ABSTRACTS OF INVITED SPEAKERS

Bill Amos	University of Cambridge	**Genetic archaeology: new approaches to find out who was where and when**	Despite huge genetic datasets on many species, but particularly humans, the goal of reconstructing accurate population histories remains frustratingly distant. In this talk I present two new approaches aimed at overcoming some of the most likely problems. First I present a spatio-genetic study of human populations, using allele frequency gradients to infer the most likely historical locations of populations and individuals. The resulting pattern indicates the presence of population clusters in the regions associated with early agriculture and with a strong affinity for coastal locations. Second, I ask whether it is possible to reconstruct how populations mix over time. I present a method based on Monte Carlo Markov chain that appears surprisingly effective at recovering the muddy history of the British Isles.	**Molecular Ecology**
Rebecca Cann & Karl Diller	University of hawaii (Manoa) Dept of cell and molecular biology, 1960 east-west road, honolulu, hawaii 96822	**Why molecular evolutionists need to reassert their independence: eurocentrism hijacks the human MSY and FoxP2**	Interest in human-specific mutations is a natural and important outcome of comparative genome sequencing in higher primates. However, in one particular case, a desire to linkinformation about the potential role of a specific transcription factor, FoxP2, to the evolution of language and emergence of socially modern behaviors led molecular evolutionists to tie their genetic data to a discredited archaeological model for the recent (40ka) spread of behaviorally modern humans. This model denies fully modern status to a number of different human aboriginal populations, based on geochemical dating for their first occurances in the fossil record. It also ignores the gradual first appearances of "modern" behaviors, now documented by prehistorians as well established in sub-Saharan Africa 150,000 years prior to their occurance in Europe and the Near East. Redating of modern skulls from Ethiopia to 195,000 also fits the original MtDNA Out of Africa model. The young dates associated with the most recent common ancestor (MRCA) in the human Y chromosome tree, said to support the relatively "young" estimates for the FoxP2 substitutions, must be recalibrated in light of the extensive pallindromic structure of the Y undergoing gene conversion. Analysis of SNP typing for the region of chromosome 7 containing FoxP2 also does not support a recent selective sweep, but suggests the FoxP2 human specific mutations may have occurred as along as 1.5mya, associated with the first spread of archaic human species from Africa.	**Evolution in the Pacific**
Richard Frankham	Key Centre for Biodiversity and Bioresources, Department of Biological Sciences, Macquarie University, NSW 2109, Australia, School of Tropical Biology, James Cook University, Townsville Qld 4811, Australia, and Australian Museum, 6 College Street, Sydney, NSW 2090, Australia	**Genetics and extinction**	The role of genetic factors in extinction has been a controversial issue, especially since Lande's 1988 paper in Science. It has been hypothesised that inbreeding depression, loss of genetic diversity and mutation accumulation increase extinction risk in wild populations in nature. There is now compelling evidence that inbreeding depression and loss of genetic diversity increase extinction risk in laboratory populations of naturally outbreeding species. There is now clear evidence for inbreeding depression in wild species of naturally outbreeding species and strong grounds from individual case studies and from computer projections for believing that this contributes to extinction risk. Further, most species are not driven to extinction before genetic factors have time to impact. The contributions of mutation accumulation to extinction risk in threatened taxa appear to be small and to require very long time spans. Thus, there is now sufficient evidence to regard the controversies regarding the contribution of genetic factors to extinction risk as resolved. If genetic factors are ignored, extinction risk will be underestimated and inappropriate recovery strategies may be used.	**Conservation Genetics**

Jennifer A. Marshall Graves	ARC Centre for Kangaroo Genomics, Research School of Biological Science, Australian National University, Canberra, ACT 2601, Australia	**Exploring genomes of weird mammals**	Marsupial and monotreme mammals fill a phylogenetic gap i vertebrate species lined up for exhaustive genomic study. Huma and mice (~70MY) are too close to distinguish signal an mammal/bird comparisons (~310MY) are too distant to allo alignment, but kangaroos (180 MY) and platypus (210 MY) may b just right. Sequence has diverged sufficiently for stringent detectio of homologies that can reveal coding regions and regulatory signals Importantly, marsupials and monotremes share with humans man mammal-specific developmental pathways and regulatory system such as sex determination