

Primary Author	All Authors	Address	Poster Title	Poster Abstract
Alansari	Aliya Alansari, Aisha Al-Khayat, Andrew Spalton, Khamis Al-Dafry, Shoab AL-Zadjali	Diwan of Royal Court, Office of the Adviser for Conservation of the Environment, Dept of Biology, Sultan Qaboos University	<b>The molecular genetics of the Arabian leopard: Preliminary study.</b>	The Arabian Leopard is endemic to the Arabian Peninsula and has decreased dramatically over the last century. This is mainly due to human activities. It is classified as critically endangered and therefore studying its population genetics using molecular techniques will allow a better understanding of its genetic diversity in the wild. Four samples (1 tissue and 3 scats) were obtained to optimize the molecular techniques conditions before screening samples collected from the wild. To investigating the genetic distinctiveness, primers were designed to amplify 572 bp from the NADH5 gene and 108 bp from the mitochondrial control region. Also, primers were designed to amplify the ZFX/ZFY region for sex determination using SSCP. Successfully DNA has been extracted from the tissue sample and the 3 scats. The PCR conditions for the three reactions have been optimized. The NADH and control region for the 4 samples have been sequenced. Analysis of the sequences showed two substitutions within the NADH5 mtDNA sequence compared to the one in the Gene Bank. This is only a preliminary study and including the samples collected from the wild and their data analysis will provide a definitive conclusion. The results of this study will be of value to the conservation of the remaining Arabian Leopard population in Oman.
Alsop	Alsop A1, Wakefield M2, Wei K-J1, Deakin J1, Koina E1, Zenger KR3, Wang C3, Cooper DW4 and Graves J1	ARC centre for Kangaroo Genomics. 1 Comparative Genomics Group, Research School of Biological Sciences, The Australian National University, Canberra Australia. 2 Division of Immunology and Genetics, John Curtin School of Medical Research, The Australian National University, Canberra Australia 3 ReproGen, Faculty of Veterinary Science, University of Sydney, Sydney Australia. 4 School of Biology, Earth and Environmental Sciences, Faculty of Science, University of New South Wales, Sydney Australia.	<b>An Integrated cytogenetic map of the tammar wallaby</b>	The tammar wallaby ( <i>Macropus eugenii</i> ), the model species of Australian marsupials, is currently being whole genome shotgun sequenced to a depth of 2x coverage by the Australian Genome Research Facility and Baylor College of Medicine, with support from the Victorian Government and US NIH. To aid the sequence assembly and enable mapping of phenotypic traits to sequenced regions we are generating an integrated cytogenetic and linkage map, including markers associated with known genes that can be used for comparative mapping between species. We have used Fluorescence in situ hybridization (FISH) to localize fully sequenced BAC clones from the NISC comparative sequencing project, and end-sequenced BAC clones. Microsatellites from these clones have been placed on the linkage map (See Zenger et al poster). Microsatellites from the first generation linkage map have been used to isolate BAC clones and these markers added to the cytogenetic map. Additional microsatellites were isolated by library enrichment from BAC clones that had been cytogenetically mapped but not fully sequenced. We will present the integrated markers in the context of the cytogenetic map of tammar wallaby and its regions of shared synteny with the human and mouse genome.
Baldo	Laura Baldo1,2, Nathan Lo3 and John H. Werren2	1Department of Biology, University of California, Riverside, CA, USA 2Department of Biology, Rochester University, NY, USA 3School of Biological Sciences, The University of Sydney, Australia	<b>The Mosaic Nature of the Wolbachia Surface Protein</b>	Lateral gene transfer and recombination play important roles in the evolution of many parasitic bacteria. Here we investigate intragenic recombination in <i>Wolbachia</i> bacteria, considered among the most abundant intracellular bacteria on earth. We conduct a detailed analysis of the patterns of variation and recombination within the <i>Wolbachia</i> surface protein (WSP), utilizing an extensive set of published and new sequences from five main supergroups of <i>Wolbachia</i> . Analysis of nucleotide and amino acid variation confirms four hypervariable regions (HVRs), separated by regions under strong conservation (CRs). Comparison of shared polymorphisms reveals a complex mosaic structure of the gene, characterized by a clear intragenic recombining of segments among several distinct strains, whose major recombination effect is shuffling of a relatively conserved set of amino acid motifs within each of the four HVRs. Exchanges occurred both within and between the arthropod supergroups. Analyses based on phylogenetic methods and a specific recombination detection program (MAXCHI) significantly support this complex partitioning of the gene, indicating a chimeric origin of <i>wsp</i> . Although <i>wsp</i> has been widely used to define macro and micro-taxonomy among <i>Wolbachia</i> strains, these results clearly show that it is not suitable for this purpose. The role of <i>wsp</i> in bacterial-host interactions is currently unknown, but results presented here indicate that exchanges of HVR motifs are favored by natural selection. Identifying host proteins that interact with <i>wsp</i> variants should help reveal how these widespread bacterial parasites affect and evolve in response to the cellular environments of their invertebrate hosts.

<p><b>Beiko</b></p>	<p>Robert G. Beiko, Timothy J. Harlow and Mark A. Ragan</p>	<p>Institute for Molecular Bioscience and ARC Centre in Bioinformatics, The University of Queensland, Brisbane 4072 Australia</p>	<p><b>Genome Partners at the Prokaryotic Dance</b></p>	<p>Lateral genetic transfer is known to have played a role in the evolution of prokaryotic genomes, but the extent to which LGT has shaped these genomes remains controversial. We carried out a detailed phylogenetic analysis of over 220 000 proteins from 144 microbial genomes, and combined the strongly supported phylogenetic relationships into a reference supertree. This reference tree was highly consistent with relationships implied by 16S rDNA sequences and taxonomy based on e.g. cell wall structure, but some regions of this tree were supported by only a weak majority or even a minority of all relevant protein relationships. Where weak support for the reference tree is observed, the conflicting phylogenetic signal often favours the grouping of genomes from similar ecological niches, such as thermophiles or soil bacteria.</p>
<p><b>Bilgmann</b></p>	<p>Kerstin Bilgmann_3, Luciana M. Möller_3, Robert G. Harcourt_ Catherine M. Kemper_ Susan E. Gibbs_ and Luciano B. Beheregaray_</p>	<p>1. Marine Mammal Research Group, Macquarie University, Graduate School of the Environment, Sydney, NSW 2109, Australia. 2. South Australian Museum, North Terrace, Adelaide, SA 5000, Australia. 3. Molecular Ecology Laboratory, Macquarie University, Dept. of Biological Sciences, Sydney, NSW 2109, Australia.</p>	<p><b>Comparative population genetic structure of bottlenose and common dolphins in South Australian waters</b></p>	<p>In coastal waters of South Australia (SA) bottlenose dolphins (<i>Tursiops sp</i>) and short-beaked common dolphins (<i>Delphinus delphis</i>) are distributed parapatrically. Several individuals from both species die each year in fisheries interactions in Spencer Gulf, South Australia. There is a concern that this mortality may negatively impact on the viability of local dolphin populations. We are conducting a comparative analysis of the genetic diversity and population structure of bottlenose and common dolphins in SA, using 467bp of the mtDNA control region and seven microsatellite markers. Tissue samples (<i>T. sp</i>=184, <i>D. delphis</i>=140) were collected from carcasses by the South Australian Museum and from free-ranging dolphins by biopsy sampling. Mitochondrial DNA sequences show greater haplotypic and nucleotide diversity for common dolphins than for bottlenose dolphins. In addition, preliminary analyses of mtDNA and microsatellite data suggest a higher degree of genetic structuring for bottlenose dolphins than for common dolphins. The implications of these findings for our understanding of cetacean population structure and for identifying conservation units in coastal dolphins are discussed.</p>
<p><b>Blair</b></p>	<p>David Blair, Kim Sewell, Lester Cannon, Keith Crandall, Tim Littlewood and Susan Lawler</p>	<p>School of Tropical Biology, James Cook University, Townsville, Qld 4811, Australia. Department of Primary Industries, Cairns, Qld. Australia, and Cooperative Research Centre for the Great Barrier Reef World Heritage Area, Townsville, Qld. Australia.</p>	<p><b>Mitochondrial DNA Diversity in the Invasive Tropical Marine Mussel, <i>Perna viridis</i> and Differentiation from other <i>Perna</i> Species.</b></p>	<p>We have sequenced portions of the mitochondrial <i>cox1</i> and <i>nad4</i> genes from samples of the invasive tropical marine mussel, <i>Perna viridis</i> from northern Australia, Hong Kong, the Gulf of Mexico and Venezuela. Sequences from all localities are almost identical, consistent with the transport of this species around the world on ships. Sequences of the same region from the remaining two species of <i>Perna</i>, <i>P. perna</i> and <i>P. canaliculus</i> are distinctly different from each other and from those of <i>P. viridis</i>, so much so that it is difficult to design primers that will amplify portions of the region only from <i>Perna</i> species. Primers with the required levels of redundancy are likely to amplify DNA also from other mytilids. We are developing a PCR-based method for identifying <i>P. viridis</i> using material from any part of its life-cycle and to distinguish this species from its congeners.</p>
<p><b>Brown</b></p>	<p>Sarah C. Brown and N. Louise Glass <b>GSA</b></p>	<p>Department of Plant and Microbiology 111 Koshland Hall University of California Berkeley, CA 94720 USA</p>	<p><b>Microarray analysis of vegetative incompatibility in <i>Neurospora crassa</i></b></p>	<p>In <i>Neurospora crassa</i>, hyphal fusion between genetically distinct individuals leads to the formation of heterokaryons. If hyphal fusion occurs between individuals with different alleles at any het locus, growth arrest, hyphal compartmentation and cell death occur. We are investigating this vegetative incompatibility using a temperature sensitive mutant capable of forming stable heterokaryons at 34°C with an otherwise incompatible partner. The incompatible phenotype becomes evident within 30 minutes of transfer to 20°C. We are using oligonucleotide arrays to compare gene expression patterns in compatible and incompatible heterokaryons made with the temperature sensitive mutant at 34°C and 20°C. Results indicate the upregulation of stress-related genes and the down-regulation of protein synthesis and cell cycling in the incompatible heterokaryon, and little or no change in the compatible heterokaryon.</p>

<p><b>Cai</b></p>	<p>James Jing Cai, David K Smith, Xuhua Xia and Kwok-Yung Yuen</p>	<p>Department of Microbiology, University of Hong Kong, Department of Biochemistry, University of Hong Kong, Department of Biology, University of Ottawa, Canada</p>	<p><b>MBEToolbox : A Matlab Toolbox for Sequence Data Analysis in Molecular Biology and Evolution</b></p> <p>Matlab is a high-performance language for technical computing, integrating computation, visualization, and programming in an easy-to-use environment. However, few functions are freely available in Matlab to perform the sequence data analyses specifically required for molecular biology and evolution. We have developed a Matlab toolbox, called MBEToolbox, aimed at filling this gap by offering efficient implementations of the most needed functions in molecular biology and evolution. It can be used to manipulate aligned sequences, calculate evolutionary distances, estimate synonymous and nonsynonymous substitution rates, and infer phylogenetic trees. Moreover, it provides an extensible functional framework for users with more specialized requirements to explore and analyze aligned nucleotide or protein sequences from an evolutionary perspective. The full functions in the toolbox are accessible through the command-line for seasoned Matlab users. A graphical user interface, that may be especially useful for non-specialist end users, is also provided.</p>
<p><b>Caramelli</b></p>	<p>David Caramelli 1, Albano Beja Pereira 2,3, Martina Lari 1, Cristiano Vernesi 4, Guido Barbujani 4, Carles Lalueza Fox 5, Gordon Luikart 2, Giorgio Bertorelle 4.</p>	<p>1Dipartimento di Biologia Animale e Genetica, Laboratori di Antropologia, Università di Firenze, via del Proconsolo 12, 50122, Firenze, Italy</p> <p>2Laboratoire d'Ecologie Alpine - Génomique des Populations et Biodiversité, CNRS UMR 5553, Université Joseph Fourier, B.P. 53, 38041 Grenoble, Cedex 9, France.</p> <p>3Centro de Investigação em Biodiversidade e Recursos Genéticos (CIBIO-UP) and Secção Autónoma de Engenharia de Ciências Agrárias, Universidade do Porto, 4485- 661 Vairão, Portugal</p> <p>4Dipartimento di Biologia, Università di Ferrara, via Borsari 46, I- 44100 Ferrara, Italy</p> <p>5Secció Antropologia, Departamento Biologia Animal, Facultat de Biologia, Universitat de Barcelona, Spain.</p>	<p><b>Italian aurochsen in the Palaeolithic had cattle-like mtDNA</b></p> <p>The genetic analysis of modern and ancient samples has been used in the last ten years to understand different aspects of the cattle domestication from its wild ancestor, the aurochs. Six aurochs samples from Britain are genetically distinct from all the modern samples. As far as Europe is concerned, this result is regarded as a strong evidence that European breeds descend from Middle-Eastern or Anatolian Neolithic immigrants, spread in the continent by humans during the demic diffusion of farmers and farming practices, with no major introgression of local aurochsen. Additional support for this hypothesis comes from the pattern of genetic variation observed within modern breeds from different regions. Here we present the genetic variation observed in five Italian aurochs specimens dated between 7,000 and 17,000 years BP. The mtDNA hypervariable control region was typed following the most stringent current standards for validation of ancient DNA. All the sequences fall within the range of variation of modern cattle, with no resemblance with the British aurochsen. Three of them are identical, and the same sequence is found in 60% of the individuals in a sample of Italian breeds but only in 30% in a sample of Middle-Eastern and Anatolian animals. The level of genetic divergence between Italian and British aurochsen is consistent with the presence of a strong and ancient geographic structure in this species. The genetic similarity between Italian (and not British) aurochsen and modern cattle argue against the simple hypothesis that European aurochsen did not contribute to the genetic composition of modern breeds.</p>
<p><b>Carlsson</b></p>	<p>Britt-Louise Carlsson1, Alan N Wilton1 and David Jenkins2</p>	<p>1School of Biotechnology and Biomolecular Sciences, University of New South Wales, NSW 2052, Australia, 2Australian Hydatid Control and Epidemiology Program, Fyshwick, NSW, Australia</p>	<p><b>The Imminent Extinction of the Australian Dingo</b></p> <p>Recent contact between European domestic dogs and dingoes has lead to a large amount of hybridisation. To examine the extent of hybridisation, 20 microsatellites with different allele profiles in dogs and dingoes have been typed in 1500 wild canids from across Australia. In most areas only 10 to 15% of animals show NO evidence of European dog ancestry. The Fraser Island population is the only east coast population tested with very low levels of dog introgression. Is the dingo doomed to extinction in the wild? It is gradually being replaced by dogs and hybrids which are likely to be larger and breed more often than dingoes, thus increasing pressure on other endangered native species. The management of these wild dog populations, which are an agricultural pest, while trying to conserve the dingo is a fine balancing act for wildlife managers. There is little in the way of practical solutions to save the dingo in the wild because it is so closely related to the dog. Additional DNA tests to improve hybrid detection are being implemented and dingo reference material other than living captive animals are being examined to better characterise the DNA profile of pure dingoes, such as museum skulls that have assessed pure by skull morphometrics.</p>

<p><b>Chen</b></p>	<p>Zhenzhong Chen, Ayscha Hill-Williams, John A. McKenzie, Philip Batterham</p>	<p>Centre for Environmental Stress and Adaptation Research (CESAR), Department of Genetics, Bio21 Institute of Molecular Science and Biotechnology, The University of Melbourne, Victoria 3010, Australia</p>	<p><b>Overexpression of cytochrome P450 genes and insecticide resistance in the sheep blowfly, <i>Lucilia cuprina</i></b></p>	<p>Cytochrome P450 enzymes provide an important mechanism of insecticide resistance in many insect species. Some cytochrome P450 enzymes are able to detoxify xenobiotic compounds. We have cloned 31 P450 genes in <i>L. cuprina</i> including members of the Cyp4, Cyp6, Cyp9 and Cyp12 gene families that have been implicated in resistance in other insect species. To identify the resistance-associated P450s, the expression levels of the Cyp6, Cyp9 and Cyp12 genes were investigated in susceptible strain (M1,5) and a recently isolated field strain (Tara), which is resistant to chemically diverse insecticides. Three genes (Cyp6a2, Cyp6a8 and Cyp12a2) are highly up regulated in the resistant field strain. One or more of these genes may be responsible for the metabolic detoxification of insecticides. <i>Lucilia</i> Cyp6g1 is not up regulated in the Tara strain, although the sequence is high identity to <i>Drosophila</i> Cyp6g1 that confers resistance in that species. Full length sequences of the Cyp6a2, Cyp6a8 and Cyp12a2 genes have revealed amino acid replacements that distinguish the resistant and susceptible strains. Analysis of PCR-RFLPs indicates that Cyp6A2 and Cyp6A8 are linked on the same chromosome as resistance (chromosome 4). All of the <i>L. cuprina</i> P450 genes and a range of housekeeping genes of have been printed on a DNA microarray to facilitate further studies on resistance phenotypes and the overexpression.</p>
<p><b>Chen</b></p>	<p>Min Chen<sup>1</sup>, Roger Hiller<sup>2</sup>, and Anthony Larkum<sup>1</sup></p>	<p><sup>1</sup>School of Biological Sciences, The University of Sydney, NSW 2069, Australia <sup>2</sup>School of Biological Sciences, Macquarie University, NSW 2109, Australia</p>	<p><b>Evolution of chlorophyll antenna complexes in oxyphotobacteria</b></p>	<p>Two light-harvesting genes have been cloned from genomic DNA in the chlorophyll d-containing cyanobacterium <i>Acaryochloris marina</i> and named pcbA and pcbC. Phylogenetic tree reconstruction using distance matrix and maximum likelihood methods indicated that these genes are homologous with the pcb and isiA genes of the oxyphotobacteria and also suggests a single origin of the pcb gene family, whether occurring in Chl b- or Chl d-containing organisms. This may indicate widespread lateral transfer of the Pcb-based light-harvesting system. Real time RT-PCR confirms that the two pcb genes in <i>Acaryochloris</i> possess different transcript levels under various iron nutrient conditions, although the two pcb genes are linked with an 270 bp non-coding nucleotides between them. Furthermore, investigation on the structure and function of Pcb proteins in <i>Acaryochloris</i> revealed that there are two types of antenna-reaction centre supercomplexes in <i>Acaryochloris</i>; 16-mer pcbs associated with a tetramer of PSII reaction core under normal culture conditions and 18-mer Pcbs associated with a trimer of PSI reaction cores under iron-stressed conditions. Using peptide fingerprinting analysis combined with RT-PCR and ultrastructural modeling analyses, we are able to identify PcbA, encoded by pcbA, as part of the structure of the Pcb-PSII core supercomplex, and PcbC, encoded by pcbC, as part of the Pcb-PSI supercomplex under iron-stress conditions. Phylogenetic tree reconstruction provides further evidence; there are two groups of pcbs in oxyphotobacteria; one is associated with PSI, which is closer to the isiA clade in phylogenetic trees, and the other may be associated with PSII supercomplexes. Comparing the structure and function of the membrane-bound photosynthetic antenna reaction centre supercomplexes present in oxyphotobacteria, we will discuss how variations in the organisation of these complexes have enabled oxyphotobacteria to exploit different ecological niches and we will also discuss the evolutionary relationships within the IsiA/Pcb family of pigment-binding proteins.</p>
<p><b>Chen</b></p>	<p>Sylvia (Xiaowei) Chen</p>		<p><b>Evolution of eukaryotic non-coding RNA: insights from the RNA library of early eukaryote <i>Giardia Intestinalis</i></b></p>	<p>In general, the evolutionary stages of eukaryotes are closely associated with the acquisition of complex organelles and integration of cellular structure and cell types. Non-coding RNAs play important roles in cellular metabolism and their functions appear to diversify as the size of genome increases, whereas most of the fundamental properties of non-coding RNAs remain unchanged. The deep-branching eukaryote <i>Giardia Intestinalis</i> had long been regarded as a model organism representing the transition state from prokaryotes to eukaryotes, until the discovery of mitochondria-like organelle and a spliceosomal intron in <i>Giardia</i>. Its "primitive" position has now been questioned. However, highly reduced ribosomal RNA and many archaeobacteria-like features of the transcription machinery still suggest that <i>Giardia</i> belongs to one of the earliest eukaryotes. In this project, a library is constructed for non-coding RNAs of <i>Giardia</i>, and secondary structures of these RNAs are proposed according to sequence motifs. The analysis focuses on small RNA species involving in cellular metabolism such as the small nuclear RNAs (snRNAs) and small nucleolar RNAs (snoRNAs). The snRNAs in <i>Giardia</i> are of particular interest since the discovery of snRNAs will lead to identification of a functional spliceosome, which is proposed to be present in <i>Giardia</i> through the discovery of a spliceosomal intron and several spliceosomal-protein gene homologues.</p>

