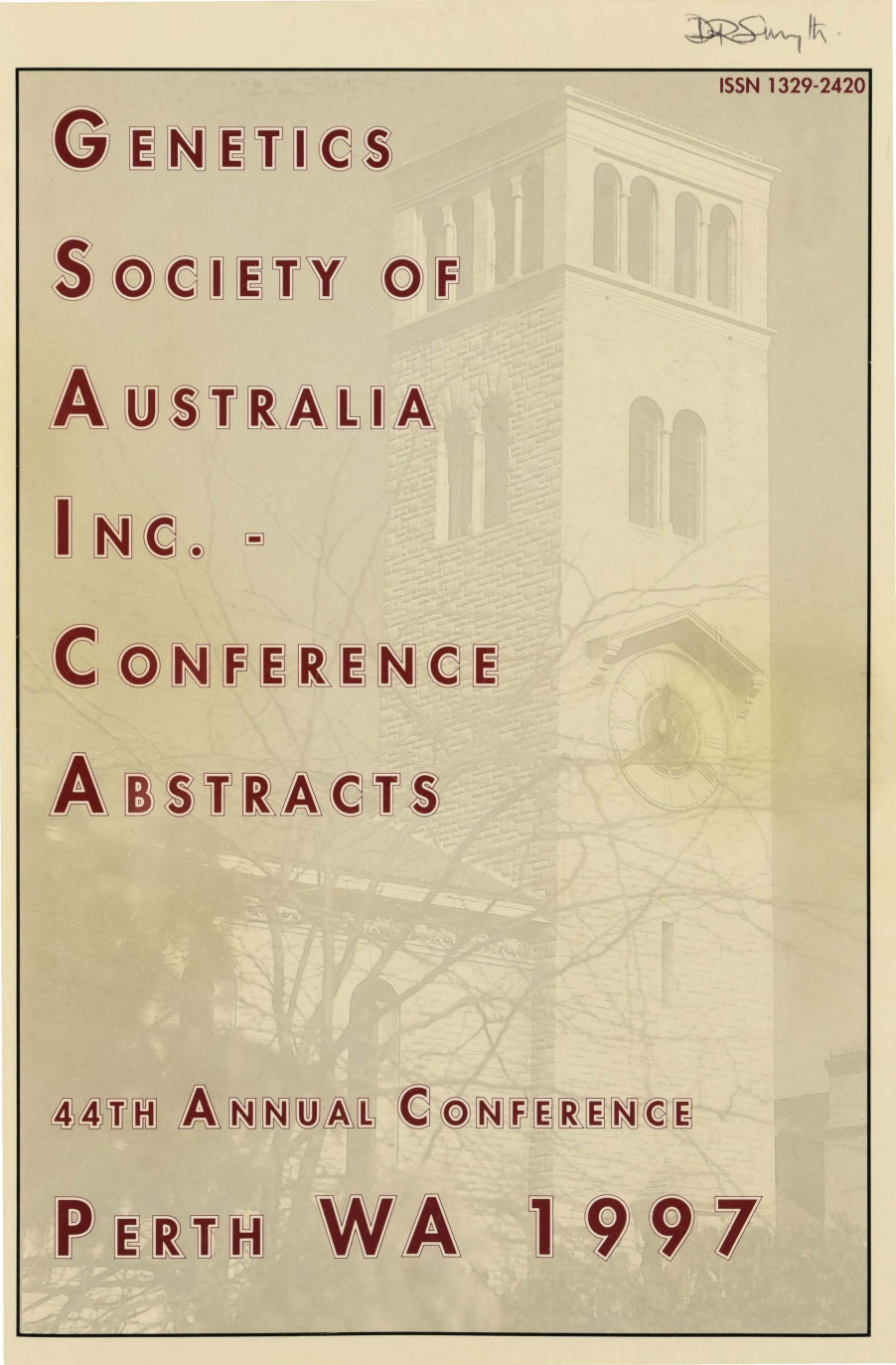
ISSN 1329-2420

GENETICS SOCIETY OF AUSTRALIA INC. - CONFERENCE ABSTRACTS



44TH ANNUAL CONFERENCE

PERTH WA 1997

Genetics Society of Australia Inc. - Conference Abstracts

Proceedings of the
44th Annual Conference of the
Genetics Society of Australia Inc.

Held in the
Weatherburn Lecture Theatre
Blakers Lecture Theatre
Maths Senior Lab
The Undercroft

at
The University of Western Australia
Nedlands, WA 6907
Australia

9 a.m. Sunday 28th September - 12.30 p.m. Wednesday 1st October 1997

Genetics Society of Australia Inc. - Conference Abstracts
ISSN 1329-2420
edited by Helen M. Stace
1997 Perth WA

44th Annual Conference of the
Genetics Society of Australia Inc.

Organising Committee

David Coates
Helen Stace
Margaret Byrne
Jennie Chaplin
David Groth
Sid James
Grace Jezierski
Tony Scalzo
Linda Broadhurst

assisted by
Jason Kennington
John Bussell
Ainsley Calladine
Clare Constantine
Joan Bot
Peta Whitaker
Rachel Pratt
Ed Demasi
Marcello Pernacchio

Contributed talks are 15 minutes + 5 minutes for questions.
Speakers are asked to keep strictly to the time limits.

PRIZES AND AWARDS

Student Members of GSA are eligible for the following prizes and awards at the 1997 GSA Annual Conference:

1. Smith-White Travel Award
2. Promega Prize for Best Student Talk
3. Cambridge University Press Prize for Best Student Poster

These will judged by the GSA Committee.
Prizes and awards will be announced in the second session of Wednesday, 1st October.

FURTHER INFORMATION

GSA ANNUAL CONFERENCE PERTH 1997

The 44th Annual GSA conference will be held at the University of Western Australia. The Weatherburn and Blakers Lecture Theatres and Maths Senior Lab are near the Physics Building. The Poster Session will be held in The Undercroft of Hackett Hall.

Sessions will begin at 9 a.m. on Sunday 28 September and will conclude at 12.30 p.m. on Wednesday 1 October. Morning and afternoon teas are included in the program. The program will be augmented by addresses given by invited local and overseas speakers. These speakers are:-

Tom Adams, Oregon State University
John Endler, James Cook University
Chris Gillies, University of Sydney
David Hay, Curtin University of Technology
Kent Holsinger, University of Connecticut
Nigel Laing, University of Western Australia
Michael Lynch, University of Oregon
John McKenzie, University of Melbourne
Gavin Moran, CSIRO Forestry and Forest Products
Jim Peacock, CSIRO Plant Industry

ACCOMMODATION

The University of Western Australia stands on the shores of the Swan River, a short busride from Perth CBD. Conference accommodation (bed and breakfast) is at nearby Kingswood College (Stirling Highway opposite Broadway) and St George's College (Stirling Highway opposite Hackett Drive).

MEALS: Lunch can be bought at the Guild Village Cafe or from University House (see map). For dinner, there are many restaurants around the University, at Nedlands and Subiaco, in the city and Northbridge, and other suburbs. See the tourist information included in your Registration pack.

CHILD CARE: Limited places are available at nearby childcare centres. For more information contact Jane on (08) 9383 2086.

SOCIAL PROGRAM

THE MIXER and Registration will be held in the Dining Hall at St George's College on Saturday evening between 7.00 p.m. - 10.00 p.m. Drinks and savories are provided.

GSA ANNUAL DINNER will be held at University House on Tuesday 30 September from 7.30 p.m. (booking required). There will be provision for quiet dining as well as music for dancing. Dinner tickets $40 each, partners are welcome to attend.

PICNIC IN KING'S PARK AND BOTANIC GARDENS on Wednesday 1 October from 12.30 p.m. (booking required). Cost including tram ride to Kings Park $15 (children $6). Spectacular views of Perth City and Swan River from the superb Botanic Gardens with rare Western Australian flora. And a DNA Tower to climb!

POST-CONFERENCE TOUR: 3 day bus tour (2- 4 October) to a world famous southwestern State Forest for numbats, spot lighting and wild flowers, with cabin accommodation and tour guides by expert officers of CALM. Booking required.

LOCAL TRANSPORT. Taxis may be phoned on 444 444 (Swan taxis), 333 3333 (Black and White taxis) or 13 2227 (Australian taxis). TransPerth buses (No. 72) travel along the Stirling Highway between the University and Perth CBD and Fremantle.

CAR PARKING. All Day Pay Parking (30 cents/hour) is available at Car Park 17 (off Cooper Street, reached from Fairway), at Car Park 14 (Fairway Entrance 4), and at Car Park 21 (off Broadway, south of Edward Street). Always use the clearly designated pay parking areas.

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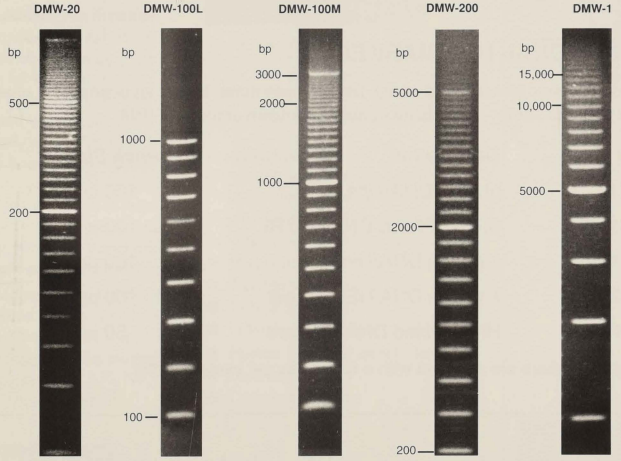

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DMW-L2	λ phage DNA/HEH Digest	100 µg	$55
DMW-M1	Hi-Lo Mixed DNA Markers	50 µg	$55

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Product Profile

Figure 5. QIAamp Blood Kit (50).

A Wide Range of Sample Sources

QIAamp Blood Kits isolate DNA from fresh, frozen or dried whole blood (with any common anticoagulant), buffy coat, bone marrow, mucus, other body fluids, or cell suspensions. Viral RNA and DNA can be efficiently prepared from plasma or serum. DNA from most human and animal tissues, such as muscle, liver, heart, brain, tumors, and mouse tails, (as well as blood and body fluids) can be purified with QIAamp Tissue Kit. Special protocols for paraffin-embedded tissue, yeast, and some bacterial species are available on request.

Sample		Total nucleic acid yield	DNA yield (with RNase A treatment)
Blood	(200 µl)	5–8 µg	5–8 µg
Buffy coat	(200 µl)	30–40 µg	30–40 µg
Cells	(1×10^7)	50–60 µg	40–50 µg
Liver	(25 mg)	150–180 µg	10–30 µg
Brain	(25 mg)	40–60 µg	15–30 µg
Lung	(25 mg)	10–20 µg	5–10 µg
Heart	(25 mg)	15–40 µg	5–10 µg
Kidney	(25 mg)	40–80 µg	15–30 µg
Spleen	(10 mg)	10–40 µg	5–30 µg
Mouse tail (1.2 cm)		40–70 µg	20–40 µg

Table 1. Yields of nucleic acids purified from various sources with QIAamp Blood Kits and QIAamp Tissue Kits.

Ordering information

Product	Contents	Cat. No.
QIAamp Blood Kit (50) for blood and body fluids	50 QIAamp Spin Columns, 100 Collection Microtubes (2 ml), QIAGEN Protease, Reagents and Buffers	29104
QIAamp Blood Kit (250) for blood and body fluids	250 QIAamp Spin Columns, 500 Collection Microtubes (2 ml), QIAGEN Protease, Reagents and Buffers	29106
QIAamp Tissue Kit (50) for tissue and mouse tails	50 QIAamp Spin Columns, 100 Collection Microtubes (2 ml), Proteinase K, Reagents and Buffers	29304
QIAamp Tissue Kit (250) for tissue and mouse tails	250 QIAamp Spin Columns, 500 Collection Microtubes (2 ml), Proteinase K, Reagents and Buffers	29306
Related Products		
QIAamp HCV Kit (50)	50 QIAamp Spin Columns, Carrier RNA, Buffers, and Collection Tubes (2 ml)	29504
QIAamp HCV Kit (250)	250 QIAamp Spin Columns, Carrier RNA, Buffers, and Collection Tubes (2 ml)	29506
Accessories		
Collection Tubes (2 ml)	1000 Collection Tubes (2 ml) for 500 preparations	19201
Buffer AW (concentrate)	390 ml Wash Buffer Concentrate for 1000 preps	19072
Buffer AL (Reagents AL1, AL2)	180 ml Reagents AL1 and 45 ml Reagent AL2 to prepare Buffer AL for 1000 preps	19075
Buffer ATL	200 ml Tissue Lysis Buffer for 1000 preps	19076
Buffer AVL	155 ml Viral Lysis Buffer and 4.2 mg Carrier RNA for 250 preps	19073

Germany: QIAGEN GmbH Tel. 02103-892-0, Fax 02103-892-222
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CONFERENCE ACCESSORIES

Genetics Society of Australia
Perth 1997 Conference
27 September - 1 October

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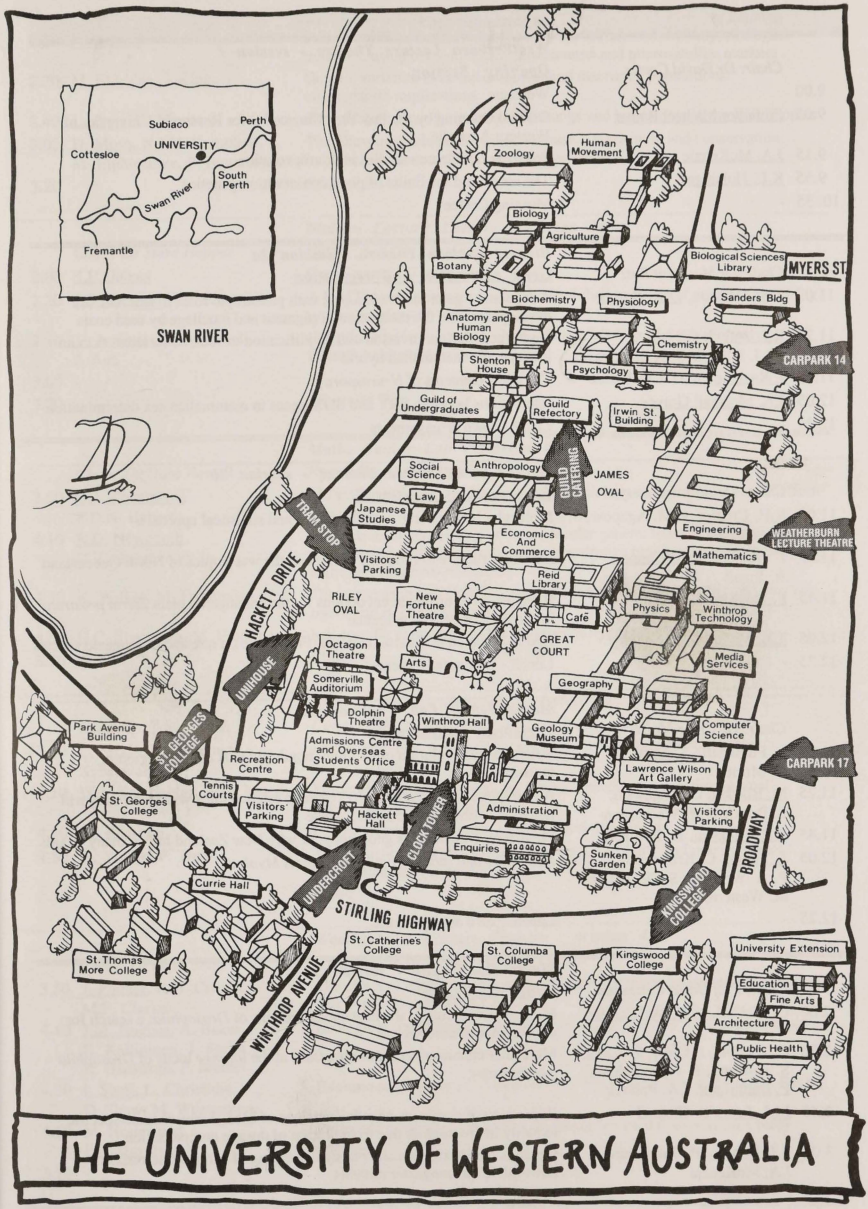

THE UNIVERSITY OF WESTERN AUSTRALIA

Program

	SUNDAY	28 September 1997
		Weatherburn Lecture Theatre - session 1
	Chair: Dr David Coates	***Opening Session***
9.00		Welcome
9.05	Professor Michael Barber	Official Opening by the Pro-Vice Chancellor for Research, University of Western Australia
9.15	J.A. McKenzie	Pesticide resistence - studies in microevolution
9.55	K.E. Holsinger	The scope and the limits of plant conservation genetics
10. 35	-	Morning Coffee
		Blakers Lecture Theatre - session 2a
	Chair: Dr Margaret Katz	***Gene expression and regulation***
11.05	C.S. Johnson, D.R. Smyth	A regulatory gene for *Arabidopsis* with pleiotropic roles in leaf hair development and the production of pigment and mucilege by seed coats
11.25	R.J. Waugh O'Neill, M. J. O'Neill, J. A. M. Graves	Undermethylation, invasion and amplification of retroviral elements in an interspecific mammalian hybrid
11.45	J. Rasmussen, D. Catcheside	The guest elements of *Neurospora*
12.05	J.A. Marshall Graves	Interactions between SRY and SOX genes in mammalian sex determination
12.25	-	Lunch - own arrangements
		Weatherburn Lecture Theatre - session 2b
	Chair: Dr Alan Lymbery	***Conservation genetics 1***
11.05	R.H. Crozier, P-M. Agapow, K. Pedersen	Molecular biodiversity: a phylogenetic and statistical approach
11.25	J. Playford, K. O'Connor, A. Small	Genetic structure of montane flora from the wet tropics of North Queensland
11.45	P. Hogbin, R. Peakall	Revaluation of management options for the endangered plant *Zieria prostrata* in the light of genetic evidence
12.05	T.L. Maguire, M. Sedgley	RAPD variation in *Banksia cuneata* (Proteaceae), a rare and endangered species
12.25	-	Lunch - own arrangements
		Maths Senior Lab - session 2c
	Chair: Dr Craig Moritz	***Vertebrate phylogeny***
11.05	L. Fumagalli, L. Pope, C. Moritz	Structure and evolution of the mitochondrial DNA control region in marsupials
11.25	M. Blacket, C. Krajewski, L. Buckley, M. Westerman	A multigene assessment of phylogenetic relationships within the dasyurid marsupial subfamily Sminthsopsinae
11.45	R.E. Hickson, K. E. Slack	Phylogeny recapitulates geography, or why New Zealand has so many lizards
12.05	J. Young, C. Krajewski, P. A. Woolley, S. Donnellan, M. Westerman	Molecules and morphology in the genus *Myoictis*
12.25	-	Lunch - own arrangements
		Maths Senior Lab - session 3a
	Chair: Prof David Catcheside	***Gene expression***
2.00	G. McColl, S.W. McKechnie	Molecular variation in the heat shock proteins of *Drosophila*: a search for developmental associations
2.20	C. Nichols, J. Crew, Z. Chen, S. Hoening, F. Cunningham, P. Batterham, J.A. Pollock	Molecular characterization of mutations at the *lozenge* locus of *Drosophila melanogaster*
2.40	M.J. Scott, S. Cleland	Expression of dominant-negative versions of MSL-1 causes male-specific lethality in *Drosophila* due to inhibition of dosage compensation
3.00	P.J. Daborn, P. Batterham, J.A. McKenzie	Genetic characterization and physical mapping of cyromazine-resistent *Drosophila melanogaster* mutants
3.20	-	Afternoon Tea

		Weatherburn Lecture Theatre - session 3b
	Chair: Dr Jenny Ovenden	***Conservation genetics 2***
2.00	P. Spencer	Patterns of dispersal and philopatry in the Allied rock-wallaby, *Petrogale assimilis*, using detailed spatial-use patterns and microsatellite markers
2.20	M. Eldridge, J. King	Genetic variation in island and mainland macropod populations: conservation implications
2.40	L. Pope, C. Moritz	Comparative phylogeography of bettongs and bandicoots in the Wet Tropics
3.00	D. Moro, N.J.H. Campbell, M. Elphinstone, P. Baverstock	The Thevenard Island short-tailed mouse - taxonomic and conservation implications from mtDNA sequence variation
3.20	-	Afternoon Tea
		Blakers Lecture Theatre - session 3c
	Chair: Dr Steve Hopper	***Plant genetic systems***
2.00	S.H. James	Consequences of inbreeding
2.20	J.D. Bussell, S.H. James	A RAPD based phylogenetic analysis of the evolution of complex hybridity in *Isotoma petraea*.
2.40	T. Armstrong, D. Rowell, J. Ash	Hybridization in Australian alpine *Ranunculus*: species maintenance through habitat selection
3.00	-	-
3.20	-	Afternoon Tea
		Maths Senior Lab - session 4a
	Chair: Dr Dave Rowell	***Reproductive genetics***
3.50	G.J. Thompson, P.D.N. Hebert	Molecular insights into the reproductive biology of an arboreal termite from Jamaica
4.10	R.D. Newcomb, D.R. Greenwood	Towards an understanding of the molecular genetic basis of odorant and pheromone reception in insects: the pheromone binding proteins of the pest leafroller, *Epiphyas postvittana*
4.30	K. Wilkes, M. Frommer	The *per* gene in two closely related species of tephritid fruit flies *Bactrocera tryoni* and *B. neohumeralis*
4.50	D.C. Shearman, M. Frommer	Sex-specific expression of the *Bactrocera tryoni* gene *doublesex*
5.10	-	Close
		Blakers Lecture Theatre - session 4b
	Chair: Dr David Groth	***Conservation genetics 3***
3.50	C. Moritz, L. Kelemen, K. McGuigan	Phylogeography, outbreeding depression and genetic guidelines for translocations
4.10	W.J. Kennington, S.H. James	Mutation accumulation and the loss of reproductive capacity in small populations of a rare eucalypt
4.30	M. Rossetto	Plant conservation genetics - the practical experience
4.50	A. Young, P. Thrall	The influence of correlated paternity on the viability and persistence of fragmented daisy populations
5.10	-	Close
		Weatherburn Lecture Theatre - session 4c
	Chair: Dr Dave Shaw	***Avian genetics and evolution***
3.50	J. Painter, R.H. Crozier, M.F. Clarke	The effect of relatedness on helping behaviour in the cooperatively breeding bell miner, *Manorina melanophrys*
4.10	J.M. Hughes, A. Baker, R. Kallioinen, J. Smith, K. Hedstrom, P. Mather	Ecological significance of back colour variation in the Australian Magpie
4.30	L. Scott, L. Christidis, D. Shaw, M. Westerman	Evolutionary history of *Daphoenositta*: How useful is mitochondrial DNA?
4.50	M. Heslewood, P.R. Baverstock	Rates and patterns of molecular evolution in Australian passerine birds - Aromatase
5.10	-	Close

MONDAY	29 September 1997	
	Weatherburn Lecture Theatre - session 1	
Chair: Dr Sid James	***Meiosis and mutation***	
9.00	C.B. Gillies	Recent thoughts on mechanisms of meiotic chromosome pairing
9.40	M. Lynch	The role of mutation in evolution and extinction
10.20	-	Morning Coffee
	Maths Senior Lab - session 2a	
Chair: Dr Chris Gillies	***Recombination and rearrangements***	
10.50	J.A. Sved, X. Liang, M.M. Tanaka, J.M.H. Gray	Recombination and chromosome changes induced by P element derivatives in *Drosphila*
11.10	H.D. Perkins, A. O'Donnell, A.J. Howells	P-elements in *Lucilia cuprina* - the final chapter
11.30	C.J. Metcalfe, M. Eldridge, P.G. Johnston	Mapping the distribution of the telomeric sequence $(T_2AC_3)_n$ in rock wallabies and pademelon by FISH
11.50	- ~~Zoltan~~ Rasmussen	- see Session 2a
12.10	- Paul	Group Photograph in the Sunken Garden
12.30	-	Lunch - own arrangements
	Weatherburn Lecture Theatre - session 2b	
Chair: Prof John Endler	***Hymenopteran genetics and evolution***	
10.50	B. Oldroyd, C. Montague	Enforcement of worker sterility in honey bees
11.10	W. Tek Tay, R.H. Crozier	Mating behaviour of the queenless ponerine ant *Rhytidoponera* sp. 12
11.30	M. Dowton, A.D. Austin	Molecular evidence for an unanticipated transition from endoparasitism to ectoparasitism in braconid wasps (Hymenoptera: Braconidae)
11.50	R.N. Johnson, R.H. Crozier	Population structure of the weaver ant *Polyrhachis doddi* using microsatellite DNA markers
12.10	-	Group Photograph in the Sunken Garden
12.30	-	Lunch - own arrangements
	Blakers Lecture Theatre - session 2c	
Chair: Dr Jane Sampson	***Population genetics***	
10.50	R.W. Slade, E. Bermingham, C.J. Schneider, I.B. Jakobsen, A. Ng, T. Littlejohn	WebPop - Population genetics on the World Wide Web
11.10	S. Krauss	An evaluation of the AFLP fingerprinting technique for the analysis of paternity in natural populations of *Persoonia mollis* (Proteaceae)
11.30	G. Starr, S. Carthew	Microevolutionary processes inferred from spatial autocorrelation of genetic variation within a population of *Hakea carinata*
11.50	L. Broadhurst, D.J. Coates, B. Tan	Genetic diversity in the monotypic Western Australian endemic, *Geleznowia verrucosa* Turcz. (Rutaceae)
12.10	-	Group Photograph in the Sunken Garden
12.30	-	Lunch - own arrangements
	Maths Senior Lab - session 3a	
Chair: Dr Helen Stace	***Cytoevolution***	
2.00	M. Eldridge, D. Pearson	Identification of a rock wallaby hybrid zone in Western Australia
2.20	J.D. Roberts	Evolution of polyploid frogs in the genus *Neobatrachus*
2.40	S.D. Hopper, S.H. James	Chromosome numbers and phylogeny in the kangaroo paw and bloodroot family Haemodoraceae
3.00	D. Shaw, F. Groeters	Chromosomes, development and climate: latitudinal clines in the grasshopper *Caledia captiva*
3.20	-	Afternoon Tea in the Undercroft