and X chromosome inactivation. The ARC Centre for Kangaroo Genomics is characterizing the genome of the model Australian kangaroo *Macropus eugenii* (the tammar wallaby), which is being sequenced by AGRF in Australia, with NIH. We are developing detailed physical and linkage maps of the genome to complement sequencing, and will prepare and array cDNAs for functional studies, especially of reproduction and development. Sequencing of the Brazilian short-tailed opossum *Monodelphis domestica* by the NIH allows us to compare distantly related marsupials. Sequencing of the genome of the platypus, *Ornithorhynchus anatinus* by the NIH is under way. We have isolated and completely characterized many BACs and cDNAs containing kangaroo and platypus genes of interest, and demonstrate the value of comparisons to reveal conserved protein domains and regulatory signals.	**Genome Evolution**
Paul Hebert	Department of Integrative Biology & Biodiversity Institute of Ontario, University of Guelph, Guelph, N1G 2W1	**DNA Barcodes and Biodiversity**	We live on a planet populated by millions of species, most of which remain unknown despite more than 250 years of scientific investigation. There is now a growing international effort to address this deficit by assembling a DNA barcode library for all eukaryotes. This work is based on the premise that sequence diversity in a short, standardized segment of the genome can reliably discriminate species in large assemblages of life. The effectiveness of this approach has now been validated for animals and pilot studies on other kingdoms of life suggest the generality of this result. As a consequence, the first global projects have been launched with plans to assemble comprehensive barcode libraries for all fishes and birds within just 5 years. Although DNA barcoding is primarily motivated by the joint goals of developing automated identification systems and completing the inventory of life, this horizontal survey of gene diversity will have broader impacts. Early results on animals have revealed a striking constraint on barcode divergences within species, suggesting either the near-universality of 'Eves' or the stripping of variation through selective sweeps. Barcode studies are also revealing new information about the ages and origins of species, the factors modulating rates of molecular evolution and shifts in nucleotide usage. As taxonomic coverage expands, there will be novel opportunities to explore evolutionary patterns on a grand scale.	**DNA Barcoding and Biodiversity**
Michael D Hendy	Allan Wilson centre for Molecular Ecology and Evolution Massey University Palmerston North New Zealand	**Rates and Dates**	The evolutionary history of a set of organisms has an historical time dimension. A putative phylogeny for these organisms should therefore also reflect a time component. When a phylogeny has been derived from comparative sequence analysis, the lengths of the branches are sometimes measured in terms of numbers of inferred substitutions. If a stochastic model of substitution with prescribed rates is assumed, then these numbers can be mapped to time intervals, from which the placement of the root, and the times of bifurcation can be inferred. The variation in path lengths from the root to the tips can suggest that the substitution rates are not uniform over the tree. We will consider how these rates could be estimated, such as using fossil evidence or in using mixtures of ancient and extant sequences. We will also consider how apparent rate variation might in fact be evidence of error in root placement, of inaccuracy in branch length estimates, or incorrect topology. The imposition of a molecular clock hypothesis reduces the number of parameters to be inferred in likelihood calculations. We have no direct evidence that a model that allows independent rates at each branch is realistic. We will also look at how bounding the rates can give useful bounds on the dates of divergence.	**Rates and Dates**
Ary A. Hoffmann	Centre for Environmental Stress and Adaptation Research, Departments of Genetics and Zoology, The University of Melbourne, Parkville 3010 Australia	**Using DNA markers for environmental monitoring: from Drosophila genes monitoring climate change to chironomid species monitoring aquatic pollutants**	Changes in the frequency of genes in populations and shifts in the distribution of cryptic species provide powerful tools to detect the impact of environmental changes at the biological level. I will illustrate these approaches by outlining the use of adaptive genetic markers in Drosophila to detect climate change, and the development of species-specific DNA markers in chironomids to detect different types of aquatic pollutants in water bodies. These approaches should prove useful in identifying subtle and diffuse environmental changes, and in isolating specific target pollutants for environmental management.	**Michael White Lecture**