	<p>(Sylvia Chen Abstract continued)</p> <p>Although the reduced genome of <i>Giardia</i> suggests reduced types of non-coding RNA, from early studies unknown small RNA species (below tRNA range) have been suggested to be present in <i>Giardia</i>, including microRNAs, however there is yet no experimental proof. In all, this study will reveal the types and functions of novel non-coding RNAs in a model organism of early eukaryotes and shed light on the evolution of non-coding RNAs through comparison with the known RNAs in higher eukaryotes.</p>
<p><b>Collinge</b></p> <p>Derek Collinge<sup>1-2</sup>, Karl Gordon<sup>1</sup>, Carolyn Behm<sup>2</sup>, Steve Whyard<sup>3</sup>.</p> <p>1. CSIRO Entomology Canberra, Australia, 2. The Australian National University Canberra, Australia, 3. University of Manitoba, Canada.</p>	<p><b>Delivering a Silent Punch: Stable Transformation and RNAi in <i>Helicoverpa armigera</i></b></p> <p><i>Helicoverpa armigera</i> is Australia's most significant pest of cotton crops causing extensive crop damage and costing millions in control measures each year. A biological alternative to the use of broad spectrum insecticides to control <i>H. armigera</i> outbreaks is very attractive due to the rapid build up of insecticide resistance. My project will assess the feasibility of using RNA interference (RNAi) to specifically knock down essential growth and development genes in <i>H. armigera</i> as a potential species-specific control measure. Microinjection is a well established method of delivering gene constructs into model insects such as <i>Drosophila</i> and <i>Anopheles</i>, however this technique is still being perfected in Lepidopterans. I have been using microinjection to deliver a transposon-based (piggyBac) GFP reporter construct into <i>H. armigera</i> eggs in an attempt to get stable integration of GFP into the hosts genome. In the same way microinjection is being used to introduce dsRNA into <i>H. armigera</i> as a way of studying the parameters of RNAi in a new insect. RNAi will also allow me to test the function of targeted genes such as the <i>H. armigera</i> orthologue to the <i>Drosophila</i> "white" gene and may ultimately help identify targets for insect control.</p>
<p><b>Cook</b></p> <p>Catherine A. Cook, Xin An, Kathryn A. Raphael.</p> <p>Fruit Fly Research Centre, School of Biological Sciences A12, University of Sydney NSW 2006</p>	<p><b>The Role of cryptochrome in Mating Time Difference in Tephritid Fruit Flies</b></p> <p>The Queensland fruit fly (<i>Bactrocera tryoni</i>) and its sibling species <i>Bactrocera neohumeralis</i> occur sympatrically in eastern Queensland. Despite being very closely related at the level of DNA sequence, the two species are reproductively isolated by time of mating, which is genetically determined. The species provide an ideal system for studying the molecular basis of a difference in mating time. The endogenous clock influences daily patterns of behaviour through molecular outputs of the central pacemaker. The cryptochrome (<i>cry</i>) gene encodes a light sensitive component of the circadian clock, involved in entraining the endogenous clock to external light. The <i>cry</i> transcript cycles in abundance in the brain and antennae of both species. <i>cry</i> mRNA is more abundant in <i>B. neohumeralis</i> than <i>B. tryoni</i>, a relationship that is duplicated in hybrid lines selected for dusk and day mating time. We are using RNA interference (RNAi) to down-regulate <i>cry</i> expression in antennae and brain in order to test the role of <i>cry</i> in determining mating time. The results of experiments designed to test RNAi in live adult flies will be reported. Double stranded RNA will be synthesised from three DNA fragments that overlap to span the entire coding region of the <i>cry</i> gene. Antennae of flies will be soaked in solutions of long double-stranded RNA fragments and/or short 21 nucleotide RNA fragments (produced by RNaseIII digestion of long fragments), then removed to test for down-regulation by real-time PCR. The effect of <i>cry</i> down-regulation on mating time of flies will be tested.</p>
<p><b>Corrigan</b></p> <p>Shannon Corrigan<sup>1</sup>, Tonia S. Schwartz<sup>1</sup>, Charlie Huvneers<sup>2</sup> and Luciano B. Beheregaray<sup>1</sup></p> <p>1Molecular Ecology Group for Marine Research, Department of Biological Sciences, Macquarie University, Sydney, NSW, 2109.; 2Graduate School of the Environment, Macquarie University, Sydney, NSW, 2109.</p>	<p><b>Conservation Genetics of Wobbegong Sharks (<i>Orectolobus</i>) in Australian Waters</b></p> <p>Compared with teleost fishes, sharks are relatively long lived, experience slow growth rates, exhibit long interbirth intervals and lower fecundity. These life history characteristics render sharks particularly susceptible to anthropogenic impacts, such as stock depletion through over fishing. The spotted wobbegong (<i>Orectolobus maculatus</i>) and the ornate wobbegong (<i>O. ornatus</i>) are examples of shark species affected in Australian waters. Wobbegongs are targeted in ocean trap and line fisheries and commercial landings of these sharks have declined substantially in recent years. Despite being a well-recognized large marine predator, basic research on aspects of wobbegong population biology is essentially non-existent. Here we present the early stages of a conservation oriented project which aims to (i) elucidate current and historical patterns of population genetic structure of wobbegong sharks and (ii) describe their mating system.</p>

	<p>(Shannan Corrigan abstract continued)</p> <p>Our study is based on a large sample of both spotted and ornate wobbegongs from the east coast of Australia and on samples of a recently identified "dwarf" morphotype that matures at a smaller size and appears to be reproductively isolated from other wobbegong species. Preliminary analyses based on mitochondrial DNA cytochrome b and control region sequences provide strong support for lineage sorting among the three morphotypes. However, regardless of using a large sample (n = 158), we detected very low haplotypic and genetic diversity within each species. We also developed an enriched microsatellite library for wobbegong sharks. Despite the success of the enrichment procedure, the identification of polymorphic microsatellite markers is proving quite problematic. Analyses based on microsatellites will not only provide an opportunity for identifying conservation units in wobbegong sharks, but also through parentage analyses will allow accurate investigations of the breeding system of these animals.</p>
<p><b>Coucheron</b></p> <p>Dag H. Coucheron, Kari Haugli, and Steinar D. Johansen</p> <p>Department of Molecular Biotechnology, IMB, University of Tromsø, Tromsø, Norway</p>	<p><b>Phylogeny of the Physaridae slime molds (and other Myxomycota) based on a combined data-set of nuclear small subunit and large subunit ribosomal DNA sequences</b></p> <p>The evolutionary relationships of the myxomycete orders, families, and taxa are largely unknown. Inference of phylogenetic relationships for a variety of species at different taxonomic levels has been based extensively on ribosomal (rRNA) gene sequences. Currently we have obtained ca. 250,000 bp unique rDNA sequences from approximately 40 different species/isolates of myxomycota, with focus on the Physaridae myxomycetes. We have performed phylogenetic analyses based on conserved sequence regions from both the small subunit (SSU) and large subunit (LSU) rRNA genes of species representing both the myxomycete, dictyostelid, and protostelid slime molds. The myxomycete taxa are: Echinosteliida (Echinostelium), Stemonitida (Stemonitis and Comatricha), and Physarida (Physarum [10 species], Badhamia [2 species], Fuligo, Physarella, Diderma, Lepidoderma, and Didymium [6 species]). In addition to the myxomycetes, one species representing the protostelids (Soliformovum) and two species representing the dictyostelid cellular slime moulds (Acytostelium, Dictyostelium) were included. The analyses indicate that the myxomycete, dictyostelid, and protostelid slime molds are early branching protists, but not of monophyletic origin. However, all the myxomycete taxa appear monophyletic. Here we discuss aspects of the phylogeny of the Physaridae myxomycetes in more detail.</p>
<p><b>Damiano</b></p> <p>JOHN DAMIANO, Trent Perry and Philip Batterham</p> <p>Centre for Environmental Stress and Adaptation Research (CESAR), Department of Genetics, Bio21 Molecular Science and Biotechnology Institute, University of Melbourne.</p>	<p><b>RESISTANCE: TO BE OR NOT TO BE – SCREENING THE GENOME FOR MUTANTS.</b></p> <p>Mutations in genes can point to their function. Many insecticides are used without the knowledge of their mode of action or of the genes that encode the target. It is only when resistance to an insecticide develops, that the mode of action and the genes involved in resistance can be determined. With this background we have performed a genome-wide forward genetics screen to discover insecticide resistant mutants.</p> <p>Drosophila melanogaster, the model genetic insect species, was employed for this screen. The Zuker collection, a series of 12,000 chromosomally balanced EMS mutagenised lines was screened for sensitive and resistant mutants. Two different insecticides were used for screening - nitenpyram, a neonicotinoid used in flea control, and cyromazine, an insect growth regulator employed for the control of fly strike in sheep.</p> <p>Sensitivity was characterized as zero emergence on an insecticide concentration that would kill 50% of wild type individuals. Resistance was determined by the emergence of greater than 5 individuals on a concentration double that required to kill 95% of wild type individuals. To date, 2,300 lines with mutations on the 2nd chromosome have been screened; putative mutants were re-screened. No cyromazine resistant mutants were recovered. However we have found 11 sensitive mutants. Several nitenpyram mutants have also been discovered, 7 which are sensitive and 9 resistant.</p> <p>The cloning of the resistance/sensitivity genes will give us a better understanding of a) the proteins that are targeted by the insecticide and b) the range of genes that can confer resistance to these insecticides.</p>

<p><b>de Salas</b></p>	<p>de Salas, M.F.1, , Koutoulis, A.1, Rhodes, L.L.2, and Hallegraeff, G.M.1</p> <p>1 School of Plant Science, University of Tasmania, Private Bag 55, Hobart 7001, TAS, Australia.</p> <p>2 Cawthron Institute, 98 Halifax St. East, Nelson, New Zealand</p>	<p><b>Genetic diversity in unarmoured dinoflagellates: design of molecular probes</b></p>	<p>A survey of unarmoured dinoflagellates in Australian waters uncovered several previously described species of fish-killing dinoflagellates in the genera <i>Karenia</i> and <i>Karlodinium</i> and <i>Takayama</i>. Species in these genera are very difficult to identify using light microscopy and have posed problems both for aquacultured and wild fish stocks. Sequencing of the large subunit (28S) ribosomal gene, which contains regions of high variability, has allowed a comprehensive picture of dinoflagellate phylogeny to be built. Comparison of sequenced species with data obtained from GenBank has allowed the development of molecular probes targeting both rRNA and rDNA. New rRNA-targeted, fluorescent in-situ hybridisation (FISH) probes have been developed for <i>Karenia umbella</i>, <i>Karlodinium micrum</i> the genus <i>Takayama</i>, and <i>Takayama tasmanica</i> (species specific), which are known fish killers, as well as <i>Gymnodinium aureolum</i>, which is sometimes confused with potentially toxic species. New quantitative PCR probes targeting the 28S rDNA have been developed for <i>Takayama tasmanica</i>, <i>Karenia umbella</i> and <i>Karenia brevisulcata</i>. The use of these probes to detect and quantify toxic species below the level at which they can generally be detected using light microscopy will help reduce their impact on wild and aquacultured fish and human health.</p>
<p><b>Docking</b></p>	<p>T. Roderick Docking and Daniel J. Schoen</p> <p>Department of Biology, McGill University, Montréal, Québec, Canada</p>	<p><b>Retrotransposon Sequence Variation in Four Asexual Plant Species</b></p>	<p>Transposable elements (TEs) are expected to spread within sexual populations, but become eliminated or inactivated within asexual populations. While previous work with animals has shown that asexual taxa may contain less TE diversity than sexual taxa, comparable work in plants has been lacking. Here we report the results of a study of Ty1/copia, Ty3/gypsy and LINE-like retroelement diversity in four asexual plant species. Retroelement-like sequences with a high degree of conservation both within and between species, were isolated from all four species. The sequences correspond to several previously annotated retroelement subfamilies, and exhibit a pattern of nucleotide substitution characterized by an excess of synonymous substitutions, suggestive of a history of purifying selection. One likely explanation for the discovery of conserved TE sequences in the genomes of these asexual taxa is that asexuality within these taxa has evolved relatively recently, such that the loss and breakdown of TEs is not yet detectable through analysis of sequence diversity. This explanation is examined using stochastic simulation of TE evolution and information obtained from molecular divergence within the asexual taxa examined.</p>
<p><b>Druzhinina</b></p>	<p>Irina S. Druzhinina, Alexei G. Kopchinski, Monika Komon, and Christian P. Kubicek</p> <p>Division of Gene Technology and Applied Biochemistry (DGTAB), Institute of Chemical Engineering, University of Technology, Getreidemarkt 9/1665, A- 1060 Wien, Austria;</p>	<p><b>An oligonucleotide barcode for species identification in Trichoderma and Hypocrea</b></p>	<p>One of the biggest impediments to studies on <i>Trichoderma</i> has been the incorrect and confused application of species names to isolates used in industry, biocontrol of plant pathogens and ecological surveys, thereby making the comparison of results questionable. Here we provide a convenient, on-line available method for the quick molecular identification of <i>Hypocrea</i> and <i>Trichoderma</i> on the genus and species levels based on an oligonucleotide barcode, a diagnostic combination of several oligonucleotides (hallmarks) specifically allocated within the internal transcribed spacer 1 and 2 (ITS1 and 2) sequences of rDNA repeat. The barcode was developed on the basis of 979 sequences of 88 vouchered species which displayed in total 142 ITS1 and 2 haplotypes. Oligonucleotide sequences which are constant in all known ITS1 and 2 of <i>Hypocrea</i> and <i>Trichoderma</i> but different in closely related fungal genera, were used to define genus specific hallmarks. The library of species-, clade- and genus-specific hallmarks is stored in the MySQL database and integrated in the TrichOKey v1.0 - barcode sequence identification program with the web interface located on <a href="http://www.isth.info">www.isth.info</a>. TrichOKey v1.0 identifies 76 single species, 5 species pairs and 1 species triplet. Verification of the DNA-barcode was done by a blind test on 53 unknown isolates of <i>Trichoderma</i>, collected in Central and South America. The obtained results were in a total agreement with phylogenetic identification based on <i>tef1</i> (large intron), NCBI BLAST of vouchered records and postum morphological analysis. We conclude that oligonucleotide barcoding is a powerful tool for the routine identification of <i>Hypocrea/Trichoderma</i> species and should be useful as a complement to traditional methods.</p>

<p><b>Duffy</b></p>	<p>Angela Duffy and Peter B. Mather <b>GSA</b></p>	<p>School of Natural Resource Sciences, Queensland University of Technology, GPO Box 2434, Brisbane, Qld 4001, Australia.</p>	<p><b>Isolation by distance at small spatial scales in lacustrine populations of freshwater turtles.</b></p>	<p>The freshwater turtle <i>Emydura krefftii</i>, is the predominant vertebrate species in the perched dune lakes of Fraser Island, Australia and as such represents an important component of the depauperate fauna in these fragile habitats. While some species of freshwater turtle are known to disperse widely among freshwater habitats, previous mark-recapture studies of <i>E. krefftii</i> in two lakes 1km apart found no evidence of dispersal between lakes. In order to get an insight into historical patterns of gene flow in these long lived animals, we examined the population genetic structure of 137 turtles from five lakes in an area 6km x 2km. Data from 555bp of control region mtDNA showed significant genetic structuring among lake populations with a pattern of isolation by distance (<math>r=0.971</math>, <math>p&lt;0.03</math>) even at this small spatial scale. These findings have significant implications for the management of turtle populations which in some lakes are threatened by the pressure of increasing tourism in the region.</p>
<p><b>Duffy</b></p>	<p>Angela Duffy, Satya Nandlal and Peter B. Mather <b>GSA</b></p>	<p>1 School of Natural Resource Sciences, Queensland University of Technology, GPO Box 2434, Brisbane, Qld 4001, Australia. Email: p.mather@qut.edu.au 2 Secretariat of the Pacific Community, BPD5, 98848, Noumea Cedex, New Caledonia.</p>	<p><b>Phylogeography of a pan tropical freshwater prawn with extensive marine larval dispersal potential.</b></p>	<p>While marine species with extensive pelagic larval dispersal potential tend to show patterns of gene flow at large spatial scales, those with a distribution that spans multiple biogeographic regions may none the less show differentiation across these regions. We examined the broadscale phylogenetic structure of the pan tropically distributed giant freshwater prawn <i>Macrobrachium</i> lar. Adults inhabit perennial freshwater streams but the species is diadromous with larvae completing at least 11 zoal stages (taking over 89 days) in the marine realm before returning to freshwater habitats as post-larvae. The life history characteristics of this species therefore result in them having the potential for extensive larval dispersal, similar to many marine species. Results to date, using a combination of 509bp 16SrRNA and 604bp COI mtDNA, have revealed the presence of four main clades across M.lar's distribution. Clade 1 was widespread containing populations from the Samoan islands in the eastern Pacific though to New Caledonia, Micronesia and New Britain and extending into Malaysia and Christmas Island (Indian Ocean). The remaining three clades were more restricted with Clade 2 containing populations from mainland Australia and Papua New Guinea, Clade 3 found only in the Madagascan samples and Clade 4 restricted to the Cook Islands. These results suggest that despite the potential for widespread dispersal, oceanographic features may restrict gene flow in some populations.</p>
<p><b>Ezawa</b></p>	<p>Kiyoshi Ezawa1, Satoshi Oota2, and Naruya Saitou1</p>	<p>1 Division of Population Genetics, National Institute of Genetics, Yata, Mishima 411-8540, Japan 2 Bioresource Center, RIKEN, Tsukuba 305-0074, Japan</p>	<p><b>An Extensive Search for Gene Conversion Events in Mouse and Rat Genomes</b></p>	<p>Gene conversion, also known as non-reciprocal recombination, is considered to play important roles in the formation of genomic makeup such as homogenization of multigene families and diversification of alleles. In order to figure out a genome-wide picture of gene conversion events, we searched mouse and rat cDNA sequences stored in the Ensembl database (<a href="http://www.ensembl.org">http://www.ensembl.org</a>) for traces of gene conversion. Our gene conversion search is based on a 2-step statistical test conducted on 'quartet's. Each quartet consists of 2 pairs of orthologous sequences supposed to have generated by a duplication event and a subsequent speciation of 2 closely related species. In order to enhance the detection sensitivity, we combined our method with S. Sawyer's GENCONV (<a href="http://www.math.wustl.edu/~sawyer">http://www.math.wustl.edu/~sawyer</a>). Out of approximately 2,500 quartets we sampled, about 300 showed highly significant signs of gene conversion. This set of positive quartets is not likely to contain more than one false positive, according to an estimation with computer simulations. We statistically analyzed how the gene conversion frequency correlates with the linkage, the physical and evolutionary distances, and the relative orientation between genes of the same species. We also examined whether or not genes of particular functional categories are prone to gene conversion.</p>
<p><b>Fang</b></p>	<p>Shu Fang, Yen-Po Lin, Yu-Po Chen, and Shun-Chern Tsaur</p>	<p>Research Center for Biodiversity, Academia Sinica, Taipei, Taiwan, ROC</p>	<p><b>Evolution of Acp26Aa, the Male Accessory Gland Protein Gene, in <i>Drosophila mauritiana</i></b></p>	<p>Many genes related to reproductive success tend to evolve rapidly. One particular group of reproductive-related proteins, the accessory gland proteins (Acp's) of <i>Drosophila</i>, has been the subject of much research. Acp's, a major component of <i>Drosophila</i> seminal fluid, have several demonstrated effects on female physiology, and sperm use. Among them, Acp26Aa has attracted considerable interest. Comparing with other members of melanogaster subgroup, a very high level of amino acid polymorphism of Acp26Aa has been observed in <i>D. mauritiana</i>. Among 22 lines surveyed, three major indel variants, namely W, D1, and D2, are highly polymorphic in both laboratory strains and natural populations. It is, therefore, our intention to identify what driving force(s) maintaining this polymorphism in the nature.</p>

(Shu Fang abstract continued)

To see if the individual numbers will finally outcompete/replace the pre-existed dominant genotypes, pairwise crossing tests among three genotypes were performed with the reciprocal proportions of 1:9, and 1:1. Two replicates were carried out for each ratio. Each fifty males and females were sacrificed for genotyping three major alleles from each cage every five plus the first two generations. Allelic frequencies of all cage devices were somehow stabilized after heterosis disappeared due to the homogenization of genetic background. It suggests that the Acp26Aa indels were either evolved neutrally or subjected to weak selection.

