ARC Research Collaboration Network: Environmental Futures

In Partnership with the Combined Invertebrates Conference

The Evolution of Australia Over The Last 25 Million Years: The Consequences of Aridification and Ice Age Cycles

Organisers: David Yeates, Margaret Byrne, Mike Crisp, Mike Lee, Steve Hopper.

Thursday 8 Dec., Manning Clarke Centre, Lecture Theatre 1 ANU.

Consequences of the Aridification of Australia since the beginning of the Tertiary: Evolutionary Radiations in the Biota (1) Lecture Theatre 1 (Co Chairs David Yeates/Mike Crisp)
8:30-9:30 **Keynote: *Robert Hill*** The Palaeobotanical record of aridification in Australia
9:30-10:00 ***James Bowler*** Threshold Events in Australia's Late Cenozoic Climatic History
10:00-10:15 ***Nick Porch*** *and* ***Peter Kershaw*** Quaternary Environments
10:15-10:30 ***David Bowman*** Extreme evolution and adaptive shock – the forging of the Australian biota by drought, fire and overkill
Morning Tea 10:30-11:00
11:00-11:15 ***Michael Bayly, Pauline Ladiges* et al.** Phylogeny of the eucalypts - from rainforest to desert
11:15-11:30 ***Daniel Murphy* et al.** Phylogeny and diversity of Australian *Acacias* (Leguminosae)
11:30-11:45 ***Mike Crisp* and Lyn Cook** When did the Nullarbor become a barrier? The timing of divergences between south-eastern and south-western Australian plant lineages
11:45-12:00 ***Ken Aplin*** Taxic to community level adaptations to aridification in the Australian terrestrial mammal fauna
12:00-12:15 ***Michael Lee*** Lineage-specific effects of aridification on agamid lizard diversification
12:15-12:30 ***Andrew Hugall*** Spatial Distribution of Phylogenetic Diversity in Camaenid Land Snails of Eastern Australia
12:30-12:45 ***Craig Moritz*** Speciation processes in the Australian rainforest biome
Lunch 12:45-2:00
Consequences of the Aridification of Australia since the beginning of the Tertiary: Evolutionary Radiations in the Biota / Fine scale Phylogeography and speciation Lecture Theatre 1 (Co Chairs David

Rowell/Margaret Byrne)	
2:00-2:30	***Sonja Scheffer* et al.** Coevolution, Host-Use Pattern, and Radiation in the *Fergusonina-Fergusobia* (fly-worm) galling mutualism on Australasian Myrtaceae
2:30-2:45	***Lyn Cook* and Penny Gullan** Radiation of gall-inducing scale insects on Myrtaceae through the Cenozoic
2:45-3:00	***Remko Leijs, Steve Cooper et al.*** Speciation modes of diving beetles in the arid zone of Australia
3:00-3:15	***Christine Lambkin, David Yeates et al.*** Divergence Time Estimates for Australia's stiletto fly radiation
3:15-3:30	***Michael McLeish and T. Chapman*** Australian gall-thrips on *Acacia* and the formation of xeric biomes
Afternoon Tea 3:30-4:00	
4:00-4:15	***Margaret Byrne*** Comparative phylogeography reveals historical fragmentation in the ancient landscape of south-western Australia
4:15-4:30	***Steve Cooper et al.*** Comparative phylogeography of stygofauna from calcrete aquifers of central Western Australia: speciation patterns in subterranean islands
4:30-5:00	***Paul Sunnucks*** Fine scale comparative phylogeography and speciation: the view from fallen timber in temperate montane Australia
5:00-5:30	***Steve Trewick*** Grasshopper speciation in semi-arid New Zealand
7:00	Dinner at Turkish Pide House Cnr Moore St and Barry Drive, phone 6249 8700