Weatherburn Lecture Theatre - session 3b

Chair: Prof John McKenzie

Population genetics of invertebrates

2.00	M.K. Robson, R. Osborne, A. Meats, R. Drew, J. Sved, H. Yu, M. Kinnear, M. Frommer	Australian distribution of fruit flies (Diptera: Tephritidiae) attracted to cue lure; microsatellite studies of *Bactrocera tryoni* outbreak flies
2.20	A.J. Lymbery	Combining quantitative and population genetics to infer transmission cycles in a parasitic tapeworm
2.40	P. Sunnucks, J. French, D. Briscoe, N. Tait, A. Wilson	Extreme genetic localization and divergence in *Euperipatoides rowelli* (Onchophora: Peripatopsidae) revealed by microsatellite and mitochondrial DNA analysis
3.00	C.C Constantine, M.S. Blouin, A.J. Lymbery, R.C. Thompson	Population genetic structure of *Ostertagi ostertagi* in Australia and USA
3.20	-	Afternoon Tea in the Undercroft

Blakers Lecture Theatre - session 3c

Chair: Dr Cedric May

Genetics in agriculture

2.00	S.J. Bennett	Genetic strategies of colonising plant species - their success in southern Australia
2.20	N. Galwey, K. Adhikari, J. Cooper, M. Dracup, B. Buirchell	Contribution of genetic studies to the development of lupin species for cultivation in Australia
2.40	S. Brien, W. Cowling, P. O'Brien, R. Potter, R. Jones, M. Shankar, M. Jones	Gene mapping in lupins
3.00	G.Yan, B.G. Murray, A. Ferguson, M. McNeilage	Cytogenetic studies to assist kiwifruit breeding
3.20	-	Afternoon Tea in the Undercroft

POSTERS

The Undercroft - session 4

T. Booth, A. Scalzo, N. Davis-Poynter, G. Shellam	Genetic Variation Among MCMV Field Isolates
F.J. Bowring, D.E.A. Catcheside	The relationship between gene conversion and crossing over at the *am* locus of *Neurospora*
S. Burrows, B. Cheetham, M. Katz	Localization of the *xpr*F gene from *Aspergillus nidulans*
B. Cardinal, D. Edwards, J. Smissen	Assessment of genetic variation within and between the three known southern Australian maternity caves of the Common Bent-Wing Bat (*Miniopterus schreibersii*)
M. Carew, R. H. Crozier	Polygyny via unrelated queens indicated by mitochondrial DNA variation in the Australian meatant *Iridomyrmex purpureus*
L. Chen, S.H. James	Genetic diversity in three tuberous and self-incompatible species of *Drosera*
M.L. Cooper	Geographic variation in the southern brown bandicoot (*Isoodon obesulus*): molecules versus morphology
S.R. Dahanayake, N.W. Galwey	Diallel analysis in spring rape (*Brassica napus* var *annua*)
D. Edwards, B. Wilson	To amplify an Antechinus ... Technical notes on DNA extraction from small field samples of *Antechinus minimus* for PCR reactions
L. Federle, R.J. Mitchell	Y-chromosome haplotypes in indigenous Siberians
W. Flood, I. Rogozin, A. Ruvinsky	Origin and evolution of LINE derived elements in mice: a novel subfamily
M. Gardner, S. Cooper, M. Bull, W. Grant	Lizards caught with their genes down: a genetic investigation of sociality in lizards of the *Egernia* group
H. Gasiamis	Polymorphisms of the *apoliprotein* B gene and their associations with lipid phenotypes in Greek and Italian migrants to Australia

J. Glaubitz, J. Strk, G. Moran	Effects of silviculture on genetic diversity in *Eucalyptus sieberi*
J. Gratten, P. Hale	Local population structure in the inshore bottlenose dolphin
P. Hale, A. Crawford, G. Ross, K. Kemper, V. Cokroft	Regional population structure in the inshore bottlenose dolphin
P. Hale, A. Crawford, G. Ross	Species subdivision in the genus *Tursiops*
R. Henry, T. Maguire, S. Lee, M. Rossetto, A. McLaughlan, L. Homer, S. Garland, S. Weining, M. Cross, R. Gupta, M. Shepherd, P. Baverstock	Analysis of Plant Microsatellites
K. Hood, M. Menzies, R. Slade	MHC genes in the European Harbor seal
G. Jezierski, P. Hood, P. Armstrong, M. Rossetto, K. Dixon	Clonality studies in conservation genetics and weed control
L. Kelemen	On the use of sister species for studies of speciation: a case study from *Drosophila serrata* and *D. birchii*
M. Kinnear, H. Bariana, J. Sved, M. Frommer	Polymorphic microsatellite markers for population analysis of the Queensland fruitfly *Bactrocera tryoni*
A. Murrell, N. Campbell, S. Barker	Phylogeny and evolution of the tick subfamily Rhipicephalinae
N. Naqui, D. Ma	Does autoregulation exist for BCL-2 gene in human lymphoma? Preliminary findings
J. Ovenden, G. Monteith, C.Moritz	Molecular biogeography of flightless beetles in the Australian Wet Tropics
N. Parker, D. Scarcella, P. Smith	Expression and imprinting of the human *stim*1 gene
C. Ranasinghe, A. Hobbs	Involvement of Cytochrome P450 CYP6B7 in pyrethroid resistence in *Helicoverpa armigera*
M. Rossetto, S. Lee, R. Henry, P. Baverstock	Population genetics of Tea Tree (*Melaleuca alternifolia*) using DNA microsatellites
I.K. Sharma, D.L. Jones, C.J. French	Patterns of genetic variability and phylogenetic relatedness among six endemic *Pterostylis* species (Orchidaceae, section Grandiflorae) of Western Australia
G. Schmidt-Adam, A. Young, B. Murray	Reproductive biology of Pohutukawa - a species under threat
L. Schmitt, S. Hisheh, A. Suyanto, Maharadatunkamsi	Biogeography of the Indonesian Archipelago: genetic diversity of vertebrate taxa
E. Sinclair	Comparison between island and mainland populations of the Quokka, *Setonix brachyurus* (Marsupalia: Macropodidae), using molecular techniques
E. Sinclair, B. Costello	Microsatellite variation in Gilbert's Potoroo, *Potorous gilbertii* (Marsupialia: Potoroidae)
R. Sladic, J. Kelly	Towards cloning of the *creC* and *creD* genes: two genes involved in carbon catabolite repression in *Aspergillus nidulans*
D. Slaney	Comparison of morphometric and molecular data sets for populations of *Paratemnopteryx stonei* Roth (Blattellidae)
C. Wood, D. Walker, M. Byrne	Genetic variation within and between populations of *Posidonia sinuosa* Cambridge and Kuo
J. Wroth	Possible role for wild genotypes of *Pisum* spp. to enhance *Ascochyta* blight resistence in pea
P.J. Yeadon, D.E.A. Catcheside	The molecular outcome of recombination events associated with the *cog* recombinator of *Neurospora*
A. Young, T. Brown, B. Murray	Viable or vulnerable: population genetics and demography of the endangered grassland daisy the button wrinklewort.

TUESDAY		30 September 1997
		Weatherburn Lecture Theatre - session 1
	Chair: Dr Tony Pryor	***Molecular plant breeeding***
9.00	W.J. Peacock	The control of genes - *in planta* and in commerce
9.40	W.T. Adams	Contributions of genetic markers to population genetics and breeding of forest trees
10.20	-	Morning Coffee
		Blakers Lecture Theatre - session 2a
	Chair: Prof Tom Adams	***Forestry genetics***
10.50	G.F.Moran	Towards molecular breeding of forest trees for quantitative traits
11.10	P.A. Butcher, G.F. Moran, S. DeCroocq	Application of RFLP and microsatellite markers in acacias
11.30	D. Kusnandar, N.W. Galwey, G.L. Hertzler, T.B. Butcher	Inheritance of growth characteristics in trees of *Pinus pinaster*
11.50	M. Byrne, G. Moran, M. Stukely, L. Emebiri, E.Williams	Identification of QTL for resistence to *Phytophora cinnamomi* in *Eucalyptus marginata*
12.10	-	Lunch - own arrangements
		Weatherburn Lecture Theatre - session 2b
	Chair: Dr Jane Hughes	***Aquatic genetics - marine populations***
10.50	R. Doupé, A.J. Lymbery	Mitochondrial genealogy of Western Australian barramundi (*Lates calcarifera*): Applications of inbreeding coefficients and coalescent analysis for separating contemporary from historical population processes
11.10	M. Kruetzen, W.B. Sherwin, R.C. Connor, R.A. Smolker	Kinship and alliance formation in male bottlenose dolphins (*Tursiops* sp.) in Shark Bay, Western Australia
11.30	N.N. FitzSimmons, C. Moritz	Microsatellites, models, mutations, and marine turtles
11.50	K. Whitaker	Glimpses into the past for soothsayers: a genetic approach to the problems of predicting dispersal and recolonization in hermatypic corals
12.10	-	Lunch - own arrangements
		Maths Senior Lab - session 2c
	Chair: Dr Marianne Frommer	***Invertebrate evolution***
10.50	A. Wilson, P. Sunnucks, D.F. Hales	Sex in New Zealand? Microsatellite evolution in parthenogenetic *Sitobion* aphids on grasses in New Zealand
11.10	L. van Herwerden, D. Blair	Comparison of nuclear and mitochondrial sequences for phylogenetic studies in human lung flukes
11.30	N.J.H. Campbell, S.C. Barker	The major mitochondrial genes of the Arthropoda can move: a large rearrangement in the cattle tick (*Boophilus microplus*)
11.50	-	-
12.10	-	Lunch - own arrangements
		Blakers Lecture Theatre - session 3a
	Chair: Dr Margaret Byrne	***Gene mapping***
2.00	C. Moran, F.W. Nicholas	Gene mapping in domestic animals
2.40	N. Maqbool, C. Moran, F.W. Nicholas, L.P. Silva	QTL studies of growth and fertility in mouse
3.00	S. Lowden, G. Davis, D. Hetzel, J. Renaud, S. Armitage, C. Mayne, C. Frost, R. Stevenson	Detection of quantitative trait loci for growth in crosses between selection lines of beef cattle
3.20	-	Afternoon Tea

		Weatherburn Lecture Theatre - session 3b
	Chair: Dr John Sved	***Aquatic genetics - evolutionary processes***
2.00	J.A. Endler	Artificial selection for spectral sensitivity and sexual selection
2.20	J.M.Arthur, J.M. Hughes, W. Hogarth	Simulation of gene flow and genetic drift in a dendritic system
2.40	D.M. Gleeson, N. Ling, R. Howitt	D-loop variation among populations of a native New Zealand fish
3.00	D.J. McGlashan, J.M. Hughes	Heirarchical analysis of genetic variation in the Pacific blue-eye *Pseudomugil signifer* (Pseudomugilidae) in northern Queensland
3.20	-	Afternoon Tea

		Blakers Lecture Theatre - session 4a
	Chair: Dr Penny Smith	***Gene mapping and resistence genetics***
3.50	W-F Hong, V. Krishnapillai	DNA sequence analysis of a conserved chromosomal segment of a bacterial plant pathogen
4.10	M. Francki, O. Crasta, D. Bucholtz, H. Sharma, H. Ohm, J. Anderson	Molecular characterization of wheat-wheatgrass Group 7 translocation lines and localization of barley yellow dwarf virus resistence gene(s) in wheat (*Triticum aestivum* L.)
4.30	N. Urosevic, S. Hodgetts, K. Mann, P. Lyons, G. Shellam	High resolution mapping and the analysis of YAC clones around the mouse flavivirus resistence locus
4.50	T. Pryor, N. Collins, M. Ayliffe, J. Ellis, S. Hulbert	Recombination and new rust resistance specificities
5.10	-	To GSA Annual General Meeting (Weatherburn)

		Maths Senior Lab - session 4b
	Chair: Prof Ross Crozier	***Aquatic genetics - freshwater evolution***
3.50	D. Hurwood, J.M. Hughes	Phylogeography of freshwater fauna from the wet tropics of northeastern Queensland
4.10	M. van Oppen, G. Turner, J. Deutsch, G. Hewitt	Unusually fine-scale genetic structuring found in rapidly speciating Malawi cichlid fishes
4.30	M. Ponniah, J.M. Hughes	Queensland *Euastacus* (spiny mountain crayfish): dispersal capabilities and evolutionary relationships
4.50	-	-
5.10	-	To GSA Annual General Meeting (Weatherburn)

		Weatherburn Lecture Theatre - session 4c
	Chair: Dr John Wetherall	***Human behaviour genetics***
3.50	D.A. Hay	ADHD as a model for what behaviour genetics can achieve
4.30	A. Page, N.G. Martin	Testing a genetic structure of blood-injury fears
4.50	J. Hallmayer	Multipoint sib-pair analysis in schizophrenia: chromosomal markers in potential candidate regions
5.10	-	To GSA Annual General Meeting (Weatherburn)

		Weatherburn Lecture Theatre
5.20	*Chair: Prof Jenny Graves*	Genetics Society of Australia Inc. Annual General Meeting

		University House
7.30	-	Genetics Society of Australia Inc. Annual Dinner

	WEDNESDAY	1 October 1997
		Weatherburn Lecture Theatre - session 1
	Chair: Dr Phil Batterham	***Past and future prospects***
9.30	P. Armstrong	Charles Darwin in Western Australia
10.00	N. G. Laing	Inherited neuromuscular diseases: beyond the genes, what do we do next?
10.40	-	Morning Coffee
		Weatherburn Lecture Theatre - session 2
	Chair: Prof Jenny Graves	***M.J.D. White Address***
11.10	D.R. Smyth	*Arabidopsis*, the green genie
12.00		Awards and Prizes
12.30	-	Close
		Kings Park and Botanic Garden
1.00	-	Picnic Lunch

Abstracts of Talks T1-T95

T1

Contributions of genetic markers to population genetics and breeding of forest trees

W. T. Adams

Department of Forest Science, Oregon State University, Corvallis, OR U.S.A.

Single-locus genetic markers in the form of allozymes have been available to forest geneticists for over 20 years, and the number and variety of markers has increased dramatically with the development, more recently, of DNA marker methods. This talk explores the contributions of genetic markers to advancing the understanding of forest genetics and to tree breeding. A major disappointment in early allozyme research was the revelation that genetic markers are largely adaptively neutral. Freedom from selection, however, makes these markers ideal for investigating other evolutionary forces (i.e., genetic drift, mating systems, and gene flow) in natural and artificial populations of forest trees. Genetic markers, mostly allozymes, have had three major applications to date: 1) Description of population genetic architecture within species; 2) Description of mating systems and patterns of gene dispersal within and among populations; and 3) Design and evaluation of gene conservation strategies. Examples of each application are presented and the potential for improving these applications with DNA methods discussed. A particularly promising application of DNA markers in the future is for genome mapping and identification of quantitative trait loci (QTLs). QTL analysis makes it possible to understand the underlying genetic basis of quantitative traits and could greatly aid in selection and breeding of forest trees.

T2

Hybridization in Australian alpine *Ranunculus* species maintenance through habitat selection

Tristan Armstrong, Julian Ash and Dave Rowell

Division of Botany and Zoology, ANU, ACT 0200

Five homoploid (2n=16) species of *Ranunculus* hybridize extensively in the alpine region of mainland Australia. All species are clearly distinguishable on gross morphological characters, with hybrids exhibiting intermediate morphology in all characters examined. Interspecific hybrids are often abundant in narrow (< 2m wide) ecotonal areas between the different microhabitats occupied by each parental species.

An allozyme study revealed that parental populations on either side of one zone exhibited fixed differences at two loci - suggesting that gene flow between the hybridizing populations is negligible, and also that narrow clines in morphology correspond with narrow clines in gene frequency. Insect mediated pollen dispersal was found to be very broad relative to hybrid zone widths and, based on strong evidence of complete interspecific reproductive compatibility, the distribution of hybrids would be expected to be much wider than observed. Indeed, given these data, the persistance of five distinct morphological forms seems anomalous.

It has been hypothesised that the stability of these hybrid zones is maintained purely as a result of habitat specialisation and intense disruptive selection against intermediate forms within each parental habitat. To test this hypothesis, parental and F1 hybrid seedlings were grown in glass house treatments designed to mimic key aspects of parental habitat. Parental forms were most successful in treatments corresponding to their natural habitat. In all habitat treatments, F1 hybrid performance was intermediate to that of the two parentals.

T3

Simulation of gene flow and genetic drift in a dendritic system

James Michael Arthur, Hughes J. M., Hogarth W.

Australian School of Environmental Studies, Griffith University, Nathan Qld 4111

The genetic structure of metapopulations associated with stream systems was investigated using a computer model simulating the interaction of genetic drift and gene flow through time. This model suggests that for neutral alleles certain intrinsic characteristics of lotic systems may be influential in the determination of the population genetic structure of a species confined to these systems. These characteristics are stream topology (ie a linear but dendritic structure), catchment position, migration strength, and migration direction (upstream/downstream).

The results of these simulation runs showed that high F_{ST} values can be maintained even under high gene flow. This study also indicates that genetic differentiation between different catchment positions (headwaters versus tailwaters) can be maintained even under different combinations of gene flow characteristics. These high levels of differentiation are maintained even for situations where simple gene flow models (Island model and Stepping Stone model) would predict no population differentiation at all. This is due to the influence of the complexity of the lotic system's dendritic topology and also to a non equilibrium gene flow pattern.

The consequence for researchers who are looking at allozyme markers for detection of migration patterns in lotic systems, or for that matter any other system that has a complex network of populations, are important. For example, the interpretation of gene flow patterns via the use of genetic differentiation between populations (ie F_{ST} values) and a simple gene flow model may be inappropriate in these systems. The use of which can lead to incorrect gene flow estimates when certain conditions are present.

T4

Genetic strategies of colonising plant species. Their success in southern Australia

Sarita Jane Bennett

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Australia has been subject to a large number of invasions of plant species since its colonisation. Some of these have been due to deliberate introductions, but many are the result of accidental introductions through the movement of animals and animal feed. The genetic strategies of a number of species of successful colonisers in Australia, both inbreeders and outbreeders, dicotyledons and monocotyledons, are discussed. The strategy adopted by each species is usually related to its breeding system. All of the successful colonisers are shown to contain high levels of genetic variation, both within and between populations which has resulted in broad-scale adaptations to the environment, and in particular, climatic variation. More localised variation in micro-habitat is controlled by high levels of phenotypic plasticity being present within a population. Many of the species show mixed mating systems to some degree. This is true of predominantly outbreeding species such as *Echium plantagineum* (Patterson's curse) and *Onopordum illynum* (thistle) and inbreeders such as *Trifolium subterraneum* (subterranean clover) and *Bromus diandrus* (great brome). It combines the advantages of outbreeders with the potential of recombination with the stability of inbreeders. Inbreeding annual species also appear to favour specific reproductive strategies, namely the production of large numbers of small seeds e.g. *Trifolium glomeratum* (cluster clover) which contain some form of dormancy ensuring the spread in time of germination and establishment. The efficient dispersal of the fruits by either the production of spiny burrs e.g. *Medicago minima* and *Xanthium strumarium* (Noogara burr) or ingestion by animals, e.g. *T. glomeratum* is also favoured.

T5

A multigene assessment of phylogenetic relationships within the dasyurid marsupial subfamily Sminthopsinae

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The Dasyurid subfamily Sminthopsinae comprises four genera *Sminthopsis*, *Ningaui*, *Antechinomys* and *Planigale* whose precise relationships to one another are unclear. Complete DNA sequences of the mitochondrial genes cytochrome b and 12S ribosomal RNA as well as from a nuclear gene - Protamine P1 were obtained for 13 species representing all four genera. The results of this study on inter and intra-generic relationships within Sminthopsinae will be discussed.

T6

Gene conversion and crossing over: associated or coincidental?

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In 1955, Mary Mitchell demonstrated that non-reciprocal recombination (gene conversion) at the Neurospora *pdx* locus was correlated with elevated levels of reciprocal exchange (crossing over) in the flanking intervals. This phenomenon was subsequently observed in numerous fungi. The association between gene conversion and crossing over is supported by a formidable body of data and underpins the most popular molecular models of recombination which mechanistically relate these manifestations of recombination. However, our work with the Neurospora *am* locus has forced us to recognise that this association may reflect only a correlation between the occurrence of distinct events. A high resolution analysis of prototrophic recombinants from a repulsion phase cross revealed that fewer than 7% of gene conversion events at *am* enjoyed a crossover close enough to be considered associated. Moreover, the data suggested a means whereby the level of association might have been consistently overestimated at the high frequency recombinators typically studied.

T7

Gene mapping in lupins

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Australia is the largest producer of sweet narrow-leafed lupins (*Lupinus angustifolius*) in the world, growing over one million hectares annually in Western Australia. Expansion in both area grown, and in yields, is taking place as plant breeders continue to develop new varieties to suit the vast range of environmental conditions throughout the state. Traditionally, however, it can take at least 10 years to release a new variety, but through the application of DNA fingerprinting techniques, investigation of the lupin genome can reduce this time period. Amplified Fragment Length Polymorphisms (AFLPs) and Random Amplified Polymorphic DNA (RAPDs) are two techniques being used to generate polymorphic DNA fragments, which are then assigned to linkage groups using the computer program, MAPMAKER. Molecular markers linked to the major domestication traits (eg. early maturity, reduced pod-shattering, low alkaloid content, permeable seed coats and white flowers) are being sought, together with markers linked to resistance to *Phomopsis leptostromiformis* (a fungal disease of lupins leading to lupinosis in sheep feeding on infected stubble) and to the trait of restricted branching. To date, nearly 300 polymorphic loci have been generated. Of these, 177 have been assigned to 28 linkage groups, including two AFLP markers and a RAPD marker that have been found to be segregating with early maturity.

T8

Genetic diversity in the monotypic Western Australian endemic, *Geleznowia verrucosa* Turcz. (Rutaceae)

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Geleznowia verrucosa Turcz. (Rutaceae) is a little known monotypic genus endemic to the sandplains north and east of Perth, Western Australia. Populations of this woody shrub are small, disjunct and morphologically variable. Three forms can be recognised in the field by height, habit, leaf size and flower size and abundance; different forms rarely co-occur. Sixteen allozyme loci in 19 populations were examined to investigate genetic diversity in disjunct and morphologically variable populations and to determine whether different taxa existed. Single locus diversity measures portrayed *Geleznowia* as a somewhat genetically depauperate genus (*A*, 1.3; *P*, 29.3%). Total genetic diversity (H_t 0.226) was partitioned among (D_{st}, 0.126) rather than within (H_s, 0.100) populations with 56% of the total genetic diversity attributable to interpopulational differences. Observed heterozygosity was significantly less than expected heterozygosity in most populations although differences ranged from no heterozygosity to levels expected under panmixia. The apportioning of genetic diversity in different ways within the forms suggest this is an enigmatic species complex consisting of at least two taxa. Possible explanations for the patterns encountered within *Geleznowia* include ancient hybridisation and introgression, differing reproductive strategies, limited gene flow and genetic drift, small population size, bottlenecks and local adaptation.

T9

A RAPD based phylogenetic analysis of the evolution of complex hybridity in *Isotoma petraea*.

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Complex hybridity is a genetic system in which true breeding for chromosomal interchange heterozygosity is maintained by autogamy and a balanced lethal system. It is proposed to originate in response to the combination of extreme inbreeding and accumulation of deleterious mutations. Recombination is restricted to fewer and larger units, such that eventually the whole genome segregates as a supergenic locus with two alleles. This genomic coalescence increases the chance of selfed progeny maintaining levels of hybridity as high as the parent.

The populations of *Isotoma petraea* (2n=14) in south western Australia provide a window on the evolutionary process involved. The species is normally outbreeding with 7 bivalents (7II) at meiosis. The Pigeon Rocks population is home to 7II and interchange heterozygote (rings of 6 chromosomes; O6) lineages characterised by varying levels of seed abortion, exceeding 50% in some cases. Complex hybridity appears to have evolved there in a sequence of steps: adoption of autogamy by 7II, accumulation of seed aborting mutations, origin of a O6 interchange heterozygote from a 7II lineage with a low level of seed abortion, and elaboration in derivative O6 lineages of fully balanced lethal systems. The complex hybrids then migrated (directly or in steps) to populations south west of Pigeon Rocks to produce hybrids in which additional chromosomes were sequentially incorporated into the rings.

RAPD data were collected for individuals representing the Pigeon Rocks lineages, primitive outbreeding populations, and a range of larger ringed complex hybrid populations. The occurrence of many complex hybrid specific RAPD fragments indicated that a single origin of the genetic system was likely. Cladistic analysis with the closely related *I. axillaris* as an outgroup fully supported the proposed model, outlined above, for the evolution of complex hybridity

T10

Application of RFLP and microsatellite markers in acacias

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With more than 1200 species in the genus *Acacia* and over 1000 endemic to Australia, the conservation and utility of molecular markers in the genus is of important practical and evolutionary interest. RFLP and microsatellite markers have been developed for studies of genetic diversity and the construction of genetic linkage maps. Testing of these markers across 15 species representing the subgenera Acacia and Phyllodineae indicated major differences in conservation of the two types of marker. RFLPs developed in *Acacia mangium* can be used across all 15 species while microsatellite loci could only be amplified in five species. When the variability of markers was compared using 20 unrelated individuals of *A. mangium* the mean number of alleles was threefold higher for 5 microsatellite loci than for 58 RFLP loci. The increased variability of microsatellite loci makes them particul!arly useful for genetic fingerprinting but their limited conservation across the genus suggests RFLPs will be of more use for comparisons across species.

A genetic linkage map is being constructed in *A. mangium* using RFLP and microsatellite markers. The aim is to produce a map with 200 codominant, highly variable markers which are scorable across a large number of acacia species. This will be used to locate traits of commercial significance such as disease resistance, pulp yield and wood density.