Michael Hofreiter	Max Planck Institute for Evolutionary Anthropology, D04103 Leipzig, Germany	**Multiplex amplification of the complete mitochondrial genome of Mammuthus primigenius and the evolutionary relationship of mammoths, African and Asian elephants**	We have developed a multiplex PCR approach that in principle allows an entire mtDNA genome of over 16,000 bp to be amplified from late Pleistocene fossil remains using just two amplifications. We used this approach to amplify the entire mtDNA (16,771 bp) of the woolly mammoth (Mammuthus primigenius) from a bone from Berelesch, Yakutia, dated by accelerator mass spectrometry to 12,000 years before present. Phylogenetic analyses show that the mtDNA of the mammoth is more closely related to the mtDNA of the Asian elephant than the African elephant. However, the length of the common branch leading to the mammoth and Asian elephant mtDNA is less than 10 % of that leading to the African elephant. Thus, all three species diverged within a fairly short time during the late Miocene.	**Ancient DNA**
Craig P. Hunter	Harvard University, Molecular and Cellular Biology 16 Divinity Avenue, Cambridge, Massachusetts 02138	**The Molecular Genetics of Intercellular RNA Transport in Nematodes**	RNAi in C. elegans, whether induced by ingestion or injection of double-stranded RNA (dsRNA), spreads throughout the organism and is even transmitted to the progeny. We are investigating how gene-specific RNAi silencing information, most likely dsRNA, is transmitted between cells. Through forward genetic screens for systemic RNAi defective (sid) mutants we have identified five sid genes. Three of these, SID-1, SID-2, and SID-5, have been cloned and their structure, subcellular localization, and expression pattern have been informative for how double-stranded RNA can be transported into and between cells. SID-1 is required for spreading of RNAi between and within all tested cells and tissues. sid-1 encodes a large membrane protein that when expressed in heterologous cells can transport dsRNA across cellular membranes. Proteins homologous to SID-1 are present and widely expressed in vertebrates. SID-2 is a transmembrane protein expressed strongly in the intestine and localized to the apical membrane, lining the lumen and, unlike sid-1, is required for ingestion mediated RNAi only. SID-2 homologs while detectable in other Caenorhabditis species do not support ingestion mediated RNAi while expression of C. elegans SID-2 in C. briggsae confers the ability to initiate RNAi by feeding. SID-5 is a small, possibly secreted, highly conserved protein within nematodes that appears to be required to mediate transport of the silencing signal between tissues. Phenotypic analysis of sid-3 and sid-4 suggest that they may have a similar requirement. These studies may have a direct impact on the treatment of human genetic disease and viral infection because, although RNAi has been shown to effectively knock-down gene expression in cultured cells, a major obstacle remains efficient in vivo delivery of dsRNA into cells.	**Genes and Gene Expression**
Martin A. Lysak	Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AB, UK	**Genome evolution in crucifers (Brassicaceae)**	The sequencing of the Arabidopsis thaliana genome and the steadily improving information on phylogenetic relationships make possible a wide range of comparative studies between Arabidopsis and more than 3,300 higly diversified cruciferous species (Brassicaceae). Arabidopsis genomic resources and tiny genomes containing a low percentage of dispersed DNA repeats enabled large-scale karyotype comparisons within Brassicaceae. Comparative chromosome painting (CCP) using chromosome-specific Arabidopsis BAC clones (Bacterial Artificial Chromosomes) is used to identify homeologous chromosomes and chromosome regions in other Brassicaceae species. Data on comparative painting shed light on the origin of the A. thaliana karyotype (n=5) from an ancestral karyotype by chromosome number reduction from n=8 to 5. Chromosome fusions were accompanied by genome reshuffling including translocations and inversions, and genome size decrease. Comparable but independent reductions in chromosome number from n=8 to n=6 and 7 also occurred in other genera. CCP in combination with phylogenetic data also provides insights into polyploid evolution in several other cruciferous groups. The tribe Brassiceae (the Brassica clade) and the New Zealand genus Pachycladon are both descendend from ancestral polyploid progenitors. Polyploid events have been followed by genome diploidization including large karyotype rearrangements and chromosome number reduction in Brassiceae.	**Genome Evolution**