Friday 9 Dec. Manning Clarke Centre, Lecture Theatre 3, ANU

Australian Phylogeography and Speciation: Co Chairs David Rowell and Margaret Byrne
9:30-10:00 **DNA Barcoding** Symposium, MCC Lecture theatre 1
10:00-10:15 ***Mark Scriber*** Recombinant hybrid mountain species of swallowtail butterfly; origins and danger
10:15-10:30 ***Alastair Richardson*** The geographic ranges of Tasmanian crayfish: extent and pattern
Morning Tea 10:30-11:00
11:00-11:15 ***Karen Edward*** Many legs … tiny distances - A study of Speciation and Biogeography of a Gondwanan millipede genus within Southwestern Australia
11:15-11:30 ***Michelle Guzik*** Identifying mechanisms of speciation in subterranean cave organisms
11:30-11:45 ***Amber Beavis*** A comparative phylogeographic study of two niche differentiated funnel web spider species
11:45-12:00 ***Jody Taylor*** A tale of two flatties: different responses of two terrestrial flatworms to past environmental climatic fluctuations at Tallaganda in south-eastern Australia
12:00-12:15 **Lyn Cook** Phylogeography of *Apiomorpha munita*: interplay between host-specificity, chromosomes and geography?
12:15-12:30 ***Hayley Sharp*** Chromosomal Phylogeography of *Delena cancerides*
Closing Ceremony, Combined Invertebrates Conference 12:30-1:00 MCC Lecture Theatre 1
Lunch 1:00-2:00
2:00-2:30 **David Yeates and Margaret Byrne** Introduction/merging activities??
2:30-2:45 **Craig Moritz** Phylogeography, recent analytical approaches and the potential to integrate paleo-environmental information with molecular data
2:45-3:00 **Leo Joseph** TBA
3:00-3:15 **Andrew Hugall** Climatic modelling in phylogeography
3:15-3:30 **Mitzy Pepper and Scott Keogh** Does Geological History Shape Genetic Diversity in Pilbara Geckos?
Afternoon Tea 3:30-4:00
4:00-4:15 **Gaye McKinnon** Eucalypt phylogeography in SE Australia
4:15-4:30 **John Chappell** Changing habitats: Late Cenozoic aridity in the Australian interior

4:30-4:45	**Paul Sunnucks** for **Luciano Beheregaray** - Aquatic phylogeography
4:45-5:00	**Dan Schmitt** Phylogeography in freshwater and marine systems
5:00-5:15	**Mark Harvey** Targetting short-range endemics to maximise phylogeographic content
5:15-5:30	**Nick Porch** The subfossil record of beetles in Australia
Evening Free	

Saturday 10 December Manning Clarke Centre, Moran G007, ANU

ARC Environmental Futures Workshop **The Evolution of Australia Over The Last 25 Million Years: The Consequences of Aridification and Ice Age Cycles**
9:00-9:15 Introduction**: David Yeates** and facilitator **Robert Marshall,** Knowledge Teams International
Morning: Seeking Synergy
9:15-10:55
Morning Tea -11:00-11:30
Forming Groups
11:30-12:30
Lunch 12:30-1:30
Developing a roadmap
2:00-3:30
Afternoon Tea 3:30-3:45
3:45-400 Final summary – activities separate, linked or joined
4:00-4:15 Final summary – activities separate, linked or joined
4:15-4:30 Next meeting planning
4:30-4:45 Next meeting planning
4:45-5:00 Delegates depart
5:00-5:30

ARC ENVIRONMENTAL FUTURES WORKSHOP

DRAFT PROGRAM FOR DAY 3

ANU, MANNING CLARKE CENTRE, MORAN G007

CANBERRA, 10 DECEMBER 2005

Objectives

1 Agree on an Agenda for the Network for the next 3 years

2 Identify opportunities for synergy in inter-disciplinary and cross organisational work teams

3 Develop and agree on a roadmap to get us to the next meeting of the network and to ensure that it is a productive and effective meeting