T11

Identification of QTL for resistance to *Phytophthora cinnamomi* in *Eucalyptus marginata*

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Dieback is a major problem in the jarrah forests of south west Western Australia. It is caused by the fungal pathogen *Phytophthora cinnamomi* and affects the dominant tree species of the forests (*E. marginata*) as well as many of the understorey species, some of which are endangered. The disease poses significant management problems for the forest and mining industries in the regeneration of forest sites and in the rehabilitation of mining sites. Identification and development of resistant planting stock of *E. marginata* has been a focus for mining companies and forest management agencies. Identification of markers for *P. cinnamomi* resistance will assist in the development and selection of dieback resistant germplasm. A genetic linkage map has been constructed for a full-sib family of *E. marginata* using nuclear RFLP markers. The progeny of this family have been screened for *P. cinnamomi* resistance using a stem inoculation method in the glasshouse. Analysis of variance between the lesion length and the RFLP markers have identified markers that are significantly associated with lesion length. The map position of these markers suggests two regions of the genome that are associated with disease resistance in this family.

T12

Population Genetic Structure of *Ostertagia ostertagi* in Australia and the USA

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Ostertagia ostertagi is a nematode parasite of cattle, found throughout the world. A recent study on the population genetics of *O. ostertagi* in the USA found high within-population diversity and no molecular genetic differentiation between populations of the parasite from farms throughout the country, despite differences in genetically controlled developmental traits (Blouin, Dame, Tarrant & Courtney 1992). Understanding the genetic structure (i.e. the amount and distribution of genetic variation within and between populations) of a parasite species is essential for effective control of parasitic disease because it enables one to predict the consequences of local control programs on long term population size and on the development of resistance to control agents. We examined genetic variation for 9-13 worms from 5 populations of *O. ostertagi* from Western Australia by sequencing a 300 bp region of the ND4 locus. From estimates of genetic diversity within and between populations, we have calculated gene flow within Australia and between Australia and the USA, effective population sizes and migration rates using both standard and coalescent approaches.

T13

The major mitochondrial genes of the Arthropoda can move: a large rearrangement in the cattle tick (*Boophilus microplus*)

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The arthropods appeared, until now, to have an arrangement of protein-coding and ribosomal RNA (rRNA) mitochondrial genes that was conserved absolutely and, thus, one which had remained unchanged for >530 million years. We have found a major gene rearrangement in the mitochondrial genome of the cattle tick, *Boophilus microplus* (Chelicerata : Arachnida), which indicates that these large genes can move in the mitochondrial genome of arthropods. There are good practical and mechanistic reasons why identical gene arrangements are unlikely to evolve independently (ie. convergently), so when rearrangements do occur they invariably diagnose real evolutionary groups. Identifying which other arachnids share this rearrangment with the cattle tick will therefore undoubtedly shed light on the phylogeny of the Arachnida. We have also found three other gene arrangements that are unique to the cattle tick among all arthropods studied to date. The implications of these data for the phylogeny of the Arthropoda are profound and raise the novel possibility that this group may have a terrestial rather than a marine origin.

T14

Molecular biodiversity: a phylogenetic and statistical approach

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The information content of the coding DNA of the Earth's organisms is the ultimate measure of biodiversity. The numbers of genes in organisms is therefore important between groups, but within groups phylogenetic relationships between organisms is the crucial aspect. Sets of habitats which preserve larger fractions of the heritable information content (in terms of sequence variation) are to be preferred over sets which preserve less, as judged from phylogeny. Two approaches in general use, namely Genetic Diversity [the probability of the preserved tree having more than one allele] and Phylogenetic Diversity [gross tree length] yield the same rank orders for sets of habitats, but differ in estimating the proportion of the total preserved[1]. In making conservation decisions, statistical sufficiency is desirable. Methods exist for setting confidence limits on the numbers of species in a habitat, although these methods seem to be underused. Species richness, however, takes no account of the evolutionary distinctiveness of the species in various habitats, a lack which can be filled by phylogenetic methods. At present there are major difficulties with the level of completeness of the knowledge required for application of the phylogenetic approach, although considerable progress is possible using indicator groups. Bacteria represent a group for which molecular methods could yield accurate estimates of both species richness and genetic diversity. An analysis of bacterial 16S rDNA extracted from groundwater sampled at the natural nuclear reactor region of Oklo, West Africa, finds statistically significant rankings of the conservation worth of the various sites studied. This demonstration indicates that at least this major source of biodiversity [eg, thousands of species per gram of forest soil] is susceptible to quantitative molecular genetic analysis, and hence that an automated or semiautomated approach to conservation assessment of a high order is possible (how well bacterial predicts eukaryotic biodiversity emerges as an important research question).

[1]Crozier RH. 1997. Preserving the information content of species: genetic diversity, phylogeny and conservation worth. Annu. Rev. Ecol. Syst. 28:in press.

T15

Genetic Characterisation and Physical Mapping of a Cyromazine-Resistant *Drosophila melanogaster* mutant

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The insect growth regulator, cyromazine, is used for controlling insect pests including the Australian sheep blowfly (*Lucilia cuprina*) and the housefly (*Musca domestica*). Cyromazine's mode of action is unknown. The genetic and molecular bases of cyromazine resistance and the molecular basis of cyromazine's mode of action are being investigated using *Drosophila melanogaster*, a model species for insecticide resistance studies. Six *D. melanogaster* mutants resistant to cyromazine have been isolated after mutagenesis and selection in a susceptible strain. In each case, resistance is monogenic. A minimum of four genetic loci conferring cyromazine resistance have been identified. Precise genetic mapping and toxicological analysis of each mutant has been conducted.

In one mutant, (*rst(1a)cyr*), resistance to cyromazine is sex linked and recessive. Analyses using duplication strains suggest that the resistance gene product is a target of cyromazine. Physical mapping of the resistance gene in *rst(1a)cyr* using deficiency strains and duplication strains has placed it in the interval 6C to 6E2. Further physical and genetic mapping is being conducted before positional cloning of the gene is undertaken.

T16

Mitochondrial genealogy of Western Australian barramundi (*Lates calcarifer*): applications of inbreeding coefficients and coalescent analysis for separating contemporary from historical population processes

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Without data on times of population separation and effective population sizes, populations cannot be adequately described by their genetic diffusion in time and space. Fisheries and other population surveys typically calculate the fraction of genetic diversity apportioned among populations, F_{ST}, to differentiate stocks by estimating gene flow. Such estimates yield a statistic that incorporates the effects of both mutation and migration. Where investigations concern the non-recombining, rapidly evolving mtDNA genome, high mutation rates can obscure the history of migration. This problem may be overcome to some extent by the genealogical or coalescent approach in population genetics, which uses only the topological information from a phylogenetic tree for the explicit counting of past migration events.

Here we investigate patterns of population subdivision and gene flow in populations of barramundi (*Lates calcarifer*), using highly variable mtDNA control region sequences to reconstruct the division of western Australian stocks during Recent interglacial episodes. We demonstrate how phylogenetic reconstructions infer historical population processes, thus providing estimates of past gene flow, whereas traditional measures of genetic diversity among populations probably remain the most appropriate indicator of contemporary population subdivision and gene flow.

T17

Molecular evidence for an unanticipated transition from endoparasitism to ectoparasitism in braconid wasps (Hymenoptera, Braconidae)

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The Braconidae are a family of ecto- and endoparasitic hymenopteran wasps, which attack narrow host ranges at the subfamily level. As such they provide an important working model in which to examine the transition between these 2 parasitic lifestyles, as well as the transition between different host groups. We sequenced an homologous portion of the 16S rDNA gene across 59 members of the Braconidae, encompassing 28 subfamilies. Parsimony analyses suggested that endoparasitism of lepidopteran or coleopteran larvae is plesiomorphic for the family. Radiation into hosts other than these (such as Diptera, aphids, other Hymenoptera) occurred relatively recently from an ancestor that attacked lepidopteran or coleopteran larvae. Surprisingly, endoparasitism appears to be plesiomorphic for the family, with our analyses suggesting a single reversion to ectoparasitism in the cyclostome braconid families, in agreement with previous suggestions that the cyclostomes represent a natural, derived braconid group. An alternative explanation, favoured in the literature, is that all of the ectoparasitic ancestors to the earlier diverging Braconidae are now extinct.

T18

Genetic variation in island and mainland macropod populations: conservation implications.

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Island populations are important to the conservation of a large number of endemic Australian species. However, island populations are vulnerable to extinction in the long term. Genetic variation is also important for the longterm survival of populations as it enables populations to adapt and evolve. Despite the importance of islands to the conservation of Australia's mammals, few studies have assessed the genetic variation of island populations. Recent studies, using (up to ten) highly variable microsatellite loci, have examined island and mainland populations of two species - the black -footed rock-wallaby *Petrogale lateralis* (2 mainland; 6 island) and the Euro *Macropus robustus* (1 mainland; 1 island). For both species the mainland populations are characterised by high levels of genetic variation, while the island populations show extremely low levels of variation. Some island populations may also be suffering from inbreeding depression. Should this level of genetic variation prove typical of other island populations it presents another challenge in the long-term management of Australia's endangered species.

T19

Identification of a rock-wallaby hybrid zone in Western Australia?

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Recent field work in the western deserts has identified an unusual population of black-footed rock-wallabies Petrogale lateralis in the Townsend Ridges near Warburton, WA. All animals examined have an unusual 2n = 21 karyotype, intermediate between the allopatric West Kimberley race (2n = 20) and the MacDonnell Ranges race (2n = 22) of *P. lateralis*. Subsequent examination of mitochondrial DNA has revealed two divergent haplotypes in this population. The most common haplotype is closely related to a haplotype characteristic of the West Kimberley race (800 km to the NW), while the rarer haplotype is typical of adjacent MacDonnell Ranges race populations. These data would strongly suggest that the highly endangered Townsend Ridges population represents a hybrid zone between the West Kimberley and MacDonnell Ranges races of *P. lateralis*.

T20

Artificial Selection for Spectral Sensitivity and Sexual Selection

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Most genetic models of the evolution of sexual selection examine the effects of female preference on male traits and vice versa. However, the joint evolution of male traits and female preferences can be affected by direct selection on the sensory system, which is also used for food finding and predator avoidance. Sensory systems can change as a species invades a new habitat, or if there is habitat change resulting from climatic change. I examined these effects by artificially selecting for different kinds of colour vision in guppies (*Poecilia reticulata*). Spectral sensitivity responded significantly to selection in 9 generations, but lines diverged markedly in how they responded. This is consistent with different known neural mechanisms, each of which can respond to the same selective pressure. Mate preferences and male traits were also tracked during the experiment and showed some correlated effects.

T21

Microsatellites, Models, Mutations, and Marine Turtles

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Microsatellites continue to gain increasing use in the study of population processes and genetic structure, yet the need remains to better understand mutational events and pattern and to test infinite allele model (IAM) vs. stepwise mutation model (SMM) approaches on real world data sets. We have developed microsatellite techniques to study the genetic structure among marine turtle populations breeding in Australian waters and to assess male-mediated gene flow. IAM and SMM measures of genetic subdivision (Fst and Rst) were applied to the population data to determine which was most appropriate when compared to ecological data from physical tagging studies. In general the IAM model was in better agreement with expectations, likely the result of moderate to high levels of gene flow, but results varied with mutation rate at the four loci. Mutation rate and pattern were examined fortuitously while using the same microsatellite loci to study clutch paternity in green turtles (*Chelonia mydas*). Mutation rate was determined from the analyses of over 900 offspring at five loci, revealing 19 mutational events observed in 27 offspring. Typically, pre-existing alleles were regenerated by mutation, contra the IAM, but only ~30% of mutations were single step events, thus the strict SMM also appears inappropriate.

T22

Molecular Characterisation of Wheat-Wheatgrass Group 7 Translocation Lines and Localisation of Barley Yellow Dwarf Virus Resistance Gene(s) in Wheat (*Triticum aestivum* L.)

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Barley Yellow Dwarf Virus (BYDV) is the most significant viral pathogen in wheat and other cereals world-wide. However, wheat germplasm collections lack suitable cultivars resistant to BYDV infection. Therefore, resistance genes are sought from wild species that can be introgressed into wheat. The intermediate wheatgrass, *Thinopyrum intermedium*, is an excellent source of resistance to BYDV and has been exploited in the soft red winter wheat breeding program at Purdue University, USA. A group 7 chromosome from *Th. intermedium* was substituted for wheat chromosome 7D by intergeneric hybridisation, generating valuable wheat germplasm resistant to BYDV. This germplasm was used as parental material in further breeding strategies to restore much of the wheat genetic background but retaining BYDV resistance. A strategy involving backcrossing the group 7 disomic alien substitution line (P29), irradiating and selfing produced a series of resistant translocation lines with reduced amounts of alien chromatin.

A preliminary molecular study using homoeologous group 7 RFLP markers has shown that the source of the alien chromosome responsible for BYDV resistance in P29 is syntenic to wheat group 7A and 7D chromosomes. This information was used for screening and identification of resistant translocation lines with the smallest amount of alien chromosome segments. Several resistant translocation lines were identified having less than half the long arm of the alien group 7 chromosome. These lines are currently being used in the Purdue wheat breeding program to introgress resistance into other elite wheat cultivars. Additional studies were done to further localise resistance genes on the long arm of the alien chromosome. Analysis of susceptible translocation lines using homoeologous group 7 markers have localised BYDV resistance gene(s) on the distal end of the long arm of the alien chromosome. Although these susceptible lines are not beneficial for breeding purposes, they are extremely useful for physical mapping of BYDV resistance.

T23

Structure and evolution of the mitochondrial DNA control region in marsupials

Luca Fumagalli, Lisa Pope and Craig Moritz

The mitochondrial DNA control region, which is the major non-coding portion of the mitochondrial genome, contains the start signals for both replication and transcription. Due to its rapid rate of evolution, the control region has widely been used for detection of nucleotide polymorphism among closely related species, or for determining intraspecific molecular population structure. Some parts of the mtDNA control region evolve much faster than others possibly due to reduced functional constraints, and many studies of intraspecific sequence polymorphism have focused on these segments. However, the variety of structures and features found in the vertebrate control regions studied so far (e.g. tandemly repeated sequences, secondary structures, substitution rate heterogeneity among sites, bias in base content) indicate that a particular care should be taken to identify the most appropriate segment for studies of control region sequence variation.

Although sequences of many mammalian mtDNA control regions have been published to date, little is known about the control region structure in marsupials . In this study, we present a comparative analysis among mtDNA control region sequences of 11 different marsupial species, and describe their main particularities, such as tandem repeats structure and evolution, localisation of conserved sequences, base content and secondary structures. Furthermore, we compare these sequences with the homologous sequences in the other major groups of mammals (eutherians and monotremes) in an attempt to understand the pattern of evolution of this complex mitochondrial region.

T24

The contribution of genetic studies to the development of lupin species for cultivation in Australia

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The cultivation of lupins is an important feature of the cereal cropping systems of Australia, particularly Western Australia. The lupin crop provides a disease break between cereal crops, and contributes to the maintenance of soil fertility. Of the several lupin species actually or potentially cultivated (which are adapted to different soil types), we will consider three which are at very different stages of development, and which together illustrate the whole process of plant domestication and improvement. *Lupinus angustifolius* is already widely cultivated and has been the subject of genetic improvement in Australia since 1960. *Lupinus albus* is cultivated only on a limited area, and on the basis of cultivars introduced from Europe. *Lupinus pilosus* is an undomesticated species. In *L. pilosus* we have identified fertile low-alkaloid mutants, completing the set of recessive mutants required for cultivation, and have identified germplasm accessions in which early flowering is associated with vigorous growth at the seedling stage. In *L. albus* we have shown that the restricted branching character, expected to raise the harvest index, has an unexpected association with late maturity, and we have broadened the range of genetic backgrounds in which this character is available. In *L. angustifolius* mild restricted branching is a feature of recently released cultivars, and we have shown that this character, which varies quantitatively and is influenced by the environment, is nevertheless sufficiently highly heritable to be a target for selection in the F_3 generation.

T25

D-Loop variation among populations of a native New Zealand fish

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There are three species of mudfish in New Zealand which are placed in the Neochanna genus of the family Galaxiidae. They are the brown mudfish (*Neochanna apoda*), black mudfish (*Neochanna diversus*), and the Canterbury mudfish (*Neochanna burrowsius*). All three are endemic and can live within the soil for long periods of time surviving drought conditions. These three species are listed as threatened by Department of Conservation, however they are the only native vertebrates in New Zealand that are not legally protected. Little is currently known about exactly how widespread or densely distributed these fish are. We have begun research on the black mudfish *N. diversus* which occurs from the Central North Island north. This species is the most specialised of the three due to its northern range where it experiences the longest aestivation times. The major existing habitat for this species is the Whangamarino Swamp and the Kopuatai Peat Dome in the Waikato. Fire is a constant threat in these habitats with a fire in the summer of 1986 burning almost two thirds of the Whangamarino wetland. In Northland, the remaining habitats for black mudfish are under threat from drainage for pasture conversion, reduction in water table levels, and the predation by mosquitofish *Gambusia* sp. We have sampled populations from both Northland and Waikato to determine the level of diversity between regions and among populations through sequencing of the entire D- Loop and a region of the 16S from the mitochondrial genome. The D-Loop has shown considerable diversity between populations and includes a 200bp repeat insertion. These results and the implications for the conservation and management of the black mudfish will be discussed.

T26

Recent thoughts on mechanisms of meiotic chromosome pairing

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The classical view of the sequence of chromosome events in meiosis I is that the achievement of homologous chromosome pairing is necessary to allow the occurrence of reciprocal crossing over in bivalents, the evidence of which is the appearance of chiasmata, which are also essential for reductional segregation at anaphase I. Electron microscopic studies of meiotic chromosome pairing have revealed that a necessary but not sufficient requirement for recombination is the formation of synaptonemal complexes (SC) during zygotene and pachytene. This view of meiotic events based on cytological and genetical studies in plants and animals has recently been challenged by data from biochemical and mutational studies in yeast *(Saccharomyces cerevisiae).* The analysis of the temporal relationships of a number of yeast meiotic mutants has revealed that certain genes controlling the initiation of recombination act before and are necessary for the occurrence of pairing. This has led to a model of yeast meiosis I in which:

- the earliest process is a search for homology involving DNA matching which, if successful, causes double stranded breaks (DSBs);
- DSB processing results in formation of Holliday junctions and heteroduplex DNA, and is coincident with SC formation;
- resolution of Holliday junctions leads to reciprocal crossovers and/or gene conversion events, which coincide with SC completion.

In this talk I will compare the evidence from cytological and biochemical studies of yeast with results from studies of rearranged and polyploid plants and animals, and discuss such topics as how chromatin packaging may influence recombination frequency; the number of DSBs, pairing sites and recombination events; the role of SC in regulating the number and position of crossovers; and the telomeric localisation of pairing and crossing over.

T27

Interactions between *sry* and *sox* genes in mammalian sex determination

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The *SRY* gene on the mamalian Y chromosome undoubtedly acts to determine testis, but it is still quite unclear how. The original supposition that *SRY* acts directly to activate other genes in the testis determining pathway seems unliikely. Here I present the hypothesis that *SRY* functions indirectly by interacting with related *SOX* genes. I propose that *SRY* inhibits the closely related X-linked *SOX3* gene from which it evolved, and *SOX3* in turn inhibits *SOX9*, an autosomal gene which appears to be intimately involved in vertebrate gonad differentiation. This hypothesis makes testable predictions of the phenotypes of XX and XY individuals with deficiencies or overproduction of any of the three genes, and is able to account for the difficult cases of XX (*SRY*-) males, and transdifferentiation in the absence of *SRY*. The hypothesis also suggests a way that the dominant *SRY* sex determining sustem of present-day mammals may have evolved from an ancient system relying on *SOX3* dosage.

Prospects and pitfalls of the new human behaviour genetics

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The aim of this session is to demonstrate that behaviour genetics has advanced well beyond the old argument over whether or not behaviour is inherited. Not only is that question naïve, since behaviours differ in the extent of their genetic determination, but also the answers have often been flawed, being based on small and selective samples. Contemporary behaviour genetic analysis requires large-scale co-operative studies involving many individuals/families and is thus a major undertaking, academically and financially. We shall demonstrate what behaviour genetics has achieved to date and speculate on what it can achieve in the future. The vital role of Australia must be recognised. Through the Australian NHMRC Twin Registry, the new WA population-based twin child health registry (WATCH), the NHMRC Network for Brain Research on Mental Disorders plus other initiatives, this country is playing a key role in the developing the large-scale databases needed to analyse both normal behaviours and the range of psychiatric conditions.

The first two papers will focus on common conditions in children and adults respectively, namely Attention Deficit Hyperactivity Disorder (ADHD) and the neuroses (the anxiety disorders and depression). While twin research has been fundamental to quantitative genetic analyses of these behaviours, there is growing emphases on molecular approaches. The third paper will focus on schizophrenia, the disorder where there has been the most intensive molecular research and describe one of the international initiatives needed to identify sufficient families with this condition.

T28

Attention Deficit Hyperactivity Disorder (ADHD) as a model for the genetic analysis of childhood behaviour

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This paper illustrates some key behaviour genetic issues, using the Australian Twin ADHD Project (ATAP) which since 1991 has been following 2000 twin pairs aged 4-12 years plus their siblings. (1) How is ADHD inherited? We have used the Defries and Fulker multiple regression approach to show ADHD is inherited as a continuum throughout the entire population rather than as a distinct disorder and that it is highly heritable (75-90%), irrespective of how it is defined. (2) Is there more than one sort of ADHD? The twin concordances demonstrate that the currently recognised Inattentive, Hyperactive/Impulsive and Combined subtypes "breed true". (3) What causes the overlap of ADHD with reading problems? Rather than ADHD causing reading problems or vice versa, multivariate genetic analysis confirms there are common genes contributing to both problems. (4) If ADHD is so heritable, what about the adult relatives? Several studies have shown repeat number polymorphism in the Dopamine D4 receptor gene to be associated both with ADHD in children and with one adult temperament trait (Novelty Seeking). Our twin-family study (in conjunction with Prof Nick Martin) allows us to test this relationship between different behaviours in different generations.

Thus the quantitative and the molecular approaches to ADHD can be complementary with the former being crucial in defining the phenotype, its changes with age and its relationship to other behaviours.

T29

Multipoint sib-pair analysis in schizophrenia: chromosomal markers in potential candidate regions

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There is general agreement that genetic factors play a major role in the aetiology of autism as well as in schizophrenia. The most plausible explanation for genetic transmission in both disorders is the action of a small number of interacting loci. Results have suggested susceptibility loci to be located on chromosome 6, 8 and chromosome 22. Evidence for a susceptibility locus for bipolar disorders had been reported in an area of 20 cM on 18p11.21-18q11.1. In order to test for a gene we employed multipoint sib-pair analysis. In sib-pair analysis one determines excess identity by descent sharing of markers linked to a disease susceptibility locus in affected siblings, allowing for the detection of linkage without requiring assumptions about the mode of inheritance. The parameterization of the model is in terms of a single parameter, the risk ratio l_S (i.e. the ratio of risk to siblings compared to population prevalence). Forty-eight pedigrees were collected in two areas in Germany (Mainz and Haar). 11 families of Sephardic Jewish origin were recruited in Israel (total 59 families). Each family included a minimum of two affected siblings, suffering from schizophrenia or schizoaffective disorder (RDC). Full parental genotype information was available for 55 families. The sample comprised 155 individuals with schizophrenia or schizoaffective disorders (schizophrenic type). Results suggest a possible susceptibility gene to be located on chromosome 6. A region of chromosome 18 may also be implicated.

T30

Comparison of nuclear and mitochondrial sequences for phylogenetic studies of human lung flukes

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The *Paragonimus westermani* species complex is medically the most important species of lungfluke. It is widely distributed from the Soviet Republic, throughout Asia and as far south as the Malay Peninsula. The species complex includes sexually reproducing diploids, which are widely distributed and parthenogenetic triploids, which are restricted to northeast Asia, and are the most pathogenic form. Although drug therapy is effective, drug-resistance is emerging and eventual vaccine development would be desirable. The primary aim of this study is to determine the extent of diversity within the species complex, particularly to distinguish diploids from triploids, which exist sympatrically in northeast Asia. Sequences were obtained from several Asian isolates of both diploid and triploid strains, from two nuclear regions (ITS1 & ITS2) and two partial mitochondrial genes (COI & ND1). These regions are frequently used to distinguish organisms both within and between species. Sequence data was analysed using both Parsimony (branch and bound) and Neighbour-Joining (Kimura 2 parameter) methods. ITS2 and COI data were unable to differentiate between diploids and triploids, however northeast Asian strains were distinct from southeast Asian strains. In addition to the two Asian strains, diploids and triploids were differentiated using ITS1 and ND1 sequences. Some of the confounding factors associated with ND1 and ITS1 data sets will be discussed.

T31

Rates and Patterns of Molecular Evolution in Australian Passerine Birds - Aromatase.

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Subsequent to last years presentation of a study of molecular evolution at the myoglobin intron in a hierarchy of Australian passerine birds, we present data for these species for a second nuclear intron - aromatase. We shall compare rates and patterns of sequence evolution at these 2 loci in passerine birds.

Initial data from the myoglobin intron suggested that it would be useful as a marker for intrageneric phylogenetics studies, but with a level of variation too low to distinguish relationships within genera. Is this a general quality of the evolution of nuclear introns? Or might there be substantial variation in rates or patterns of evolution across loci?

T32

Phylogeny recapitulates geography, or why New Zealand has so many lizards

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The evolutionary history of 25 New Zealand scincid lizards in the endemic genera *Oligosoma* and *Cyclodina* was examined using 380 base pairs of 12S rRNA sequence data. Phylogenetic resolution was poor, despite there being up to 9% sequence divergence between taxa. A relative rates test established that rates of nucleotide substitution in the skinks are similar to birds, and this was used to estimate that divergence of many extant *Oligosoma* skinks occurred 27 - 42 million years ago. The pattern of relationships and the timing of this diversification are interpreted as resulting from rapid allopatric speciation during the Oligocene (25 - 35 million years ago) when New Zealand may have been fragmented into many relatively small and low lying islands. A second major phase of speciation involving the *Cyclodina* seems to have occurred during the Miocene (15 - 23 Ma), perhaps as a consequence of increasing land area and habitat diversity. This pattern of skink evolution contrasts with the Oligocene "environmental crisis" hypothesis of Cooper & Cooper (Proc. R. Soc. Lond B. **261**, 293-302), but could be associated with differences in the ecology of lizards and birds. This can be tested by examination of other groups, such as geckos and land snails. The large number of lizard species in New Zealand can be considered an adaptive radiation, a legacy both of past geography and the absence of small insectivorous mammals.