Feng

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**A Computational Pipeline for the Rapid Identification of Candidate Disease Genes**

We are currently developing a computational pipeline to aid in the discovery of disease genes within specific chromosomal intervals identified by linkage analysis. Given a novel chromosomal interval as input the computational pipeline aids in the discovery of disease genes by automatically predicting candidate genes within the interval. The predictions are based on known disease genes or previously determined disease intervals. If little or no information has been previously determined for the disease, the pipeline provides assistance by allowing the researcher to sift through the genes in the interval using criteria such as tissue expression data, protein structure information and keywords. The pipeline consists of three major parts: 1. An annotation engine which draws on numerous bioinformatics tools from around the world in order to characterise each gene and its associated product. 2. A prediction engine that directly selects candidate genes by comparing annotations in the interval of interest with annotations of known disease genes, or other known intervals associated with that disease. 3. A search engine that enables investigators to filter the dataset and view annotations for specific genes by querying an SQL database through a web interface. The pipeline is currently in use at VCCRI in the discovery of genes involved in inherited heart diseases but can be applied to any multigenic disease. We present results from our benchmarking process on multigenic diseases with known disease genes.

Froula

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**Testing for over/under-representation of sigma 70 promoter-like signals in different genomic regions.**

The consensus binding site for sigma 70 is 5'-TTGACA-3' and 5'-TATAAT-3' which is -35 and -10 base pairs upstream respectively from a gene or operon. It has been previously shown that the sigma 70 consensus sequence is under represented in non-regulatory DNA and coding DNA. In practice, the consensus binding sequence itself is rarely involved in sigma 70 binding but rather variations of it are used which have lower but more functional binding strengths. Additionally regulatory regions contain high densities of overlapping and probably competing promoter-like signals, in contrast to coding regions and non-regulatory regions. We will therefore use the more biologically relevant promoter-like sequences and not the consensus sequence to analyze whether selection pressures have resulted in an over-representation of all potential sigma 70 binding sites in regulatory regions and/or under-representation in coding and non-regulatory regions. To prove under or over-representation, we will compare the expected and observed binding site frequencies using log likelihood analysis, for each of the three categories of sequence, coding, regulatory, and non-regulatory. The observed frequencies will be compared to expected frequencies generated by multiple methods. First, the Markov maximal order model can calculate expected word frequencies from the known frequencies of di and tri-nucleotide sub-sequences that make up the word. A second method for obtaining expected frequencies is through applying an algorithm that finds putative promoter-site signals from random sequences that have the same di and tri nucleotide bias. These random sequences will be generated separately for coding, regulatory, and non-regulatory regions.

<p><b>Gaddam</b></p>	<p>Ravikumar Gaddam, Tim White, Simon Hills, Barbara Holland, David Penny</p>	<p>Allan Wilson Centre for Molecular Ecology and Evolution, Institute of Molecular BioSciences, Massey University, Palmerston North, New Zealand</p>	<p><b>Deep Divergence in Green Plant Phylogeny</b></p>	<p>Flowering plants dominate terrestrial flora with a large number of species, but their origin and early evolution are still poorly understood. The question of the origin and early diversification of green plants is one of the most intriguing issues due to the lack of reliable paleobotanic evidence and it leads to speculation about their origins. Phylogenetic relationships among different groups of bryophytes (Mosses, Liverworts, Hornworts) and vascular plants are not clear. The base of the land plant phylogeny has been controversial for many years. Many studies addressed these relationships using single genes with many taxa or several genes with fewer taxa. In our view there is as yet no clear answer, therefore we are conducting an analysis with 30 taxa and 50 genes with four subsets of flowering plants, land plants, greens including green algae, and plastids with glaucocystophytes. This increased taxon sampling which includes more representatives of all the major lineages of plants ultimately provides ample opportunities for addressing phylogenetic questions way back in time. We are studying different measures of how phylogenetic signal is lost as we go further back in time.</p>
<p><b>Gibb</b></p>	<p>Gillian C. Gibb, Olga Kardailsky, Edward Braun, and David Penny</p>	<p>Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Palmerston North, New Zealand,</p>	<p><b>Avian Evolution Using Complete Mitochondrial Genome Sequences</b></p>	<p>Good phylogenetic trees are required to test hypotheses about evolutionary processes. We wish to know how many lineages of birds survived from the Cretaceous to the present, and when they diverged, in order to test models of apparent 'mass extinctions' and 'explosive radiations', and also to test biogeographic and ecological hypotheses. We have five hypothetical models, each with different implications for the mechanisms of macroevolution. Before these models can be fully explored, there needs to be good resolution in the avian evolutionary tree. We have found that sufficiently long DNA sequences, for example complete mitochondrial genomes, are capable of resolving the branching of the avian tree. RY coding of the third position, and avoiding long branch attraction by using pairs of distantly related species have proven helpful in stabilizing the tree.</p> <p>We improve the taxon sampling for bird phylogeny by analyzing six new mitochondrial genomes for birds (osprey, lined forest falcon, adélie penguin, white-faced heron, ivory-billed aracari (toucan) and pileated woodpecker). There are three main effects of the improved taxon sampling. Firstly, the forest falcon and osprey increase the stability of the position of the falcon. Secondly, the heron and additional penguin mt genomes stabilize the position of the stork. Finally, the aracari and woodpecker start resolving the proposed six-way split within Neoaves (Cracraft 2001). In addition, because there is a complete duplication of the control region in some birds (for example the aracari and the osprey) we now find three main gene orders within birds. There is some evidence for continued gene conversion between parts of the duplicated control regions, resulting in parts of the duplicates being highly similar. These gene rearrangements are not informative for deep phylogeny, as they appear to have occurred multiple times during avian evolution.</p>
<p><b>Gleave</b></p>	<p>Andrew Gleave, Charles Dwamena, Bhawana Nain, Ross Crowhurst, Annette Richardson, Daya Dayatilake, Phillip Martin, Michael Clearwater, Bart Janssen, Robert Schaffer, Kate Thodey, Rebecca Bishop, and Robin MacDiarmid.</p>	<p>The Horticulture and Food Research Institute of New Zealand Ltd., 120 Mount Albert Rd, Auckland, New Zealand.</p>	<p><b>Identification of small RNAs in fruit crops</b></p>	<p>Small RNA molecules have been shown to be key regulators of gene expression in eukaryotic systems. HortResearch is undertaking research to determine how small RNA-mediated gene regulation in fruit crops and in particular the non-coding RNAs termed microRNAs (miRNAs). Guided by sequence complementarity, the miRNAs interact with target mRNA transcripts to negatively regulate their expression.</p> <p>Based on the apparent conservation of miRNAs between different plant genera, we have taken the approach of using Arabidopsis miRNA sequences to search the HortResearch Fruit EST databases and identify potential targets. Using various bioinformatics tools a significant number of ESTs/genes whose transcripts are the potential targets for miRNA-mediated regulation have been identified. These putative targets were predicted based on their degree of sequence complementarity to the Arabidopsis miRNA and their putative function.</p> <p>To complement the bioinformatics approach, and thereby verify the potential miRNA targets, and to discover new targets we have also adopted a direct cloning approach. This has involved the isolation of small RNA molecules from specific fruit tissues. Small RNA molecules have been isolated and sequenced from critical stages of fruit development as determined by the microarray analysis.</p>

<p><b>Goldberg</b></p>	<p>Julia Goldberg and Steve Trewick</p>	<p>Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Palmerston North, New Zealand</p>	<p><b>Rates of Speciation – patterns of diversification among New Zealand insects</b></p>	<p>Isolated island systems provide a good opportunity to determine rates of speciation. For this study the Chatham Islands (located approx. 850 km to the east of New Zealand) are employed to gather data from an environment with a secluded island biota. Although widely assumed to be a stable land surface since the break up of Gondwana (~ 85 Ma), the Chathams may have emerged by regional tectonic uplift no more than 3.6 to 3.0 Ma ago. If the Late Pliocene origin of the Chathams is verified, the arrival and colonization of all terrestrial plants and animals in the Chathams has been recent. This concept has major implications for understanding mechanisms and rates of dispersal over large distances, speciation on oceanic islands and interpretation of the biological history of New Zealand. Genetic data across a broad sample of insect taxa is used to obtain evidence for ancient divergences and the extent of genetic distance between taxa on the Chatham Islands and their closest relatives on mainland New Zealand. Mitochondrial and nuclear gene regions that have been used widely in phylogenetic studies and population genetics (e.g. COI, 16S, 18S) are utilized.</p>
<p><b>Goode</b></p>	<p>Matthew Goode, Howard Ross, Helen Sherman, C. Scott Baker, Shane Lavery, Allen Rodrigo</p>	<p>School of Biological Sciences, University of Auckland, New Zealand</p>	<p><b>DNA-Surveillance –creating curated databases for molecular taxonomy using phylogenetic identification</b></p>	<p>The DNA-Surveillance project (<a href="http://www.dna-surveillance.auckland.ac.nz">www.dna-surveillance.auckland.ac.nz</a>) provides a tool for taxonomic identification, using molecular sequence data. The identification methods employed use phylogenetic techniques, in contrast with for example similarity matching techniques such as Blast. In particular, the underlying database employs program derived phylogenetic trees and sequence alignments. The flagship identification technique tests the placement of a query sequence at all possible locations on a database tree. Placement is scored with maximum likelihood, and the Shimodaira-Hasegawa test provides a statistical assessment of species identification.</p> <p>The original version of DNA-Surveillance functioned purely as a tool for the identification of cetaceans. The latest version is now general and extensible, allowing individual third-parties to configure and develop their own particular databases. Administrators, who obtain accounts on the DNA-Surveillance server, can upload the required phylogenetic data, and enter the related documentation, via an easy to use web interface. The resulting customised database is then available to general users.</p>
<p><b>Grady</b></p>	<p>Deborah L. Grady<sup>1</sup>, Maria M. Corrada<sup>2</sup>, Valentina Ciobanu<sup>1</sup>, Claudia Kawas<sup>2</sup>, James Swanson<sup>3</sup>, and Robert K. Moyzis<sup>1,3</sup></p>	<p><sup>1</sup>Department of Biological Chemistry, <sup>2</sup>Department of Neurology, <sup>3</sup>Department of Pediatrics, University of California, Irvine, California 92697 USA</p>	<p><b>A Recently Selected Human Dopamine Receptor Variant (DRD4 7R) is at Higher Frequency in Individuals Over 90 Years Old.</b></p>	<p>Associations have been reported of the 7-repeat (7R) allele of the human dopamine receptor D4 (DRD4) gene with both the personality trait of novelty seeking (NS) and attention deficit/hyperactivity disorder (ADHD, Grady et al., Molecular Psychiatry 8, 536-545, 2003). Recently, based on the unusual DNA sequence organization of the DRD4 7R locus, we proposed that the 7R allele originated as a rare mutational event (approximately 40,000-50,000 years ago) that increased to high frequency by positive selection (Ding et al., Proc. Natl. Acad. Sci. USA 99, 309-314, 2002; Wang et al., Am. J. Hum. Genet. 74, 931-944, 2004). We suggested that the faster reaction time exhibited by individuals with a 7R allele (Swanson et al., Proc. Natl. Acad. Sci. USA 97, 4745-4759, 2000) might be of advantage in certain environmental/cultural contexts. In order to determine if DRD4 7R variants are related to human longevity, 200 individuals greater than 90 years of age (the "oldest-old", mean 94.26 years) were genotyped/sequenced. Seventy-one percent of this oldest-old sample are female, and over 95% are of European ancestry. In comparison to European ancestry controls (N=1,652, &lt;20 years of age), the DRD4 7R/n genotype frequency was over 50% elevated in this oldest-old sample (0.214 versus 0.333). This observed increase was due to an increased frequency of 7R/n genotypes in females versus males (0.404 versus 0.226). While one could hypothesize that an allele associated with NS and ADHD would be underrepresented in the oldest-old (due to an increased death rate caused by such behavior), the data support the opposite hypothesis. In females in particular, DRD4 7R is disproportionately represented in those attaining 90+ years of age.</p>
<p><b>Grams</b></p>	<p>Raymond W. Grams II, David A. McClellan</p>	<p>Department of Integrative Biology, Brigham Young University, Provo, UT 84602, USA</p>	<p><b>Adaptation of physicochemical properties of competing proteins TNF-<math>\alpha</math> and LTA</b></p>	<p>TNF-<math>\alpha</math> is a cytokine released by activated macrophages and lymphotoxin-<math>\alpha</math> (LTA) is a cytokine released by activated lymphocytes. Both proteins act as modulators of the immune response and competitively bind to the same protein receptors TNFR-1 and TNFR-2. TNF-<math>\alpha</math> and LTA are responsible for the lysis of certain types of cells, with specificity for tumor cells. Target therapies of these proteins against multiple diseases have been unsuccessful due to a lack of understanding of protein properties, such as receptor binding and differentiation, and cytotoxicity. This analysis takes a phylogenetic approach to characterize the molecular adaptations of TNF-<math>\alpha</math> and LTA. Using this method a comparison study of TNF-<math>\alpha</math> and LTA with affected amino acid residues and corresponding physicochemical properties have been identified.</p>

<p><b>Guzik</b></p> <p>Michelle T. Guzik1, 2, Steven J.B. Cooper2, William F. Humphreys3, Chris H.S. Watts4 and Andrew D. Austin1</p>	<p>1 Centre for Evolutionary Biology and Biodiversity and School of Earth and Environmental Sciences, The University of Adelaide, Adelaide, South Australia, 5005  2 Evolutionary Biology Unit (and Centre for Evolutionary Biology and Biodiversity) South Australian Museum, North Terrace, Adelaide, South Australia 5000.  3 Western Australian Museum, Francis Street, Perth, Western Australia, 6000.  4 Department of Entomology, South Australian Museum, North Terrace, Adelaide, South Australia 5000.</p>	<p><b>Identifying mechanisms of speciation in subterranean cave organisms</b></p>	<p>Closed ecosystems offer a unique opportunity to investigate mechanisms of speciation. In such systems, confounding factors like dispersal and many stochastic variables are naturally excluded, such that extrinsic variables can be measured and assessed as factors leading to genetic isolation and potential speciation within the system. A diverse aquatic invertebrate fauna was recently discovered in calcrete aquifers of the Yilgarn region, Western Australia. Individual calcretes are thought to comprise unique 'subterranean islands' in which high numbers of endemic fauna are observed. Dytiscid water beetles are a dominant component of the calcrete fauna, with 80 species now described from 34 isolated calcretes. Many subterranean dytiscid species share epigeal ancestors but appear to have evolved and diversified independently of taxa in other calcretes. Interestingly, three distinct size classes of dytiscid species are a common feature within calcretes. Many of these have been identified as sister taxa but the modes of speciation within individual calcretes governing their evolution is yet to be identified. To explore whether allopatric or sympatric processes are operating on present day taxa we use newly developed microsatellite markers to investigate the population genetic structure of dytiscid species within calcretes. The aim is to determine whether individual calcretes contain panmictic populations of dytiscids or show genetic substructuring strong enough to indicate isolating processes that could lead to allopatric speciation of dytiscids within calcretes. Here, we present our experimental design and preliminary results regarding levels of gene flow and population genetic structure in stygobitic dytiscid species within a single calcrete aquifer.</p>
<p><b>Hara</b></p> <p>Yuichiro Hara, Kanako O. Koyanagi and Hidemi Watanabe</p>	<p>Division of Bioengineering and Bioinformatics, Graduate School of Information Science and Technology, Hokkaido University, Sapporo Japan.</p>	<p><b>Significant contribution of gene conversion to the evolution of tandemly duplicated genes</b></p>	<p>It is known that there are many duplicated genes in the vertebrate genomes, and that each of them has complicated function. Some duplicated genes are clustered by tandem gene duplication, and there are almost 3,300 tandemly duplicated genes in the human genome. These tandem clusters are often conserved beyond a certain lineage. This is of interest in explanation for the evolution of the function of the tandemly duplicated genes; some of them may adopt a new function after gene duplication and gene conversion event as seen in olfactory receptor genes. Here, we analyzed the evolution of such clustered genes in the human and the mouse genomes. As a result, we found the strong evidence of gene conversion in many tandem clusters. This suggests that the gene conversion events have some important contribution to the evolution of tandemly duplicated genes.</p>
<p><b>Haynesh</b></p> <p>Gwilym D. Haynes*, Peter Grewe **, Dean Gilligan† and Frank W. Nicholas*</p>	<p>*Reprogen, Faculty of Veterinary Science, University of Sydney, Sydney, NSW **CSIRO Division of Marine Research, Hobart, Tasmania †NSW Department of Primary Industries (Fisheries), Narranderra, NSW</p>	<p><b>Population Genetics of common carp in the Murray-Darling Basin</b></p>	<p>Common carp are a major freshwater pest in Australia. Thriving in disturbed habitats, they degrade waterways and compete with native fish for resources. They are currently spread throughout most Australian river systems. Their broad tolerance to salinity and temperature gives them the potential to occupy possibly all permanent freshwater habitats in Australia. Effective control of carp will require understanding their population biology, which can be revealed by population genetic studies.</p> <p>This study aims to gain a detailed picture of the population genetics of carp in the Murray-Darling Basin. Fin-clips are being collected from carp in every major river in the Murray-Darling Basin, and above and below every major dam. In addition carp DNA samples are being collected from numerous localities around the Sydney basin, and samples are being sent from Europe and Asia. Genetic variability will be assessed using microsatellite genotyping, and sequence data from mtDNA loci and the ovarian aromatase gene. It is anticipated that between 13 and 20 microsatellite markers will be required for a comprehensive genetic study.</p>
<p><b>Hedges</b></p> <p>S. Blair Hedges1,*, Joel Dudley2, Davide Pisani1, Vinod Swarna2, Graziela Valente2, and Sudhir Kumar2.</p>	<p>1Department of Biology and Astrobiology Research Center, Pennsylvania State University, University Park, PA 16802, USA, and 2Center for Evolutionary Functional Genomics, The Biodesign Institute, Arizona State University, Tempe, AZ 85287-5301, USA.</p>	<p><b>TimeTree: A Database of Species Divergence Times</b></p>	<p>Knowledge of the evolutionary timescale of life is increasing at a rapid pace, creating the need for a database that assembles and compares divergence times scattered in the scientific literature. The TIMETREE database uses a hierarchical system (taxonomy tree) to identify all pertinent molecular time estimates bearing on the divergence of two taxa (e.g., species) in question. The web interface includes a primary search query for the taxa being compared and allows for the use of scientific and common names. The resulting time estimates are presented along with associated data, including standard errors, numbers of genes, the type of molecular data used (e.g., amino acid or nucleotide), cellular location (e.g., nuclear, mitochondrial, etc.), year of publication, and the PubMed-linked reference. Summary statistics are provided for divergences involving multiple studies and time estimates.</p>