FACILITATORS' BRIEF

Day 3 – Saturday, 10 December 2005

DAY/ TIME	TOPIC	PURPOSE – KEY POINTS	PROCESS	RESOURCES
9.00 am	**Introduction and Welcome** **David Yeates** **Bob Marshall**	Outline of Objectives of the Day Outline of Processes for the Day Inter-disciplinary Research Principles of Dialogue	Brief presentation and questions	Network Goal Posters
9.15 am	**Information Preparation**	Sharing information about participants' capabilities and interests	Prepare "Aprons" or Sandwich Boards What I what to explore in this network What I can contribute What I can commit to What I would like form others	Flip Chart Paper 3M post it flip chart paper (5X) Flipchart pens
9.35 am	**Sharing Information**	Mingle and greet	Participants mingle and greet one another. Interact with people that you know less well. Read aprons, explore etc	Floor space
9.50	**Seeking Synergy**	Formation of groups of potential synergy **Rule**: You can accept, bid but not reject	Various Groups, 4 or 5 iterations, eg Max diff, Disc, Geol period, Shoe style Focus Questions for group formation Groups form talk What is the logic or organising principle of each group?	Floor Space
10.30	**"Finalisation" of Groups**	Final Mix	Form groups that you would like to work with for the rest of the day and leading up to next meeting.	

DAY/ TIME	TOPIC	PURPOSE – KEY POINTS	PROCESS	RESOURCES
10.40	**Morning Tea**			
11.00	**Groups Meet**	What can we know? What do we know now? What do we need to get there? Do we have the resources?	Breakouts Appoint Facil, Recorder, Spokesperson Rotate Use affinity diagrams?	Flip Charts Post its?
12.00	**Report Back to Plenary**	Brief report back from each group on progress		
12.30	**Lunch**			
1.30	**Check In**	Brief check on progress and processes for the afternoon. Outline next steps	Identify best way to go forward, Together as one group or two affiliated groups?	
1.45	**Developing a Roadmap to the Next Meeting**	Groups meet to develop a roadmap to the next meeting	**Focus Questions:** What info or data do we need to have by then? What can we commit to Who do we need to invite? When ? Where? Host? Who is going to do what?	
3.00	**Report Back to Plenary**	Report back on focus questions		
3.30	**Afternoon Tea**			
3.45	**Summary & Next Steps**	Summary of agreements and commitments		
4.30	**Departures**			

ARC Environmental Futures Workshop
The Evolution of Australia Over The Last 25 Million Years: The Consequences of Aridification and Ice Age Cycles

Group 1 South West and Arid Zone David Yeates

How have Ice Age climatic change shaped patterns of speciation and diversification on the arid zone?

Relative influence of historical Quaternary processes on biota of SW WA

Do Australian evolutionary radiations interact synergistically and catalytically?

Evolution of the flammable biomass (i.e. non-rainforest)

How was the biota of arid-zone refugia (eg C.Aust, Pilbara) assembled and over what time frame

What have been the mechanisms of differentiation in the arid zone? History vs ecology

What has shaped present day genetic architecture of the arid zone species?

Is the onset of intense aridification at 15mya reflected in radiations of biodiversity?

Do radiations in animal taxa correlate with radiations in plant taxa?

How do evolutionary processes affecting vegetation in the South-West differ from those in South-Eastern Australia?

Group 2 Monsoon Tropics **David Bowman**

Evolutionary impact of the Australia Summer monsoons. When was the monsoon onset?

Relative influence of historical Quaternary processes on biota of Northern Australia

Group 3 Eastern Mesic including Wet Tropics **Dot Steane**

How much of the Australian Forest biota is ‘semi-arid’ origin vs. true relictual forest origin?

Group 4 Methods **Mike Lee**

Data Layers Dan Rosauer

Molecular divergence estimation Mike Lee

Are there concordant splits at certain points in time between unrelated groups?

How do patterns of diversification compare for different organisms? Congruence/differences

What can we learn from overlapping spatial patterning in diverse phylogenies?

Do arid and mesic clades have consistently different diversification patterns?

Did the onset of aridification 25mya cause a pulse of diversification across the biota?

To what extent did evolutionary dynamics over the mid-Miocene → late Quaternary differ between mesic and arid biomes?

Coalescence and speciation Craig Moritz

Have common speciation processes driven Cenozoic diversification of the biota? Or did each group do its own?