T33

Re-evaluation of management options for the endangered plant *Zieria prostrata* in the light of genetic evidence

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Zieria prostrata (Rutaceae) exhibits extreme endemism being known from only 4 headlands along a 3 km stretch of coastline near Coffs Harbour in northern New South Wales. The species was also presumed extinct at a fifth headland, 23 kilometres south of its present distribution. A translocation program commenced in 1993 (enhancing two populations and re-introducing individuals to the extinct population sourced from a plant apparently sampled prior to extinction). Subsequently a genetic study was undertaken to assess patterns of genetic variation both in the wild and in the ex situ collection used for the translocations.

An extreme level of genetic divergence among populations was revealed by allozymes and RAPD marker analysis. An Analysis of Molecular Variance (AMOVA) for the RAPD data revealed 66% divergence among populations. The strong population genetic differentiation among *Z. prostrata* populations, despite their close proximity, is probably due to isolation of the populations as a result of high selfing rates and perhaps also to genetic drift in these small populations.

In addition, genetic analysis revealed the individual reported to be from the extinct population shared the same DNA profile with an individual from one of the other sites. Since extensive genetic divergence occurs among populations within this species the probability of sharing DNA profiles among populations is extremely low. This led to a search for hard evidence supporting the prior existence of the fifth population, the lack of which resulted in the abandonment of reintroduction at that site and suspension of the entire translocation program. Genetic findings have thus had important practical conservation implications for this species, leading to an important change in the management plan.

T34

The scope and the limits of plant conservation genetics

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Plant conservationists have often concerned themselves with loss of genetic diversity in rare plants, but loss of diversity is more likely to be a symptom of endangerment than its cause. Loss of self-incompatibility alleles or genetic assimilation through hybridization may threaten some species with extinction, but genetic threats to persistence generally pale in comparison to threats posed by loss and alteration of habitat. Managing the genetic structure of endangered plant populations will often be less important than managing demographic structure or habitat. Nonetheless, genetic principles should play a role in the design of re-introduction/augmentation efforts. Similarly, genetic tools may help to identify evolutionarily distinct populations worthy of conservation concern and to unravel the extent of demographic connections among existing populations. Data from molecular markers must be carefully interpreted, however, because patterns of variation for those markers may be quite different from those for polygenic traits likely to be involved in future adaptive responses.

T35

DNA sequence analysis of a conserved chromosomal segment of a bacterial plant pathogen

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Ralstonia (previously *Pseudomonas*) *solanacearum* is an important plant pathogen. We have identified a chromosomal *Spe*I fragment which contains virulence and essential genes. A DNA fragment from this region was sequenced. Seven short segments of DNA at the 5' end of the sequence have high homology with a virulence gene (*hrp)* cluster. Downstream from it a 360 bp sequence was found to be highly homologous with the *ssrA* gene which codes for a small stable RNA(10 Sa RNA). Identity is higher with that of the soil bacterium *R. eutropha* than with that of the human bacterial pathogens *E.coli, M. tuberculosis* and *V. cholerae*. A theoretical RNA transcript of this sequence can be arranged into a half-molecule of tRNA, suggesting a functional *ssrA* gene. A prophage attachment site overlapped with the *ssrA*. The site contains part of 3' end of a tRNA gene. These elements may represent target sites for the chromosomal integration of virulence genes. These observations suggest that fundamental aspects of the genome organization of plant and animal bacterial pathogens might be highly conserved from the perspective of the evolution of virulence.

T36

Chromosome numbers and phylogeny in the kangaroo paw and bloodroot family Haemodoraceae

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The Haemodoraceae is a small monocotyledon family of 14 genera and 102 species, the vast majority of which are found in south-western Australia, with the remainder elsewhere in Australia, New Guinea, South Africa, the New World tropics and eastern North America. Chromosome numbers are known for 12 genera and 58 species, and range from n=4 to n=24. Dysploid reduction series and limited polyploidy occur in the large SW Australian genus Conostylis (n=8[16], 7[14,21,28], 6, 5, 4[8]). Descending dysploidy and genomic coalescence also may underpin generic divergence in the Haemodoraceae. The small sister family Philydraceae has counts of n=8, 16 and 17. Previous authors have proposed numbers of n=8, 7 or 4 as ancestral for the Haemodoraceae. However, recent molecular phylogenetic analysis suggest that n=16 is more probable. This conforms with the wider hypothesis that the primitive chromosome numbers in angiosperm families are high and chromosome number evolution is characterised by descending dysploidy.

T37

Ecological Significance of Back Colour Variation in the Australian Magpie

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The Australian Magpie varies in back colour across its range. In northern Australia all birds are black-backed, in the south east birds are white-backed and in the southwest males are white-backed and females are black-backed. In the east, the white-backed and black-backed forms meet in a hybrid zone in northern Victoria. This project is examining explanations for the variation in eastern Australia. Is the hybrid zone an area of secondary contact or is it a primary contact zone, with the colour distribution determined by variation in environmental factors affecting back colour. The hybrid zone was first mapped in 1975. In 1996 it was remapped and the results suggest that genes for black-backs may be moving south, right across the zone. At the northern extreme of the zone, no consistent pattern was seen. Analysis of nuclear gene markers (allozymes and three microsatellite loci) and mitochondrial control region suggest no evidence of past separation of white-backed and black-backed forms. Analysis of various components of fitness of black-backs, white-backs and hybrids in the hybrid zone will also be presented. These results indicate no evidence of selection against hybrids. There is limited evidence that selection may act against white-backs in the hybrid zone, as territories with white-backed males produce fewer fledglings and fledgling survival is lower than in other territories. There is no evidence to suggest that sexual selection favours white-backs because of their brighter colour. Specifically, white-backs do not have larger territories, they are not more likely to hold a territory and they do not have more females in their territories. We cannot yet test whether or not they achieve more matings than other back colours.

T38

Phylogeography of Freshwater Fauna from Northeastern Queensland

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It is generally accepted that population genetic structure of freshwater fauna should fit the hierarchical model of gene flow which reflects the dendritic nature of river drainages (i.e. genetic similarity is high between populations within a stream and low between populations from different drainages). Previous allozyme studies in the Tully and Herbert Rivers indicated that populations in some Tully streams were genetically more similar to populations in the adjacent drainage than they were to other populations in the Tully. This genetic structure suggests that the current drainage patterns were different in the past.

Using phylogeographic techniques, this project aims to investigate the distribution of mtDNA lineages of three fully aquatic species in this region in order to determine the relative roles that gene flow and genetic drift and historical geomorphological barriers have played in determining current spatial patterns.

T39

Consequences of inbreeding

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Classical population genetics informs us that inbreeding will promote homozygosity, generate inbreeding depression, purge deleterious recessives from gene pools and lead to population differentiation. Analysis of genetic systems in Australian native plants indicates that this is only half the story. Inbreeding depression, which is the segregational genetic load exposed by inbreeding, provides the fuel driving the engine of evolution towards its own minimization. Adaptive devices minimizing the genetic load include mechanisms promoting outbreeding such as spectacular pollination mechanisms, prezygotic self-incompatibility and dioecy; mechanisms promoting the efficiency of post-zygotic selection systems including early acting seed aborting recessive lethals and sibling competition; mechanisms which reduce the number of independently segregating units at meiosis (genomic coalescence or supergene formation) including chiasma localization, chromosome structural hybridity, dysploidy and heterogamy; polyploidy and apomixis. In this talk, several case histories of cytoevolutionary interest will be briefly reviewed and illustrated. The principles that emerge have obvious implications for conservation practice, but perhaps they confuse the picture rather than simplifying it.

T40

A regulatory gene from *Arabidopsis* with pleiotropic roles in leaf hair development and the production of pigment and mucilage by seed coats

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A mutant arose in an Ac transposon tagging experiment that modified three aspects of Arabidopsis development. The leaf and stem hairs (trichomes) were reduced in number and mostly unbranched. Pigmentation of the seed coat (testa) was reduced from brown to a light tan. Seed coats also lacked the mucilage normally produced upon wetting. The gene was named TRANSPARENT TESTA GLABRA2 (TTG2), as it is the second, non-allelic gene to show this spectrum of mutant defects. The TTG2 gene was disrupted by the endogenous transposable element Tag1 rather than the transgenic Ac element. Tag1 was apparently activated by the regeneration of transformed plants during the insertion of Ac. The disrupted gene was cloned by inverse PCR. It was shown by complementation to correspond to the gene that gave all three phenotypic changes when in mutant form. A cDNA clone was isolated, and sequence comparisons revealed that Tag1 had inserted into the second exon. The TTG2 product shares similarities with transcription factors recently isolated from plants with a unique CCHH zinc-finger motif. These factors are involved in the induction of amylases, and in response to pathogen attack. Thus it seems that this family of genes regulates a wide range of cellular and developmental processes in plants. In situ hybridisation on wild type plants detected TTG2 expression in developing leaf hairs, and in a layer of cells in the inner seed coat where pigment is generated. However, no expression was seen in the outer seed coat from which mucilage is produced, suggesting that it has a non-cell autonomous action in regulating mucliage production.

T41

Population structure of the weaver ant *Polyrhachis doddi* using microsatellite DNA markers

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The formicine ant *Polyrhachis doddi* belongs to an arboreal group of species found in the subgenus Cyrtomyrma. *P. doddi* workers weave their nests from leaves with the aid of silk produced by cocoonless larvae. Previous behavioural studies (V. Hinman, 1994) have indicated that the polygynous colonies of this species can be established pleometrotically (new colonies are established by multiple egg layers) with no preference to kin, as well as exhibiting polydomous colonies (multiple nest units forming a colony). Genetic analysis can provide additional insight into possible modes of colony foundation as well as colony and population sub-structure. Specifically, our microsatellite markers for *P. doddi* should provide a means for assessing the average number of matings per queen, the extent and conditions of pleometrosis, and the mode of polydomous colony establishment. Additionally, at a higher level of spatial resolution, these markers have the potential to delimit colony boundaries and define population substructuring. Currently we have three polymorphic microsatellite loci in use. Further sequencing of positive clones is being carried out to obtain at least five markers to obtain an accurate analysis. The microsatellites developed here may provide similar insights into the breeding system of other species in the genus as has been the case for microsatellite markers origionally developed for the bumble bee *Bombus terrestris* which also served for four other *Bombus* species to determine the average number of queen matings in these species (Estoup et al, 1995).

Estoup, A., Scholl, A., Pouvreau, A. and Solignac, M. (1995) Monoandry and polandry in bumble bees (Hymenoptera; Bombinae) as evidenced by highly variable microsatellites. Molecular Ecology, 4, 89-93.

Hinman, V. (1994) Pleometrosis and polygyny in *Polyrhachis doddi* (Formicidae: Formicinae). Honours thesis, University of Queensland.

T42

Mutation accumulation and the loss of reproductive capacity in small populations of a rare eucalypt

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Although there has been much recent theoretical interest in evaluating the risk of extinction of small sexual populations via the accumulation of deleterious mutations, there is a notable absence of empirical data on this subject. Further, there seems to be some debate as to whether deleterious mutations will become fixed and accumulate in small populations, or whether they will be purged through natural selection. In this study, pollen viability was used to assess the accumulated genetic load in different-sized populations of two closely related eucalypt species (*Eucalyptus argutifolia* and *E. obtusiflora*). The results revealed significantly lower pollen viability in small populations ($\leq$ 12 genets) of the rare *E. argutifolia*, relative to those found in the large populations (> 400 genets) of *E. argutifolia* and the widespread *E. obtusiflora*. In addition, the (sexual) reproductive capacity of small populations was significantly reduced relative to that found in the large populations, and it was suggested that they are currently in the later stages of a 'mutational meltdown' process. These results strengthen the concerns expressed in recent studies that the accumulation of deleterious mutations may be a significant source of extinction vulnerability to small populations.

T43

An evaluation of the AFLP fingerprinting technique for the analysis of paternity in natural populations of *Persoonia mollis* (Proteaceae)

Siegfried Krauss, *ANU*

The accurate assignment of paternity in natural plant populations is required to address important issues in evolutionary biology, e.g. factors that affect reproductive success. New molecular fingerprinting techniques offer the potential to address these aims more completely than previously possible. Here, I evaluate the utility of the new PCR-based multi-locus fingerprinting technique called Amplified Fragment Length Polymorphism (AFLP) for paternity studies in *Persoonia mollis*. AFLPs are generated by the selective PCR amplification of restriction fragments from a total digest of genomic DNA. Fragments were flourescently labelled and visualized using an ABI 377 sequencer and Genescan software. In a pilot study, individuals representing four hierarchical levels were compared for each of 64 AFLP primer pairs: between species (*P. mollis* and *P. levis*), between subspecies (*P. mollis* subsp. *nectens* and subsp. *livens*), between individuals within a single *P. mollis* population, and between a mother and its naturally pollinated seed. Results to date show 793 polymorphic fragments (23.5% of all fragments) between species, 537 (16.0%) between subspecies, 280 (8.9%) between individuals within a single population, and 214 (6.7%) between a mother and its seed. Based on these observations, it will be feasible to generate, from a subset of these 64 AFLP primer pairs, 100 polymorphic AFLP loci that will be sufficiently polymorphic to assign paternity unambiguously to more than 99% of all seed in current experiments involving small, known paternity pools. More generally, the AFLP procedure is well suited to molecular ecological studies, because it produces more polymorphism than allozymes or RAPDs, but unlike conventionally developed microsatellite loci, it requires no prior sequence knowledge and minimal development time.

T44

Kinship and alliance formation in male bottlenose dolphins (*Tursiops* sp.) in Shark Bay, Western Australia

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Male bottlenose dolphins in Shark Bay form two levels of alliances. Almost all males form first-order alliances; pairs or triplets, which are stable over many years. Male dolphins within such an alliance cooperate to sequester and control females in reproductive condition. First-order alliances cooperate with other first-order alliances, forming so-called second-order alliances. However, second-order alliance partners may be on the same side on one context and on opposite side in another. Evolutionary explanations of these context dependant hostile and affiliative interactions depend critically on the genetic relatedness of cooperating males and their reproductive success. Therefore, the following kinship hypotheses need to be tested: First-order alliance members will be more closely related than would be expected by chance; and second-order alliances should involve first-order alliances that are more closely related than expected by chance. For a preliminary study, a panel of ten microsatellite loci was cloned and characterized from genomic libraries of *Tursiops* spp. For the four polymorphic loci found, the population appears to be in Hardy-Weinberg equilibrium ($p<0.05$; n=17; Ho=0.53-0.73) and no linkage disequilibrium was observed ($p<0.05$). Using LOD-scores, maternity was analyzed for three suspected mother-offspring relationships and could be supported in all of the cases. Paternity analyses that do not include the necessity of data such as allele frequencies were performed. By investigating 45 possible father-offspring relationships, paternity could be excluded in 96.4% of all of the cases. We show that microsatellites are a useful genetic approach to test the kinship hypotheses.

T45

Age trends in variances and heritabilities for height and diameter in maritime pine (*Pinus pinaster* Ait.)

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The inheritance of variables related to growth was studied in a progeny trial of maritime pine (*Pinus pinaster* Ait.) in Wanneroo, Western Australia. The trial consists of the progeny of three parent trees used as females and five used as males, crossed in 14 of the 15 possible combinations (full-sib families). There are 108 trees/cross, planted at a spacing of 3 m × 3 m. The height of each tree was measured at ages 4, 6, 9 and 25 years, and the diameter at ages 9, 12, 16 and 25 years. Genetic and environmental variance components of heights and diameters were estimated using restricted maximum likelihood (REML). Phenotypic and additive-genetic variances increased as trees became older, rapidly up to age 6 years, then more gradually. Heritabilities were fairly constant, in the range 0.11 to 0.14 (for height) and 0.14 to 0.16 (for diameter). This is in contrast to other studies of pines in which heritability increased with age, and was greater for height than for diameter, possibly because the trees were planted at narrower spacings. Certain full-sib families were consistently tall and had consistently large diameters, indicating that early selection between families may be effective. In a principal component (pcp) analysis the first pcp explained 93 % of the variation in the diameters (i.e. they were consistent over time). However, the second pcp, though it explained only 6 % of the variation, was more heritable (1st pcp: $h^2 = 0.14$; 2nd pcp: $h^2 = 0.37$). This pcp contrasted early and late measurements. A similar pattern was found in a pcp analysis of the heights. It is suggested that the second principal component could be of use as an indicator of the closeness of the genetic relationship between trees, in order to maintain genetic diversity in a breeding program.

T46

Detection of quantitative trait loci for growth in crosses between selection lines of beef cattle

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Closed selection lines of Angus cattle were established at the Agricultural Research Centre in Trangie, New South Wales in 1974. Fifteen years of selection for either increased or decreased yearling growth rate resulted in a divergence in growth rate of over 30% between high and low selection lines. Detection of Quantitative Trait Loci (QTL) for growth was carried out using progeny from seven sires resulting from the reciprocal crosses between the high and low lines. The sires were backcrossed to approximately 250 dams from both the high and low selection lines. A total of 314 progeny were produced in two cohorts over two consecutive years (1993-94). The offspring were raised to one year of age in Hamilton (Victoria) where birth, weaning and yearling weights, and pre-and post-weaning gain were measured. In this half-sib design, only the sires and progeny were genotyped. A total of 10, 509 genotypes were collected from 49 microsatellite markers typed manually and using an automated sequencer. Sires were allocated by DNA fingerprinting using unlinked polymorphic markers. QTL for growth traits were analysed by interval mapping. From analysis of the first cohort, growth QTL were detected on regions of chromosomes 19 and 21. Additional mapping of these two regions using the same and additional markers on both cohorts resulted in a total of 2314 genotypes being obtained from eight markers. The characteristics and localisations of the QTL will be discussed.

T47

Inherited Neuromuscular diseases: beyond the genes, what do we do next?

Nigel G Laing

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The theoretical basis for localising disease genes using DNA polymorphisms was put forward in 1980. This led to the "new genetics" and the huge expansion in knowledge of human disease genes. More and more mutated genes significant in human diseases are being identified, and more patients and their families are benefiting from this new knowledge. The benefits take the form of more accurate diagnosis and prevention of further affected family members through prenatal diagnosis. Prenatal diagnosis and termination brings significant trauma, but is the preferred route of most, when the alternatives run the risk of inflicting a serious inherited disease on one's children through playing genetic roulette or abstention from having children. The aim of finding disease genes was however to provide more than "death before life". The hope was to obtain better treatments and even cures through understanding of the pathogenic mechanisms of each inherited disease. The problems which have led to little or nothing in the way of successful new treatments to date revolve round lack of understanding of the cell biology of the protein products of the identified disease genes. In many cases, the protein product of the disease gene was previously unknown. For other diseases, although the protein product was previously identified, the exact function of the mutated amino acid is unknown. Finally the disease-causing mutation may confer a new ability on the protein a so-called "gain of function" mutation. Treatments for inherited diseases require normalisation of the affected protein function. Treatments may involve transplantation, eg heart, liver, bone marrow; gene therapy with viral vectors; antisense technology or upregulation of alternate genes. All these routes have been, or are being attempted in various inherited diseases. All require great investments in time and money in understanding the cell biology of the particular disease protein. Replacing a missing protein by transplantation or gene therapy introduces the further complication of immune response to a protein which the patient's immune system has never seen and means that patients given such treatments will require immunosuppression. Antisense technology and upregulation of alternate genes should not require immunosuppression. Which approach if any will be effective in a particular disease, will have to be determined over a considerable period of time. There is bound to be a lengthy hiatus between gene discovery and any resultant treatment.

T48

Combining quantitative and population genetics to infer transmission cycles in a parasitic tapeworm

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Species of *Echinococcus* (Cestoda: Taeniidae) require two mammalian hosts to complete their life cycle; a carnivorous definitive host in which the adult develops, and a herbivorous or omnivorous intermediate host in which the larva (hydatid cyst) develops. For most species of *Echinococcus*, the definitive host range is restricted to one or a few species, but the intermediate host range is very broad. Programs to control hydatid disease attempt to break the life-cycle of the parasite and their effectiveness therefore requires an understanding of local patterns of transmission. It is known that the rostellar hooks of larvae may be directly influenced by the species of intermediate host in which they develop. This knowledge has not so far been very useful for inferring transmission cycles, because it has not been possible to isolate the intermediate host effect from other environmental and genetic components of phenotypic variance. I present here a method for separating these potentially confounding genetic and environmental effects, which combines a quantitative genetic approach with data on population structure from neutral genetic markers. For populations of *E. granulosus* in Australia, the method estimates that 49-60% of the variance in hook length is due to intermediate host origin. These data suggest that hook length measurements of adult worms from naturally infected definitive hosts could be used to determine the intermediate host species from which infection was acquired, with a single-trait accuracy (correlation between trait morphology and correct host assignment) of 0.70-0.79. I discuss ways by which accuracy of assignment may be improved.

T49

The Role of Mutation in Evolution and Extinction

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A broad overview will be presented on our empirical and theoretical work on spontaneous deleterious mutations. Data from species ranging from *Daphnia pulex* to *Caenorhabditis elegans* to *Arabidopsis thaliana* support the idea that on the order of 0.1 to 1.0 new deleterious mutations arise per genome per generation in eukaryotes, with the average mutation causing an approximately 2% decline in fitness. Such mutation pressure has important implications for the viability of populations, especially those that are small (endangered species) and those for which selection pressures are temporarily relaxed (humans, and species in captive breeding programs). Theory also suggests that the efficiency of selection against deleterious mutations is particularly reduced for genes residing in nonrecombining portions of the genome, a prediction that is well supported by comparative studies on aspects of molecular evolution in organelle and nuclear genomes of the same species. Evidence will be presented that the vast majority of segregating variation for quantitative characters in natural populations may simply represent transient cohorts of deleterious mutations enroute to elimination by natural selection. If this interpretation is correct, then conventional measures of variation, such as heritabilities, may be highly unreliable indicators of the adaptive potential of populations. The talk will conclude on a more optimistic note --- an overview of a new model which demonstrates how deleterious mutations accumulating in duplicate genes can promote the origin of evolutionary novelties and perhaps play a role in the process of speciation.

T50

RAPD variation in Banksia cuneata (Proteaceae), a rare and endangered species.

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Random amplified polymorphic DNA (RAPD) markers were investigated as a tool for estimating genetic diversity in all ten known populations of *Banksia cuneata*, a rare and endangered species. B. cuneata has a restricted geographic distribution in south western Australia, totalling about 550 plants, in an area of approximately 90 km 2. Estimates of genetic diversity ranged from 0.65 - 0.74, which is high for a rare and endangered species. Analysis of molecular variance (AMOVA) was used to partition RAPD variation within and between populations. Nearly all of the variation was attributable to individuals within populations, indicating a lack of population divergence. It is suggested that the combination of bird pollination and high outcrossing rates in *B. cuneata* maintain genetic diversity and cohesion between the populations.

T51

QTL studies of growth and fertility in mouse

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F_1 females from divergent inbred strains, C57BL/6J (small body size & low fecundity) and Inbred Quackenbush Swiss 5 (IQ5) (large body size and high fecundity) were backcrossed to either C57BL/6J or IQ5 males. Litter size (number of pups born alive) and body weight (mating weight and post-partum weight after four consecutive litters) were recorded for the female backcross progeny.

Initially, microsatellite markers were selected from chromosomal regions where other mouse studies had indicated the presence of QTLs. In addition, markers adjacent to the *estrogen receptor* locus, shown to be a QTL for litter size in pigs, were examined. Preliminary analysis showed the presence of only one region on chromosome 4 influencing variation in both body weight and litter size.

Subsequently with the availability of an automated genotyping facility, a genome scan has been commenced. Over fifty markers spaced at approximately 30cM are progressively being genotyped, with genotyping completed for twelve and in progress for the remaining 39. Results from a full interval analysis to detect QTLs for body weight and litter size will be presented.

T52

Molecular variation in the heat shock genes of *Drosophila*: a search for environmental associations

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Strains of *Drosophila melanogaster* show heritable variation for tolerance to various environmental stresses - stresses that are of likely ecological significance. Often positive associations are found between tolerance levels and particular climatic regions where such stresses are frequent. In an attempt to find some of the underlying genes involved in this variation we are examining polymorphic variation in candidate heat shock genes. In particular we focus on *hsr-omega* and *hsp-68*, two genes that have been shown to respond to laboratory selection for adult resistance to a knockdown heat stress. Allelic variation is detected using PCR to amplify a part of each gene which is characterised for sequence variation by denaturing gradient gel electrophoresis (DGGE). Here we report the development of a DGGE method to expediently estimate allele frequencies at the *hsr-omega* locus and we look for temporal, spatial and climatic associations in natural populations. Marked allelic frequency variation among populations along the eastern coast of Australia suggests this locus contributes to a phenotype that is subject to differential natural selection.

T53

Hierarchical analysis of genetic variation in the pacific blue-eye *Pseudomugil signifer* (Pseudomugilidae) in northern Queensland, Australia.

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Dendritic river systems provide a useful opportunity to study the consequences of varying levels of isolation and gene flow on population genetic structure. The pacific blue-eye *Pseudomugil signifer* is a small freshwater fish common to coastal drainages of eastern Australia and some offshore islands. Using a hierarchical sampling design, levels of genetic divergence within and among populations from five drainages in northern Queensland were estimated by cellulose acetate electrophoresis. Analyses using *F* statistics revealed extensive genetic differentiation among drainages, with less within and between subcatchments within a drainage. This is concordant with the degree of physical isolation between populations and suggests that dispersal is restricted among drainages. Other results indicate that a population in the South Johnstone subcatchment may be introduced, and the relatively high degree of similarity of the Mulgrave/Russell Rivers and Barron River populations raises questions about possible historical connections between these systems.

T54

Pesticide Resistance - Studies in Microevolution

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Studies of adaptation attempt to provide a mechanistic understanding of the role of natural selection during evolution. However, in many systems it is not possible to unambiguously identify the selective agent, a difficulty overcome in studies of the evolution of pesticide resistance. Such studies have further advantages. Physiological and biochemical differences between phenotypes are frequently known. Selection coefficients may be large enough to generate rapid changes in allele frequency in natural populations but, at lower pesticide concentrations, may also be sufficiently small to enable subtle interactions between genotypes to be investigated. These differences enable components of fitness to be measured in both the field and the laboratory and related to genetic change over experimentally tractable time scales.