Uwe Maier	Philipps-University Marburg, Germany	**Primary, secondary and tertiary endosymbiosis**	Primary plastids, which are found in green algae, land plants, red algae and glaucocystophytes, are surrounded by a double membrane (plastid envelope) and evolved by the incorporation of a cyanobacterium-like cell and its reduction to a plastid. Other plastids, the complex plastids, originated from secondary endosymbiosis. Here, a eukaryotic phototroph with primary plastids was engulfed and reduced to a plastid surrounded by three or four membranes. Finally, few algae integrated a secondarily evolved alga and use it as a solar-powered factory (tertiary endosymbiosis). Some secondarily evolved algae harbour very small genomes. The resulting genetic compartmentalization and its implication for protein targeting will be presented by two examples, the cryptophytes and the dinoflagellates. No free-living cyanobacterium is known, which can be assigned as the closest relative to primary plastids. This situation complicates the reconstruction of genomic evolution in early steps of intracellular co-evolution. However, several intracellular cyanobacteria are identified, which can be used as model systems for the transition of free-living organisms to permanent intracellular symbionts. Results from a comparative genome project on an intracellular symbiont and its free-living relative will be furthermore presented.	**Genome Evolution**
John S. Mattick	Institute for Molecular Bioscience, University of Queensland, Brisbane QLD 4072, Australia	**The hidden layer of noncoding RNA in the evolution and development of complex organisms**	Recent evidence suggests that at least half of the genes in the mammalian genome do not encode proteins. Most of the mammalian genome is transcribed, the vast majority (~98%) of which is non-protein-coding RNA (comprising introns of protein-coding genes and introns and exons of ncRNA genes). These transcripts include complex clusters of overlapping and antisense transcripts, "intergenic" transcripts and pseudogene transcripts that appear to participate in both local and long-distance regulatory networks. Many of these transcripts are processed to smaller RNAs, called microRNAs, that control many aspects of development, including haematopoietic differentiation, adipocyte differentiation and insulin secretion, and are perturbed in cancer. MicroRNAs also regulate a variety of developmental processes in plants, and the RNA signaling is clearly involved in chromosome dynamics and epigenetic modification in plants, animals and fungi. In addition, a significant proportion of the mammalian genome appears to be under evolutionary selection, both positive and negative, including thousands of ultra-conserved sequences and transposon-free regions that have remained essentially unchanged throughout mammalian evolution. These observations, and the increasing number of complex genetic phenomena shown to be directed by regulatory RNAs, suggest that the majority of the genomes of mammals and other complex organisms is devoted to an advanced genetic operating system that is primarily transacted by RNA, which comprise a highly parallel network of quasi-digital, feed-forward regulatory signals that control the trajectories of differentiation and development via epigenetic memory, promoter selection and alternative splicing. Further evidence in support of this, including an information theoretic analysis and empirical data which show that regulatory networks are accelerating networks, and that introns contain sequences that are conserved elsewhere in the genome in functionally congruent clusters, will be presented. This system appears to occur in all multicellular organisms, as well as in a primitive version in yeast, and to progressively dominate genomic programming as complexity increases. If this is correct, our current conceptions of the genomic information content and the genetic programming of complex organisms will have to be radically reassessed, with implications for many aspects of animal and plant biology, including the genetic basis of quantitative trait variation.	**RNA World**
Axel Meyer	Lehrstuhl für Zoologie und Evolutionsbiologie Universität Konstanz, D-78457 Konstanz, Germany	**The evolution cichlids and their genomes: from trees to comparative genomics**	The species flocks of cichlid fishes in the large East African Lakes Victoria, Malawi and Tanganyika are well-known examples of adaptive radiations and explosive speciation. These species assemblages are the most species-rich and the most diverse, morphologically, ecologically and behaviorally among vertebrates. The understanding of the phylogenetic relationships among cichlid fish species flocks and the underlying evolutionary processes that might be responsible for their evolutionary success has increased dramatically during the last 15 years. Phylogenetic analyses of recent molecular data in the context of the geological history of the East African lakes helped to elucidate some aspects of the population history and the evolutionary processes that might have led to the extremely fast origination of these extraordinary fish faunas. I will review some of the recent advances and insights that were made both in terms of phylogenetic patterns as well as evolutionary processes. I will highlight promising research directions in comparative developmental and genomic approaches that already yielded insights into the genetic and genomic underpinnings of the phenotypic diversity of cichlid fish species flocks. I will also point out which avenues of research are still unexplored and suggest which type of future work might yield interesting insights into the origins of the adaptive radiations of the East African cichlid fishes.	**Bioinformatics and Phylogenetic Methods**