<p><b>Horn</b></p> <p>Thorsten Horn<sup>1,2</sup>, Christopher Robert Bridges<sup>2</sup> and Neil Gemmell<sup>1</sup></p>	<p><sup>1</sup>School of Biological Sciences, University of Canterbury, Private Bag 4800, Christchurch 8020, New Zealand; <sup>2</sup>Institut für Zoophysiology, Lehrstuhl für Stoffwechselphysiologie, Heinrich-Heine Universität, D-40225 Düsseldorf, Germany</p>	<p><b>Telomere length change in vertebrates - A new aging-tool for field studies</b></p>	<p>Telomeres are found at the ends of chromosomes and consist of a repetitive DNA sequence, TTAGGG in vertebrates, and associated proteins. Their functions include preventing the degradation and fusion of chromosome ends, regulating the expression of subtelomeric genes and positioning chromosomes during cell division. They also act as a buffer against loss of DNA sequences due to the inability of the DNA polymerase to replicate the end of the chromosomes. Telomere length has been proposed as a marker not only for estimating the replicative age of tissues and cell lines but also for the age of whole animals. Measurement of telomere length provides an easy and none-lethal possibility for aging animals in field study, because it can be undertaken with just few microliters of blood. We used the standard Telomere Restriction Fragment (TRF) analysis to study the dynamic of telomere length in European sea bass (<i>Dicentrarchus labrax</i>) and intend to expand our research to native vertebrate species of New Zealand using TRF and a more recent developed approach called Single Telomere Length Analysis (STELA).</p>
<p><b>Huerta</b></p> <p>Araceli M. Huerta, Pilar Francino</p>	<p>Evolutionary Genomics Department, DOE Joint Genome Institute and Genomics Division, Lawrence Berkeley National Laboratory, Wainut Creek CA, USA.</p>	<p><b>Comparing the fine structure of promoter regions across bacterial species.</b></p>	<p>The selective mechanisms operating in regulatory regions of bacterial genomes are poorly understood. In <i>Escherichia coli</i>, we have found that regulatory regions contain high densities of overlapping and probably competing promoter-like signals, in contrast to coding regions and regions located between convergently-transcribed genes. Functional promoter sites identified experimentally are often found in the subregions of highest density of signals, even when individual sites with higher binding affinity for RNA polymerase exist elsewhere within the region. For each of the 532 regulatory regions in <i>Escherichia coli</i> that contain at least one experimentally-mapped sigma-70 promoter, we will perform a detailed structural analysis in terms of sequence, location, relative distribution and binding strength of the different promoter-like signals present. In order to explore the relative functional relevance of these different structural and organizational factors, we will then analyze their level of conservation across the orthologous regulatory regions of all enteric species for which complete genome sequences are available. We will also look for correlations between different types of regulatory region organizations and different classes of genes, in terms of function, level of expression, type of regulation and coexpression patterns. Together, these analyses will shed light on the molecular and selective mechanisms that generate and maintain the observed levels of signal redundancy in regulatory regions.</p>
<p><b>Janssen</b></p> <p>Bart Janssen, Robert Schaffer, Kate Thodey, Shavindra Bajaj, Lena Balakrishnan, Ross Crowhurst, Judith Bowen, Susan Ledger, Yar- Khing Yauk, Shayna Ward, Steve McCartney, Jens Wunsche</p>	<p>Genomic Technologies HortResearch Private Bag 92169 Auckland Ph 8158852 Fax 8154201</p>	<p><b>MICROARRAY ANALYSIS OF FRUIT DEVELOPMENT IN APPLE</b></p>	<p>Apple fruit develop over a period of 150 days from pollination to full tree ripeness. Cell division occurs early during development and the basic pattern of the apple fruit is established before any significant cell expansion occurs. The receptacle (the fused base of the petals and sepals) is expanded to become the cortex, vascular traces are established and the ovary tissue divides to become the core of the apple. At about 24 days after pollination cell expansion starts. As the fruit expands during development starch is built up and then as the fruit finally ripens sugars increase and the flavour components develop. In order to begin to understand the molecular events that control and define this developmental process we have collected samples at 7 stages through apple development during the season, RNA from those samples have been used to probe a microarray of 5000 apple oligonucleotides representing approximately 4000 unigenes. Analysis of this preliminary experiment has identified clusters of genes whose expression peaks at distinct stages of development. This year a second series of samples was collected and has been used to probe a 16500 oligo array representing approximately 13000 unigenes. Quantitative PCR has been used to confirm gene expression patterns for some of the genes. Results from these experiments will be presented and discussed.</p>

<p><b>Johansen</b></p> <p>Steinar D. Johansen 1, 2, Ragna Breines 1, Anita Ursvik 1, and Dag H. Coucheron 1,</p>	<p>1 University of Tromsø, Tromsø, Norway; 2 Bodø Regional University, Bodø, Norway</p>	<p><b>Mitochondrial genomics of Gadidae fishes: molecular phylogeny and evolution based on complete mtDNA sequences</b></p>	<p>The order Gadiformes includes several well-known families with a number of commercially important codfish species. About 25 species of the larges gadiform family (the Gadidae) are present in Norwegian waters. However, evolutionary relationships of the gadids and related taxa are still not well resolved. Most previous works on gadiform systematics have been based on morphology and/or life history, but an increasing amount of DNA sequence data are now being added in order to improve the phylogenetic resolution. We recently sequenced selected regions of three mitochondrial genes (mtSSU, mtLSU, and cytb) from 20 species representing 5 gadiform families, and reconstructed a phylogenetic relationship of the Gadiforms [Bakke &amp; Johansen (2005)]. Molecular phylogenetics of the Gadidae and related Gadiformes based on mitochondrial DNA sequences. Marine Biotechnology, In press]. Ten gadid species were included, representing 8 of the 12 known genera recognized in the Gadidae. In order to further resolve the phylogenetic relationships, we have performed mitogenomic analysis based on the complete mtDNA sequences from several closely related Gadidae species and stocks. Here we discuss recent findings including the genera Gadus, Theragra, Arctogadus and Boreogadus.</p>
<p><b>Johnston</b></p> <p>Kate Johnston, Patrick Dicker, Richard Edwards &amp; Denis Shields.</p>	<p>Bioinformatics Core Group, Department of Clinical Pharmacology, Royal College of Surgeons in Ireland, Dublin 2, Ireland.</p>	<p><b>The Evolution of Specificity</b></p>	<p>The functional divergence of specificity-conferring residues in duplicated proteins is an important process in evolution, giving rise to key differences between members of protein families which have adopted different functional niches. A number of models have been proposed, including adaptive "pre-duplication" anticipatory sequence changes (i.e. introduction of a strong selection pressure leading to multiple functions for a single protein, then followed by duplication to allow separate proteins fulfil these separate functions), "post-duplication" fixation of adaptive changes, and "neutral" models of relaxed selection post-duplication. In vertebrates, recent adaptive evolutionary changes are detectable as an excess of amino acid altering substitutions in protein-coding DNA, but recent duplications may have less relevance to long-term evolution of specificity, since the dynamics of gene turn-over suggest that many recent duplications may have only a short-term adaptive advantage. We contrast the more short-term DNA-based measures of adaptation (e.g. the ratio Ka:Ks) with protein-based longer-term evolutionary measures (e.g. Burst After Duplication statistics) using a database containing multiple-species protein family alignments and their respective phylogenetic trees. An assessment of evidence for the "pre-duplication" adaptive hypothesis over a variety of evolutionary time-spans is presented.</p>
<p><b>Jones</b></p> <p>Julia C. Jones<sup>1</sup>, Benjamin P. Oldroyd<sup>1</sup> and Ryszard Maleszka<sup>2</sup> GSA</p>	<p>1. Behaviour and Genetics of Social Insects Laboratory, School of Biological Sciences, Macleay Building A12, University of Sydney, Sydney 2006, NSW, Australia. 2. Visual Sciences Group, Research School of Biological Science, GPO Box 475, Canberra, ACT 2601, Australia.</p>	<p><b>The Genetics of Thermoregulation in Honey bee Colonies</b></p>	<p>Honey bee workers maintain the temperature of their brood nest within a very narrow range (34.5 ± 1.5°C). We have shown that individuals of different patriline have variable thresholds for starting to cool or heat their colony. We are currently identifying the genetic basis of individual threshold differences. To do this we will individually mark all individuals in a colony and then record which workers perform the thermoregulatory behaviour of fanning at a low and high temperature. We will then genotype all workers observed fanning to determine if there are patriline with distinctive low and high temperature thresholds for fanning. If the latter is true we will age match and mark individuals from the same colony, in two two-frame hives. We will heat one hive to the same low temperature, from the previous experiment, and the other to the same high temperature. Immediately before fanning behaviour commences we will place the colony in liquid nitrogen and then compare individuals from the high and low thresholds patriline using microarrays.</p>
<p><b>Kopchinskiy</b></p> <p>Alexey Kopchinskiy, Monika Komo, Christian P. Kubicek and Irina S. Druzhinina</p>	<p>Division of Gene Technology and Applied Biochemistry (DGTAB), Institute of Chemical Engineering, University of Technology, Getreidemarkt 9/1665, A-1060 Wien, Austria</p>	<p><b>TrichoBLAST: a multiloci database of phylogenetic markers for Trichoderma and Hypocrea powered by sequence diagnosis and similarity search tools</b></p>	<p>Hypocrea/Trichoderma is a genus of soil-borne or wood-decaying fungi, which contains members that are important to mankind. Today the identification of Hypocrea/Trichoderma chiefly relies on the use of DNA sequence data. The most common approach for molecular identification is that by local alignment comparison. A popular tool for this task is BLAST. Unfortunately, results from such large public databases like GenBank, which already contains about one million of only fungal nucleotide sequences, can be flawed for two main reasons: (i) most public databases are riddled with misidentified sequences (~40% for Hypocrea/Trichoderma in GenBank), and (ii) not all public databases fully cover the sequences and species of a given genus.</p>

(Alexey Kopchinskiy abstract continued)

In order to eliminate the later two difficulties with respect to Hypocrea/Trichoderma, we have developed TrichoBLAST: a publicly available database supported by sequence diagnosis and the similarity search tools, which covers all 88 genetically characterized species of the genus and contains almost complete sets of 5 most frequently used phylogenetic markers: the internal transcribed spacers 1 and 2 – ITS1 and 2; two introns (tef1\_int4(large), tef1\_int5(short) ) and one exon tef1\_exon6(large) of the gene encoding translation elongation factor 1-alpha and, a portion of the exon between the 5th and 7th eukaryotic conserved amino acid motives of subunit 2 of the RNA polymerase gene(rpb2\_exon). TrichoBLAST is located on the website of the International Subcommittee of taxonomy of Trichoderma and Hypocrea (ISTH; www.isth.info) of the International Commission of Fungal Taxonomy (ICFT). To increase the accuracy of the similarity search we have enforced TrichoBLAST by TrichoMARK, a script specifically written for detection and retrieval of phylogenetic markers in query sequences, and for the subsequent individual submission of them to the similarity search. Since hypotheses of relationships should not be always inferred directly from similarity indices, but use phylogenetic inference methods. To this end, we have finally developed a third module of TrichoBLAST, i.e. a publicly available Multiloci Database of Phylogenetic Markers, a relational database built on a MySQL platform. It is accessed through a web interface system written in PHP scripting languages. This database serves as a reference database for the similarity search and allows retrieving any custom set of sequences in FASTA file format for phylogenetic analysis. A search option by any keyword is included to speed up the access to sequences from known strains, species or GenBank accession numbers.

Kumar

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**MEGA3: An Integrated Software for Molecular Evolutionary Genetics Analysis and Sequence Alignment**

With its theoretical basis firmly established in molecular evolutionary and population genetics, the comparative DNA and protein sequence analysis plays a central role in reconstructing the evolutionary histories of species and multigene families, estimating rates of molecular evolution, and inferring the nature and extent of selective forces shaping the evolution of genes and genomes. The scope of these investigations has now expanded greatly owing to the development of high-throughput sequencing techniques and novel statistical and computational methods. These methods require easy-to-use computer programs. One such effort has been to produce Molecular Evolutionary Genetics Analysis (MEGA) software, with its focus on facilitating the exploration and analysis of the DNA and protein sequence variation from an evolutionary perspective. Currently in its third major release, MEGA3 contains facilities for automatic and manual sequence alignment based on CLUSTALW, web-based mining of databases, inference of the phylogenetic trees, estimation of evolutionary distances and testing evolutionary hypotheses. This poster provides an overview of the statistical methods, computational tools, and visual exploration modules for data input and the results obtainable in MEGA3. MEGA3 can be downloaded free of charge from <http://www.megasoftware.net>.

Kumar

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**Launch of the FlyExpress Resource: The Drosophila in situ Gene Expression Pattern Database and Search Tool**

We announce the release of the first edition of the FlyExpress resource. The FlyExpress project goals are to curate all images containing embryonic gene expression patterns, develop methods for standardizing gene expression patterns, build efficient image-retrieval systems to quickly identify best-matching expression patterns, and to deliver the database along with a gene expression search tool in an effort to accelerate the developmental biology research. This first edition includes a large sampling of the early stage (1-8) images derived from the Berkeley Drosophila Genome Project (BDPG). Using this web resource, investigators are able to query the database and to find other images whose expression patterns overlap the query gene expression patterns. The search is based on image searching rather than on text searching. Facilities will also be included to sketch the query gene expression pattern using a gene expression paint tool and the embryo template, and to conduct a search. In addition to this, text searches based on gene names and other attributes can also be conducted. Searches can be restricted to specific developmental stages and views. Future releases of this software will provide access to late stage BDGP as well as to all fly embryo images published in the literature. The FlyExpress Consortium currently consists of intra- and extramural scientists and students instrumental in developing this resource (see [www.flyexpress.net](http://www.flyexpress.net) for a list).

<p><b>Kuraku</b></p>	<p>Shigehiro Kuraku,<sup>1</sup> Junko Ishijima,<sup>2</sup> Shigeru Kuratani,<sup>1</sup> and Yoichi Matsuda<sup>2, 3</sup></p>	<p><sup>1</sup>Laboratory for Evolutionary Morphology, RIKEN Center for Developmental Biology, 2-2-3 Minatojima-minami, Chuo-ku, Kobe 650-0047, Japan; <sup>2</sup>Laboratory of Animal Cytogenetics, Center for Advanced Science and Technology, Hokkaido University, North 10 West 8, Kita-ku, Sapporo 060-0810, Japan; <sup>3</sup>Chromosome Research Unit, Faculty of Science, Hokkaido University, North 10 West 8, Kita-ku, Sapporo 060-0810, Japan</p>	<p><b>Chromosome size-dependent GC-compartmentalization in sauropsids estimated by cDNA sequencing and gene mapping in Chinese soft-shelled turtle <i>Pelodiscus sinensis</i></b></p>	<p>Mammalian and avian genomes are composed of several classes of chromosomal segments that dramatically vary in GC-content, namely "isochores". In order to understand evolutionary history of the intra-genome GC-heterogeneity along amniote evolution, it is necessary to take reptiles, from which avians diverged, into account. In this study, we newly isolated and sequenced cDNAs from Chinese soft-shelled turtle <i>Pelodiscus sinensis</i>, and performed gene mapping with fluorescent in situ hybridization (FISH). Estimated distribution of GC-rich and GC-poor regions based on GC-content of exonic third positions (GC3) throughout the genome highlighted two modes of chromosomal evolution in amniote karyotypic evolution.</p>
<p><b>Lasser</b></p>	<p>Elyse Lasser, Frances Terry, Jessica Grant and Laura A. Katz</p>	<p>Department of Biological Sciences, Smith College, Northampton MA</p>	<p><b>Diversity of amoebae among eukaryotes: insights from multigene analyses</b></p>	<p>As part of an on-going project, Assembling the Tree of Eukaryotic diversity, we are sequencing multiple genes from amoeboid organisms. Our focus is two fold: (1) placing enigmatic taxa on the eukaryotic tree of life, and (2) testing hypotheses for supergroups containing amoeboid taxa. To address these hypotheses, we are analyzing a combination of rDNA and protein coding genes using a variety of evolutionary models. To date, our analyses reveal that there is considerably more morphological diversity underlying proposed clades of eukaryotes than had previously been believed.</p>
<p><b>Laukien</b></p>	<p>Frank H. Laukien</p>	<p>University of Amsterdam; Swammerdam Institute for Life Sciences, The Netherlands</p>	<p><b>Postulate of an Externally-Driven Irreversible Transferable Adaptation (EDITA) Mechanism As a Second Generator of Evolutionary Change</b></p>	<p>The present implicit assumption that evolutionary change prior to selection is exclusively generated by random DNA mutations may be insufficient to explain various phenomena observed in evolutionary biology. Here it is postulated that an externally-driven irreversible and transferable adaptation mechanism, called EDITA mechanism, can be a second generator of biological change and diversity prior to natural selection.</p> <p>Various examples from developmental biology, as well as from immunology and infectious disease transfer will be presented, where external or environmental factors can drive or induce irreversible changes in molecular systems, cells or higher level organisms. In many cases these externally-driven irreversible changes first occur in one or just a few molecules or cells, but are then transferred to others and propagate this externally-driven adaptation. Examples of this apparently quite general EDITA mechanism at work include 'healthy' biological processes like stem cell differentiation, immunological response or processes in developmental biology, as well as 'disease' processes like prion proliferation, bacterial or viral infections, and uncontrolled cancer cell division.</p> <p>It is implausible for this EDITA mechanism to not also play a role in evolutionary biology, as a second generator of change and diversity that is complementary to the random mutation generation of change prior to selection. Darwin's original theory, conceived long before the discovery of DNA, is much broader in its generalized concept of change followed by selection, and it is applicable also outside of biology. Thus, it is proposed here to reinterpret Darwin's theory of evolution more broadly with EDITA as an additional transfer mechanism for heritable information. As the EDITA mechanism can contribute to periods of rapid evolution, it may provide an even more satisfactory explanation on how evolution has succeeded in creating such a diversity of complex traits and species, as well as the molecular and cellular machinery of life.</p> <p>A second intertwined postulate is then that not all inherited information needs to reside strictly in the genome, and that non-DNA molecular storage, e.g. in RNA, proteins, metabolic equilibria, etc. can be carriers of heritable information. This implies that the Central Dogma of molecular biology perhaps represents just the dominant direction of a two-way transfer of heritable information. This certainly must have been true historically in the early stages of evolution prior to the emergence of our present day molecular machinery for DNA information storage, followed by transcription and translation. If the EDITA mechanism played an important role in the emergence and early evolution of life, then it would be implausible to assume that it has vanished altogether. The EDITA concept as a second generator of change, that is complementary to random mutations, could considerably accelerate our understanding of evolutionary biology. Moreover, the generalized EDITA mechanism postulated here may also have broader implications for basic biological research as well as for medical discoveries.</p>

