Technologies, Lincoln University, New Zealand; Biotype biodiversity supported and revealed by DNA barcoding	
1.00pm	Conference ends			