Thus, the evolution of pesticide resistance provides the opportunity to define the precise environmental conditions that determine the genetic and molecular bases of adaptive change and therefore to make a significant contribution to fundamental studies of the influence of selection during microevolution. Furthermore, as will be argued in this paper, pest- and resistance-management strategies are most likely to be effective when based on a foundation of ecological and evolutionary genetics (McKenzie, 1996).

McKenzie, J.A. (1996). Ecological and Evolutionary Aspects of Insecticide Resistance. R.G. Landes/Academic Press.

T55

Mapping the distribution of the telomeric sequence (T_2AG_3) in rock-wallabies, *Petrogale* by fluoresence *in situ* hybridization (FISH): The *xanthopus* and the *lateralis/pencillata* groups; plus a comparision with the pademelons, *Thylogale* and the swamp wallaby, *Wallabia bicolor*

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School of Biological Sciences, Macquarie University, North Ryde 2019

The sequence $(T_2AG_3)_n$ has been found to be the predominant telomeric sequence in all examined vertebrate species. Non-telomeric sites of this sequence have been shown to arise by tandem and centric fusions in chromosomes from some species, including the Indian muntjac, giraffe, opaki and Venezuelan gekkos. However, in some cases the$(T_2AG_3)_n$ sequence has not been detected at known fusion sites, such as in the mouse and the short-tailed shrew. *Petrogale* (rock-wallabies) are chromosomally diverse and their pattern of chromosome evolution is well established. The rate of chromosome evolution within *Petrogale* is variable, with three distinct groups being recognised. The distribution of the $(T_2AG_3)_n$ sequence in chromosomes from the *lateralis/pencillata* group and the *xanthopus* group was examined by FISH and compared with the distribution of the telomeric sequence in chromosomes from 3 *Thylogale* species, which retain the presumed macropodid ancestral karyotype and *Wallabia bicolor,* a macropodid with a highly derived karyotype characterised by extensive chromosome fusions and other rearrangements.

T56

Gene mapping in domestic animals

Chris Moran and Frank Nicholas

Department of Animal Science, University of Sydney NSW 2006

In the past decade, the gene maps of domestic animal species have developed from virtually a zero base to become relatively dense resources for the identification of economically important quantitative trait loci (QTL). Highly informative type II (anonymous) loci, particularly microsatellites, have played a major role in the development of useful linkage maps and are now being actively used in several species (cattle, sheep, pigs and chickens) for identification of QTL. However many type I (known function) markers are also included on the domestic animal maps. The positioning of these type I markers on linkage and physical maps, together with the results of ZOO-FISH, has resulted in increasingly precise comparative maps of domestic animal genomes relative to human and mouse maps. An extremely important practical outcome of the availability of good comparative maps is the ability to identify "comparative positional candidate loci" for any QTL identified in a domestic animal, by mining the outcomes of the vast investment of resources and effort in human and mouse mapping. If you know where the domestic animal QTL is located in humans, you can eliminate a huge number of potential candidate loci and refine the list of candidates to a manageable number from this restricted region. This will hopefully eliminate much of the need for positional cloning. Another important and intriguing outcome of QTL mapping in domestic animals is the increasing recognition of "cryptic QTL alleles" or transgressive segregation. These terms describe the origin of an allele whose phenotypic effect is opposite to what would be expected from the overall phenotype of the parental strain of origin. In pigs for example, alleles for leanness have been found in an excessively fat parental breed. Such discoveries provide compelling evidence for the preservation of rare and endangered but uncompetitive breeds of domestic animals.

T57

Towards Molecular Breeding of Forest Trees for Quantitative Traits

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Tree breeding is characterised by long breeding cycles and selection for phenotypic traits which are nearly all quantitatively inherited. Field-based assessment after several years is the norm for commercially important traits such as growth, form, branching, wood properties, pulp yield and disease tolerance. For a number of species and breeding programs of forest trees throughout the world molecular marker technologies are being used to characterise and locate QTL controlling these traits.

With potentially unlimited DNA markers framework genetic linkage maps have been constructed in *Eucalyptus nitens*, *Pinus radiata* and *Acacia mangium*. Within pine and eucalypt genera the extent of synteny between species genomes is being established with the hope of developing generic maps. The maps are being used to determine regions of the genome controlling important commercial traits. Using codominant markers the mode of gene action of these QTL can being determined and tested. Examples will be drawn from, *E. nitens* and *E. marginata*. Future directions of of research and potential applications to breeding programs will be discussed.

T58

Towards an understanding of the molecular genetic basis of odorant and pheromone reception in insects: the pheromone binding proteins of the pest leafroller, *Epiphyas postvittana*

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Odorant binding proteins are essential elements in the highly sensitive and specific semiochemical detection system used by insects to detect food, oviposition sites, and potential mates. In many male moths specialised sensory organs (sensilla) in their antennae are tuned to respond to components of the sex pheromone blend produced by females. Pheromone molecules diffuse through wax-filled pores into the aqueous lumen of these sensilla where they are sequestered by pheromone binding proteins (PBPs). These proteins are thought to facilitate the transport of pheromone molecules to membrane-bound receptors.

The odorant binding proteins of the leafroller moth, *Epiphyas postvittana* were isolated from homogenised antennae by size exclusion and ion exchange HPLC. Five odorant binding proteins were detected by native PAGE (14 - 17 kDa) and their N-terminal sequence obtained. The two distinct male specific proteins showed similarity in primary and secondary structure to other lepidopteran PBPs. Oligonucleotide primers, designed to their N-terminal sequence and a conserved C-terminal region were used to amplify the *E. postvittana* PBP gene from cDNA. Two approaches have been initiated to determine residues involved in pheromone binding and specificity. One involves expression of *E. postvittana* PBP alleles in baculovirus to allow binding and structural studies of these proteins and the second is a comparative approach among PBPs of some of New Zealand's native leafroller species.

T59

Phylogeography, outbreeding depression and genetic guidelines for translocations

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Wildlife management in Australia and elsewhere is making increasing use of translocations as a tool for restoring endangered species, but there is considerable uncertainty about how to use genetic information to guide translocations. For animal species, mitochondrial gene trees overlaid on geography can provide insights into current and historical gene flow and biogeographic history. As a component for defining Evolutionarily Significant Units, such "phylogeographies" might also be used to guide translocation programs. However, we could have more confidence in this approach if the relative importance of differential adaptation along environmental gradients vs. historical isolation in determining the extent of outbreeding depression was understood more clearly. This talk will review the conceptual issues and outline our current research on two species complexes, the Drosophila serrata group and rainbowfish (*Melanotaenia eachamensis*).

T60

The Thevenard Island mouse - taxonomic and conservation implications from mitochondrial DNA sequence variation.

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Until recently, the conservation significance of an island population of the Short-tailed mouse *Leggadina lakedownensis* remained ambiguous. Individuals were genetically isolated and larger in body-size, and yet showed no allozyme variability compared to their mainland counterparts. The level of genetic differentiation between the island and mainland populations of *L. lakedownensis* was determined using mitochondrial DNA Control Region sequencing. Temperature gradient gel electrophoresis using outgroup heteroduplex analysis detected eight haplotypes. These were sequenced for 362 base-pairs, and a parsimony analysis identified two robust lineages within *L. lakedownensis*: a northern lineage comprising samples from the Kimberley region to Kakadu National Park, and a western lineage comprising samples from Thevenard Island and the adjacent Pilbara region. Conservation and taxonomic implications arising from this phylogeny are discussed.

T61

Molecular characterization of mutations at the *lozenge* locus of *Drosophila melanogaster*

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[2]*Department of Genetics, University of Melbourne, Parkville 3052, Victoria, Australia*

In the developing retina of *Drosophila melanogaster, lozenge* (*lz*) mutants exhibit defects in the recruitment and differentiation of cone cells, pigment cells, and photoreceptor neurons. The locus maps to position 1-27.7 (8D8-8D9) and has been divided into four sub-loci spanning a distance of 0.14 mu. Complementation studies reveal two cistrons, A and B, with respect to eye phenotype but one for antennae (Batterham et al., 1996). Cistron A alleles affect eye and antennal morphology and map to the spectacle sub-locus. Cistron B alleles map to each of the four sub-loci and affect several phenes including eyes and antennae. We are mapping various *lz* alleles with respect to a *lz* transcription unit characterized by Daga et al. (1996), the product of which is a transcription factor with homology to the Acute Myeloid Leukemia 1 (AML1) protein of humans. *lz* has been shown to regulate a number of genes critical for normal eye development including *seven-up* and *Bar* (Daga et al., 1996; Crew et al., 1997). Several cistron B mutations have been mapped within the Daga transcription unit. Two cistron A mutants have have deletions of the second intron. Models for the molecular basis of complementation at the *lz* locus will be presented.

Batterham, P., Crew, J. R., Sokac, A. M., Andrews, J. R., Pasquini, G. M. F., Davies, A. G., Stocker, R. and J. A. Pollock (1996). Genetic analysis of the *lozenge* gene complex in *Drosophila melanogaster*: adult visual system phenotypes. J. Neurogenet 10: 193 - 220.

Crew, J. R., Batterham, P., and J. A. Pollock (1997). Developing compound eye in *lozenge* mutants of *Drosophila*: *lozenge* expression in the R7 equivalence group. Dev Genes Evol 206: 481 - 493

Daga, A., Karlovich, C. A., Dumstrei, K., and U. Banerjee (1996). Patterning of cells in the *Drosophila* eye by Lozenge which shares homologous domains with AML1. Genes Dev 10: 1194-1205

T62

Unusually fine-scale genetic structuring found in rapidly speciating Malawi cichlid fishes

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Mechanisms behind the explosive radiation of over 500 cichlid fish species from a single founding population in Lake Malawi during the last 700,000 years are poorly understood. Recent studies have suggested that the degree of population subdivision among the habitat patches within the lake may be responsible, but the evidence has been circumstantial: lack of a dispersal stage in haplochromine cichlids; genetic and colour variation among populations separated by large-scale geographical barriers; and fluctuating lake levels. One reason for the rapidity of speciation in these fishes may be that population subdivision is on a much finer scale than previously thought. Here we quantify the level of population subdivision and estimate migration at a scale of 700-1,400 m, in order to investigate whether cichlid populations are sufficiently isolated from each other for allopatric divergence and perhaps speciation to take place. Using six microsatellite loci, we demonstrate the existence of highly significant genetic differentiation between subpopulations on adjacent headlands in each of four rock-dwelling haplochromine cichlid species. Our results suggest that these fish populations are divided into thousands of subunits among which genetic divergence is currently occurring and that this may provide unprecedented opportunities for allopatric speciation.

T63

Enforcement of worker sterility in honey bee colonies

Ben Oldroyd and Claire Montague

School of Biological Sciences, University of Sydney, N.S.W. 2006

Worker honey bees are capable of laying eggs, and often do so in queenless colonies. Although these eggs are unfertilised, they give rise to normal haploid males. However, most workers in most colonies enjoy very little personal reproduction. An attractive solution to this conundrum is the 'worker policing hypothesis'. This idea suggests that, because eggs laid by fellow workers have low relatedness, worker sterility is maintained by reciprocal control of worker egg production. Any eggs that are laid by workers are immediately eaten by other workers, thus greatly reducing the attractiveness of doing so in the first place. Worker policing is very effective, and in colonies with a queen, workers contribute < 0. 1% of males.

By advertising widely in beekeeping journals, we located a colony in which worker policing had failed. Using microsatellites, we determined that male brood in this colony originated from worker-laid eggs. Moreover, of the 12 worker subfamilies present in this colony, only one laid eggs. We conclude that one of the males that mated with the queen of this colony passed a genetically-determined ability to his offspring to evade worker policing. A second colony showing aberrant worker egg-laying behaviour again showed that one subfamily dominated in egg production. When this colony was dequeened, worker egg production developed much faster than in three control colonies. A single subfamily dominated in egg production when the colony was queenless, but this was not the same subfamily as dominated when the queen was present. The significance of these results for the evolution and maintenance of worker sterility will be discussed.

T64

Undermethylation, invasion and amplification of retroviral elements in an interspecific mammalian hybrid

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The epigenetic alteration of genomic sequences by DNA methylation is believed to be a major regulatory force in gene expression and genome evolution. It has been proposed that methylation evolved as a response to the incorporation and spread of selfish elements, such as retroviruses. Such a host defense mechanism would employ methylation as a means to inactivate transcription-mediated amplification of these parasitic elements, thereby protecting the genome from deleterious mutations.

We propose that an extension of the host defense theory of methylation patterns in the genome may explain hybrid dysgenesis and genome remodelling by causing the expression and mobility of otherwise inactive mobile elements in hybrid genomes. Our studies of a marsupial interspecies hybrid male (*Macropus eugenii* x *Wallabia bicolor*) has uncovered inter genome-mobility, insertion *in trans* and large scale amplification *in cis* of at least two genetic elements, one of which has been characterized as a retroviral element. Closer examination provides clear evidence that this element is unmethylated in the hybrid. However, it is methylated and in low copy number in only one parent species, *Wallabia bicolor*, while absent from the other parent, *Macropus eugenii*. Such transposition events, which cause genome remodelling and hybrid dysgenesis, may ultimately reinforce reproductive barriers and lead to speciation.

T65

Testing a genetic structure of blood-injury fears

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Techniqes in quantitative behaviour genetics were used to examine the extent and nature of the heritability of fears of blood, injury and injections in 659 twin pairs who completed questions concerning fear and fainting around blood, injury and injections. Univariate analyses indicated that blood fears were best explained by a model assuming uniqueenvironmental plus additive genetic and/or shared environmental variables.

Multivariate genetic analyses indicated that the variance in blood fears were principally attributable to unique environmental events specific to blood fears and additive genetic factors shared with fainting. The data will be discussed in the context of models of blood-injury phobia that identify the need to consider separate genetic and environmental etiological mechanisms for fear and fainting.

T66

The effect of relatedness on helping behaviour in the cooperatively breeding bell miner, *Manorina melanophrys*

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The bell miner has a social system atypical of cooperative breeders as individual helpers may provision nestlings at a number of different nests belonging to different breeding pairs. Individuals can act as either major or minor helpers, varying the amount of aid they give to particular breeding pairs. The theory of inclusive fitness predicts that in order to perpetuate their own genes through raising relatives, nonbreeding helpers should, on average, be more related to the individuals they help than they are to others in the population. The bell miner offers a unique system with which to investigate the effect of relatedness on helping behaviour in a cooperatively breeding species.

A key element in the evolution of altruistic behaviours by kin selection is high relatedness within social groups. We have used DNA microsatellite data to estimate levels of relatedness between helpers, breeders and nestlings within various subdivisions of bell miner colonies. The relatedness of helpers to the breeding male has a significant effect on the provisioning behaviour of helpers. Relatedness between individuals attending nests is significantly higher than the average level of relatedness within a colony. Among the contigent of helpers at a nesting attempt individuals who are most closely related to the breeding male tend to give the most aid. These results suggest an important role for kin selection in the evolution and maintenance of cooperative breeding in this species.

T67

The control of genes - *in planta* and in commerce

Jim Peacock

CSIRO Plant Industry

The first transgenic crop, cotton containing a *Bt* gene, has been grown and harvested in Australia - 30,000 hectares with a market value of approximately $150 million. Next year double this amount will be grown and soon other transgenic crops and food products will enter our market place. The build-up to commercial operations through the various regulatory controls was handled well in this country but **Control** is still the operative word. Control of the potential for pest resistance is the main concern. In this first year of widespread cropping the control of gene action in the plant has also been a focus; our research data have emphasised that we have still a lot to learn about the nuances of the interactions of the transcriptional and translational machines with plant developmental stages and with environmental conditions confronting the plant. But there are some exciting developments. I will discuss some of our lab's recent findings on coordinate gene control in a plant's response to low oxygen levels, one of the major environmental stresses encountered both in agriculture and in nature.

T68

P-elements in *Lucilia cuprina* - the final chapter

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The P-element of *Drosophila melanogaster* has been used for well over a decade as a gene transformation vector for this species, enabling huge advances in genetic analysis, mutation induction and detection, and gene cloning. Unfortunately, the P-element is functional essentially only in *D. melanogaster*. We have therefore sought P-like elements in *Lucilia cuprina*, the Australian sheep blowfly, in an attempt to provide a transformation vector for this important pest species.

Three distinct subfamilies of P-like elements (Lu-P1 Lu-P2 and Lu-P3) have been characterised from *L. cuprina*, however none appears to be entirely structurally complete. The two variants of the Lu-P1 element represent near-intact transposase genes, as does one of the Lu-P2 elements, however, none contains inverted terminal repeats. Another clone contains two apparently duplicated Lu-P2 elements in opposite orientation, both of which contain a variety of internal deletions and other defects. Lu-P3 is also represented by two apparently duplicated elements, this time in direct orientation, again with various defects. None of these elements appears to be capable of producing a functional transposase transcript, and the apparent lack of any terminal inverted repeats renders them immobile. *In situ* chromosome data and transcriptional analysis data will also be presented.

PCR amplification of P-like sequences containing various defects from other Calliphorid species suggests that P-elements are of ancient origin in the Diptera, and have probably been non-functional relicts in the Calliphorid lineage for a considerable period of time. These findings suggest that transposons other than P-elements are more likely to provide the basis of transformation systems for non-drosophilid insects.

T69

Genetic Structure of Montane Flora from the Wet Tropics of North Queensland

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Seven species of mountain-top restricted plants were collected from five major mountain tops in the wet tropics of north Queensland. The peaks range in altitude from 1026-1615m and host a distinctive montane vegetation type. Allozyme electrophoresis was used to analyse genetic variation in these species. Allele fixation occurs at different sites for several species, for example *Leptospermum wooroonooran* showed complete fixation at the only variable locus. The high levels of fixation may be attributable to genetic drift. In addition, some species have allelic variants at a site which do not occur elsewhere. Levels of gene flow are very low between populations, even for species such as *Agapetes meiniana* which are presumed bird-dispersed (Nm=0.02). The small within-population variation and the emergence of independent evolutionary lineages on each mountain for some species highlights the conservation significance of each mountain-top.

T70

Queensland *Euastacus* (Spiny Mountain crayfish): Dispersal Capabilities and Evolutionary Relationships

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Euastacus Clark is a genus of endemic, freshwater crayfish. There are fifteen species described from Queensland.They occur in rainforest streams on isolated mountaintops along the east coast. This project is examining the dispersal capabilities of selected species and the phylogenetic relationships among species. Dispersal capabilities are being assessed at two levels: 1) capacity for dispersal between mountains and 2) the capacity for dispersal between streams from different catchments on the same mountain. The dispersal capabilities of *E. robertsi* and *E. fleckeri* are being assessed. Both of these two species are endemic to the Wet Tropics and are of high conservation significance. Allozyme and mtDNA results indicate that dispersal is limited between mountains and even between streams on the same mountain where there is a lack of appropriate habitat (cool, rainforest streams). The implications of these findings for conservation management will be discussed. The molecular phylogeny generated from mtDNA 16s sequence data suggests that this group shared a common ancestor, with speciation probably occurring during the Pliocene or Miocene. The possible origins of the ancestor of this group and possible modes of speciation (e.g. vicariance or stepwise colonisation) will be discussed, especially in relation to the dispersal capabilities of present *Euastacus*.

T71

Comparative phylogeography of bettongs and bandicoots in the Wet Tropics

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The Northern bettong, Bettongia tropica, is one of the most endangered species in the Wet Tropics of North Queensland with only three remaining isolated populations. It is currently found in wet sclerophyll forest within a few kilometres of rainforest but what limits its current distribution and whether the species was in low numbers prior to European settlement are unknown. As the Northern bettong is currently closely associated with rainforest, it was hypothesised that it may have been restricted to the margins of remnant rainforest fragments during contractions of rainforest in the late Pleistocene. Northern brown bandicoots, Isoodon macrourus, are common and sclerophyll generalists and so might not be expected to show the same degree of fragmentation. The dispersal abilities of both species are little understood and more information on local scale population structure of Northern bettongs is necessary for management.

MtDNA control region sequence was obtained from sixty-six bettongs and seventy-eight bandicoots from five populations in the Wet Tropics: these represent two proposed historical Pleistocene refuges and three locations spaced 7 km apart within one 'refuge'. In both species there was a large amount of local scale geographic structure, but this was not seen at the broader geographic scale and so the basic hypothesis of diversification via rainforest refuges was not supported. There is a surprising amount of genetic diversity within B. tropica given it's current small population size. Local scale distributions of alleles indicate some dispersal and this, in combination with demographic data on individual movements and comparison with Northern brown bandicoots, is used to infer the previous structure and population size of the Northern bettong as well as to determine current local population structure in this endangered species.

T72

Recombination and new rust resistance specificities

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In the gene for gene rust resistance system, plant resistance occurs when a product of a rust resistance gene recognises the product or function of a rust avirulence gene. Evidence is accumulating that new rust resistance specificities can arise de novo as a consequence of rearrangements with in the resistance gene.

The maize gene *Rp1-D* specifying resistance to the rust *Puccinia sorghi* has been cloned using a PCR based approach based on Nucleotide Binding Site conserved amino acid motifs and also by transposon tagging. The transposon tagged mutants and revertants provide a genetic confirmation of the identity of *Rp1-D*. The *Rp1-D* specificity resides in one member of a small gene family located at the *Rp1* locus.

Genes in the *Rp1* complex including *Rp1-D* are unstable. In this case, about 1/15000 gametes from the *Rp1-D* parent give rise to susceptible progeny. In 25 cases, all involved the deletion by unequal crossover of some members of the gene family. There is evidence for cross over and non crossover (gene conversion) events. In four cases, crossover events produced variants with new resistance specificity providing resistance against rust races to which the parental alleles were susceptible. An understanding of mechanisms of generating new specificity in vivo may permit in vitro engineering for novel resistances.

T73

The *Guest* element of *Neurospora crassa*.

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Guest[1] is a Class II transposable element present in about 30 scattered copies, ranging in size from ~100 to 2000 bp, in laboratory and wild strains of *Neurospora crassa*. All characterised *Guest* iterations are deletion derivatives of a progenitor element possibly no longer active in this species.

Guest has the hallmarks of a Class II transposable element. It is flanked by a target site duplication, GTA, and has a terminal inverted repeat (TIR). The TIR varies from 20 to 100 bp in the five iterations sequenced and although unlike that of any other known element, has homology to sequences found in *N. sitophila* and *N. intermedia*. Homology searches within the fragmentary internal sequences available reveal functional sequence motifs consistent with a DNA inter-mediate cycle of replication that have homology to other Class II elements from filamentous fungi. Although these are scrambled in the smaller iterations, a large *Guest* iteration now cloned has a CAAAT promoter and a consensus translat-ional start site in the correct orientation, suggesting it has coding potential. More sequence information is required to determine if there are open reading frames.

Neurospora has a mechanism, repeat-induced point-mutation (RIP) that is active in the sexual cycle during the expansion of dikaryotic tissue preceding karyogamy and meiosis, which inactivates duplicated sequences by numerous transition mutations of cytosine to thiamine, particularly in CpA dinucleotides. The activity of extant *Guest* iterations has not yet been assessed. If *Guest* is still active within any of its hosts, the mechanism by which it escapes gene silencing by RIP is open to study. If *Guest* is now silent in all strains, its remnants will provide a revealing record of the mode of inactivation.

1. PJ Yeadon and DEA Catcheside (1995) MGG 247: 105 - 109.

T74

Evolution of polyploid frogs in the genus *Neobatrachus*.

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Polyploidy is one route to sympatric speciation. Ueda experimentally produced triploids and tetraploids of the frog*Hyla japonica*. There were graded reductions of pulse rates in male call, the signal used for mate attraction. In the north American frog species pair, *Hyla chrysoscelis* and *H. versicolor*, phylogenetic studies indicate multiple origins of the tetraploid *H. versicolor*. However, in all cases the terraploid has an almost identical, reduced pulse rate. Field and laboratory data therefore suggest a causal relationship between polyploidy and call structure. This talk will compare patterns of call structure evolution in tetraploid *Neobatrachus* with available phylogenetic data. The expected patterns of pulse rate reduction do not always occcur in this genus. Obligate changes in call structure, and therefore potential premating isolation, may not be associated with tetraploidy. This generates additional problems for the establishment of tetraploid forms interacting with sympatric diploid progenitors leading to the possibility of call strucure evolution by reinforcement.

T75

Australian distribution of fruit flies (Diptera: Tephritidiae) attracted to cue lure: microsatellite studies of *Bactrocera tryoni* outbreak flies

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This is the first widespread survey of tephritid fruit flies attempted in a single period. It forms the basis for microsatellite endemic population studies. 1,471 cue lure traps caught 17 species. Extensions to previously recorded geographical ranges were detected for seven species: *Bactrocera tryoni*, *B. neohumeralis*, *B. frauenfeldi*, *B. aeriginosa*, *Dacus absonifascies*, *D. aequalis* and *D. newmani*. The traps also unexpectedly caught several *B. cacuminata*, and also both males and females of *Dirioxa pornia* and *Ceratitis capitata*. The geographical variation in the relative abundance of *B. tryoni* and *B. neohumeralis* in the region of their co-occurrence was in substantial agreement with earlier estimates. The regional variation in the abundance of *B. tryoni* in the eastern states was in accordance with the predictions of a published bioclimatic model. Furthermore, the spread of this species to several locations in the Northern Territory is recorded for the first time.

This sample, and subsequent samples collected from the same geographic range in the last four summers, are being analysed for microsatellite variation to map the population of *B. tryoni*. The microsatellite variability is also being used to indicate whether outbreak flies have over-wintered in an area or migrated into it, and to show the likely region of origin of outbreak flies.

T76

Plant conservation genetics - the practical experience

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The resources available for conservation of rare flora are often limited given the large number of taxa involved. As a result, the principal aim of conservation geneticists participating in recovery programs is to define specific goals that lead to practical outcomes. Following definition of these goals, the best approach to be taken can be devised while considering the many restrictions that apply to rare species work. Such restrictions and limitations will affect the selection of techniques to be used in the project. Many techniques are available, each with various benefits and drawbacks affecting their suitability depending on the circumstances.