<p><b>Lawrence</b></p>	<p>Hayley Lawrence, Graeme Taylor, Dr Craig Millar and Prof David Lambert</p>	<p>Allan Wilson Centre for Molecular Ecology and Evolution  Institute of Molecular BioSciences  Te Kura Putaiao Koiora-a-Ngota  Massey University  Auckland  New Zealand</p>	<p><b>Conservation Genetics of New Zealand's rarest seabird; Whakapapa o te Taiko (<i>Pterodroma magentae</i>)</b></p>	<p>The Chatham Island Taiko (<i>Pterodroma magentae</i>) is New Zealand's most endangered seabird. It is so rare that blood samples have been obtained from the entire known living population of ~75 birds, in addition to samples from birds now deceased. Microsatellite DNA and mitochondrial DNA variation has been studied in the Taiko to increase knowledge of biology and ecology, and to assist conservation practice. DNA sexing and parentage data will help to characterise this petrel's mating system. Relatedness estimates can aid practical conservation measures such as the search for undiscovered breeding burrows, by identifying individuals with rare genotypes to track using radio telemetry. These data are also generally relevant to conservation efforts to select chicks for translocation to an area free of introduced predators. Understanding the extent of philopatry (tendency to return to natal location) will be important for these efforts, another area where genetic analysis can assist. Assessment of overall genetic variation and population structure in Taiko could indicate inbreeding risk and/or the existence of another colony. In the future, ancient DNA from subfossil Taiko bones will be used to understand past genetic variation, population size and structure, and past breeding distribution. Mitochondrial DNA analysis will confirm whether the type specimen of the Magenta Petrel (held in Turin museum, Italy) and the Taiko really are of the same species.</p>
<p><b>Lea</b></p>	<p>Rod A Lea<sup>1,2</sup></p>	<p><sup>1</sup>The Institute of Environmental Science and Research Ltd. Wellington, New Zealand.  <sup>2</sup> Genomics Research Centre, Griffith University, Australia</p>	<p><b>Tracking the evolutionary history of the Warrior gene across the South Pacific</b></p>	<p>Historically, the NZ M_oris were extremely adventurous risk takers and fearsome warriors. A DNA repeat polymorphism in the neuronal Monoamine Oxidase (MAO) gene on the X chromosome is strongly associated with risk taking and aggressive behaviour. Hence, the gene has been dubbed the "Warrior" gene. The MAO gene is known to be highly polymorphic in human populations and there is new evidence that the full spectrum sequence variation across MAO exhibits unusual patterns of linkage disequilibrium (LD) indicative of positive selection. Interestingly, our preliminary studies have revealed striking over-representation of the MAO repeat polymorphism in the M_ori male population compared to Caucasian males. Cultural, linguistic and genetic evidence points to Formosa (Taiwan) as the staging post of Maori (Polynesian) voyages between 5000-10000 years ago. In light of this, we will present full comparative genomic data of the MAO gene in M_ori and Taiwan aboriginal tribes in an effort to elucidate the evolutionary history of the Warrior gene in the South Pacific.</p>
<p><b>Lightfoot</b></p>	<p>Damien Lightfoot, Sharon Orford, Jeremy Timmis  GSA</p>	<p>School of Molecular and Biomedical Science, The University of Adelaide, Adelaide, S.A., 5005.</p>	<p><b>Development of cotton boll wall-specific promoters</b></p>	<p>The cotton boll contains the seeds of the plant to which long, white fibres are attached. The cotton industry takes advantage of these fibres to spin yarns for textile production. Despite the fact that Australian cotton growers spend more than 10 million dollars per year on insect control, it is estimated that 20% of the annual crop is lost to insect attack. The insects specifically attack the boll, causing damage to the commercially important part of the plant. The recent introduction of Bollgard® and BollgardII® transgenic cotton varieties, containing one or two cry genes, respectively, from the soil bacterium <i>Bacillus thuringiensis</i>, has had very positive impacts in terms of insect control and reductions in pesticide usage. The cry genes are under control of constitutive promoters, producing protein in all parts of the cotton plant. There is evidence that this constitutive expression (~1% of total soluble protein) results in a yield penalty to the plant, is likely to increase the rate of development of insect resistance to the toxins and has negative effects on non-target species. For these reasons, our aim is to identify promoters that could be used for tissue specific expression of the Bt (or other) toxin in only the boll wall of the cotton plant. We have used a differential screening method to screen a 5 days post anthesis boll wall cDNA library. Several putative boll wall specific mRNAs have been identified and isolated and their expression patterns analysed by Northern analysis. Transient transformations of cotton tissues are currently being performed to test the specificity of these promoters.</p>

<p><b>Maxwell</b></p>	<p>Peter Maxwell, Matthew Wakefield, Brett Easton, Gavin Huttley</p>	<p>Centre for Bioinformation Science, John Curtin School of Medical Research and Mathematical Sciences Institute, Australian National University, Canberra, ACT 0200, Australia</p>	<p><b>PyEvolve: a toolkit for statistical molecular evolutionary analysis of genomes</b></p> <p>The number of genes and species for which DNA sequence data are now available is enormous compared with just five years ago. This data present an opportunity for statistical dissection of molecular evolutionary processes. The ability to exploit the data is limited, however, by the poor scalability and extensibility of existing software. As a result, developments in distributed high performance computing cannot be efficiently exploited. We present a description of the functionality and performance of PyEvolve, software we have developed in response to these challenges. PyEvolve is a toolkit designed to perform existing, and for the development of new, methods of molecular evolutionary analysis. It can operate on a single CPU or take advantage of multi-CPU hardware. The functional capabilities of PyEvolve are centered on its ability to perform phylogeny-based maximum-likelihood calculations. PyEvolve implements a range of existing and several novel Markov models of substitution (nucleotide, dinucleotide, codon, protein, and models for measuring interactions between sites) that can be used for these calculations. Other features include allowing parameter heterogeneity (per site or across a tree), ancestral sequence reconstruction, and sequence simulation. Example analytical applications of PyEvolve are testing for evidence of selection using codon substitution models, identifying positively selected sites, or performing relative rate tests. The toolkit can also be employed for the development of novel models of substitution, or phylogenetic reconstruction applications.</p>
<p><b>Meneses</b></p>	<p>Isabel Meneses1, Rodrigo Vidal2 and Macarena Smith1</p>	<p>1Departamento de Ecología, Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile, Santiago, Chile. 2Departamento de Biología, Facultad de Química y Biología, Universidad de Santiago, Santiago, Chile</p>	<p><b>PHYLOGEOGRAPHY OF THE SPONGITES GENUS (CORALLINALES, RHODOPHYTA): HOW MANY POPULATIONS AND HOW MANY SPECIES EXIST IN THE COASTS OF CHILE?.</b></p> <p>Spongites, a genus of calcified non-geniculated red algae, represent a very well- defined morphological group within the order Corallinales (Rhodophyta). Understanding the phylogeography of this group, requires not only identifying the possible evolutionary events generating its relationships, but also analyzing patterns of genetic structure among populations. We undertook a comprehensive study of the genus Spongites along the Chilean coasts, using this genus as model to evaluate these aspects and to gain insight into the biogeographic distribution of calcified non-geniculated species of the southern hemisphere and possible modes of dispersal. Individuals were sampled in several locations along the coast of Chile and in selected sectors of New Zealand and South Africa. The mitochondrial spacer region between the COX2 and COX3 genes and the first half of the 18S gene were chosen. The selection of these molecular markers provide a progression from phylogenetic, demographic to population genetic analysis. The combination of these analyses revealed: (1) the genus Spongites presents a complex history of vicariant and dispersal events; (2) the taxon of Spongites present in the coasts of Chile will represent a new species with a wide latitudinal distribution and elevated molecular variability.</p>
<p><b>Möller</b></p>	<p>Luciana Möller1,2, Jennifer Kingston2, Shannon Corrigan2, Joe Waas3, Mark Hindell4, Luciano Beheregaray2, Robert Harcourt1</p>	<p>1Marine Mammal Research Group, Graduate School of the Environment, Macquarie University, Sydney NSW 2109 Australia; 2Molecular Ecology Group, Dept of Biological Sciences, Macquarie University, Sydney NSW 2109 Australia; 3Dept of Biological Sciences, University of Waikato, Hamilton 3105 New Zealand ; 4School of Zoology, University of Tasmania, Hobart TAS 7701 Australia</p>	<p><b>Are there genetic benefits from mate choice in marine mammals?</b></p> <p>Benefits from female multiple mating are easy to understand in species where males provide resources to females because material benefits are often conspicuous. However, in many species, including in marine mammals, females appear to gain nothing more from mating than the male's sperm. For these species it is assumed that females derive genetic benefits from multiple mating and mate choice. We are using large genetic and behavioural databases for Weddell seals (<i>Leptonychotes weddelli</i>) and Indian Ocean bottlenose dolphins (<i>Tursiops aduncus</i>) to investigate whether female marine mammals gain genetic benefits from multiple mating and mate choice. We are combining microsatellite DNA markers and major histocompatibility complex (MHC) genes with modern analytical approaches to test the heterozygosity and genetic diversity hypotheses. If females are found to exert choice, we will attempt to identify the strategies employed by females to maximize offspring heterozygosity and to assess the two proposed roles of the MHC in mate choice. Preliminary results based on microsatellite loci found no evidence that female dolphins were selecting genetic dissimilar partners.</p>

<p><b>Montaño</b></p>	<p>Adriana Maria Montaño, Naoyuki Takahata and Yoko Satta</p>	<p>Department of Biosystems Science, The Graduate University for Advanced Studies (Sokendai), Shonan Village, Hayama, Kanagawa 240-0193, Japan</p>	<p><b>ORIGIN OF PEPTIDOGLYCAN RECOGNITION PROTEINS IN VERTEBRATES</b></p>	<p>Innate immune system recognizes microorganisms through a series of pattern recognition receptors that are highly conserved in evolution. This system surveilles the presence of bacteria by targeting peptidoglycans (PGNs) which are an essential and unique cell wall component of all bacteria. Peptidoglycan recognition proteins (PGRPs) are pattern recognition molecules that bind to PGNs, and are present in mammals as well as insects. In humans, there are only four PGRP genes (L, S, Ia and Ib), in contrast to 13 paralogs in Drosophila. The purpose of this study is to clarify the origin and evolutionary relationship of PGRPs in vertebrates. Our analysis suggests that there were already three paralogous loci (S, L and I) prior to the emergence of vertebrates, some 500 million years ago (MYA). The PGRP-S and -L duplicated first and afterwards PGRP-I duplicated from S. The divergence time of PGRP-Ia and -Ib was dated to 107~143 MYA. After duplication events there was an accumulation of changes through time: an intensive analysis of amino acid sequences was performed to understand their effect on PGRP proteins. We found the presence of several parallel and convergent amino acid substitutions in different lineages suggesting that either the functional constraint has changed or this gene family has undergone positive Darwinian selection.</p>
<p><b>Muirhead</b></p>	<p>K. A. Muirhead, A. D. Austin, M. N. Sallam, S. C. Donnellan GSA</p>	<p>Centre for Evolutionary Biology &amp; Biodiversity, School of Earth &amp; Environmental Science DP 418, The University of Adelaide, SA, 5005,</p>	<p><b>Genetic variation in the Cotesia flavipes complex of parasitic wasps: towards the effective biological control of stemborer pests in Australia</b></p>	<p>The <i>Cotesia flavipes</i> species complex of parasitic wasps are economically important worldwide for the biological control of lepidopteran stemborer species associated with gramineous crops. The complex, characterised in part by a dorsoventrally flattened body, currently comprises three species: <i>C. flavipes</i> Cameron, <i>C. sesamiae</i> (Cameron) and <i>C. chilonis</i> (Matsumura), which are morphologically similar. The absence of clear diagnostic characters to separate the species and inaccurate identification have confounded past efforts to assess the impact of specific introductions. Moreover, small- and large-scale geographic populations have exhibited differences in host/habitat preference and host range. Founder effects, drift, inbreeding and adaptation to new environments can occur during the introduction and establishment of biological control agents and may promote the genetic divergence of populations. Molecular markers are being developed to characterise genetic variation and phylogenetic relationships among these and other species and among worldwide populations of <i>C. flavipes</i>, and correlate these with host and/or habitat preference. The status of <i>C. flavipes</i>-like species in Australia will be determined for the preparedness of stemborer incursion into Australia. Genetic differentiation between populations may have potentially important implications for host utilisation and thus, the diagnosis of appropriate strains for biological control against specific host species.</p>
<p><b>Muller</b></p>	<p>Chris Muller1, Lesley Hughes2 and Luciano B. Beheregaray1</p>	<p>1Molecular Ecology Group, Department of Biological Sciences, Macquarie University, Sydney NSW 2109 Australia; 2 Ecology Group, Department of Biological Sciences, Macquarie University, Sydney NSW 2109 Australia</p>	<p><b>The Phylogeny of the Butterfly Genus <i>Delias</i> (Lepidoptera) * a Biogeographical Perspective</b></p>	<p>The genus <i>Delias</i> comprises 251 described species, making it the largest known genus of butterflies. Previous studies based on morphological characters have classified all known <i>Delias</i> taxa into 23 species groups. Although <i>Delias</i> is distributed throughout the Indo-Pacific region, at least half of the known taxa are confined to mainland New Guinea and its satellite islands. Large numbers of cryptic species with restricted ranges at high altitude make <i>Delias</i> an ideal subject for biogeographical analysis. Extensive fieldwork by the author conducted throughout the region since 1984 (focusing on Indonesia, Papua New Guinea and the Solomon Islands) has yielded samples of approximately 180 species. The aims of this study are (i) to complete a taxonomic revision of <i>Delias</i>, (ii) to reconstruct a phylogeny for the genus using a combination of molecular and morphological characters, and (iii) to elucidate the biogeographic history of the genus. Preliminary morphological and molecular phylogenetic analyses (based on mitochondrial DNA sequences) reveal that <i>Delias</i> constitutes several well-defined species groups often with overlapping ranges. Large numbers of species with apparently little morphological divergence occur in the central cordillera of mainland New Guinea. Older lineages appear to be represented by species occurring in China and throughout South-East Asia. Future work will focus on amplification and sequencing of mitochondrial and nuclear DNA genes and on analyses of their phylogenetic usefulness. Geological maps and structural interpretations of the Indo-Pacific region will be used to determine distinct geological terranes (micro-plates) for comparison with the biogeographic patterns inferred by this study.</p>

<p><b>Murray</b></p>	<p>Brent W Murray<sup>1</sup>, John Wang<sup>2</sup>, John Stevens<sup>3</sup> and Ross Daley<sup>3</sup>, Jim Reist<sup>4</sup>, Aaron Fish<sup>5</sup>, Bill Bechtol<sup>6</sup>.</p>	<p><sup>1</sup>University of Northern British Columbia, 3333 University Way, Prince George, Canada, V2N 4Z9.  <sup>2</sup>, National Museum of Marine Biology &amp; Aquarium, Taiwan.  <sup>3</sup>CSIRO Marine research, Australia.  <sup>4</sup> Department of Fisheries and Oceans, Canada.  <sup>5</sup>, National Water Research Institute, Environment Canada.  <sup>6</sup> Alaska Department of Fish and Game, USA.</p>	<p><b>Mitochondrial Cytochrome b variation in sleeper sharks (Somniosus), subgenus Somniosus.</b></p>	<p>Sleeper sharks of the subgenera Somniosus are relatively poorly studied, large (adults ~4m) deep-sea sharks. The subgenus, Somniosus, contains three species: S. microcephalus found in the Arctic and North Atlantic; S. pacificus in the North Pacific; and S. antarcticus in the South Indo-Pacific and South Atlantic. These sharks have been reported mainly in temperate to polar waters, however, S. pacificus has been found as far south as Baja California in the Western Pacific and recently in the subtropical waters off the Island of Taiwan. This study investigates the relationships of the North Pacific and South Indo-Pacific populations through analysis of the mitochondrial cytochrome b gene. Twenty-six sharks from subtropical waters of Taiwan, 15 from the North Pacific off the coast of Alaska, and 16 from the South Indo-Pacific were examined. Twenty-two haplotypes were found with an average sequence difference of 0.56%. Analysis of molecular variance (AMOVA) showed no evidence for genetic structure among the populations. Despite the presence of genetic variation within the populations, no evidence for genetic structure was found among these samples.</p>
<p><b>Nielsen</b></p>	<p>Rasmus Nielsen<sup>1</sup> and Mikhail Matz<sup>2</sup></p>	<p><sup>1</sup> Department of Biological Statistics and Computational Biology, Cornell University, Ithaca, NY 14853, USA and Center for Bioinformatics, University of Copenhagen Universitetsparken 15, 2100 Copenhagen, Denmark; <sup>2</sup> Whitney Laboratory and Department of Molecular Genetics and Microbiology, University of Florida, 9505 Ocean Shore Blvd, Saint Augustine, FL 32080, USA.</p>	<p><b>Statistical approaches for DNA barcoding</b></p>	<p>The weakest spot of DNA barcoding is the fact that no gene can serve as an actual barcode, i.e. be always invariant within species but different among species. In theory, different species may share identical sequences, and on another hand, two sequences from the same species can be notably different, depending on the life histories of species and populations. Clearly, there is a need for statistical methods for assessing if a sampled query sequence is sufficiently identical to a particular data base sequence to justify a species assignment of the sequence. Here we discuss the statistical problems associated with DNA barcoding and illustrate the need for population genetic thinking when applying DNA barcoding to real data. We then propose possible solutions to the problem of establishing measures of statistical uncertainty for DNA barcoding based on the coalescent theory, using frequentist and Bayesian approaches.</p>
<p><b>Noda-Ogura</b></p>	<p><sup>1</sup>,<sup>2</sup>Akiko Noda-Ogura, <sup>1</sup>Kazuho Ikeo, <sup>2</sup>Etsuko Matsuura, <sup>1</sup>Takashi Gojobori</p>	<p><sup>1</sup> Center for Information Biology and DNA Data Bank of Japan, National Institutes of Genetics, Mishima 411-8540, Japan.  <sup>2</sup> Graduate School of Humanities and Sciences, Ochanomizu University, Bunkyo-ku, Tokyo, 112-8610, Japan</p>	<p><b>Comparative Genome Analyses of Nervous System-Specific Genes</b></p>	<p>To elucidate the evolutionary process of the nervous system (NS), we determined the emergence times of human genes expressed specifically in the NS (NS-specific genes) and examined their functions and genomic locations. We obtained 255 NS-specific genes from the gene expression data of the Human Full-length cDNA Annotation Invitational database. We then searched for their orthologues in 13 species using complete genomes and phylogenetically examined their emergence times. As a result, we found that 14% of the NS-specific genes had already emerged before the divergence of yeast and human. This suggests that a common ancestor with no nervous system possessed a portion of NS-specific gene homologues, the original functions of which have changed differentially during NS evolution. In other words, the remaining 86% of the 255 NS-specific genes have newly emerged. In particular, 26% of the 255 NS-specific genes had emerged after divergence of urochordata and human but before divergence of fishes and human. This suggests that the evolution of NS during this period needs the emergence of many NS-specific genes. Thus, evolution of the NS came about both by emergences of novel genes and functional changes in existing genes. We also found regions where NS-specific genes are concentrated in human chromosomes. We report the relationship between the emergence times of NS-specific genes and their functions or genomic locations in the poster.</p>
<p><b>Nowick</b></p>	<p>Katja Nowick, Joshua Pollack, Florian Heissig, Hilliary Creely, Philipp Khaitovich, Birgit Nickel, Svante Pääbo</p>	<p>Max-Planck-Institute for Evolutionary Anthropology, Deutscher Platz 6, D-04103 Leipzig, Germany</p>	<p><b>Identification of genes regulated by FOXP2</b></p>	<p>FOXP2, the first protein discovered to be involved in the acquisition of speech and language, is of great interest in evolutionary and developmental biology. However, the molecular function of this transcription factor and its role during development is still largely uncharacterized. To investigate FOXP2's function and its target genes, we established a human neuroblastoma model system with inducible FOXP2 expression. Using micro arrays, we identified genes with specifically altered expression at 3, 8 and 24 hours after FOXP2 induction. We next applied a bioinformatics approach to scan the promoter sequences of these candidate genes for the putative FOXP2 binding site and found a significant overrepresentation of these sites in upregulated genes at early time points. Further, a highly significant fraction of the upregulated genes are involved in the cell cycle, suggesting that FOXP2 may be important for cell proliferation. To gain insight on the role of FOXP2 in the evolution of speech, we also compared the effects of human and chimpanzee FOXP2 in our system and found indications that they differently regulate the expression of target genes.</p>