What is the role of long distance dispersal during climate driven speciation and adaptation?

What were the dynamics and processes of species range change since the last glacial maximum?

Can we map biodiversity processes?

Palaeoenvironments Margaret Byrne

Can we create a robust model of Quaternary climate and vegetation change and test impacts on biota?

What can geological history and data tell us about diversification in the arid zone?

Did the onset of aridification coincide with arrival of new migrants from outside Australia?

Are desert regions all related? i.e. monophyletic or not?
What is the relative influence of two major aridification periods on species radiations?

What are the main periods of climatic change in different parts of Australia in the past 30-25my?

What climatological and environmental processes drove radiations in the Australian biota ~9-3mya – were these different South vs. North?

Were deep splits within taxa with diverse life histories and from different parts of the continent (Pliocene/Miocene) caused by the same process and at the same time?

Filling the ‘gap’ in the fossil record from the Karstic landscapes of Australia

How does New Caledonia relate to Australia? (biogeographic links)
-need geoplogy
-need phylogenies of a range of organisms
-need time scale

How do the divergences of Australian fauna reflect the geological separation of Australia from the various continents?

Does the Paleo environment record predict the relative diversification and extinction patterns in organismal groups according to their ecology?

Can or How do we develop spatial-temporal analysis of bioregional scales?

How can we combine paleo-environmental and phylogenetic/phylogeographic knowledge to better predict biodiversity response to climate change?

Differential effects of climate change on modern biota (ie will groups respond differently?)

Group 5 Conservation Dan Faith

What are the conservation and management implications of our knowledge of range changes in the past?
What do we need to know to minimize species extinctions as the climate changes?

Does phylogeny/phylogeography help us with planning for overall biodiversity?

Do environmental/habitat gradients contribute to speciation process?

Altitude vs. Latitude migrations as a result of climate change

Co-incidence of major radiations?

Coincidental patterns of diversification across groups across regions

What does the past mean for the future? Can our knowledge of he past changes help us to predict future changes?

Matrix to Operationalise Activities based on Questions

	SW+Arid Zone	Monsoon	E Mesic (+WT)
Palaeontological data	-- ---------→		
Fossils Soils Climate Time scales			
Methods + data analysis	--→		
Conservation	--→		
Phylogenies + distn (Clades->populations)	--→		

5 Subgroups coalesced:

Group 1 South West and Arid

Coordinator David Yeates

Ken Aplin
Jim Bowler
Margaret Byrne
Steve Cooper
Leo Joseph
Scott Keogh
Remko Leijs
Dan Murphy

Group 2 Monsoon Tropics

Coordinator David Bowman

Gillian Brown
Pauline Ladiges
Gary Nelson
Dan Schmidt

Group 3 Eastern Mesic including Wet Tropics

Coordinator Dot Steane

Andy Lowe
Rene Vaillancourt

Group 4 Methods and Data Analysis

Coordinator Mike Lee

Lyn Cook
Mike Crisp
Ross Crozier
Andrew Hugall
Chris Lambkin
Matt Phillips
Dan Rosauer
Mike Schwarz

Group 5 Conservation

Coordinator Dan Faith

Don Driscoll
Gay McKinnon
Craig Moritz
Paul Sunnucks

Sharing Information

Sharing Information

The questions are sorted into categories

Arid Zone group listening to Jim Bowler

Conservation Group making plans

Methods Group in the sun

What were the responses of the Australian biota to climatic change during the Tertiary and Quaternary?

What evidence would we need to establish this?

What do we know?
What do we need to know?
What can we know?
How do we get there?

Establish concise narrative of climatic change

- Determine chronology of aridification events (number and time)
- Determine magnitude of climatic change (how strong, seasonality and aridity)
- Determine spatial patterns in onset of aridification at continental scale (where/when)
- Determine climatic cycles in the Quaternary (duration, intensity and tempo)
- Determine spatial extent of climatic cycles, different influences in different regions?