Some of these techniques and their direct applications to rare flora conservation projects will be reviewed through practical examples. The conclusions drawn clearly demonstrate that practicality and reliability need to be emphasised in conservation genetics. Often a combination of simple techniques satisfies these requirements.

T77

Evolutionary history of *Daphoenositta*: How useful is mitochondrial DNA?

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The varied sittella (*Daphoenositta chrysoptera*) complex presents several intriguing evolutionary questions. While the taxonomic affinities of the group have historically been the source of confusion, it is the unique distributional pattern of the Australian taxa which has caused most interest.

Five morphologically distinct taxa are distributed peripherally around mainland Australia and intermediate forms occur where their ranges are parapatric. These hybrid "zones" converge in central Queensland where morphological mosaics have been recovered. The observed pattern has been explained both in terms of a radiation (polytomy) and as a strict, hierarchical tree. Given the apparent confusion surrounding the origins and relationships among the extant taxa we evaluated the utility of two mitochondrial markers to recove

T78

Expression of dominant-negative versions of MSL-1 causes male-specific lethality in *Drosophila* due to inhibition of dosage compensation

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The finding that transcription coactivators such as CBP and TAFII250 are histone acetyl transferases has highlighted the importance of histone acetylation and gene expression. Dosage compensation (equalisation of X-linked gene products) in the fruit fly *Drosophila melanogaster* is an excellent model system for studying how histone acetylation is controlled. Dosage compensation involves the binding of a group of four proteins called the Male-Specific Lethals (MSLs) to hundreds of sites along the length of the male X chromosome. The MSLs in turn recruit MOF, a histone acetylase. We are interested in studying the role of one the MSLs, MSL-1, in dosage compensation.

The approach we have taken involves over-expressing different regions of MSL-1 in transgenic flies. Males which cannot dosage compensate die. Thus, we expected that high levels of expression of an MSL-1 domain may cause male-specific lethality due to its binding of a factor required for dosage compensation. We found that high levels of expression of two domains (one epitope tagged) caused males to die. Genetic analyses indicates that one domain interacts with MSL-2 but the other domain does not appear to interact with any of the known MSLs (e.g. males cannot be rescued by co-expression of high levels of any of the other MSLs). We are currently testing if either domain binds to MOF. We are also carrying out screens for dominant mutations which either enhance or suppress lethality due to expression of a dominant-negative version of MSL-1. Such screens may lead to the identification of new factors which are required for dosage compensation.

T79

Chromosomes, development and climate: latitudinal clines in the grasshopper *Caledia captiva* (Orthoptera:Acrididae)

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Chromosomal variation within the Moreton subspecies of *Caledia captiva* involves the transposition of the centromere from terminal (telo/acrocentric) to medial (metacentric) locations on all of its 24 chromosomes. At each end of its distributional range, covering 1500km along the east coast of Australia, populations show fixed differences in chromosome structure. Between these two extremes, populations are characterised by complex chromosomal polymorphisms that take the form of latitudinal clines along which the entire complement of chromosomes changes gradually and systemically from metacentric to acrocentric. To date over 600 different chromosomal rearrangements have been identified. Using a series of mtDNA, rDNA and allozyme markers, we have previously shown that gene flow is uninterrupted between populations along the cline suggesting that the establishment and maintenance of these concerted patterns of chromosomal change has involved selective rather than stochastic events. Moreover, we have also revealed that chromosomal change is associated with significant changes in embryonic development time. Development time along the cline gradually decreases as a result of the fourfold reduction in the number of 0days available for successful completion of the life cycle and probably represents an adaptive response to seasonality changes with increasing latitude. This unusual relationship between genome organisation, development time and adaptation to seasonality is currently being investigated in the context of its cellular basis (cell cycle times and cell size) using chromosomally divergent populations to determine any causal relationship and its adaptive significance.

T80

Patterns of dispersal and philopatry in the Allied rock-wallaby, *Petrogale assimilis*, using detailed spatial-use patterns and microsatellite markers

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Both demographic and genetic methodologies were used to investigate patterns of philopatry and dispersal in the Allied rock-wallaby, *Petrogale assimilis*. The findings show several important processes of dispersal occuring at the intracolony and between colony scale. Within a rock-outcrop (colony), males are moving from their natal rock home range (RHR) as they reach sexual maturity. Females, however, tend to remain with their mothers. Consequently, females in a subsection of the rock-outcrop show a higher level of relatedness than males habituating the same area. The relative genetic estimates of migration rates between colonies of *P. assimilis* is high. The amount of genetic exchange between these colonies may be sufficient to maintain the high levels of genetic diversity observed in subpopulations. In addition, the talk will also discuss the management and conservation implications for *Petrogale* secies.

T81

Sex-specific expression of the *Bactrocera tryoni* gene *doublesex*

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In the sex determination pathway of *Drosophila melanogaster*, *Sex-lethal* (*Sxl*) has been identified as the key binary switch. Homologues of this gene have been reported in other insect species; however sex-specific expression of this gene appears to be limited to drosophilids. The *doublesex* (*dsx*) gene of *D. melanogaster* is the last gene in the heirachy of genes that control somatic sexual differentiation. The sex specificity of the proteins is brought about by differential splicing of the pre-mRNA which results in products each with a common amino terminus and a sex-specific carboxyl terminus. In females this splicing is activated by the binding of the protein products of the *transformer* (*tra*) and *transformer*-2 (*tra*-2) genes to 13 nucleotide repeats in the non-coding region of exon 4. Male-specific splicing is the default process, in the absence of functional TRA protein. Two 3' RACE fragments of 1.4kb and 1.85kb, isolated from adult *B. tryoni* RNA, show a significant degree of homology at the amino acid level to the female-specific and male-specific transcripts of *D. melanogaster* respectively. Northern blot analysis confirms that these fragments represent a female-specific and male-specific transcript expressed in the adult. Analysis of the 3' non-coding region of the putative female transcript has identified four 13 nucleotide repeats which are 8/13 bases identical to the *tra*/*tra*-2 recognition sites found in exon 4 of *dsx* in *D. melanogaster*. This would suggest that homologues of the *tra* and *tra*-2 genes also exist in *B. tryoni*. We propose that the pathway is the same from the bottom up, despite a difference in the initial sex-determination signal — the X:A ratio in *D. melanogaster* and a dominant male-determiner on the Y-chromosome in *B. tryoni*.

1. Bopp, D., Calhoun, G., Horabin, J. I., Samuels, M. and Schedl, P. (1996) *Development* 122, 971-982; **2**. Burtis, K. C. and Baker, B. S. (1989) *Cell* 56, 997-1010. **3**. Inoue, K. Hoshijima, K., Higuchi, I., Sakamoto, H. and Shimura, Y. (1992) *Proc. Natl. Acad. Sci. USA* 89, 8092-8096. **4**. Chen, H-J. and Burtis, K. C. (1993) *Abstracts of the 34th Annual Drosophila Research Conference*.

T82

WebPop - Population Genetics Analysis on the World Wide Web

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The breadth and depth of population genetic studies has expanded dramatically with the incorporation of DNA sequencing and microsatellite technologies, and these data have necessitated the development of many new analytical methods. However, many of these analyses are either not readily accessible to biologists or, if computer programs do exist, they run on a variety of hardware platforms and use a variety of input formats each of which must be learned by the user. What is needed is a single integrated computer package that will allow users to rapidly, thoroughly, and properly analyse their data. We are developing an integrated bioinformatics package, within the framework of the Australian National Genomic Information Service (ANGIS), that will incorporate these new analyses and integrate them into a user-friendly, interactive suite of programs running on any computer that can run popular Web browser software such as Netscape. WebPop will ultimately incorporate all of the modern analyses for determining population genetic parameters, detecting geographic structure, detecting selection and recombination, etc, as well as maintaining flexibility of input and output for linking with other, more restricted, programs. The advantages of a centralised web-based package are (i) accessibility from all common computer platforms, (ii) rapid development using existing WWW technologies at ANGIS, (iii) improvements quickly incorporated and distributed as there is no software to update on the users' computer, (iv) integration into the broader WebANGIS system of databases and sequence analysis tools, and (v) users will be able to share information about methods of analysis.

M.J.D. White Address

T83

Arabidopsis, the green genie

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In genetics, model organisms have played a key role in unlocking the principles of molecular, cellular and developmental biology. After several early moves, *Arabidopsis thaliana* has recently taken off as the geneticists' model plant. This small mustard is a weedy species of temperate regions of Eurasia. Its genome is now tagged, RIed, ESTed and contigged, and large scale sequencing has begun. The challenge now is to understand how the 20,000 or so genes being defined go about assembling their encoded information into the living, transpiring plant.

Morphogenesis is an area that has particularly benefitted from a molecular genetic approach. In *Arabidopsis*, as in *Drosophila*, homeosis has been important. The study of homeotic flower mutants, in which organs develop in inappropriate places, has revealed that their products form an 'ABC' plan of overlapping fields in the developing flower meristem. These combine to control the identity of the four classes of floral organ that arise. The genes encode transcription factors, mostly of the MADS family. Thus the proteins controlling this morphogenetic pathway in plants are different from those involved in segementation in animals, where homeodomain proteins predominate. Mutli-cellularity arose independently in plants and animals after their split around 1,000 million years ago. Thus it seems that differentiation may involve similar principles of combinatorial gene action in each kingdom, although different gene families may be involved.

T84

Microevolutionary processes inferred from spatial autocorrelation of genetic variation within a population of *Hakea carinata*

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Spatial autocorrelation of genetic variation expresses similarity between geographically neighbouring data points. These similarities can arise through forces that differ in space, such as selection, and those that are true autocorrelational phenomena, such as isolation by distance (Sokal *et al.* 1997). These forces can theoretically be distinguished by a combined analysis of spatial autocorrelation and spatial surfaces (Sokal and Jacquez 1991).

This study investigated the genetic structure in one population of a sclerophyllous perennial shrub, *Hakea carinata* (Proteaceae). Consistent and significant spatial autocorrelation across loci suggests that related individuals occur in clusters measuring approximately 50m in diameter. Gene frequency surfaces however differ significantly across replicate loci. This pattern suggests that isolation by distance is the force determining spatial structure in this population. The random force produces uncorrelated replicate surfaces, yet because the spatial process is the same at all loci we expect similar correlograms.

Sokal R.R. and Jacquez G.M. (1991) Evolution **45:** 152-168.

Sokal R.R., Oden N.L. and Thomson B.A. (1997) Biol. J. Linn. Soc. **60:** 73-93.

T85

Extreme genetic localization and divergence in *Euperipatoides rowelli* (Onychophora: Peripatopsidae) revealed by microsatellite and mitochondrial DNA analysis

Paul Sunnucks, Jordan French, Dave Briscoe, Noel Tait and Alex Wilson

Peripatus or velvet worms (Phylum Onychophora) inhabit moist terrestrial habitats including the interiors of rotting logs. Australian species exhibit an extreme degree of local endemism and cryptic speciation, as judged by allozyme analysis. Very high fixed gene differences occur among allopatric populations of the same morphospecies. This genetic differentiation probably reflects the antiquity of the group, and also their extremely low vagility associated with suceptibility to desiccation. Allozyme heterozygosity is extremely low, and most loci are fixed for single alleles within cryptic species. We used microsatellite loci and SSCP / sequencing analysis of a 456 bp region of mtDNA COI to investigate population processes in a 300 individuals of one allozyme species *Euperipatoides rowelli*. Samples were taken over a 38km transect in Tallaganda State Forest (NSW). While the microsatellites had a modest 6-7 alleles per locus, there were 27 distinct mtDNA haplotypes showing up to 15% nucleotide divergence. Both types of genetic marker were highly localized, but this was more true for mtDNA than for microsatellites, suggesting that males perform breeding dispersal more readily than do females. The microsatellite loci showed isolation-by-distance to 10km, and almost complete discontinuity between the ends of the transect. Isolation-by-distance was marked for females but less so for males. This very surprising finding implies that dispersing males are not very successful in achieving reproductive success at their destination, corroborated by other data. Males appear usually to mate near their birthplace. However, microsatellite analysis showed that females typically mate with multiple males, which may help to diversify their offspring. The localization of mtDNA appears to be unusually long-lived: e.g. one clade of 6 haplotypes showing up to 10% divergence was restricted to a few square kilometers. Thus nuclear and mtDNA frequency and mtDNA phylogenetic data all point to extreme and long-term genetic localization, which may help to explain the extensive local endemism in peripatus.

T86

Recombination and chromosome changes induced by P element derivatives in *Drosophila*

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P elements which lack either end are known to be inactive in the presence of P transposase. However activity can be restored if a right-end element on one chromosome is combined with a left-end element at the same site of a homologous chromosome. The result implies that the two ends are capable of finding each other even if they are not physically on the same element. Analysis of the recombinant products reveals that the ends 'excise' as in a normal element, and that two processes are involved in the resolution of the excision event, both of which can lead to recombination: (1) the two ends remain associated as a 'hybrid element' and insert somewhere nearby in the chromosome (Hybrid Element Insertion - HEI), (2) the ends which do not contain P elements are joined through repair and ligation (Hybrid Excision and Repair - HER). Evidence is also presented, obtained primarily by W.R. Engels and C.R. Preston, that the HEI process is the likely cause of recombination induced by single P elements. In this case, the two ends which associate are from sister chromatids rather than from homologous chromosomes. The HEI process leads to novel 'elements' in which a left and right end are both present, but pointing in opposite directions to the ends of a normal element. We report on the levels of activity of such elements as measured by their ability to induce recombination. The use of very closely linked RFLPs has been important in understanding the mechanism of recombination and the role of DNA repair associated with a single P element. These markers were found by surveying a range of wild type strains, from which a set was chosen which differed maximally from the original P element insertion. To date, RFLPs have not been available for end-deleted elements. We describe a method which will allow us to incoporate the same set of markers into crosses involving the end-deleted elements, to confirm details of the HER process.

T87

Mating behaviour of the queenless ponerine ant *Rhytidoponera* sp. 12

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The mating behaviour of the queenless, polygynous ant *Rhytidoponera* sp. 12 was investigated using five highly polymorphic microsatellite markers. Relationships between the sexuals were inferred using sperm DNA isolated from spremathecae of individual gamergates (mated workers). Intracolony relatedness estimates of gamergates fell into two distinct catagories, suggesting that co-existing reproductives were either full sisters or from different matrilines. Mating frequencies in both males and females were also determined, and whilst gamergates are usually monandrous, polyandry can sometimes occur. In both within and between colony analyses, low frequencies of sprem DNA samples from individual gamergates have identical allele frequencies over five microsatellite loci. This strongly suggested that given the opportunities, males could mate with more than one female. *R.* sp. 12 is essentially an outbreeding ant species as indicated from analyses of worker allele frequencies. However, results from microsatellite analyses indicated that matings between males and gamergates that were related often occurred within a colony. The results demonstrated the difficulties of accurately estimating the levels of inbreeding and polyandry using population genetic data in polygynous hymenopteran species, and further confirmed microsatellite markers as powerful genetic tools for the investigation of social insect biology.

T88

Molecular insights into the reproductive biology of an arboreal termite from Jamaica

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Monogamy and inbreeding are often thought to characterise the breeding system of termite societies. However, few studies have employed molecular markers to ascertain either the genetic structure of single colonies or the extent of local inbreeding. This study employs allozyme and mtDNA analysis to investigate the breeding system of *Nasutitermes nigriceps* with respect to the number of reproductives contributing to single colonies, and the level of inbreeding within and among colonies. The majority of the 136 nests examined from three study sites on Jamaica showed patterns of protein polymorphism consistent with their origin from a single mated pair, establishing that monogamy is indeed the predominant mode of reproduction. A small proportion of nests (N=7) had genotypic frequencies suggesting that offspring were not full siblings. The extent to which the variance in allelic frequencies among non-monogamous colonies was less than that among monogamous colonies suggests an average of 3 to 5 reproductives. However, mtDNA analysis revealed that all colonies are restricted to a single matriline indicating that secondary reproductives are recruited from within the natal nest. Wright's (1978) *F*-statistics showed moderate gene flow among sites and the occurrence of inbreeding at a regional scale. However, mating appeared to be random at single sites as the inferred genotypic frequencies of colony progenitors did not deviate from Hardy-Weinberg expectations.

Wrights, S. 1978. Evolution and the genetics of populations. Vol 4: Variability within and among populations. University of Chicago Press, Chicago.

T89

High resolution genetic mapping and mouse YAC library screening for the markers closely linked to the flavivirus resistance locus (*Flv*)

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Resistance to flaviviruses in mice is a dominant genetic trait which is controlled by a single autosomal locus *Flv*. Genetic analysis using different mouse strains and different strains of flaviviruses have revealed the presence of at least three allelic forms at the *Flv* locus conferring susceptibility (Flv^s), resistance (Flv^r) or minor resistance (Flv^{mr}) to flaviviruses. Using backcross linkage analysis we have mapped this locus to distal portion of mouse Chromosome 5 between the anchor loci *rd* and *Gus*. This chromosomal interval spans a minimum 15 cM genetic distance which corresponds to an average of 30 Mb segment of genomic DNA. In an effort to get closer to *Flv* and identify tightly linked loci we have genotyped a number of microsatellites in 1325 progeny of backcross matings (C3H/HeJxC3H/RV)F1 X C3H/HeJ and (BALB/cxC3H/RV)F1 X BALB/c. Two microsatellite markers were identified to be very closely linked to *Flv* (less than 0.1 cM) since no recombinations were detected with *Flv* in 1325 backcross mice. These markers were used further to screen a mouse YAC library (Research Genetics) and 5 positive YAC clones were recovered. Two of them were shown to be chimeric by FISH analysis while the remaining three are currently being used for physical mapping of the region in the vicinity of *Flv*.

T90

Glimpses into the past for soothsayers: a genetic approach to the problems of predicting dispersal and recolonization in hermatypic corals

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Seventy-five percent of the live coral cover on the backreef of Ningaloo Reef, Western Australia, has been eaten by the gastropod *Drupella cornus*. Predictions regarding recolonization of the reef by corals are difficult because the spatial scale of destruction and the dispersal potential of corals with different life histories are variable. Allozyme electrophoresis was used to infer the dispersal and recolonization potential of five species of coral at Ningaloo Reef that differ in their life histories. *Acropora digitifera* and *Acropora aspera* have external fertilization and development, and are expected to disperse widely. *Stylophora pistillata* and *Seriatopora caliendrum* brood their larvae and are expected to disperse less widely than the broadcasters. *Pocillopora damicornis* has mixed development, as colonies brood asexual planulae as well as broadcast spawn. Asexual reproduction should be important for local proliferation, whilst sexual reproduction should be important for dispersal. Despite their contrasting life histories, all five species have broad Indo-Pacific distributions, implying at least occasional widespread dispersal, but how often this occurs is unknown. The two broadcasting species, *A. digitifera* and *A. aspera* had the lowest levels of population subdivision (F_{ST} values: 0.010 and 0.067 respectively) compared to the two brooders, *S. pistillata* and *S. caliendrum* (*FST* values: 0.096 and 0.260 respectively) and the mixed developer *P. damicornis* (F_{ST} values: 0.338 including asexual recruits and 0.190 sexual recruits only) as expected. However, all species, even the two broadcasters, had significant levels of genetic subdivision among samples. Dispersal is not as widespread as previously thought, even among broadcasting species. Recolonization is expected to heavily depend on local recruitment rather than larvae from a wider pool.

T91

The *per* gene in two closely related species of tephritid fruit flies, *Bactrocera tryoni* and *Bactrocera neohumeralis*

Keryn Wilkes and Marianne Frommer

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Two closely-related Australian tephritid fruit fly species, *Bactrocera tryoni* and *Bactrocera neohumeralis*, can be mated in the laboratory to yield viable, fertile hybrids. In the wild, the distribution of *B. neohumeralis* is contained within the distribution of *B. tryoni* and morphological intermediates are identified. However, a definite mechanism of mating isolation based on specific time of mating, persists between the two species. The *period* gene (*per*) in *Drosophila melanogaster* plays a major role in setting up the circadian clock and may be involved in pre-mating reproductive isolation between two *Drosophila* species. As such, it is a good candidate gene to study mating isolation between *B. tryoni* and *B. neohumeralis*. Rapid Amplification of cDNA ends (RACE) was used to isolate a large region of the 3' end of the *per* gene in *B. tryoni*. A PCR-based assay, which used *per*-specific primers in replicate reactions over a variable number of cycles, was developed to selectively amplify *per* gene cDNA from samples of both *B. tryoni* and *B. neohumeralis* that had been collected at regular intervals over a 36 hour time course. The PCR products were resolved by agarose gel electrophoresis and relative levels of cDNA calculated as a measure of circadian patterns of gene expression. These showed that *per* gene expression in *B. tryoni* and *B. neohumeralis* cycles in a circadian manner. Expression levels in both species are in accordance with those observed in *D. melanogaster*, peaking during the first 2-5 hours of the dark cycle and falling to a minimum around the beginning of the light phase. Therefore, the phase of cycling is not correlated with mating time, although there may be a two to three hour phase difference in peak *per* expression between the two species.

T92

Sex in New Zealand? Microsatellite evolution in parthenogenetic *Sitobion* aphids on grasses in New Zealand

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Using microsatellite and mitochondrial DNA markers we explore the geographic distribution and evolution of New Zealand Sitobion aphids and their Australian relatives. There are four chromosomal races of *Sitobion miscanthi* and one of *S.* near fragariae in Australia, each of which is distinguishable on the basis of two microsatellite markers. The relatedness between the races suggests that S. miscanthi is the result of two colonisation events and S. nr fragariae is the result of a single colonisation. Recent field collections of Sitobion aphids from New Zealand have revealed additional genotypes not yet found on the Australian mainland. We present a nuclear phylogeny based on 15 microsatellite loci of the Australian and New Zealand genotypes. Two S. miscanthi genotypes present on the Australian mainland were also present in New Zealand. An additional four closely related genotypes were also identified, two of which appear to be sister lineages of one of the Australian genotypes. The other two genotypes display exceptional homozygosity at microsatellite loci and may possibly be the result of an historic recombination event. There are two main explanations for the observed levels of homozygosity in these lineages; automixis, and recombination followed by exteme selection for homozygosity. It is improbable that such extreme levels of homozygosity can solely be explained by the presence of null alleles in these lineages. S. nr fragariae is represented by two genotypes in New Zealand, one identical to the single Australian genotype and another similar widespread genotype. Most of these lineages have arisen by mutation alone. Thus, the potential of this system to understand the processes of microsatellite evolution will be addressed.

T93

The influence of correlated paternity on the viability and persistence of fragmented daisy populations

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Fragmentation and destruction of native grasslands in southeastern Australia over the past century has been severe. Populations of many grassland species are now restricted to small isolated habitat remnants. The grassland daisy *Rutidosis leptorrhynchoides* is one such species. Genetic markers indicate that fragmentation has resulted in a loss of genetic diversity, as well as a significant shift towards greater correlation of outcrossed paternity (r_p), in small isolated populations of this species. This will increase biparental inbreeding through mating among full sibs. In this study we use computer simulation models to compare the demography of populations with low r_p values to those with high r_p values; the models were parameterised with data from a long-term study of natural populations of *R. leptorrhynchoides*.

T94

Cytogenetic studies to assist kiwifruit breeding

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Kiwifruit (*Actinidia*) is a recently domesticated fruit crop relying mainly on a single cultivar 'Hayward'. Breeding programs for cultivars with novel fruit characteristics, such as yellow or red flesh, easy peeling or improved postharvest shelf life, require a better cytogenetic understanding of the genus.

Chromosome numbers are recorded for the first time for six taxa, including the first report of naturally occurring octoploids, in *A. arguta* var. *purpurea*. A survey of 191 plants found new polyploids, e.g. fifteen tetraploid accessions in *A. chinensis*, previously thought to be a diploid species. Intraspecific ploidy variation was common. Metaphase I in tetraploid *A. chinensis* revealed mainly bivalent formation. Univalents and bivalents were observed in one *A. chinensis* (2*x*) x *A. eriantha* (2*x*) hybrid, and trivalents, bivalents and univalents were observed in an artificially produced triploid *A. chinensis*. These results suggest that the constituent genomes of diploid and tetraploid *A. chinensis* are homologous, whereas those of diploid *A. chinensis* and *A. eriantha* showed less homology. *In situ* hybridisation and dot-blotting with several genomic probes suggested that *A. deliciosa*, diploid and tetraploid *A. chinensis* and tetraploid *A. chrysantha* had considerable genomic homology. However, a repeat sequence cloned from *A. deliciosa*, pKIWI516, divided these plants into two groups: one group (*A. deliciosa*, some tetraploid *A. chinensis* accessions ($4x^+$) and *A. chrysantha*) was positive to the repeat, whereas the other group (diploid and some other tetraploid ($4x^-$) *A. chinensis* accessions and eight other *Actinidia* taxa) was negative. *In situ* hybridisation with this repeat sequence revealed six hybridisation sites on six different chromosomes of both $4x^+$ *A. chinensis* and hexaploid *A. deliciosa* . Both male and female plants produced functioning unreduced gametes, as shown in meiosis and progenies of controlled crosses. Such functioning unreduced gametes in *Actinidia* could account for the high frequency of polyploid plants in the genus, the multiple origins of tetraploid *A. chinensis*, and the evolution of a simple XY sex determination system at the diploid and polyploid levels. The results of these studies will be discussed in relation to the present kiwifruit breeding programs.

T95

Molecules and morphology in the genus *Myoictis*

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The genus *Myoictis* is one of four endemic genera of dasyurid marsupials found in Papua New Guinea. Currently only one species (*Myoictis melas*) is recognized, though a second (*Myoictis wallacei*) may be valid.

We have examined DNA sequences from two mitochondrial genes (cytochrome b and 12S ribosomal RNA) as well as allozyme data from four populations. The results will be discussed and suggestions made about the possible taxonomic status of these animals.

Abstracts of Posters P1-P38

P1

Genetic Variation Among Murine Cytomegalovirus Field Isolates

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Murine cytomegalovirus (MCMV) is a betaherpesvirus which establishes a persistent and latent infection in its natural host. The genome of MCMV is a single unique double-stranded sequence of 230 kb that shares significant homology with other members of the herpesvirus family. Previous studies have shown that significant variation is present between strains of MCMV isolated from wild mice (*Mus domesticus*) (1). To further characterize this variation the genome of a collection of field isolates was mapped by Southern blot hybridization. Using a panel of specific probes, distinct areas of genotypic variation were identified which correlated to regions coding for MCMV-specific genes. This heterogeneity may be functionally significant as it correlates with the phenotype of field isolates *in vivo*.