Jeffrey Mower	Department of Biology and School of Informatics Indiana University Bloomington, IN 47405 USA	**Quick and Accurate Prediction of RNA Editing Sites in Plant Mitochondrial Genes**	In plants, RNA editing is a post-transcriptional process that converts specific cytidines to uridines in transcripts from virtually all mitochondrial protein-coding genes. It is well established that this process tends to increase protein conservation across species by "correcting" codons that specify unconserved amino acids. Exploiting this principle and the codon-position-specific frequencies of RNA editing, a program (PREditor: Predictive RNA Editor) was developed that predicts sites of RNA editing for any known protein-coding gene in plant mitochondria. To test the program, edit sites were predicted for nearly 400 sequences using PREditor, and these predictions were then compared to the experimentally determined editing positions listed in Genbank or the literature. The test results show that PREditor correctly predicted the editing status for 98% of all cytidines in the tested sequences. Furthermore, editing site prediction took much less than one second for each gene. An online version of the program is available at http://www.preditor.org.	**Protein Evolution**
David Penny	Allan Wilson Center for Molecular Ecology and Evolution Massey University, P O Box 11-222 Palmerston North, New Zealand	**RNA-world and deep eukaryote evolution – the role of theory.**	Many models for the origin of eukaryotes are post-hoc in the sense that they are proposed after data has been collected. Here we explore an alternative approach where we start from theoretical limitations to sequence length in an RNA-world (the Eigen limit) and experimental results about the relative efficiencies of RNA and protein catalysis. From these observations, a natural extension is proposing a positive feedback loop, the Darwin-Eigen cycle, which allows successive increases in replication accuracy and coding capacity. Given the relative efficiency of protein catalysis compared with RNA catalysis, it is a prediction that RNA cannot take back a catalytic function that protein is already doing. Therefore, examples of widely dispersed RNA catalysis are good candidates for relics of an RNA-world. The unexpected result is that eukaryotes have far more ribozymes than 'prokaryotes', and is in RNA processing. The simple-minded prediction from a theoretical view is that these RNA processing RNA reactions are relics from the RNA-world, and that eukaryotes thus retain many ancestral features. A summary of predictions from the Eigen limit is presented.	**RNA World**
AK Prashanth	UC Davis Genome Centre	**Socio-behavioral variation and rapid evolution: DNA duplex destabilization at Regulatory DNA microsatellites as aN Underlying mechanism.**	Mutation by expansion and contraction of repeat DNA occurs at higher rates than single nucleotide mutations. Such mutations in microsatellite regions that may be present in regulatory regions of genes can contribute to the alteration of gene expression. In vole species, variation in the length of a microsatellite upstream of the vasopressin V1a receptor gene (avpr1a) has been associated with variation in social behavioral traits such as paternal care and social bonding (via variation in V1a receptor expression patterns in the brain). The repetitive nature of the microsatellite makes it unlikely that differences in cis regulatory elements are responsible for the differences in expression. Structural properties of DNA (such as ease of strand separation of the duplex) can be altered by repetitive DNA motifs, and such increased ease of strand separation can radically affect gene expression. To examine the susceptibility of the DNA duplex to separate to single strands, we have developed methods for calculating the stress-driven strand separation. Since stresses imposed on the DNA in vivo create long range coupling of the strand-opening behaviors of all base pairs that experience the stresses, in vivo, susceptibility to strand separation does not depend only on local DNA properties such as A+T content or thermodynamic stability. Here we apply these methods to assess the structural properties underlying DNA function at the polymorphic microsatellite region upstream of avpr1a gene. Our calculations show that the DNA sequences carrying a longer microsatellite allele in the vole displays more than a 2000-fold difference in propensities to unwind to single strands than the shorter allele. This difference could result in alteration of protein binding (e.g. transcription factors) in the neighborhood, and thus alter gene expression profiles in a cell-type specific manner. This difference in duplex destabilization between long and short microsatellite alleles may explain the differential gene expression of avpr1a and thus the differing social-behavioral traits. The avpr1a 5' regulatory region is very highly conserved between humans, bonobos and chimpanzees, with the exception of a 360bp microsatellite element that is missing in chimpanzees. This difference causes a zone of destabilization in the humans and bonobo microsatellite region, but not in the chimpanzee. These findings raise the possibility that in primates, as in voles, DNA duplex destabilization caused by microsatellite mutations in the avpr1a gene alter gene expression patterns and influence socio-behavioral traits.	**Molecular Ecology**