<p><b>Ottewell</b></p>	<p>Kym Ottewell, David Ayre and Rob Whelan GSA</p>	<p>Institute for Conservation Biology, University of Wollongong, Northfields Avenue, Wollongong, New South Wales, 2522</p>	<p><b>The Genetic Composition Of A Canopy Stored Seed Bank: Variation Across Years And With Plant Reproductive Effort.</b></p>	<p>The canopy-stored seed of serotinous plants, such as <i>Banksia spinulosa</i>, potentially represent a buffer against the stochastic effects of annual variation in reproductive effort and output. Individual plants may produce multiple inflorescences per year that, in turn, generate multiple woody 'cones' (infructescences) containing hundreds of seed that are expected to be released and germinated only following a fire. We have been conducting demographic surveys of ~ 350 hermaphroditic plants within one such population for 14 years and have found that the likely effective population size varies dramatically from year to year, with some year's inflorescence production dominated by a very few plants. However, even across all 14 flowering years only 20% of all plants account for 50% of inflorescence production and 15% of plants account for 50% of infructescence production. This skewing of reproductive effort and perhaps reproductive output (since male reproductive success is unknown) confounds any predictions about the real diversity of the seed bank. Here, we compare genetic diversity estimates across each of several years, with patterns of flowering and fruit production and we use a more detailed survey of genotypic variation within the year 2000 seed cohort to determine how outcrossing rates and levels of genotypic diversity vary among seed produced by plants with single and multiple inflorescences.</p>
<p><b>Oxley</b></p>	<p>Peter Oxley, Ben Oldroyd, Jürgen Paar, GSA</p>	<p>Behaviour and Genetics of Social Insects Lab, School of Biological Sciences, A-12 Macleay Building, University of Sydney, NSW 2006 Australia</p>	<p><b>The Genetics of Hygienic Behaviour of Honey Bees (<i>Apis mellifera</i>)</b></p>	<p>Hygienic behaviour is a genetically influenced, complex behavioural trait of honey bees (<i>Apis mellifera</i>), and a primary component of natural resistance to various parasitic and pathogenic organisms. Variations in behaviour are influenced by both genetic and environmental factors. As a result, measuring the genetic influence of this complex behaviour is difficult. Despite much study on animal behaviour and genetics, there are few examples of variation in the genome having a direct influence on behaviour. Bee hygienic behaviour provides us with an excellent opportunity to study how complex social behaviours can be influenced by genotypic variation. This project aims to identify candidate genes and the allelic variations responsible for influencing hygienic behaviour. This is being achieved through fine mapping suggestive quantitative trait loci (QTLs) that have been recently identified. A more robust PCR test for identification of hygienic alleles in honey bee colonies is also being developed, for use in marker assisted selection.</p>
<p><b>Pingault</b></p>	<p>Pingault, N.M1., Lehmann, D2., Bowman, J.3 and Riley, T.V3.4.</p>	<p>1School of Biomedical Sciences, Curtin University of Technology, Perth, Western Australia, 2Telethon Institute for Child Health Research, Perth, Western Australia, 3Western Australian Centre for Pathology and Medical Research, Perth, Western Australia, 4School of Biomedical and Chemical Sciences, University of Western Australia, Perth, Western Australia</p>	<p><b>Comparison of Molecular Typing Methods for <i>Moraxella catarrhalis</i></b></p>	<p>A number of molecular typing techniques were examined to determine which method was the most discriminatory in order to perform epidemiological typing of <i>Moraxella catarrhalis</i>. Twenty five <i>M. catarrhalis</i> isolates obtained from nasopharyngeal aspirates from Aboriginal and non Aboriginal children were subjected to random amplified polymorphic DNA analysis (RAPD), automated ribotyping and pulsed field gel electrophoresis (PFGE). RAPD analysis determined two <i>M. catarrhalis</i> types, automated ribotyping with Pst1 determined four <i>M. catarrhalis</i> ribogroups and PFGE analysis with Not1 determined 21 pulse field groups within the 25 isolates examined. This study confirms that PFGE is the most discriminatory method for the typing of <i>M. catarrhalis</i>.</p>
<p><b>Pocwierz-Kotus</b></p>	<p>A. Pocwierz- Kotus1, A. Burzynski1, W. Makalowski2 R. Wenne1,3</p>	<p>1- Institute of Oceanology, PAS, Powstancow Warszawy 55, 81-712 Sopot, Poland 2- 514 Mueller Lab, Pennsylvania State University, University Park, PA 16802, USA 3- Institute of Biology, University of Gdansk, Kladki 24, 80-822 Gdansk, Poland</p>	<p><b>Occurrence of Tc1 transposons in commercial fish species from the Baltic Sea</b></p>	<p>Transposable elements (TEs) are mobile segments of DNA that are present in most genomes. They play a significant role in genomic evolution by generating different kind of mutations including chromosomal aberrations. They are present in multiple highly similar copies scattered in a genome that enables recombinations that may lead to gene shuffling and change of gene expression. Interestingly, they are also subjected to horizontal transfer between unrelated species and in consequence they can increase genetic variability of infected species. Tc1-like transposons, related to Tc1 elements that were discovered in nematode <i>Caenorhabditis elegans</i>, are present in most metazoan genomes and they seem to be especially successful in colonising genomes of different fish species. Typically, they are about 1600 bp long and their terminal inverted repeats (ITR) are flanking a single transposase gene. For the first time, we investigated Tc1-like element distribution in populations of number of commercially important fish species from the brackish water Baltic Sea. Following species were studied: flounder <i>Platichthys flesus</i>, plaice <i>Pleuronectes platessa</i>, turbot <i>Scophthalmus maximus</i>, halibut <i>Reinhardtius hippoglossoides</i>, herring <i>Clupea harengus</i>, salmon <i>Salmo salar</i>, land locked trout <i>Salmo trutta</i>, perch <i>Perca fluviatilis</i>, pikeperch <i>Stizostedion lucioperca</i>, pike <i>Esox lucius</i>, cod <i>Gadus morhua</i>, hake <i>Merluccius merluccius</i>, bream <i>Abramis brama</i>, and round goby <i>Neogobius melanostomus</i>.</p>

			(A. Pocwierz-Kotus abstract continued)
			<p>Based on Tc1 sequences deposited in the GenBank a pair of primers (APK1 and APK2) was designed that enabled amplification of DNA fragment that encodes for a transposase. A primer complementary to reversed repeats was also used (Leaver, 2001), and PCR product size was 1630 bp. Presence of Tc1 transposon using PCR was confirmed for plaice, turbot, herring, salmon, pike, land locked trout, round goby and perch. Additionally, a Southern hybridisation was performed between genomic DNA, digested by restriction enzymes PvuII, BamHI, and HindIII, and the transposase gene fragment with size 814 bp as a probe labelled with DIG-dUTP. These procedures enabled us to detect Tc1 transposons in flounder, plaice, salmon, pike, land locked trout, round goby and perch genomes. We are planning to analyse these genomes for the distribution and sequence polymorphism of Tc1 transposons.</p>
Pratt	Renae Pratt, Mary Morgan-Richards and Steve Trewick	Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Palmerston North, New Zealand	<p><b>Weta worldwide - systematics and biogeography of the Anostostomatids</b></p> <p>New Zealand is well known for its endemic weta, Anostostomatidae. These large flightless orthoptera (crickets) play important ecological roles in the environment, but the group is not restricted to New Zealand, with extant endemic taxa present in other Gondwanan regions. Weta may therefore provide valuable data for the study of Gondwanan biogeography and the evolution of endemic biota. Previous studies have assessed taxonomy and biogeography of the New Zealand species using morphological traits, cytology, allozymes, mitochondrial DNA sequence, and sexual behaviour.</p> <p>The phylogenetic relationships within and between Anostostomatid genera are still poorly resolved. Using larger sequence fragments, and a combination of nuclear and mitochondrial DNA, three distinct lineages in New Zealand have been identified; Giant/Tree weta (Deinacrida/Hemideina), Ground weta (Hemiandrus) and Tusked weta (Anisoura, Motuweta) that appear to have diverged prior to the Miocene. These groups each appear to have affinities with genera outside New Zealand.</p> <p>A combination of phylogenetic methods with molecular clock calibrations and morphological characteristics are helping to elucidate evolutionary relationships for New Zealand weta and their relatives.</p>
QIN	JINYI QIN, CHEE YANG LEE, JOHN WETHERALL & DAVID GROTH	1School of Biomedical Science, Curtin University of Technology, Western Australia, 2Centre for High Throughput Agricultural Genetic Analysis, Murdoch University, Western Australia.	<p><b>Identification of Clones Spanning the Sheep MHC Gene Region</b></p> <p>This project aims to study the association between parasitic nematodes and sheep MHC class III region by using single nucleotide polymorphisms (SNP's) as markers for haplotypic variation. Mouse mRNA sequences were aligned with human MHC genomic DNA sequences to identify highly conserved exons, which served as DNA templates for designing PCR primers as well as overlapping primers ("overgo primers"). 9 probes developed from PCR of a merino sheep DNA were hybridised with sheep cosmid library, while 20 sets of overgo primers were hybridised with sheep BAC library. 2 positive cosmid colonies and 108 positive BAC colonies have been identified containing the entire MHC class III region and parts of class I and II regions. Subcloning and sequencing of 1 cosmid colony has revealed the end part of MHC class II region spanning from B3GALT4, BING4, HKE2, RGL2, TAPBP, and BING1 gene. Previously identified cosmids containing genes from C2 to TNXB within the class III region have also been subcloned and sequenced, upon which a SNP marker within Tumour Necrosis Factor (TNFa) gene has been discovered. Identification of additional SNPs markers is underway.</p>
Raterman	Raterman Denise, M. S. Springer	University of California-Riverside, Riverside, CA	<p><b>A comparative genomics approach to elucidating acrosin's role in mammalian fertilization</b></p> <p>Mammalian fertilization has been extensively studied yet the proteins involved and the roles certain proteins play in the process remain contentious. This complex, species-specific process is mediated by molecular interactions between the egg and sperm. Given the extreme importance of this pathway, the discovery that many fertilization proteins show rapid divergence linked to positive selection is intriguing. It has been speculated that this divergence results from male-female protein interactions. Acrosin, a male reproductive protein located in the sperm acrosome, may perform dual functions when acrosome-reacted sperm contact the zona pellucida. One function may be that of a serine protease. Acrosin is also believed to be involved in secondary binding interactions with the zona pellucida. Since acrosin has been suggested to play an integral role in fertilization, is important to understand this gene's structure and function. We obtained sequences from a diverse range of mammalian species for several regions of acrosin. This data was then used to identify sites under positive selection.</p>

(Denise Raterman abstract continued)

These sites were examined in the context of the known molecular structure to determine whether their positions within the molecule are amenable to protein-protein interaction. A preliminary analysis identified one site under positive selection that occupies an external position on the molecule. Furthermore, residues indicated to be involved in acrosin's function were examined to determine their level of conservation. High amino acid conservation was detected at the serine catalytic triad sites and many of the basic residues believed to play a role in zona pellucida binding.

Roach

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**Phylogenomics: Isolation  
and Evolutionary Analysis  
of Random EST  
Sequences**

Phylogenetic information is often determined from morphological and molecular traits. The most common molecular traits are from mitochondrial DNA and occasionally nuclear DNA sequences are also used. Phylogenetic information based on nuclear genes is often limited to a few loci for many taxa or many loci (including genomes) for a few taxa. To characterize molecular traits from a wide variety of nuclear genes, we have isolated cDNA sequences from several hundred mRNAs in species of the teleost fish *Fundulus*. In this approach, we randomly isolated and sequenced cDNAs from non-normalized libraries. Libraries are biased toward a few genes that are highly expressed: a few hundred genes represent 70-85% of the all expressed mRNAs. Thus, many of the randomly chosen cDNAs encode the same gene. Using a high-throughput approach, approximately 100 different orthologous genes from each taxa are identified and used for analyses. For example, orthologous sequences are aligned and used to describe evolutionary relationships among taxa. These relationships are compared among genes to identify genes with unusual patterns of evolution. The ratio of non-synonymous to synonymous substitutions is used to investigate the evolutionary processes affecting the phylogenetic relationships.

Robbens

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**Genome analysis of the  
world's smallest free-  
living eukaryote  
*Ostreococcus tauri*  
unveils unique genome  
heterogeneity**

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In collaboration with the Laboratoire Arago, Banyuls, France, we are performing the full genome annotation of the unicellular green alga *Ostreococcus tauri*. This alga is the smallest eukaryotic organism described until now (its size is comparable to that of a bacterium) and has a nuclear genome of about 12.65 Mb, divided over 19 chromosomes. *Ostreococcus tauri* was discovered in the Mediterranean Thau lagoon (France) in 1994. Its cellular organisation is rather simple: *O. tauri* has a relatively large nucleus with only one nuclear pore, a single chloroplast, one mitochondrion, one Golgi body and a very reduced cytoplasmic compartment. The presence of only one chloroplast and mitochondrion makes it interesting to use not only for experimental studies, but also for evolutionary studies. Phylogenetic analysis placed *Ostreococcus tauri* within the Prasinophyceae, an early branch of the Chlorophyta (green algae). Morphologically, the absence of flagella is the most typical characteristic compared to other green algae. Regarding the genome itself, there are a number of very unexpected and unique findings that have never been observed in any of the eukaryotic genomes sequenced to date. The most striking is the genome heterogeneity, where the chromosomes 2 and 18 are surprisingly different from all other 17 chromosomes. Genes on chromosome 2 have unique intron features, unlike the genes found on the other chromosomes. Also, most of the transposable elements in *Ostreococcus* are found on both aberrant chromosomes. Another unique and important aspect of this genome is the extreme simplification of the gene complement. For many pathways and cellular processes (one example being the cell cycle where only one member of each cell cycle gene family was detected), the number of genes is kept to an absolute minimum. The genome of *Ostreococcus* is also exceptionally compact. The result is that gene transcripts, and sometimes even the CDS themselves, are overlapping, a feature rarely observed in eukaryotes. Furthermore, we observed the clustering of functionally related genes comparable to bacterial organization. In addition to the nuclear genome, the chloroplast and mitochondrial genome were also sequenced and annotated. The circular chloroplast genome is about 60,600 bp long with an overall GC content of 43% and contains 93 genes. The mitochondrial genome with its 66 genes is about 42,500 bp long and has an almost identical gene repertoire compared to *Nephroselmis olivacea*, another green alga. In order to classify *Ostreococcus tauri* within the tree of life, an extensive phylogenetic analysis was performed. Phylogenies were inferred on the basis of concatenated chloroplast genes, concatenated mitochondrial genes, and a combination of chloroplast, mitochondrial and nuclear genes. All datasets and methods confirmed *Ostreococcus* being a basal green alga, closely related to *Nephroselmis*.

<p><b>Rogers</b></p>	<p>Stephanie A. Rogers<sup>1,2</sup>, Sudhir Kumar<sup>1</sup>, and Jeffrey W. Touchman<sup>1,2</sup></p>	<p>1. The Biodesign Institute, Arizona State University, Temp, AZ; 2. The Translational Genomics Research Institute (TGen), Phoenix, AZ.</p>	<p><b>PRIMATE LINAGE SEQUENCE CONSERVATION IN PROMOTER REGIONS</b></p>	<p>Identifying regions of cross-species conservation specifically amongst primates promises to identify functional sequences that make humans distinct from other animals. Here we report an extensive analysis of the complete 2-kb promoter region of ten neighboring genes in a comparison study within and between the two groups: primates and non-primates. We compared the ten promoter regions across 36 different genomes that included 13 primate species and 23 non-primate species. Using a novel computational method that relies upon using a score comprised of the summed divergence age of each base pair in the human promoters, we were able to create a primate sequence conservation map for each promoter. The identification of numerous candidates for primate-specific regulatory regions that are not conserved in other vertebrates was detected by looking at both the "mutual information content" between primates and non-primates and the age-profile previously produced. With this approach, regions that were significantly incongruent between the two groups and highly conserved in primates were highlighted. The resulting putative primate-specific elements were compared to previously identified promoter elements and these results are discussed. Identified sequences are being studied actively to assess their regulatory activity in humans versus non-primates.</p>
<p><b>Roy</b></p>	<p>Scott William Roy</p>	<p>Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA</p>	<p><b>Low level of polymorphism in the untranslated regions of three highly polymorphic genes of the human malaria parasite, Plasmodium falciparum</b></p>	<p>The Plasmodium falciparum protein merozoite surface protein-1 is one of the most polymorphic genes known in any species, with different alleles being so divergent as to be unalignable in some regions. Surprisingly, nearby regions including other sections of the coding sequence and the gene's one intron have previously been found to have low levels of polymorphism. We show here that the 5' and 3' UTRs of the gene also have very low levels of polymorphism, with no SNPs observed among six widely divergent strains. Along with previous data, this strongly suggests that the different alleles diverged only recently and that their high level of sequence divergence is due to strong and recent diversifying selection. To assess the generality of this pattern, we sequenced the UTRs of two other surface antigens whose coding sequences show extremely high levels of polymorphism. These regions too showed low levels of polymorphism. These results strongly suggest that selection for novel alleles by the immune system and not balancing selection explains high levels of surface antigen polymorphism in P. falciparum.</p>
<p><b>Roy</b></p>	<p>Scott William Roy</p>	<p>Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA</p>	<p><b>Parallel gain can not explain the level of intron conservation between eukaryotic orthologs</b></p>	<p>A large body of work has shown that a large fraction of introns in eukaryotic genes are at the same positions of introns in widely diverged homologs. This pattern may be explained either by retention of ancestral introns or by independent homoplastic insertions into homologous sites along various lineages. The latter, termed parallel insertion, postulates a highly specific intron insertion mechanism favoring so-called "protosplice sites", leading to a high degree of coincidence in intron position between homologs. However, I show here that parallel insertion is highly unlikely to be a major factor in the pattern of intron coincidence for several reasons: 1) there are too many coincidences between pairs of widely divergent species to be explained by biased insertion into protosplice sites; 2) there are too many three-way coincidences between trios of widely diverged species to be explained by observed numbers of two-way coincidences; 3) numbers of introns shared between species vary widely between genes, as expected by differences in rates of intron evolution between genes or if introns are lost in concert but not by parallel insertion; and 4) introns present in multiple outgroup species and a sister are not particularly more likely to be retained in a species than are those found in only a sister and single outgroup, suggesting that the latter class do not contain significant numbers of parallel insertions.</p>