(1) Booth, T.W.M. *et al.*, Arch. Virol. 132, 209-220.

P2

Localisation of the *xprF* gene from *Aspergillus nidulans*

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Aspergillus nidulans secretes several extracellular proteases in response to an absence of preferred low molecular weight carbon, nitrogen, and sulphur sources. It is our aim to isolate and characterise genes involved in extracellular protease regulation. Using UV mutagenesis, a mutant was identified that exhibited very high levels of extracellular protease production in response to carbon starvation. This strain was shown to carry a mutation in a single gene, *xprF*. The mutation, *xprF1*, also has a negative effect on the utilisation of alternative nitrogen sources, especially hypoxanthine. The *xprF* gene was isolated by cotransforming a strain (AM5) containing the *xprF1* mutation, with chromosome VII cosmid DNA from an *A. nidulans* chromosome-specific cosmid library. The transformants were screened for wild type levels of protease production, and wild type growth on hypoxanthine. A cosmid, L32F12, was isolated using this method.

The aim of this study was to specifically localise the *xprF* gene on the L32F12 cosmid. A number of strategies were utilised to produce clones to test for cotransformation of strain AM5, and possible complementation of the *xprF1* mutation. A) Construction of partial *Hind*III deletions of L32F12; B) subcloning of large restriction fragments from L32F12 into pUC18; and C) isolation of cosmids that overlap L32F12 using version 2.0 of the *A. nidulans* physical map. The use of overlapping cosmids was the most useful in localising *xprF*. Sequencing and characterisation of a 7.0 kb *Hind*III fragment, which is believed to contain part of the gene, is in progress.

P3

The assessment of genetic variation within and between the three known Southern Australian maternity caves of the Common bent-wing bat (*Miniopterus schreibersii*)

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The Common bent-wing bat, *Miniopterus schreibersii*, is a small, insectivorous, cave-dwelling bat. Female bats use specific caves throughout Australia for the birth of their young. These maternity caves possess the correct conditions to allow the growth and development of the young. In Southern Australia (Victoria and South Australia) there are only three maternity caves, located at Warrnambool, Naracoorte and Lakes Entrance. It is due to the reliance on these few maternity caves, that this species is regarded as threatened.

M. schreibersii is capable of long distance movement, with distances of 50 to 100 km not uncommon. However, it is not yet known if individuals routinely travel between maternity caves. An investigation of microsatellite DNA is being conducted in order to determine whether the three maternity caves constitute three distinct populations or whether they are one large interbreeding population.

P4

Polygyny via unrelated queens indicated by mitochondrial DNA variation in the Australian meat ant *Iridomyrmex purpureus*

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Populations of the Australian meat ant *Iridomyrmex purpureus* are known from observations and allozymes data to consist of many mature polygynous (multiple queen) colonies and a small proportion of mostly monogynous incipient colonies. This distribution, along with observations of nuptial flights, suggest secondary polygyny, with additional queens adopted into mature colonies (Greaves and Hughes, 1974; Halliday, 1983). It is not known whether the adoption process discriminates among potential supernumerary queens on the basis of kinship. This factor is likely to influence patterns of intercolonial competition and cooperation (Crozier and Pamilo, 1996). We therefore used mt DNA analysis to determine the matrilineal relationship among queens in polygynous associations. Restriction fragment length polymorphism revealed a total of four haplotypes. The majority of the nests surveyed were monomorphic, but one contained two haplotypes. Given the number of nests surveyed and the haplotype frequencies, this result suggests that a high proportion of mature nests contain unrelated queens.

Crozier, R.H. and P. Pamilo 1996. *Evolution of social insects colonies. Sex allocation and kin selection.* Oxford University Press, Oxford, UK.

Greaves, T. and R.D. Hughes 1974. The population biology of the meat ant. *Aust. J. Zool.* 13:329-351.

Halliday, R.B. 1983. Social organisation of meat ants, *Iridomyrmex purpureus* analysed by gel electrophoresis of enzymes. *Insectes Soc.* 30:45-56.

P5

Genetic diversity in three tuberous and self-incompatible species of *Drosera*

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The level and distribution of genetic diversity at 9 allozyme loci in six populations of *D. rosulata*, one of *D. tubaestylis* and four of *D. macrantha* ssp. *macrantha* and the genotypic diversity in the Blue Rock population of *D. tubaestylis* were estimated. Chromosome numbers and pollen stainability (pollen fertility) were also determined in these taxa. Estimates of the mean expected panmictic heterozygosity (H_e) ranged from 0.29 in *D. macrantha* ssp. *macrantha* to 0.37 in *D. rosulata* and 0.45 in *D. tubaestylis*. The proportion of diversity between populations or sampled sites (G_{ST}) varied from 9.5% in *D. rosulata* and *D. macrantha* ssp. *macrantha* to 5.2% in the population of *D. tubaestylis*. The proportion of distinct genotypes (proportion distinguishable; *G/N*), measures of genotypic diversity (*D*) and evenness (*E*) and the mean size of clone in the Blue rock population of *D. tubaestylis* were 0.61, 0.98, 0.92 and 1.6, respectively. These observations reflect the accumulation of mutations as a consequence of clonal spread and the longevity of tuberous tubers. The accumulation of mutations in the clonal lineages of these taxa was also supported by male sterility and significant pollen abortion in some diploid individuals. In addition, occasional seedling establishment and high gene flow within or between populations may also be contributable to high levels of genetic or genotypic diversity in these tuberous droseras. The basic chromosome numbers of x = 13, 14 and 15 were observed in *D. rosulata*, *D. tubaestylis* and in *D. macrantha* ssp. *macrantha*, respectively. The populations of *D. rosulata* and *D. macrantha* ssp. *macrantha* were predominantly diploidy whereas the population of *D. tubaestylis* consisted of diploidy and triploidy. These cytogenetic features, together with self-incompatibility, suggest that lethal polymorphisms associated with the accumulation of mutations provide selection pressures for systems minimizing the associated genetic load.

P6

Geographic Variation in the Southern Brown Bandicoot (*Isoodon obesulus*): Molecules Versus Morphology

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The southern brown bandicoot is a threatened species, with a significant decline in its range in Western Australia over the past few decades. Despite this decline, the distribution of this species is still continuous with no major physical barriers (although there may be behavioural barriers) to migration in the region. Body size and shape, and blood protein loci of *I. obesulus* specimens were examined for geographic variation in an attempt to determine the degree and patterns of genetic subdivision in this species in Western Australia. Body size analyses showed significant geographic variation, with a two-fold difference in adult body size between some locations. Shape (ear size compared to body size) also displayed significant geographic variation. However, an examination of 44 blood protein loci produced a different picture. Very little variation was found: only 6.82% of loci were polymorphic, with a mean heterozygosity of 0.0056. Just one locus displayed significant geographic variation. The F_{ST} value of 0.0034 suggests that there is no significant genetic subdivision over the range of locations sampled. The discrepancy in results from the two types of analyses suggests that either one or both of these (molecules or morphology) does not provide an accurate picture of the extent of genetic variation in this species. Both methods have their disadvantages and it seems that in order to gain a true understanding of evolutionary processes in this (or any) species several sets of characters, both adaptive and molecular, need to be analysed.

P7

Diallel analysis of vernalization responses in spring rape (*Brassica napus* var. *annua*)

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The effect of vernalization on the pattern of plant development varies substantially among cultivars of spring rape (*Brassica napus* var. *annua*) grown in Western Australia. In particular, time to flowering and stem height at flowering are influenced by genetically controlled, temperature-dependent mechanisms. In order to explore the genetic effects of these and related characters, a complete diallel cross was made among five fully-inbred spring rape genotypes, differing in sensitivity to vernalization, derived from the cross Target x Bronowski, and the F_1 generation was grown under non-vernalizing and vernalizing conditions. In non-vernalized plants, number of leaf nodes at flowering, time to flowering, stem height at flowering and time to initiation of stem elongation were highly heritable, both additive and dominance effects being significant. However, none of these characters showed directional dominance. There were clear differences between reciprocal crosses for all characters studied, indicating the presence of a maternal influence or cytoplasmic inheritance. Graphs of Wr against Vr indicated that number of leaf nodes at flowering and time to initiation of stem elongation are controlled by genes exhibiting overdominance whereas time to flowering and stem height at flowering are controlled by genes exhibiting partial dominance. Analysis of the difference in performance between vernalized and non-vernalized plants revealed that time to initiation of stem elongation is not a vernalization-sensitive character. However, for the other three characters response to vernalization is highly heritable, genetic variation being largely additive. The response to vernalization can therefore be readily manipulated in a plant breeding programme.

P8

To amplify an Antechinus... Technical notes on DNA extraction from small field collection samples of *Antechinus minimus* for PCR reactions

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Presently, we are investigating genetic variation at the population level in selected populations within Victoria of the Swamp Antechinus (*Antechinus minimus*). Technical problems have arisen in obtaining high quality DNA for use in amplification of the microsatellites via the polymerase chain reaction (PCR). The first of these is the use of 70% ethanol in collection of the samples in the field. Ethanol appears to hinder the recovery of DNA, with yields being much lower than would be expected from the size of the tissue samples used. Washing the samples overnight in a series of TE buffers with decreasing amounts of ethanol can be used to reduce the ethanol present in each sample, dramatically increasing the yield obtained.

Another problem is that a standard phenol/chloroform extraction method does not produce DNA of high enough quality to ensure the amplification of the desired marker, in this case microsatellite DNA. Other extraction methods such as DNAzol™ have not, on there own, been successful in producing the desired result either. A combination of Proteinase K digestion followed by a second method such as DNAzol™ or Gene Clean™ has proven successful in extracting DNA of high quality which is readily amplified via PCR.

P9

Y-chromosome haplotypes in indigenous Siberians

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Male-specific DNA polymorphisms are proving highly informative to our understanding of both human evolution and present day patterns of variation in *Homo sapiens*.. Because the male-specific portion of the Y-chromosome escapes recombination with the X-chromosome any changes to the DNA sequence occurring upon it are preserved as a unit, or haplotype, and so it uniquely records the paternal lineage. Two types of polymorphism are observed on the Y, those that are unique or very rare, and those subject to recurrent mutation, such as microsatellites. The former, comprising sequence variants and insertion/deletions, are used to construct haplotypes. The principal features of the distribution of these Y-specific haplotypes are a) they tend to be population specific and b) each population tends to have a distinctive set of Y-haplotypes.

We scored several unique Y markers and one tetranucleotide microsatellite in three linguistically distinct indigenous groups of Siberia, the reindeer-herding Tungusic speaking Evenki, the hunter-fisher Kets who speak an enigmatic language, and the pastoralist Altai who speak Altaic a member of the Turkic phylum. We found a number of different Y-haplotypes in each group. While some of these haplotypes were shared across the three populations, the frequencies differed markedly among them. Some of these Y-haplotypes are associated with a particular microsatellite allele and this relationship is found regardless of the Siberian population. Other haplotypes, however, are associated with a variety of microsatellite alleles. The frequency distributions of the Y-haplotypes in Siberians are compared with those observed in the major neighbouring groups, Europeans and Asians.

P10

Origin and evolution of LINE derived elements in mice: a novel subfamily

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Tu80 and NOV1 are hybrid sequences comprised of an L1 homologous region and a region homologous to the first intron of the mouse C_{ε} immunoglobulin gene. PCR was used to isolate 11 additional elements across six murine species. All observed sequences maintain the putative site of recombination without shifts in either the 5' or 3' direction, supporting the explanation that a solitary recombination event generated an ancestral sequence which was later a subject of amplification. Through database searches we located another hybrid sequence, *Tcr*, which displays the attributes of a transposed element including short direct repeats and a poly-A signal and tail. These results argue that the sequences comprise a novel family of murine mobile genetic elements which we propose to call LINE Derived Elements, or LDEs. It is possible that these elements conform to the master gene model however the possibility that they are pseudogenes remains. The estimated time that the ancestral LDE may have arisen is roughly 15-20MYA. The *Tcr* sequence has given tentative indication that LDEs may be family of mobile elements

P11

Lizards caught with their genes down - a genetic investigation of sociality in lizards of the Egernia group

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Flinders University / South Australian Museum

Previous research has shown that species of the genus *Egernia* vary in their degree of sociability - some are completely solitary while others are colonial. *Egernia stokesii,* is often reported as occurring in family groups, however the genetic relationship among individuals is unknown. The first topic in this doctorate study will investigate the genetic relationship among and between supposed family group members of *E. stokesii* using microsatellites markers. As such the major focus of the poster will be the isolation of microsatellites using an adapted enrichment technique. The second aim is to reconstruct the phylogeny of the *Egernia* group by sequencing a mitochondrial gene and a nuclear gene. The *Egernia* group comprises approximately 45 species in four genera. The genus *Egernia* is morphologically a varied assemblage unlike its relatives within the *Egernia* group. The main objective of this section is to produce a species tree, enabling a decision on the paraphyly or otherwise of *Egernia*, and for a comparative analysis of the evolution of social behaviours.

P12

Polymorphisms of the apolipoprotein b gene and their associations with lipid phenotypes in Greek and Italian migrants to Australia

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The transport of lipids in the bloodstream is a process carried out by lipoproteins; macromolecular complexes containing lipids and apolipoproteins. Apoliporoteins can be divided into numerous classes, all of which have specific physiological roles in lipoprotein metabolism. One of these apolipoproteins, apolipoprotein B (apoB) plays an important role in the homeostasis of plasma cholesterol. Two primary forms of apoB have been identified, apoB-100 and apoB-48. Both are produced by the apoB gene located at human chromosome 2 p23-24. Elevated levels of apoB-100 are associated with both increased total cholesterol and low density lipoprotein cholesterol (LDL-cholesterol) levels in humans, which in turn are risk factors for coronary heart disease. Numerous studies have investigated the associations between polymorphisms of the apoB gene and lipid concentrations. The findings however, have been equivocal.

This poster presents the results of a study in a sample of Greek and Italian migrants investigating the associations between lipid phenotypes and two restriction site polymorphisms of the apoB gene, the silent *Xba* I point mutation at the third base of codon 2488 and the *Eco*R I base substitution mutation which changes codon 4154 from glutamic acid to lysine. The only statistically significant association detected was that between total cholesterol, and the apoB *Eco*R I polymorphism in Italian males.

P13

Effects of silviculture on genetic diversity in *Eucalyptus sieberi*

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We are employing DNA markers to examine the effects of silvicultural treatments on genetic diversity and spatial genetic structure in *Eucalyptus sieberi*. The field site for this experiment is provided by the Silvicultural Systems Project of the Victoria Department of Natural Resources and Environment, near Orbost, Victoria. Regeneration has been sampled from 2 coupes each from the following silvicultural treatments: clearfelling with aerial resowing, seed tree system with site preparation by burning, and seed tree system with mechanical site preparation. One hundred saplings have been sampled from each coupe. Genetic diversity in the regeneration is being measured with 30 RFLP and 10 microsatellite marker loci and will be compared to the diversity found in 225 mature trees (100 trees from each of 2 adjacent unharvested control stands and the 25 *E. sieberi* seed trees from the seed tree coupes). Spatial genetic structure will also be examined in the unharvested control stands as well as in the regeneration on the coupes. Our up to date results from this project will be presented and discussed.

P14

Local population structure in the inshore bottlenose dolphin

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The genetic population structure of bottlenose dolphins along the south-east and southern coastlines of Australia was investigated using mitochondrial DNA (mtDNA) sequence and nuclear DNA microsatellite (nDNA) genotypes. The aim was to establish the geographic range of genetic populations and to investigate in detail possible biogeographic barriers to gene flow. Dolphins were distinguished at post-mortem or in the field by their morphology. MtDNA sequence and haplotype analysis revealed population subdivision along both the south and south-east coasts, where it approximated a pattern of isolation by distance. However, a phylogeographic break (Da>5%) was apparent among taxa from the two coastlines, occurring within a maximum of 200 nautical miles and centred on Cape Howe. In contrast, the pattern revealed by analysis of five nDNA loci was one of isolation by distance, both within and between south-eastern and southern Australia. The geographic range of genetic populations on the south-east coast was about 300 nautical miles for both nDNA and mtDNA. The phylogeographic break for mtDNA between the south-east and southern coasts may be the result of an historical geographic barrier to the migration of *T.aduncus*, from the formation of a land bridge in Bass Strait during Pleistocene glacial maxima. The break is likely to be maintained currently by female natal philopatry. The distribution of mtDNA variation within eastern Australia may be a consequence of population contraction and expansion during Pleistocene glacial cycles and female natal philopatry.

P15

Regional population structure in the inshore bottlenose dolphin

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Inshore forms of the bottlenose dolphin occur along tropical and temperate coastlines throughout the world. We have studied the genetic population structure of the inshore form found along coastlines of the Indian, Western Pacific and Southern Oceans, where they have a continuous distribution. The aim was to investigate whether the form found in these regions comprises a single species and to determine the extent of gene flow among regions, by analysis of mitochondrial DNA (mtDNA) sequence and nuclear DNA microsatellite (nDNA) genotypes. Dolphins were distinguished at post-mortem or in the field by their morphology. The phylogeny constructed from mtDNA control region sequence revealed 4 distinct monophyletic clades that were concordant with the region of origin of the samples; the Western Pacific, Southern and eastern and western Indian Oceans. To determine whether or not the inshore form comprises a single species throughout this range, 6 nDNA loci were analysed in these populations and in three other Delphinid species found in the region, the common dolphin (*Delphinus delphis*), the Indo-Pacific humpback dolphin (*Sousa chinensis*) and the offshore bottlenose dolphin (*Tursiops truncatus*). The nDNA analysis revealed that the inshore bottlenose populations are more closely related to each other than to the other species, and the conclusion is that they comprise a single species (*Tursiops aduncus*). The pattern of nDNA variation among sites is consistent with a model of population structure based on isolation by distance. Results are discussed with regard to historic biogeographic barriers to dispersal, female natal philopatry and the dispersal of male *T.aduncus*.

P16

Species subdivision in the Genus *Tursiops*

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The species status of the two forms of the bottlenose dolphin, the inshore and offshore forms, which have sympatric distributions in eastern Australia, was assessed by comparison with two other species of Delphinid from the region, the common dolphin (*Delphinus Delphis*) and the Indo-Pacific humpback dolphin (*Sousa chinensis*), by analysis of mitochondrial DNA (mtDNA) sequence and genotypes from nuclear DNA microsatellite (nDNA) loci. Dolphins were distinguished at post-mortem or in the field by their morphology. The two forms, if a single species, should be genetically more similar to each other than to other species where their distribution is sympatric. The phylogeny constructed from mtDNA control region sequence showed the four groups, the two forms of *Tursiops* and the other two species, to comprise four distinct monophyletic clades, with the genetic distance among the two *Tursiops* forms not less than the other pairwise distances. The result from analysis of cytochrome-B sequence supports this finding. The phylogeny constructed from 6 nDNA microsatellite loci also showed that the genetic distance among the two *Tursiops* forms was not less than the other pairwise distances. It is concluded that the two *Tursiops* forms are distinct species, even though they interbreed freely in captivity and produce fertile female offspring. Morphological data supports this conclusion. We propose that the tentative species names *T.aduncus* and *T.truncatus*, for the inshore and offshore forms respectively, should be adopted. The results are discussed with reference to speciation in Delphinids and the problems and utility of using mtDNA and microsatellite loci in identifying species boundaries.

P17

Isolation and characterization of the expressed Mhc class II genes in the Harbor seal

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Mhc genes encode specialized receptor glycoproteins that bind antigen fragments in the antigen binding site (ABS) and present them to lymphocytes. In humans, the Mhc is located on the short arm of chromosome 6 and contains about 3.5 megabases. The major histocompatibility complex contains three classes of genes. Class I genes code for Mhc molecules on nearly all nucleated cells. Class II genes code for Mhc molecules on the surface of macrophages, B-cells and dendritic cells. The less studied class III genes code for soluble proteins that are not directly involved in antigen presentation, such as proteins associated with the complement pathway. The Mhc in humans contains around 20 class I genes (all of which are not expressed). Class I and II Mhc molecules are very polymorphic with over 100 alleles per locus in some species. Human class II α and β chain Mhc genes will be used as a probe to screen a previously constructed Harbor seal cDNA library in order to isolate the respective class II genes in the harbor seal. Once isolated, the genes will be sequenced and characterized. If necessary, two other strategies may be used to isolate the class II genes: (i) Anchored PCR with degenerate primers using the cDNA library as a template, (ii) 3` RACE and 5`RACE with sets of degenerate primers using spleen derived polyA RNA as template. If there is time, the introns flanking the ABS - coding exon 2, will be isolated and characterized by PCR using primers in exons 1, 2 and 3. The aim of the entire group is to identify the Mhc allele associations between Harbor seals and Phocine distemper virus. Critical to this endeavour is the characterization of the Mhc genes.

P18

Clonality Studies in Conservation Genetics and Weed Control

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Understanding the genetic basis of clonality can have diverse purposes in conservation genetics, from the protection of endangered species to the control of weeds. This work illustrates how Genetic Markers were used to understand the basis of clonal behaviour in a rare mallee eucalypt (*Eucalyptus phylacis*) and four *Grevillea* species in order to understand their growth and reproductive strategies and detect potential links to rarity. Genetic markers were also used to understand the spread and origins of the Century plant (*Agave americana*, Agavaceae) a weedy species threatening native communities with its vigorous growth. It was found that RAPD and/or AFLPs produced markers characteristic to each clone within the different species. The identification of different clones within these species with restricted genetic variability facilitated the study of clonal spread. The extent of the range varied substantially between the species studied being between 30 and 500 m. Surprisingly, over an extended sampling range of 800 km, insignificant amounts of variation were found for *A. americana*, indicating clonal division and transport to new sites as the most probable means of dispersal. *E. phylacis* was found to represent a 'super-mallee', possibly derived from one seedling and now extending over 30 m. *Grevillea* species showed a continuum of microsite and between site variation. This study highlights the use of genetic markers in the study of clonal species.

P19

On the use of sister species for studies of speciation: a case study from *Drosophila serrata* and *D. birchii*

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Drosophila serrata and *D. birchii* are thought to be recently speciated sister species which are classified within the same (*serrata*) complex on the basis of morphological and reproductive criteria. Yet, they have very different ecologies. They have been used in a number of studies looking at the evolution of pre-mating isolation during speciation. These studies hinge on the close relationship between the two species. As a result, a recent study which found no evidence for a close relationship within the *serrata* complex at mtDNA, posed a threat to the validity of the conclusions drawn from these quantitative genetic studies. In order to investigate the causes for this pattern, the population level genetic structure within both species was examined. To obtain the best estimates of phylogenetic relationships, the molecular pattern of sequence evolution of the chosen mitochondrial marker (ND5) was investigated. The mtDNA marker was also tested for neutrality, to assess the validity of the conclusions drawn about population history. The intraspecific phylogeography held plenty of surprises: the pattern in both species was inconsistent with all predictions based on ecology. *D. birchii*, a rainforest specialist, showed low diversity and no evidence for a population genetic structure. *D. serrata* on the other hand, a habitat generalist, showed strong phylogeographic structuring that was not geographically concordant with any previously identified biogeographic barrier. A recent range expansion was proposed to account for the lack of mtDNA structure within *D. birchii* and a number of suggestions were put forward to explain the position of the geographic break within *D. serrata*. The implications of the findings for further studies of speciation are discussed.

P20

Polymorphic microsatellite markers for population analysis of the Queensland Fruitfly *Bactrocera tryoni*

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The Queensland fruitfly *Bactrocera tryoni* occurs within a range extending from Darwin through coastal and central Queensland and along the NSW coast as far as eastern Victoria. Analysis of the distribution of *B. tryoni* within this range using four Restriction Fragment Length Polymorphism loci failed to detect any population subdivision. To obtain a more informative set of nuclear genetic markers, a size selected genomic library was screened with a selection of di and tri nucleotide probes to detect microsatellite sequences. Sequencing recovered 22 simple sequence repeat loci from which 16 PCR primer sets were designed. These primer sets were tested on a collection of 55 *B. tryoni* flies obtained from 6 widely separated trap sites, (Darwin, Cairns, Rockhampton, Toowoomba, Brisbane and Sydney), to determine the extent of polymorphism in the natural population. All of the loci amplified showed some degree of polymorphism in the population sample with the number of alleles ranging from 2 to 18. The microsatellite sequences which we cloned were all short, with repeat numbers ranging from 7 to 11, and the distribution of alleles is in several cases extremely steep, with one frequent allele and a number of rare alleles. Several dinucleotide repeat microsatellite sequences have alleles separated by single base differences suggesting that they have evolved by a mutation process which is more complex than the stepwise mutation model often used in population analysis using microsatellite markers.

P21

Analysis of Plant Microsatellites

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Microsatellite (SSR) markers have many potential applications in plant genetics. However the difficulty of discovery of microsatellite loci has limited their use. Recent improvements in methods for the production of enriched microsatellite libraries has increased the range of potential applications of microsatellite markers. We are applying microsatellites to analysis of plant population genetics, identification of plants and mapping of plant genomes. Species currently under investigation include, barley, mangroves, grapes, rice, sugarcane, tea tree and wheat. Advantages of microsatellite markers compared to some alternative methods include, a high degree of polymorphism, the co-dominance of microsatellites, the ability to automate much of the analysis and the potential to analyse microsatellite loci across a wide range of genotypes within a species. The abundance and nature of microsatellite loci in different species revealed by comparison of the composition of a large number of plant microsatellite libraries indicates the wide utility of these markers in plants.