Establish evidence from fossil assemblages

- Establish precise dates of macrofossil assemblages and palynology
- What major groups went extinct?
- Establish impacts on fossil assemblages by temporal comparison
- Establish the ecological impact on biomes
    - Is there physical evidence from fossils of climatic regime?
    - What was the role of nutrient poor soils-did it preadapt plants for aridification?
- What is the role of fire in defining biomes?
- What happened in mesic habitats (rf, etc)
- What was the extent of arid landscapes before 25 mya?
- What are the spatial changes in fossil assemblages

Establish evidence of radiation from phylogenies of major biotic lineages

- What do we mean by evolutionary radiations?
    - Are they adaptive radiations? How different does the rate of lineage splitting need to be?
- What groups are best to test the hypothesis?
    - A broad sample of dominant/iconic plant and animal lineages spanning different ecological guilds/functional groups, most diverse in xeric habitats.
    - Need to be groups with well understood taxonomy and distributions, with molecular data sets available, or available soon (at least 3 genes, appropriate taxon sample for question).
- For example:
    1. Acacia, Eucalyptus, another plant-pea group
    2. Phytophagous insects (on Acacia/Eucalyptus), predatory insects
    3. Vertebrates such as marsupials, bird lineages, lizards
    4. Snails from fragmented mesic patches??
- What pairs or other combinations may provide evidence of synergy or feedback loops between radiations?

- Do groups that radiated into the new xeric habitats diversify at a different (?greater) rate (or have a different signature of diversification) than those that diverged through fragmentation of an ancestral habitat (e.g. rainforest patch snails)?
- Is there evidence for major diversification in the Quaternary, or is this a period of lineage sifting, range modification, and some extinction?
- Not only concerned with arid-adapted groups. For example, mesic adapted groups may have radiated via habitat fragmentation and allopatric divergence during the Tertiary. Are these “evolutionary radiations”? What happened to rainforest adapted groups - extinction and fragmentation??

Establish evidence from phylogeographic studies

- What species groups are most impacted (less mobile?)
- What were the impacts (fragmentation, range contraction, extinction)?
- What regions were impacted?
- Was the scale of impact different between regions?
- Identification of major events through comparative studies across major groups of organisms (plants/animals)?
- Are the distributions of relict and recently evolved species comparable with major events

Are there different environmental factors at play in the Tertiary and Quaternary?

- Tertiary-increasing aridification and seaonality of rainfall over 25 mya
- Quaternary- 18 repeated cycles of hot/wet-cool/dry climates over 1.6 my
- Are these reflected in different impacts on the biota:
    - Tertiary extinction, evolutionary radiation into new biomes, range contraction and expansion
    - Quaternary range expansion/contraction, some extinction and little speciation via drift in allopatry?

To what extend does this unique history make the Australian biota unique?

- Old, stable landscape
- History of major climatic change leading to relatively recent major biomes containing major radiating groups, and fragmentation in old biomes
- Quaternary events leading to microstructuring of fragmented populations
- Scale and depth of genetic structuring different from that found in many other well studied systems (such as Europe and N America)

What methods need to be established or developed in the network?

- The best methods of dating lineage splits from molecular data (Sanderson, etc Thorne,Cooper, Bromham, Rambaut)
- The best methods of measuring changes in divergence rate, lineage-through-time analysis.
- Historical climatic modeling
- Dating of phylogenetc divergences
- Establishing and distinguishing between influences of processes (range expansion, contraction, colonization)

Palaeobotanical record of aridification

Robert S. Hill
Centre for Evolutionary Biology and Biodiversity, School of Earth and Environmental Sciences, University of Adelaide, SA 5005, and South Australian Museum, North Terrace, Adelaide 5000