<p><b>Salaün</b></p>	<p>Laurence Salaün (1,2), Fabrice Mérien (1), Guy Baranton (2) and Mathieu Picardeau (2)</p>	<p>(1) Laboratoire de Recherche en Bactériologie, Institut Pasteur de Nouvelle-Calédonie (2) Laboratoire des Spirochètes, Institut Pasteur, Paris</p>	<p><b>Genotyping of pathogenic Leptospira based on tandem repeat polymorphism</b></p>	<p>Leptospirosis, an infectious disease caused by spirochetes belonging to the genus <i>Leptospira</i>, is presumed to be the most widespread zoonosis in the world. <i>Leptospira</i> infects a large number of wild and domestic animals that constitute the reservoir of pathogenic leptospires for humans. Among the numerous species of this genus, seven are described as pathogens. The epidemiology and clinical features of leptospirosis are usually associated with the serovars and serogroups of <i>Leptospira</i>. Because this serovars determination requires tedious and time consuming serological procedures, a new typing method based on the amplification of polymorphic loci containing variable number of tandem repeats (VNTR) was recently developed on <i>L. interrogans</i> species. Here we propose to extend this method to other species of pathogenic <i>Leptospira</i>, and to apply this tool for broad epidemiological studies.</p> <p>Methods: The whole sequences of the two available genomes of <i>L. interrogans</i> were analysed using the Repeat Finder software and the Tandem Repeat database. Three VNTRs previously proved to be discriminant for <i>L. interrogans</i> typing were redefined to amplify other species of pathogenic <i>Leptospira</i> (<i>L. kirschneri</i>, <i>L. borgpetersenii</i>, <i>L. noguchii</i>). Those primers were used on a hundred field isolates from New-Caledonia. Copy number of repeats of each VNTR locus was deduced from data sequencing and size of the amplified products. Data were analysed using Bionumerics software package. Relationships among the genotypes recorded were depicted by the neighbor joining method.</p> <p>Results-Conclusion: Collection strains of <i>L. kirschneri</i> and <i>L. borgpetersenii</i> as well as most of field isolates could be rapidly and efficiently identified with only PCR and agarose gel migration apparatus. The availability of such a fast and simple typing system is of great interest for the identification and epidemiological study of <i>Leptospira</i> in laboratories located in high incidence areas such as South Pacific.</p>
<p><b>Santure</b></p>	<p>Anna Santure</p>	<p>Department of Zoology, University of Otago, Dunedin, New Zealand</p>	<p><b>Influence of Mum and Dad: Imprinting and Maternal Effects</b></p>	<p>Expression of an imprinted gene depends on the sex of the parent from which it was inherited. As a consequence, reciprocal heterozygotes may have different genotypic values. Single genes may have a significant effect on the phenotype of an individual, but in general traits are influenced by a large number of loci, each with small effect. The interaction between these loci and with the environment produces continuously varying characters, or quantitative traits. The majority of imprinted loci currently characterised are examples of single genes with large effect, but an increasing number of studies are suggesting that imprinted genes may have an influence on both economically and socially important quantitative traits, such as disease severity and livestock production traits. However, it is unclear whether imprinting can be distinguished from other paternal influences such as maternal effects. This research aims to develop a statistical test that can assess whether or not a quantitative trait is influenced by imprinted genes. Development of such a test requires deriving quantitative genetic models for imprinting, including maternal effects and interactions between loci, and calculating breeding values, components of variance and covariances between relatives.</p>
<p><b>Schliep</b></p>	<p>Klaus Schliep, Barbara Holland, Mike Hendy and David Penny</p>	<p>Allan Wilson Centre for Molecular Ecology and Evolution, Institute of Molecular Bioscience Massey University, New Zealand</p>	<p><b>Some connects between Hadamard conjugation and regression models</b></p>	<p>Hadamard conjugation (Hendy et al. 1994) is a framework to describe the transformation between site patterns and an edge length spectrum. We will show how to estimate phylogenetic trees and networks on the basis of Hadamard conjugation and (generalized) linear models. The strong connection to both regression and distance matrix models allows us to adapt many tests procedures and to develop a tool for estimation phylogenetic networks. We will present some theoretical results as well as some analysis of real datasets.</p> <p>Keywords: Phylogenetic tree estimation, maximum likelihood, Hadamard conjugation, distance matrix methods, covariance</p>
<p><b>Schliep</b></p>	<p>Klaus Schliep, Barbara Holland, Mike Hendy and David Penny</p>	<p>Allan Wilson Centre for Molecular Ecology and Evolution, Institute of Molecular Bioscience Massey University, New Zealand</p>	<p><b>Some connections between Hadamard conjugation and regression models</b></p>	<p>Hadamard conjugation (Hendy et al. 1994) is a framework to describe the transformation between site patterns and an edge length spectrum. We will show how to estimate phylogenetic trees and networks on the basis of Hadamard conjugation and (generalized) linear models. The strong connection to both regression and distance matrix models allows us to adapt many tests procedures and to develop a tool for estimation phylogenetic networks. We will present some theoretical results as well as some analysis of real datasets.</p> <p>Keywords: Phylogenetic tree estimation, maximum likelihood, Hadamard conjugation, distance matrix methods, covariance</p>

<p><b>Shaw</b></p>	<p>Matthew Shaw, Robert Cruickshank, Adrian Paterson</p>	<p>Bio-Protection and Ecology Division, Lincoln University, PO Box 84, Lincoln, Canterbury, NEW ZEALAND, shawm2@lincoln.ac.nz</p>	<p><b>Multiple episodes of reversibility of parasitism in dermanyssoid mites (Acari: Mesostigmata)?</b></p> <p>The Dermanyssoidea is a large group of mesostigmatid mites that contains both free-living and parasitic species. It has generally been assumed that the free-living dermanyssoids represent the ancestral form from which one or more clades of parasites have arisen. We have constructed a molecular phylogeny for this group that suggests there have been several origins of parasitism as well as a number of reversals to the free-living state. Loss of parasitism is almost completely unknown in other groups of parasites due to loss of the adaptations necessary for life away from the host. Most examples cited in the literature actually represent loss of feeding during a parasitic stage in the life cycle rather than genuine evolutionary transitions from parasitism to other modes of feeding. Dermanyssoid mites appear to represent a unique example of extraordinary plasticity in parasitism.</p>
<p><b>Simons</b></p>	<p>Jo Simons<sup>1, 2</sup>, Kerry Templeton<sup>1</sup>, Kim Plummer<sup>2</sup>, Christine Beveridge<sup>3</sup>, Kimberley Snowden<sup>1</sup></p>	<p><sup>1</sup>Gene Technologies Group, HortResearch, Auckland, New Zealand; <sup>2</sup>School of Biological Sciences, University of Auckland, Auckland, New Zealand; <sup>3</sup>Department of Botany, University of Queensland, Brisbane, Australia.</p>	<p><b>CHARACTERISATION OF THE GENETIC AND HORMONAL CONTROLS OF PLANT BRANCHING.</b></p> <p>Branching is a fundamental process affecting plant form and is a source of much of the wide variety of plant architecture seen in nature. Our aim is to understand the function of genes involved in branching using petunia as a model system. This research involves the study of the decreased apical dominance (dad) mutants in petunia, which have increased basal branching compared with wild type. It also involves the investigation of genes known to affect branching in other plant species to discover their effects in petunia. One of these genes, MAX2, was identified from an increased branching mutant of Arabidopsis, and its effects are being investigated by misexpression of the gene in petunia. Previous grafting experiments using the dad mutants in petunia have shown that a graft-transmissible signal is involved in causing the increased branching phenotype. Hormone levels play important roles in the control of apical dominance, one of the most studied controls in lateral branching. Auxin and cytokinin levels in dad mutant and wild type plants were investigated, but the levels of these hormones were not consistent with them being the graft transmissible signal modified by the DAD genes. In order to investigate the relationships between the DAD genes, the branching phenotypes of the single and double dad mutants were characterised and analysed. This work has revealed interactions between the DAD genes and provided evidence for the order of action of these genes.</p>
<p><b>Steeves</b></p>	<p>Tammy Steeves<sup>1</sup>, Richard Maloney<sup>2</sup>, Glenda Singleton<sup>1</sup>, Maureen Waite<sup>1</sup> and Neil Gemmell<sup>1</sup></p>	<p><sup>1</sup>School of Biological Sciences, University of Canterbury, Christchurch, NZ <sup>2</sup>Department of Conservation, Twizel Area Office, Wairepo Road, Twizel, NZ</p>	<p><b>Conservation genetics of a critically endangered New Zealand endemic, the black stilt (Himantopus novaezelandiae)</b></p> <p>The New Zealand endemic black stilt or kakī is one of the world's rarest birds and an international icon for conservation. Once widely distributed, this critically endangered braided river specialist is currently restricted to the Upper Waitaki Basin. Although intensive management has increased population size from ~ 23 adults in 1981 to 76 adults (55 wild and 21 captive) in 2004, the species remains at risk of extinction. Introduced predators, widespread habitat loss, small population size, and hybridization with self-introduced pied stilt or poaka imperil species recovery and survival. Currently, the extent of hybridisation between these two closely related species remains unclear. Hybrids were first recorded in the late 19th century, but their relative numbers increased in the mid 20th century, as kakī numbers declined. Until recently, hybridisation appeared to be driven by a male-biased sex-ratio. However, recent evidence suggests the skewed sex-ratio was likely an artifact of small population size. In addition, while more male kakī tend to mate inappropriately, both males and females form mixed-pairs. Thus, despite years of direct observation, molecular genetics may be the most effective method to gauge the extent of hybridisation between kakī and poaka. Expanding on previous studies by using both maternally-inherited mitochondrial and bipaternally-inherited nuclear genetic markers, we hope to determine: 1) if kakī are genetically distinct from poaka; and 2) the "genetic status" of hybrids, data that are fundamental for future conservation management strategies.</p>

<p><b>Stiglec</b></p>	<p>Rami Stiglec<sup>1</sup>, Shargal Tsend-Ayush<sup>1</sup>, Frank Grützner<sup>1</sup>, Tariq Ezaz<sup>1</sup>, Anne Gaeth<sup>1</sup>, Steve Sarre<sup>2</sup>, Arthur George<sup>2</sup>, Jennifer A. Marshall Graves<sup>1</sup>.</p>	<p>1. Comparative Genomics Group, Research School of Biological Sciences, The Australian National University, Canberra A.C.T. 2601, Australia. 2. Applied Ecology Research Group, University of Canberra, Canberra A.C.T. 2601, Australia</p>	<p><b>DMRT1 in the tiger snake</b></p>	<p>Like birds, snakes have ZZ male/ZW female sex chromosomes. Snakes and bird sex chromosomes are similar in size and morphology, so it is possible that they are genetically homologous and share the same sex-determining gene. A putative avian sex-determining gene DMRT1 maps to the chicken Z in a region homologous to a sex-reversal region on human 9p. Unlike other Z chromosome genes, DMRT1 shows no dosage compensation in males, and is expressed in the testes during gonadogenesis, suggesting an important dosage sensitive role in male determination and differentiation.</p> <p>As with birds, snake families differ in the degree of differentiation between the Z and W. The Boidae possess sex chromosomes that are virtually homomorphic, whereas others (such as the more derived tiger snake <i>Notechis scutatus</i>) have strongly heteromorphic sex chromosomes. We have karyotyped male and female tiger snakes and identified heteromorphic Z/W sex chromosomes. We have cloned tiger snake DMRT1 and fully sequenced it, the first time the entire cDNA of this gene has been sequenced from any reptile or bird. Using FISH, we mapped DMRT1 to the short arm of the tiger snake Z and the terminal region of the W. This is the first time a gene has been shown to be conserved between avian and reptilian sex chromosomes. Our results support homology between bird and snake sex chromosomes.</p>
<p><b>Tay</b></p>	<p>Gajanan Behere, Wee Tek Tay, Sandhya Kranthi<sup>1</sup>, Phil Batterham and Derek Russell</p>	<p>ARC Special Research Centre for Environmental Stress and Adaptation Research (CESAR), Department of Genetics, Bio21 Institute of Molecular Science and Biotechnology, The University of Melbourne, Victoria 3010, Australia. <sup>1</sup>Central Institute for Cotton Research, Nagpur, India.</p>	<p><b>Mitochondrial DNA analyses of <i>Helicoverpa armigera</i> populations from Australia, India and China</b></p>	<p>The cotton bollworm <i>Helicoverpa armigera</i> is a serious agricultural pest found in the old world - Africa to Europe, Asia and Australia. Although wide spread in Australia, the population genetics and founding history of <i>H. armigera</i> have not been studied with respect to female movements. The maternally inherited mitochondrial DNA (mtDNA) has been used extensively in many animals as the genetic marker of choice for tracing female movements due to its almost exclusive female mode of inheritance (i.e., mother – offspring) and the lack of genetic recombination with nuclear DNA. In this study, we isolated mtDNA from individuals sampled from Chinese, Indian and Australian localities representing different <i>H. armigera</i> populations, and analysed the mtDNA cytochrome b (cyt b) and the cytochrome oxidase I and II (COI – COII) regions for single nucleotide polymorphisms (SNPs) to determine the relationships between female founders in the three countries. Preliminary analyses indicated the presence of multiple SNPs in both cyt b and COI - COII regions in our study populations, and indicated the feasibility of using mtDNA to study the population movement of <i>H. armigera</i> over time and space.</p>
<p><b>Tay</b></p>	<p>W. T. Tay<sup>1,2</sup>, E. M. O'Mahony<sup>1</sup>, J. Klee<sup>1</sup>, S. Walker<sup>1</sup> and R. J. Paxton<sup>1</sup></p>	<p><sup>1</sup>School of Biology and Biochemistry, Queen's University Belfast, Belfast BT9 7BL, U.K. <sup>2</sup>ARC Special Research Centre for Environmental Stress and Adaptation Research (CESAR), Department of Genetics, Bio21 Institute of Molecular Science and Biotechnology, The University of Melbourne, Victoria 3010, Australia.</p>	<p><b>Single spore DNA analyses indicate that the multiple copies of rRNA genes in <i>Nosema bombi</i> (Microsporidia: Nosematidae) have different sequences</b></p>	<p>Ribosomal RNA genes (rRNA) that typically exist in tandem arrangements in the genome of prokaryotes and eukaryotes have become the paradigm for concerted evolution and are widely used in phylogeny reconstruction. Microsporidia are microscopic obligate intracellular parasites found in most eukaryotic organisms. To-date, the microsporidian rRNA genes from pooled-genomic DNA isolated from individual hosts have been used extensively for differentiating between genera and species. This is due in part to the limited availability of morphological characters in Microsporidia for taxonomic classification purposes, plus the ease of PCR amplification of rRNA genes, and the assumed homology between intra-genomic copies of rRNA genes by the action of concerted evolution; pooled-genomic DNA has also been necessary due to the difficulties of isolating single spores. In this study, we used laser microscopy to isolate single spores from the bumble bee (<i>Hymenoptera</i>, <i>Bombidae</i>) infecting microsporidia <i>Nosema bombi</i> for DNA analyses. Sequence data from partial small subunit rRNA (SSU-rRNA), the complete internal transcribed spacer region (ITS) and partial large subunit rRNA (LSU-rRNA) genes derived from single spores confirmed the presence of multiple non-homogeneous copies of rRNA genes in <i>N. bombi</i>, while different spores from a single bumble bee host also exhibited different rRNA haplotypes. Our study raises issues concerning the use of rRNA genes as the genetic marker of choice and the use of pooled-genomic DNA in the study of <i>N. bombi</i> and related unicellular eukaryotes.</p>

<p><b>Travers</b></p>	<p>Simon A. A. Travers and Mario A. Fares</p>	<p>Molecular Evolution and Bioinformatics Laboratory, Biology Department, National University of Ireland, Maynooth, Co Kildare, Ireland</p>	<p><b>Uncovering new cofactor-interacting regions in Heat-shock proteins (Hsps) using inter-molecular coevolutionary analyses.</b></p>	<p>The detection of coevolution between amino acid sites is an important factor to take into account in evolutionary analyses as well as in protein-protein interaction prediction. To date, several methods have been developed to detect coevolution between amino acid sites however, the results have so far been rather ambiguous and inconclusive. Here we present a novel method developed to detect coevolution between amino acid sites within and between proteins. This method also utilises protein three-dimensional information, where available, to examine coevolving amino acid sites within the context of a protein structure. Using simulated data sets we show that the main advantage of this method is the incorporation of correction parameters that ensure a high sensitivity and specificity to detect actual coevolutionary events. Previous analysis, applying the method to the 90 Kda (Hsp90) and 60 Kda (GroEL) heat-shock proteins, exhibited high correlation between coevolution analysis and previously determined functional data. These analyses indicated that the method provides a good measure of inter-protein coevolution. We applied this new method to detect protein-protein coevolution in the Hsp-cofactor system to test the hypothesis of the existence of cryptic cofactor binding sites. A new parameter is developed to determine whether or not two proteins are physically interacting and is used to detect regions within Hsp molecules that potentially interact with cofactors.</p>
<p><b>VanWye</b></p>	<p>Jeffrey D VanWye, M Danielle McDonald, Patrick J Walsh and Douglas L Crawford</p>	<p>Division of Marine Biology and Fisheries, NIEHS Marine and Freshwater Biomedical Sciences Center, Rosenstiel School of Marine &amp; Atmospheric Science, University of Miami, Miami, FL 33149</p>	<p><b>Biological Variation in Gene Expression</b></p>	<p>Previous work has shown a large variation in gene expression within and among populations of <i>Fundulus heteroclitus</i>. Much of this variation in gene expression seems to be biologically relevant because it explains metabolic rates and it appears to evolve by natural selection. These above measures of gene expression were on fish raised in a common environment, yet are from natural outbred populations and thus no two individuals are genetically similar. This presents a problem with the data: differences between individuals could be due to genetics, irreversible developmental effects, or random biological variation. To address random biological effects, we sampled blood from 10 individual fish, four times with a two-week interval between samplings. The red blood cells (RBC, which are nucleated and transcriptionally active) were separated from white blood cells and serum. RNA was isolated from the RBCs to measure gene expression using a <i>F. heteroclitus</i> microarray. The serum was used to test for cortisol levels by immunoassay and glucose levels by an enzymatic assay to determine the level of stress. Measures of stress and gene expression from replicate samples from 10 individuals were used to identify the biological variation.</p>
<p><b>Vargas</b></p>	<p>Iris M. Vargas Jentsch, Angelika Merkel, Emmanuel Buschiazio, Neil J. Gemmell</p>	<p>School of Biological Sciences, University of Canterbury, Christchurch, New Zealand</p>	<p><b>Do simple sequences evolve simply?</b></p>	<p>Microsatellites are one kind of repetitive DNA sequence widely distributed throughout eukaryotic and prokaryotic genomes, outstanding in terms of variability and still one of the most enigmatic sequences in terms of function and mutation process. These sequences, based on perfect or near-perfect tandem iterations of sequence motifs 2-6 base pairs in length, derive in multiple alleles of differing repeat length, which makes them exceptionally suitable as molecular markers for population genetics, linkage and mapping analysis. Despite a high number of ingenious studies, the mutation process and relation of microsatellites to coding regions is still not fully understood, and theoretical models fail to explain observed patterns of variation. We are using a blend of comparative genetics and bioinformatics to study microsatellite evolution using three different approaches as follows: 1) Genome-wide comparison of microsatellite conservation across duplicated regions in yeast (<i>Saccharomyces cerevisiae</i>) to evaluate the effect of genomic position on microsatellite instability; 2) Classification of microsatellite loci based on mammalian genomic comparisons to analyze observed and expected variation of different classes of microsatellites in relation to genomic position; and 3) Study of the extent, genomic distribution and variability of conserved microsatellite loci across major mammalian groups in a phylogenetic context.</p>