P22

Does autoregulation exist for BCL-2 gene in human lymphoma: preliminary findings

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It has been recently reported that an antisense RNA exists in a t(14;18) non-Hodgkin's lymphoma (NHL) cell line, but not present in the cell lines without t(14;18),(1). The aim of this study was to demonstrate the existence of this autoregulatory gene product in human NHL samples and that this is not an artefact found only in cell lines. All RNA samples were treated with DNase1. The existence of the hybrid gene, bcl-2/IgH, and antisense RNA transcript was identified by the strand specific reverse transcriptase-polymerase chain reaction method. SU-DHL-4 and WL-2 cell lines were used as positive and HL-60 as negative controls. Initial experiments indicated the presence of antisense RNA in t(14;18) +ive but not in -ive samples. However, it was observed that a PCR product, for a region shared by both t(14;18) -ive and +ive samples, appears even in the absence of strand specific primer at the reverse transcription stage. This means PCR can amplify RNA from any sample irrespective of translocation, despite the exclusion of any contamination error. To further characterise this issue, (i) affinity column method was used, to first isolate the specific antisense RNA using antisense specific column, and then apply PCR, but the results were inconclusive. (ii) SSDNA probe analysis for the antisense RNA after fractionation of RNA was used. This resulted in a negative signal, possibly due to very low expression of the transcript. (iii) Use of RNase1 after reverse transcription to remove any RNA, eliminated the false positive results. The antisense message was detected 1/3 experiments on the same t(14;18) positive sample. Other authors also found northern blots to be insensitive for the detection of rare antisense RNAs. Our study so far concludes that results obtained using RT-PCR for the detection of antisense transcript should be analysed with caution and proper controls should be employed to avoid any chance of PCR artefacts. Further experiments are underway to confirm the existence of this rare antisense transcript.

(1) Nicolin et al; *Oncogene*, July 96

P23

Phylogeny and evolution of the tick subfamily Rhipicephalinae

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Some of the world's most important species of tick from a medical, veterinary and economic perspective are contained within the subfamily Rhipicephalinae. It is surprising, then, that virtually nothing is known about the phylogenetic relationships within this subfamily. The present classification system within the Rhipicephalinae clearly needs revision. For example, the first molecular phylogenetic study on ticks indicated that this subfamily may be paraphyletic with respect to some members of Hyalomminae. To address this hypothesis with a different molecular marker, and do a preliminary assessment of the relationships among the major Rhipicephaline genera, we sequenced a 330bp fragment of the 12S ribosomal RNA gene from 15 species of Rhipicephalinae (representing four genera), two Hyalommine species and two Haemaphysaline outgroups. The congruent results of all analyses (N-J, ML, MP) confirmed that the Rhipicephalinae are paraphyletic with respect to the Hyalomminae. Moreover our data indicated that groupings within the genera *Dermacentor* and *Rhipicephalus* may need to be re-evaluated, and that *Rhipicephalus* and *Boophilus* may not be distinct genera. Our results suggest that our understanding of this speciose group is still in its infancy.

P24

Molecular Biogeography of Flightless Beetles in the Australian Wet Tropics

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Molecular phylogenetic analyses of the biogeography of vertebrates from the Australian Wet Tropics have shown pronounced divergences between populations from the same geographical regions, for example on either side of the 'Black Mountain Barrier', just to the north of Cairns. The calibrated size of the breaks suggest that ancestral populations were isolated by biogeographical events which pre-date the Pleistocene when the rainforest was known to be more fragmented and restricted than it is now. The evolutionary relationships of the numerous flightless, non-vagile beetle species with restricted, mostly disjunct, high altitude distributions in the Wet Tropics provide an ideal opportunity to test hypotheses of speciation by vicariance in the region. Molecular phylogenies constructed from nucleotide sequence variation in the mitochondrial genome are being determined for selected taxa [Carabidae; Pterostichini, Leiradira (9 species in the wet tropics, four unamed), Notonomus (11 species, 2 unamed), Trichosternus (10 species, 3 unamed), Castelnaudia (4 species); Cychrini, Pamborus (4 species)] for comparison to large and fine scale area cladograms. DNA from pinned museum specimens is being used as a template for the amplification of mitochondrial genes. Initial results suggest that speciation amongst flightless beetle taxa may have been rapid and recent, possibly during the most recent constriction of the rainforest in the Pleistocene.

P25

Expression and imprinting of the human *STIM1* gene

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During analysis of the promoter region of *RRM1*, the novel gene *STIM1* (**st**romal **i**nteraction **m**olecule) was found[1]. These genes lie at 11p15.5; a region associated with Wilms' tumour (WT) and several other malignancies including rhabdomyosarcoma, breast and lung cancer. Pulsed field electrophetic analysis indicated that *STIM1* was located immediately telomeric to *RRM1*[1]. Sequence analysis of *STIM1* cDNA indicates a transmembrane protein with no significant homology to any known protein. This was also indicated by the murine homologue (*Stim1*[2]). The genomic structure of *STIM1* is currently being determined, preliminary data suggests that the 5' half of the gene is composed of many small exons while the 3' 1.9 kb are present as a single exon.

Northern analysis of *STIM1* revealed expression in both adult and foetal tissues. Of note was significant expression in foetal kidney but minimal levels in adult kidney. The relevance of this observation may become clear when the function of the protein is determined. 11p15.5 is associated with WT; we don't yet have evidence to indicate that *STIM1* is involved with this disease. Imprinting studies have been performed and in 2/11 informative WT patients monoallelic expression of *STIM1* was found: one showed monoallelic expression in normal tissue and biallelic in the tumour suggesting LOH; the other showed biallelic expression in normal tissue and monoallelic in the tumour. We are investigating these patients for mutations and possible reasons for *STIM1*'s monoallelic expression.

[1] Parker *et al. Genomics* **37:**253 (1996) [2] Oritani and Kincade *J. Cell Biol.* **134:**771 (1996)

P26

Involvement of cytochrome p450 cyp6b7 in pyrethroid resistance in *Helicoverpa armigera*.

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Helicoverpa armigera is one of the major insect pests affecting Australian cotton crops and the development of insecticide resistance, particularly to pyrethroids, has become a serious problem in controlling this pest. Increased activity of detoxification enzymes is thought to be the most important mechanism of pyrethroid resistance, and inhibitor studies have suggested that cytochrome P450 plays a major role in resistance. We have isolated cDNA clones for three H. armigera cytochrome P450s which are members of the CYP6 gene family. The three cytochrome P450s, CYP6B2, CYP6B6 and CYP6B7, show about 86% sequence identity between them. This level of identity allows all three cDNAs to cross hybridize with all of the mRNAs. However the 3' non coding regions of each mRNA do not cross hybridize and can be used to quantitate each mRNA separately. Using the 3'-noncoding specific probes we have shown that CYP6B7 mRNA is over-expressed in many resistant individuals collected from the field. Southern blot analysis on these same individuals clearly indicated that the over-expression was not related to a gene amplification. This overproduction is not an induction phenomena due to insecticide in the resistance test since F1 individuals that were not exposed to insecticide also showed a twenty fold increase in CYP6B7 mRNA. We have concluded that CYP6B7 is involved in conferring insecticide resistance in *H. armigera*. Further studies are now underway to examine how widespread this over-expression of cytochrome P450 is in different field populations and to determine whether the mutation causing over-expression is genetically linked to this P450 gene or is likely to be in a controlling gene.

P27

Population genetics of Tea Tree (*Melaleuca alternifolia*) using DNA microsatellites

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Tea Tree oil production from the leaves of *Melaleuca alternifolia* is rapidly growing into a significant agricultural industry with the establishment in recent years of large areas of plantation crops in north-eastern New South Wales. The considerable differences in oil yield and composition are of particular interest to commercial producers, and suggest significant genotypic variability. To date however, limited varietal selection or breeding work has been conducted. This population genetics project involves sampling *M. alternifolia* leaf material from throughout the geographic range of the species, which is endemic to north-eastern New South Wales and far south-east Queensland. Genotypic diversity within the species is being studied utilising microsatellite DNA markers. A microsatellite library was prepared and will be used to study genotypic variability within and between the species population and subpopulations. In a second stage, the data will be correlated with oil yield and quality analyses in order to identify superior varieties for future commercial production. These varieties will also provide the foundation for a tea tree breeding program to pursue further varietal improvement.

P28

Patterns of genetic variability and phylogenetic relatedness among six endemic *Pterostylis* species (Orchidaceae, series *Grandiflorae*) of Western Australia

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Starch gel electrophoresis was employed to investigate the patterns of genetic variation and phylogenetic relationships among 35 populations covering six closely related Western Australian endemic *Pterostylis* species (series *Grandiflorae*) viz. *P. rogersii, P.aspera, P.angusta, P.hamiltonii P.scabra*, and *P.* sp.aff. *scabra*. The frequency of 56 alleles at 12 enzyme systems coded by 15 loci were determined along with a mean intra-specific genetic identity value. Allozyme markers clearly discriminated populations belonging to different species. Nei's genetic distance/identity co-efficient was used to measure the level of genetic differentiation among populations and species. Based on these values, a dendrogram was constructed which revealed that all the populations clustered into groups corresponding to the respective species. Gene diversity analysis revealed heterozygosity to be higher within populations than among populations. Total genetic diversity was high (H_T=0.311) with over 45% of diversity present between species. Mean genetic variability (H_e=0.136, P= 40%) was also higher than for other outbreeding plant species. Mean genetic identity of populations of all species was 0.859 which was increased to 0.926 upon exclusion of *P.* sp. aff. *scabra*, indicating a high degree of similarity among all the species except *P.* sp. aff. *scabra* which segregated distinctively from the rest. Overall the investigation provided an independent evidence for the groupings that were originally based on morphological studies.

P29

Reproductive biology of pohutukawa - a species under threat

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Pohutukawa (*Metrosideros excelsa*), a member of the Myrtaceae, is a large, mass flowering tree of coastal broadleaf forests in northern New Zealand. This species has been severely affected by forest destruction and is now the subject of a national revegetation project. We used controlled pollinations and allozyme markers to investigate the breeding system of five populations of this species.Three of these were fragmented mainland populations where two of the three likely native bird pollinators are known to be extinct. The other two were island populations with the full suite of these pollinators. It is possible, however, that introduced birds, native and introduced bees as well as geckos also play an important role in pollination. Crossing results indicate that Pohutukawa shows varying levels of self-compatibility but most trees are largely self-incompatible. Despite this, outcrossing rates are very low for a tree, ranging from tm=0.2 to tm=0.5, indicating that geitonogamy is an important component of the reproductive biology of the species. There was no obvious effect of reduction in the number of bird pollinators on the frequency of selfing. Large differences between progeny and maternal fixation indices suggest that selection eliminates most of the inbred individuals prior to reproductive maturity.

P30

Biogeography of the Indonesian archipelago: genetic diversity of vertebrate taxa

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The Indonesian archipelago is a dynamic and complex zone of faunal exchange and has particular significance due to its position at the interface of the two distinct biogeographic regions of Asia and Australia. Several features of the archipelago make the study of its fauna particularly interesting and informative. These include the complicated geological history of the region, the strongly linear orientation of fragmented land masses and the gradient of environmental and ecological parameters from east to west.

Genetic studies of endemic mammalian and reptilian species have revealed considerable information about the prevailing evolutionary forces shaping genetic diversity in this region. Evidence exists for isolation-by-distance and island size effects and east-west patterns of differentiation. Some species also demonstrate a correlation of genetic and environmental/ecological diversity. In addition, evidence of the colonization history of species through the archipelago and the influence of historical (Pleistocene) island connections are observed. These islands have also proven significant for the speciation of vertebrate taxa. In summary, concordant patterns are emerging from a number of species reflecting the influence of common historical and environmental factors on genetic variability in this region.

P31

A comparison between island and mainland populations of the Quokka, *Setonix brachyurus* (Marsupialia: Macropodidae), using molecular techniques

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Associations between patterns of genetic variation within species and historical biogeography have been observed in a wide range of species. In natural populations, which are almost invariably fragmented to some extent, interaction among genetic drift, natural selection and gene flow determine these patterns. In terrestrial vertebrates with limited mobility, genetic differentiation often increases with the distance between populations or corresponds to the extent of topographic and/or habitat barriers. In a Western Australian endemic, the Quokka (*Setonix brachyurus*), patterns of genetic variation were assessed using allozymes and mitochondrial DNA. Island populations were separated from the mainland between 7 000 and 10 000 years ago. Both islands are listed as reserves and in the absence of introduced predators, the Quokkas remain in relatively large numbers. Mainland populations have signficantly declined with increasing fragmentation and the introduction of feral predators since European settlement. The aims of this study were to determine (I) whether there has been significant differentiation among island and mainland populations of *S. brachyurus* since isolation and (II) whether the more recent isolation and small population sizes due to fragmentation are reflected in the pattern of genetic variation.

P32

Microsatellite variation in Gilbert's Potoroo, *Potorous gilbertii* (Marsupialia: Potoroidae)

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Gilbert's Potoroo was rediscovered in 1994 (Sinclair *et al.* 1996) in the Two Peoples Bay Nature Reserve. Genetic evidence strongly suggest that is should be recognized as a separate species (Sinclair and Westerman, in press). As it is still only known by the single population of less than thirty individuals, the long term conservation of this species in the wild is of major concern. A captive breeding program was set-up by CALM with two important aims: to provide a second colony as a back-up to the wild population and to increase numbers so that they can eventually be reintroduced back into the wild. Microsatellite DNA was used to assess the level of variation in this species. Microsatellites had been isolated from a closely related species, the Long-footed Potoroo (*Potorous longipes*) (Luikart *et al.* 1996). Three specific issues were addressed: (I) What was the level of variation within *P. gilbertii* (II) Are animals in the captive population adequately reflecting levels of variation in the wild population? and (III) determine the paternity of some captive animals.

Luikart, G., Painter, J., Crozier, R. H., Westerman, M. and Sherwin, W. B. (1997). Characterization of microsatellite loci in the endangered long-footed potoroo *Potorous longipes*. *Molecular Ecology* **6**: 497-498.

Sinclair, E. A., Danks, A. and Wayne, A. F. (1996). Rediscovery of Gilbert's potoroo, *Potorous tridactylus* in Western Australia. *Australian Mammalogy* **19**: 69-72.

Sinclair, E. A. and Westerman, M. (in press). Phylogenetic relationships within the genus *Potorous (Marsupialia*: Macropodidae) using allozyme electrophoresis and sequence analysis of the cytochrome *b* gene. *Journal of Mammalian Evolution*

P33

Towards cloning of the creC and creD genes: two genes involved in carbon catabolite repression in *Aspergillus nidulans*

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To gain undersatnding of the mechanism of carbon catabolite repression in *Aspergillus nidulans*, various mutants were selected which demonstrated a reduced ability to repress genes normally under carbon catabolite repression. A number of mutations generated mapped to a locus on chromosome II and named *creC* (Hynes and Kelly 1977). All strains containing mutations in *creC* displayed a reduced ability to repress a number of genes in glucose containing media. The *creD34* mutant was selected as a suppressor of the *creC27* mutant and mapped about 5 map units from *creC* (Kelly and Hynes 1977).

A molecular approach is currently underway to clone the *creC* and *creD* genes. The approach makes use of a previously cloned *A. nidulans* gene *glnA* which is located one map unit from *creC* on chromosome II. Cosmids containing the glnA gene have provided a starting point for a chromosome walk to the *creC* gene. The cosmids containing *creC* have been identified via complementation of mutant phenotypes caused by *creC*.

P34

Comparison of morphometric and molecular data sets for populations of *Paratemnopteryx stonei* Roth (Blattellidae)

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Adults of the tropical cave cockroach *Paratemnopteryx stonei* (Blattellidae) were collected from 7 caves covering 4 karst regions in tropical North Queensland to investigate the degree of geographical variation between populations at the morphological and molecular level. Measurements were made on 11 body dimensions (body length; femur, tibia, and tarsus length of hindleg; cercus length; eye length and width; tegmen length and width; and pronotum length and width), and analysed using Canonical Discriminant Analysis (CDA). Plots of the CDAs for males and females showed a clear separation of the populations with respect to geographic location, and to a lesser degree between caves within the same karst region. Currently, sequence data from the second internal transcribed spacer region of the nuclear ribosomal DNA are being analysed, and the results will be discussed in conjunction with that of the morphological studies.

P35

Possible role for wild genotypes of *Pisum* spp. to enhance *Ascochyta* blight resistance in pea

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Current field pea cultivars lack sufficient resistance to control ascochyta blight caused by *Mycosphaerella pinodes* (Berk. & Blox.) Vestergr. in Western Australia. Higher levels of resistance occur in *P. sativum* landraces and *Pisum fulvum* L. but possible linkages between resistance genes and undesirable agronomic traits and difficulties in crossing the two species have deterred this approach to improving disease resistance. *P. fulvum* JI 1006, as the pollen parent, was crossed to *P. sativum* cv.Wirrega using the wildtype *P. sativum* JI 252 as a bridging cross. JI 1006 and JI 252 both respond to *M. pinodes* infection by inducing a rapid hypersensitive response, one mechanism of resistance. The F_2 from Wirrega x (JI 252 x JI 1006) was screened as 17 - 20 day old seedling for responses to *M. pinodes* infection in a controlled environment. Plants with the highest levels of resistance were screened as F_3 progenies in a field trial for their responses to natural *M. pinodes* infection. Compared to cv. Wirrega, 9% of the lines were more resistant for leaf and stem disease and nine lines flowered at the same time or earlier than Wirrega. However, even the most resistant line had 30% of the foliage destroyed by disease. Therefore, a second resistance mechanism which retarded *M. pinodes* hyphal penetration in leaves (*P. sativum* SA 1160) was combined with the hypersensitive response in the cross SA 1160 x (JI 252 x JI 1006). Despite the wildtype growth habit of these plants when compared to cv. Wirrega, the level of resistance to disease was significantly higher than for any plant in the original F_3 population. It is suggested that breeding programs should concentrate first on maximising field resistance through isolation of some optimal combinations of resistance mechanisms before turning to improvement in agronomic performance through backcrossing to a commercial cultivar.

P36

Genetic variation within and between populations of *Posidonia sinuosa* Cambridge and Kuo

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Posidonia sinuosa is a hermaphroditic seagrass which is endemic to southern Australia. The genetic system of *P. sinuosa* has not been studied. Some populations of a closely related species, *Posidonia australis* Hook.*f.*, have been found to be highly genetically variable, with variation between populations. Given that the two species occur sympatrically and have similar breeding systems, it was expected that *P. sinuosa* would also have a highly variable genetic system. Isozyme analysis of a large monospecific *P. sinuosa* meadow in Warnbro Sound, Western Australia, found polymorphism at only 1 locus out of 19 examined. Although more extensive sampling of other populations of *P. sinuosa* is required, preliminary surveys have failed to reveal allelic differences between populations. The decreased variation in *P. sinuosa* compared with *P. australis* may be attributed to differences in their mating systems and disturbance ecology. Both species flower simultaneously. In June, 1997, lower flowering frequencies were observed for *P. sinuosa* than for *P. australis* populations in Shoalwater Bay, Western Australia. Both species have been observed in disturbed habitats but the rhizome of *P. sinuosa* is more robust. These two factors may explain the differences between these two species. General conclusions regarding seagrass genetic systems should not be drawn on the basis of habitat and breeding system similarity. The low level of genetic variation observed in *P. sinuosa* suggests that a combination of factors other than breeding system may be responsible for decreased variation in this species.

P37

The molecular outcome of recombination events associated with the *cog* recombinator of Neurospora

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Multiple polymorphisms distinguish Emerson and Lindegren strains of *Neurospora crassa* within the *histidine-3* gene and in its distal flank. Restriction site and sequence length polymorphisms in an overlapping set of PCR products covering this region have been used to identify the parental origin of DNA in histidine-prototrophic recombinant progeny of crosses between the strains. 38% of conversion tracts are interrupted. In progeny from *rec-2*$^{+}$ crosses, where the recombination hotspot *cog* is inactive, conversion tracts are short, most are not initiated at *cog* and either chromosome seems equally likely to be converted. Where the absence of *rec-2*$^{+}$ permits activity of *cog*, conversion appears to originate at *cog* and conversion tracts are up to 5.9 kb long. The chromosome bearing *cog*^{L}, the dominant allele which confers a high frequency of recombination, is almost invariably the recipient of information.

Although 47% of the prototrophs have at least one crossover between the flanking markers, only 29% of conversion events have a crossover sufficiently close to the conversion tract for association to be likely. This may suggest that a conversion intermediate containing paired Holliday junctions is frequently resolved in a way which cannot give a crossover, such as by a topoisomerase or by scission of one junction and migration of the second to the resulting nicks. Less frequent scission of both junctions, which may always result in a crossover, could explain the association. However, since crossing over and conversion appear unassociated at the *am* locus of Neurospora, the two events may proceed via unrelated mechanisms at both loci. The apparent association at the *his-3* locus may be a result of the relatively high frequency of both events in this region.

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Viable or Vulnerable: Population Genetics and Demography of the Endangered Grassland Daisy the Button Wrinklewort (*Rutidosis leptorrynchoides*)

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Habitat fragmentation is a major threatening process for species occupying Australia's native grasslands. Genetic erosion, inbreeding depression and increased demographic stochasticity can reduce the viability of small remnant populations. In this study we estimated genetic and demographic parameters for remnant populations of the endangered grassland daisy *Rutidosis leptorrhynchoides* ranging in size from 5 to > 100 000 plants. The species is cytologically complex with northern populations being primarily diploid (2n=22) and southern populations being mainly tetraploid (2n=44). Allelic richness at allozyme loci is positively related to the log of population size. Outcrossing rate is uniformly high (*t*m1), regardless of population size or geographic isolation. In contrast, size and isolation interact strongly to affect the degree of outcrossed paternal correlation (*r*p) within open-pollinated arrays such that small (<10) and medium sized (100's) populations isolated by >5 km have increased frequencies of full-sib families. Seed set in small diploid populations is on average lower and more erratic than that in larger populations, and measurements of pollen deposition onto stigmas suggests that this could be due to pollinator limitation. Variation in pollen viability was unrelated to population size. Thus, isolated remnant populations of less than 200 plants are likely to be genetically depauperate, to be prone to biparental inbreeding and to have reduced viability.

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Population Genetics of Tea Tree (*Melaleuca alternifolia*) using SSRs

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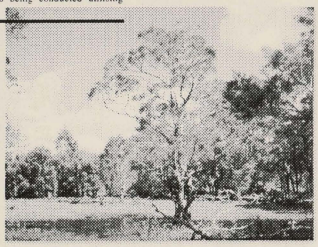
Tea Tree oil production from leaves of *Melaleuca alternifolia* is rapidly growing into a significant agricultural industry with the establishment in recent years of large areas of plantation crops. The oil contains monoterpene alcohols that are potent antibacterial and antifungal compounds, and is used in a growing variety of cosmetic and pharmaceutical products. Empirical observations over many years suggest that there is significant phenotypic diversity within the species. Considerable differences in oil yield and composition are of particular interest to commercial producers and suggest significant genotypic variability. As a result, an investigation of genetic diversity in *M. alternifolia* is being conducted utilising microsatellite DNA markers.

The aim of this project is to characterise a *M. alternifolia* microsatellite library for studying population genetics and relating genetic markers to oil quality attributes. Plant material is being sampled from the entire distribution range of the species. Leaf material has been collected for genetic analysis and oil yield and composition studies. This investigation will also provide preliminary information on the use of recently developed enrichment techniques for large scale microsatellite characterisation.



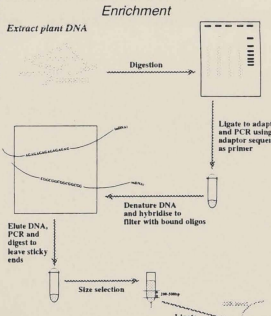
DNA microsatellite technology produces one of the most useful molecular marker systems developed to date. Also known as Simple Sequence Repeats (SSR), microsatellites are 2–6 bp recurring-sequences grouped in 10 or more tandem repeats. In plants, the frequency of SSRs has been estimated at 2·5 to 8·0 per centiMorgan, making SSRs relatively common and widespread.

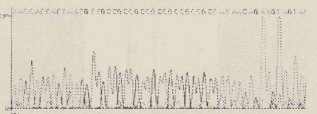
These regions, inherited in Mendelian fashion, are codominant and show high levels of heterozygosity. High polymorphism originates from slippage events during DNA replication resulting in changes in the number of repeats. The regions flanking repetitive sequences are conserved and can be used to design primers. As a result the detection of SSRs polymorphism requires simple PCR technology. The size difference of amplified products represent allelic variation and can be detected by gel electrophoresis (conventional or automated).

Once loci have been identified, SSR technology is simple and highly informative. Microsatellite markers are hypervariable, codominant, widespread, abundant, highly reproducible and amenable to automation. However, until recently, the identification of loci has been highly labour intensive and costly.

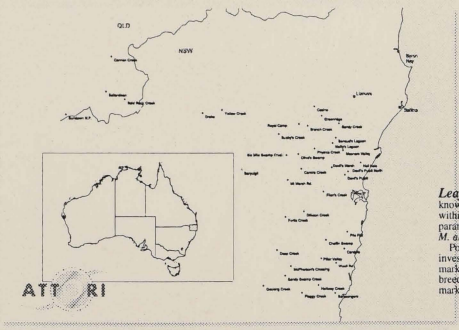
New enrichment techniques have considerably accelerated the detection of useful microsatellite loci. Conventional protocols involved the preparation of a DNA library containing size selected DNA fragments of the organisms under study. Large numbers of successfully transformed colonies were screened for the presence of useful repeat sequences within their insert.

Modern enrichment techniques pre-screen the DNA fragments prior to transformation. This way, only inserts containing selected repetitive sequences are used for the transformation process, highly increasing the rate of successful SSR characterisation.





Two-hundred sequences of inserts originated through the enrichment technique have been analysed so far for *M. alternifolia*. Of these, 87% contain unique microsatellites, with an average of 15 repeats per SSR. Equal amounts of dinucleotide and trinucleotide repeats have been obtained with $[AG]_n$ being the most frequent repeat. Primer design is currently defining how many of these SSRs can be used as functional markers for population genetics studies and mapping purposes.



Leaf samples have been collected from 15 trees at each of 40 sites throughout the know geographic range of Tea Tree providing information from 600 trees. Relatedness within and between discrete populations will be investigated and population genetics parameters will describe polymorphism, heterozygosity, inbreeding and genetic flow in *M. alternifolia*.

Potential association of microsatellite markers with specific chemotypes will also be investigated. Microsatellite technology will provide a powerful tool for analysing marker distribution throughout *M. alternifolia* as the foundation for a very productive breeding program. Ultimately a Tea Tree genetic map will be generated based on SSR markers linked to specific oil phenotypes.

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