The Early Cainozoic (Palaeogene) of Australia was characterised by warm, wet and humid conditions, and complex rainforests flourished despite prevailing high latitudes. The plant macrofossil record of this vegetation is well preserved in southeastern Australia, because abundant water is conducive to fossilisation. However, aridification of Australia commenced during the middle Cainozoic, possibly as long ago as 35 million years, and it became widespread by 20 mya. The record of arid-adapted Australian vegetation is not widespread, but some important indications exist. Even in the Palaeogene rainforests there is abundant evidence of scleromorphy, which is a primary response to low soid phosphorus, and these taxa appear to have been exapted for xerophytic (low water) conditions as they arose. The transition can be most clearly seen in the way the new species evolved to protect stomata from excessive transpirational water loss. The demise of species that had no capacity to adapt to dry conditions is also now reasonably well understood, and is best demonstrated amongst the many conifers that have a Palaeogene record in southern Australia, but are now extinct there, although they continue to survive in wetter environments elsewhere. There is little direct evidence of major evolutionary change (e.g. at the generic level) in response to aridification in Australia. However, evidence is mounting that this may have occurred within the Casuarinaceae, where *Allocasuarina* and *Casuarina* may be the result of aridification. A more tenuous example is the possible presence of a relative of *Callitris* in Early Oligocene rainforests in Tasmania. These specimens are very similar to *Callitris*, but probably cannot be placed in that genus. They are more than double the age of the oldest know *Callitris* macrofossils, and may provide direct evidence of the origin of at least one arid zone tree genus in Palaeogene rainforests.

Threshold Events in Australia's Late Cenozoic Climatic History

Bowler, J.M., School of Earth Sciences, University of Melbourne

Warm humid environments in Miocene time near 20Ma favoured widespread deposition of rainforest fed swamps and coals on land, with time-equivalent vast limestones at sea. These conditions, particularly well represented in southern Australian basins, terminated in Upper Miocene – Lower Pliocene time some 10-7 million years ago. This coincided with a global reduction in sea level associated with an isotopic signature of expanded Antarctic ice. This event, with immense implications for global carbon budgets, was associated with vegetation changes reflecting changes in E/P ratios with implications of at least temporarily increased hydrologic stress.

Major changes of this interval (10-7Ma) gave way to the return of warm, humid conditions coincident with the later collapse of Antarctic ice and global rise in sea levels near 6Ma. For the next 4-5 million years, small amplitude climatic oscillations are reflected in both isotopic and sea level records; earlier marine limestone deposition gave way to widespread siliceous sands. Relatively warm humid conditions are substantiated by deep lateritic weathering reflecting acidic soil profile conditions, by expansion of fresh water lakes and by evidence of mega-channel conditions in the early Murray River history.

Major change in Mid-Pleistocene (near 1Ma) are registered in the widespread appearance of alkaline (calcareous) soil profiles, simultaneously with the onset of major dune building, the signature of major aridity. This entirely new set of landscape conditions coincided with the onset of 100Ka cyclicity 1 million years ago, with major changes in wind and wave regimes suggesting important cause and effect relationships. Seasonal to decadal amplification of E/P variability became a characteristic feature of Late Pleistocene glacial-interglacial cycles.

Within the last glacial cycle, major changes in lake water balance defines greatly amplified aridity during the glacial maximum near 20Ka.

Responses of the Australian Quaternary flora and vegetation to climate forcing and human impact

Peter Kershaw, Nick Porch (presenter) et al.
School of Geography and Environmental Science
Monash University, Clayton, Vic. 3800.

Northern hemisphere insolation is the dominant signal in most marine and terrestrial climate proxies due to the strong influence of ice volume and temperature variation over much of the globe. This signal is most diluted in low latitudes, where precipitation is the dominant climatic variable, and especially in the southern hemisphere low latitudes where competing regional atmospheric and ocean circulation system influences are also effective. The situation is complex.

In the northern Australian region, terrestrial pollen and charcoal records, largely from marine cores covering the last 150,000 to 500,000 years, exhibit a mix of signals that have appear to reflect ice volume, northern and southern hemisphere monsoon, and El Niño-Southern Oscillation (ENSO) forcing with the ENSO signal most pronounced in the Pacific region and the southern hemisphere monsoon signal dominant adjacent to the Indian Ocean. Complexity is also evident with changes in the influence of climate forcing factors through time. Clear changes in forcing within the Australian region centred on about 300,000 years ago suggest that the so-called 'Mid Bruhnes Event' may result from atmospheric and oceanic changes associated with alteration of the Indonesian Throughflow as Australia continues its continental movement into Southeast Asia. Vegetation changes are particularly marked within the last 50,000 years and have been attributed to increased biomass burning with the arrival of people in Australia rather than climate, although recent evidence suggests that variation in ENSO activity may have been a contributing factor.