<p><b>Vaughan</b></p>	<p>Meredith Vaughan and Douglas Crawford</p>	<p>Rosenstiel School of Marine and Atmospheric Science, University of Miami, 4600 Rickenbacker Cswy, Miami, FL 33149</p>	<p><b>A Nuclear Gene Phylogeny for Fundulus</b></p>	<p>Phylogenetic information serves many purposes: establishing relationships between taxa, statistically correcting for shared evolutionary history, or measuring divergence times. For ongoing studies of Fundulus, we are examining the ecological effects on phenotypes and genotypes, and need to account for neutral divergence among natural populations. This can be accomplished using phylogenetic relationships and the approximate genetic distance among closely related Fundulus species. To begin to resolve the relationships among populations and among seven species, we have isolated and sequenced nuclear DNA from two introns: triosephosphate isomerase (TPI) intron 3, and ribosomal protein L7a (RPL7a) intron 3. Intron locations and primer pairs were determined by comparison with known locations in Danio rerio and Fugu rubripes. In order to distinguish fixed differences from shared polymorphisms among species, we sequenced both alleles from the two loci from a minimum of ten individuals from each of seven species. These analyses were used to derive evolutionary relationships and relative distances among species. These data will allow for better comparative functional genomic analyses.</p>
<p><b>Whittall</b></p>	<p>Justen B. Whittall, Claudia Voelckel, Scott Hodges</p>	<p>University of California Santa Barbara, Department of Ecology, Evolution and Marine Biology, Santa Barbara, CA 93106</p>	<p><b>The molecular basis of convergent evolution: Loss of floral anthocyanins in Aquilegia.</b></p>	<p>The ability to reconstruct phylogenies has allowed considerable progress in identifying whether similar traits in different species arise through convergent evolution. The mechanisms, by which these convergences are achieved however, remain elusive. Thus whether a single or several different molecular mechanisms account for convergent evolution is an unanswered question. Using a phylogeny of all extant species in the North American clade of Aquilegia, we have determined that the loss of floral anthocyanin production evolved multiple times resulting in shifts from red/blue to yellow/white flowers. These shifts in color are usually associated with a shift in pollination syndrome. Because the anthocyanin biosynthetic pathway is well characterized, we conducted a gene expression study using degenerate primers and qualitative RT-PCR involving the pathway's major structural genes (CHS, CHI, ANS, F3H, F3'H, F3'5'H, DFR, UF3GT) and two of its trans-regulators (myb, myc). Initially, we monitored the expression of these genes during floral development and in various tissues of A. canadensis, a species, which produces anthocyanins. Subsequently, we will measure gene expression across multiple white- or yellow-flowered species. By comparing expression patterns across species we will learn i) whether the loss of anthocyanin production may be driven by a loss of gene expression, ii) if so, whether the different anthocyanin-less species have convergent expression profiles and iii) whether cis- or trans-regulation is important in each particular case. Not only will this allow us to identify candidate genes underlying each shift but it will also contribute to unraveling the mechanisms of convergent evolution across plant model systems.</p>
<p><b>Wikmark</b></p>	<p>Odd-Gunnar Wikmark, Peik Haugen, Anna Vader, Dag H. Coucheron, Eva Sjøttem and Steinar Johansen.</p>	<p>RNA Group, Dept. of Molecular Biotechnology, Institute of Medical Biology, University of Tromsø, N-9037 Tromsø, Norway.</p>	<p><b>The recent transfer of a homing endonuclease gene between distantly related group I introns.</b></p>	<p>The myxomycete Didymium iridis (isolate Panama 2) contains a mobile group I intron named Dir.S956-1 with a twin-ribozyme organization. It is inserted after position 956 in the nuclear small subunit (SSU) rRNA gene. The intron is efficiently spread through homing into all intron-minus alleles in genetic crosses between amoeba cells of the Panama 2 strain and an intron-lacking strain. Homing is promoted by the intron-encoded homing endonuclease (HE) I-Dir1. Although homing endonuclease genes (HEGs) usually spread with their associated introns as a unit, accumulating evidence suggest that they infrequently spread independent of introns (or inteins). Clear examples of HEG mobility are however sparse. Here we provide evidence for the recent transfer of a homing endonuclease gene into a group I intron named Dir.S956-2 that is inserted into the SSU rDNA of the Costa Rica 8 isolate of D. iridis. The intron is inserted into the same SSU site (956) as the Dir.S956-1 intron in the Panama 2 isolate. Remarkably, the group I introns encode distantly related splicing ribozymes with phylogenetically related HEGs inserted on the opposite strands of different peripheral loop regions. The HEGs are both interrupted by small spliceosomal introns that need to be removed before functional HE proteins can be expressed.</p>

<p><b>Wilson</b></p>	<p>Neil Wilson<sup>1,2</sup>, Sasha Tetu<sup>2</sup>, Nick Coleman<sup>2</sup>, Michael Gillings<sup>1</sup>, Andrew Holmes<sup>2</sup>.</p>	<p>1. Department of Biological Sciences, Macquarie University, 2109, Australia. 2. School of Molecular and Microbial Biosciences, University of Sydney, 2006, Australia.</p>	<p><b>The significance of integrons outside the clinical environment</b></p>	<p>Integrons have played a central role in the emergence and dissemination of multiple antibiotic resistance in many pathogenic bacteria and have been the focus of much research. More recently, integrons have been found to be common outside the clinical environment. The role of integrons in non-clinical bacteria remains unclear. However, several characteristics of integrons from non-pathogenic bacteria suggest that their impact on bacterial evolution has been different to that of antibiotic resistance associated integrons. The <i>Pseudomonas stutzeri</i> species complex is, in terms of allelic diversity, the most diverse bacterial species currently known, and provides a unique opportunity to investigate the significance of integrons to bacterial diversity. Members of the complex are not defined by an exclusively shared set of phenotypic characters, although are obviously closely related. Fine scale taxonomy has distinguished 9 different groups (termed genomovars) based on total DNA:DNA similarity. We tested for the presence of integrons in different genomovars and their contribution to the evolutionary radiation of this species complex. Using PCR, hybridisation and cloning, integron-like sequences have been detected in all 20 <i>Ps. stutzeri</i> strains screened. Phylogenetic analyses indicate that within the <i>Pseudomonas</i> genus, the core integron is monophyletic with respect to other known integrons. Within members of <i>Ps. stutzeri</i>, the same pattern was not observed; results suggest that integrons have been acquired independently on two occasions. All strains so far screened contain different gene cassette arrays. While the cassette arrays from members of a single genomovar are different, the integron backbone is conserved, indicating that in comparison to the integron backbone, cassettes are transient members of the genome. Further, the average G + C content of most cassettes found is significantly lower than that of the genome, suggesting that they may have been acquired through lateral gene transfer. Collectively, these data indicate that integrons are significant contributors to intra-genomovar diversity in the <i>Ps. stutzeri</i> species complex.</p>
<p><b>Winder</b></p>	<p>Louise Winder, Frances Wall<sup>1</sup>, Craig Phillips, Stuart Young and Stephen Goldson</p>	<p>AgResearch, Biocontrol and Biodiversity, Gerald St, PO Box 60, Lincoln, Canterbury, New Zealand 1Christchurch Polytechnic Institute of Technology, School of Applied Science, PO Box 540, Christchurch, New Zealand</p>	<p><b>Nuclear and mitochondrial DNA sequence and ISSR variation in the Argentine Stem Weevil (<i>Listronotus bonariensis</i>) from South America and New Zealand</b></p>	<p>Argentine stem weevil, <i>Listronotus bonariensis</i> (Kuschel) (Coleoptera: Curculionidae), was accidentally introduced to New Zealand about 80 years ago and became a severe pasture pest. The parasitoid wasp, <i>Microctonus hyperodae</i> Loan (Hymenoptera: Braconidae), was collected from eight disparate southern South American locations and introduced to New Zealand during the 1990's for biological control of Argentine stem weevil. Morphometric, allozyme and DNA-based approaches have shown that <i>M. hyperodae</i> which originated from east of the Andes have generally been more successful in New Zealand than those which originated from west of the Andes in Chile.</p> <p>To evaluate the importance of host-parasitoid (weevil-wasp) coevolution to the success of the east of the Andes strain of <i>M. hyperodae</i> in New Zealand, it is necessary to identify the South American origin of New Zealand's Argentine stem weevil population. DNA sequencing and inter-simple sequence repeats (ISSRs) were therefore used to compare New Zealand and South American populations of the pest. Insects from all populations had identical 28S rDNA sequences. Most DNA sequences from the nuclear internal transcribed spacer 2 (ITS2) and mitochondrial cytochrome oxidase 1 (CO1) genes showed only minor variation between all populations collected in New Zealand and South America. However, an exception involved specimens from San Carlos de Bariloche in the Argentinean Andes whose sequences varied from all other specimens by approximately 3% in both gene regions. In contrast, ISSR banding identified considerable inter- and intra-population genomic variation.</p> <p>Sequence analysis indicates that New Zealand populations of Argentine Stem Weevil are unlikely to originate from San Carlos de Bariloche. Additionally, there appears sufficient weevil genomic variation for ISSR markers to further identify the South American origin of the New Zealand pest population.</p>

<p><b>Wolff</b></p> <p>Jonci Wolff</p>	<p>School of Biological Sciences, University of Canterbury, Christchurch, New Zealand</p>	<p><b>When good molecules go bad: how common are paternal inheritance of mitochondria and mitochondrial recombination ?</b></p>	<p>Animal mitochondrial DNA (mtDNA) has become the marker of choice for studies of phylogeography and phylogenetics because of its supposed striking characteristics, such as its higher mutation rate (compared to nuclear genes) and the lack of recombination and paternal transmission. Arguing against these commonly accepted characteristics, recent studies suggest that paternal leakage could be a much more common feature of mtDNA inheritance than previously supposed. It has been reported for mammals (sheep, humans, mice), insects (<i>Drosophila</i>) and birds (Great Tit). Further, mtDNA recombination has been demonstrated in at least three different phyla: in chordata, in mollusca and in nematoda. These results suggest that more studies on mtDNA inheritance are required to prove the accuracy of evolutionary relationships inferred using mtDNA. In particular, it is crucial to reveal the frequency of paternal leakage and recombination of mtDNA as it might have serious consequences for reconstructions of evolutionary contexts. Here, we present an approach to examine the extent of these events in chinook salmon (<i>Oncorhynchus tshawytscha</i>). Our work is based on a hatchery population, already genotyped for single nucleotide polymorphisms (SNPs). We will construct crosses between males and females homoplasmic for different mtDNA haplotypes to generate offspring that will be examined for heteroplasmy and recombination. During our experiments we will investigate the stability and prevalence of mtDNA heteroplasmy among different somatic and gametic tissues in mature fish and during different stages of embryogenesis. Furthermore we will determine the number of mtDNA molecules present in sperm and eggs to estimate the influence of egg-sperm-ratios on the probability of paternal inheritance of mtDNA.</p>
<p><b>Woods</b></p> <p>Ryan Woods, Mark Ponniah and Jane M Hughes GSA</p>	<p>Centre for Riverine Landscapes, Faculty of Environmental Sciences, Griffith University, Nathan, Queensland, Australia 4111.</p>	<p><b>Fine Scale Population Structure In the Widely Distributed Freshwater Fish: Australian smelt (<i>Retropinna semoni</i>)</b></p>	<p>The population genetic structure of the freshwater fish, <i>Retropinna semoni</i> was examined to investigate the levels of connectivity both among and within three subcatchments of the Murray Darling Basin (MDB) in south-eastern Australia. Previous biological studies have suggested that this species is widely distributed across the basin. Annual high flow events potentially provide the opportunity for individuals to disperse to populations that are temporarily isolated into refugial pools in the drier months of the year. We used allozymes, a fragment of the ATPase 6 and ATPase 8 mitochondrial genes and four microsatellite loci. Based on the predictions of the Stream Hierarchy Model (SHM) we predicted that genetic variation would be larger at higher hierarchical levels of analysis such as among subcatchments relative to the levels detected among populations within subcatchments. Contrary to these predictions the results for all three molecular markers indicated that gene flow at the finest scale of analysis was significantly restricted. However at the larger scale of analysis no significant population structure was detected suggesting this species is virtually panmictic across the MDB. Investigation of the demographic history suggests that significant population growth has historically occurred. We suggest that this population expansion has occurred too recently to allow populations to reach gene flow-drift equilibrium at larger spatial scales thus obscuring recent restrictions to gene flow. Among populations within subcatchments it is likely however that equilibrium is approached much faster and therefore the current patterns of restricted gene flow at this scale are a much more informative indicator of the levels of connectivity for this species.</p>
<p><b>Yockey</b></p> <p>Heather Yockey, Graham Thompson, Ben Oldroyd GSA</p>	<p>School of Biological Sciences, University of Sydney, 2006 NSW Australia</p>	<p><b>Control of worker sterility in honey bees (<i>Apis mellifera</i>): differential gene expression in queens and workers.</b></p>	<p>The honey bee (<i>Apis mellifera</i>) is characterized by extreme reproductive skew, whereby the workers forego personal reproduction in favour of the queen's. This is the basis of the existence of social insects, allowing for a division of labour. The aim of this study is to discover genes important to the regulation of worker sterility, as evidenced by their differential expression in ovary activated vs. ovary non-activated individuals. Preliminary quantitative RT-PCR data suggests that transferrin and vitellogenin are two genes whose activity changes with the reproductive state of individuals, at least in workers. Changes in the expression profiles of these, plus other genes, in both queens and workers undergoing ovary activation, will help test the role these genes have in the regulation of worker sterility in honey bees, and potentially other social insects.</p>

<p><b>Zamora</b></p> <p>Alejandro Zamora*, §, Qi Sun†, Charlotte Acharya*, Martha Hamblin*, Rebecca Nelson, Sharon Mitchell* and Stephen Kresovich1, §.</p>	<p>*Institute for Genomic Diversity, Cornell University, Ithaca, NY 14850; †Computational Biology Service Unit (CBSU), Cornell Theory Center, Cornell University, Ithaca, NY 14850 and §Department of Plant Breeding, Cornell University, Ithaca, NY 14850</p>	<p><b>A comparative evolutionary genomic approach identifies rapidly evolving genes in the genome of Sorghum bicolor (L.) Moench, involved in biotic and abiotic stresses</b></p>	<p>Rapidly evolving, positively selected genes have been shown to be involved in disease resistance, reproduction and other aspects of adaptation. We used a series of BLASTs to isolate highly divergent ESTs from <i>S. bicolor</i>, with no significant similarity (<math>E &gt; 10^{-5}</math>) to sequences in GenBank. We identified library-specific ESTs and constructed a total of 558 strict contigs representing putative genes. Of these, 96 were unique to the pollen library (POL), 82 from the salicylic acid library and 76 from the water stress library. Using a garden array dotblot, we hybridized <i>S. bicolor</i> probes these candidates to <i>S. bicolor</i>, <i>S. prostratum</i>, <i>Saccharum giganteum</i>, <i>Zea mays</i> and <i>Pennisetum glaucum</i> genomic DNA and identified candidates which showed the expected pattern of gradual decrease in the intensity of the blot, due to increasing evolutionary divergence. Six candidates derived from four libraries, namely pathogen incompatible (PI, anthracnose resistance, <math>n=2</math>), pathogen compatible (PIC, <math>n=2</math>), and POL (<math>n=2</math>) were sequenced in a panel of accessions including 3 landraces and 14 individuals from wild populations of <i>S. bicolor</i>, as well as <i>S. prostratum</i>, and <i>S. giganteum</i>. Of these genes, POL1, PI7 and POL163 have high <math>Ka/Ks</math> values, 0.76, 0.7 and 0.33 respectively, when compared to <i>S. prostratum</i>. PI5 is highly conserved for most of the putative ORF except for 3 non-synonymous substitutions, two of which occur in the same codon, one within <i>S. bicolor</i> and other in <i>S. prostratum</i>. POL163 and PI7 have a ratio of replacement to synonymous fixed differences greater than that of replacement to synonymous polymorphisms, suggesting that many non-synonymous substitution events have occurred in these genes, consistent with positive selection. The identification of genes involved in disease resistance (PI5, PI7) which may have evolved through positive selection at some key amino acid residues is consistent with other studies and can lead to the introgression of different alleles into the genome of the elite germplasm. Association genetics tests are underway to validate the candidate genes and determine their effect on anthracnose resistance.</p>
<p><b>Zenger</b></p> <p>Zenger KR1, Wang C1, Wei K-J2, Wakefield M3, Deakin J2, Koina E2, Alsop A2, Cooper DW4 and Graves J2</p>	<p>ARC centre for Kangaroo Genomics.1 ReproGen, Faculty of Veterinary Science, University of Sydney, Sydney Australia.2 Comparative Genomics Group, Research School of Biological Sciences, The Australian National University, Canberra Australia.3 Division of Immunology and Genetics, John Curtin School of Medical Research, The Australian National University, Canberra Australia.4 School of Biology, Earth and Environmental Sciences, Faculty of Science, University of New South Wales, Sydney Australia.</p>	<p><b>An integrated genetic linkage map of the tammar wallaby</b></p>	<p>The tammar wallaby (<i>Macropus eugenii</i>) is the Australian marsupial model for genetic mapping studies. This unique species offers an untapped resource for intensive genomic investigations, and provides a great benefit to our understanding of the organization, function and evolution of the mammalian genome. The production of a dense genetic map is perhaps one of the most important first objectives in mapping the marsupial genome. Previously, 64 genetics markers were used to create the first tammar wallaby genetic linkage map, comprising 9 linkage groups spanning more than 70% of the genome. These groups ranged in size from 15.7 to 176.5 cM and have an average distance of 16.2 cM between adjacent markers. This study aims to create a second generation genetic linkage map, by focusing on map saturation and map integration through the physical localization and genetic linkage mapping of novel genetic loci. In particular, we will concentrate on tammar wallaby chromosome 5 and X which together make up the human X chromosome. We present here the most up to date linkage map and discuss its significance.</p>
<p><b>Zufall</b></p> <p>Rebecca A. Zufall, Casey McGrath, and Laura Katz</p>	<p>Department of Biological Sciences, Smith College, Northampton, MA, 01060, USA</p>	<p><b>Exploring Genome Landscapes: Evolution of Proteins and Processing in Extensively Fragmenting Ciliates</b></p>	<p>We are exploring the hypothesis that differential selection on dual genomes allows for unusually rapid evolution in extensively processing ciliates. Ciliates are microbial eukaryotes defined by the presence of two distinct genomes within every cell: one in the germline micronucleus and the other in the somatic macronucleus. During development of the macronucleus, ciliates process their genomes by chromosomal fragmentation, excision of internal excised sequences, and amplification of chromosomes. Some ciliates undergo extensive processing to generate macronuclei containing thousands of gene-sized chromosomes. Such "extensive fragmenters" are found in three classes of ciliates. Our hypotheses is that paralogs can be hidden from selection in the unprocessed, unexpressed micronucleus, while being subject to selection only in the highly processed macronucleus. To test this hypothesis, we examine the rates of protein evolution in several genera of extensive fragmenters. We find a pattern in duplicated genes whereby one paralog is both overrepresented in the macronucleus and relatively conserved, while other paralogs are highly divergent. Further, the presence of gene-sized chromosomes in the macronuclei of extensive fragmenters enables both exploration of protein coding domains and untranslated regions.</p>