Paul Rainey	1Department of Plant Sciences, South Parks Road, Oxford OX1 3RB 2Glycobiology Institute, Department of Biochemistry, South Parks Road, Oxford OX1 3QU 3RMF Dictagene S.A., 4, Chemin de la Vulliette, CH-1000 Lausanne, Switzerland 4School of Biological Sciences, University of Auckland, P.O. Box 92019, Auckland, New Zealand	**Extensive pleiotropy underlies the evolutionary transition from single cells to simple undifferentiated groups**	The pleiotropic effects of adaptive mutations are key to the trade-offs thought to underpin evolutionary change. However, whilst such effects have frequently been inferred or invoked, they have rarely been studied in molecular detail. Mutations facilitating the evolutionary transition from single cells to simple undifferentiated groups in experimental populations of the bacterium Pseudomonas fluorescens are associated with deleterious pleiotropic effects. For one such mutation, a single base pair substitution in a gene encoding a component of a signalling pathway, the pleiotropic effects on protein expression have been characterised: 52 statistically significant changes in protein expression were detected (corresponding to 43 identifiable proteins). No overlap was observed between this set of proteins and proteins encoded by the many genes shown previously by suppressor analysis to be essential for the evolutionary transition. Correlation analysis of the expression patterns of these 52 proteins from independently derived genotypes, combined with data on environmental responsiveness, shows that this subset of proteins forms a single genetic module that encompasses specific metabolic pathways associated with amino acid degradation. Subsequent analysis shows that the underlying causal mutation 're-wires' the ancestral expression network by drawing specific proteins into tighter co-expression relationships.	**Microbial Evolution**
Hamish Spencer	Allan Wilson Centre for Molecular Ecology and Evolution, Department of Zoology, University of Otago, P.O. Box 56, Dunedin, New Zealand	**Polymorphism of Imprinting Status: What Does it Mean?**	Polymorphism of imprinting status is the situation in which, in a certain tissue at some stage of development, some members of a population have two active copies of a gene at an imprinted locus and other members have just one. I look at two different causes of such variation in levels of expression: (i) a heritable failure to imprint maintained by mutation-selection balance and (ii) a selectively balanced outcome of the evolutionary process that led to the evolution of imprinting. The first cause may be important in diseases in which biallelic expression is implicated, and I examine how well two theoretical models match the observed data for Wilms Tumour. The second cause allows discrimination among different hypotheses for the origin of imprinting, and I examine the possible examples of polymorphically imprinted loci. I conclude with a plea for molecular biologists to be more alert to the possibility of polymorphic imprinting status.	**Genetics of Disease and Human Evolution**
Theresa Wilson	Biochemistry, University of Otago, Dunedin, New Zealand	**Genomics of Livestock: the New Century**	The vast array of new genomic tools have led to a revolution and revitalisation of livestock genetics with the real possibility of determining the genetic basis that surrounds many of the complex traits of interest. Our group aims to utilise our core capabilities in genomics to identify genes conferring quality and production advantages to improve the competitiveness of New Zealand's sheep, cattle and deer industries. Thousands of years of animal breeding have led to genetic gains for desired traits and improving productivity has been the engine of growth in agriculture for the past 50 years. For the future, marker assisted selection, genomics and bioinformatics will be essential tools for offering new opportunities to make stepwise changes in livestock industries. Successes so far have included have been the identification of several genes involved in sheep prolificacy and beef meat tenderness. With the full sequencing of the bovine genome soon to be completed we will have new resources available including thousands of mapped validated SNPs. Significant research effort is required to track down the genetic basis of many complex traits, but we are fortunate in New Zealand to having a very receptive agricultural industry that provide sizable in-kind animal resources which enable genetic solutions to be tested.	**Agricultural Genomics**