In southeastern Australia, pollen records, from volcanic crater lake sediments, cover a substantial proportion of the Quaternary period, i.e. the last 1.8 million years. One record has revealed remarkably rapid oscillations between rainforest and sclerophyll vegetation at the very beginning of the Quaternary that demonstrate regional insolation forcing before the northern hemisphere ice volume became such a powerful driving force. Another site indicates that the change from southern to northern hemisphere insolation forcing occurred about a million years ago, at the transition from the Early to Mid Pleistocene, and was accompanied by the demise of the 'last' Tertiary taxa and emergence of, during wet interglacials, present day cool temperate rainforest. For some reason, possibly related to vegetation sensitivity, there is no clear signal of alteration of vegetation and biomass burning with the arrival of people in the southern part of Australia.

Extreme evolution and adaptive shock - the forging of the Australian biota by drought, fire and overkill

David M.J.S. Bowman
Wildlife and Landscape Science
School for Environmental Research
Charles Darwin University
Darwin
Northern Territory 0909
Australia

Summary

The many peculiarities of Australian biogeography are explicable in terms of evolutionary response to ecological extremes. I demonstrate this point by considering three related cases: (1) the dominance of evergreen trees in the Australian monsoon tropics, one of the most extreme seasonal climates on Earth; (2) the unique tolerance of eucalypts to landscape fire; and (3) the successful introduction of large herbivorous mammals that have filled niches made empty following the extinction of the late-Pleistocene megafauna. The success of evergreens in the Australian monsoon tropics is consistent with theoretical cost-benefit analysis of leaf function only if the extremely capricious nature of rainfall patterns and the deep weathering of the Tertiary regolith are acknowledged explicitly. Both anatomical and molecular phylogenies do not support the widely held view that the geologically recent Aboriginal landscape burning was a major driver in the evolution or geographic dominance of eucalypts. Rather these patterns are ancient and were possibly driven by ignitions from lightning storms associated with the Australian summer monsoon. Nonetheless, the colonisation of Australia by humans around 40-50,000 years ago changed fire regimes and it is possible that this contributed to the overkill of the marsupial megafauna. Modelling shows that this extinction event preferentially affected animals of large body mass, a pattern consistent with a chronic mortality pressure from the human colonists. Large animals were more vulnerable to extinction because they have longer generation lengths than their smaller counterparts and were less able to adapt to a novel chronic selection pressure. Although some of the mammal populations survived Aboriginal impacts, their populations were rendered vulnerable to the chronic ecological impacts that followed European settlement, such as the introduction of predators, stock and changed fire regimes. This latter point is illustrated with the impact of introduced Africa grasses that have triggered a grass-fire cycle. The case study underscores the need to contextualise ecological extremes in terms of both evolutionary history and population ecology.

Biosketch

Professor David Bowman is the former Director of the Australian Research Council Key Centre for Tropical Wildlife Management and leader of Wildlife and landscape Science Theme, School for Environmental Research, Charles Darwin University. He is also an adjunct professor at Centre for Resource and Environmental Studies, The Australian National University. In collaboration with numerous colleagues he uses a range of tools, including remote sensing and geographic information analyses, stable isotopes, ecophysiological analyses, mathematical modelling, biological survey and molecular analyses to understand how Australian landscapes have evolved in response to climatic change, varying fire regimes, the introduction of large vertebrate herbivores and the impacts of contemporary and prehistoric management.

Phylogeny of the eucalypts — from rainforest to desert

Ladiges, Pauline Y. [1], Michael Bayly[1], Carlos Parra-O[13] and Frank Udovicic[2]

[1]School of Botany, The University of Melbourne, Vic. 3010, Australia: p.ladiges@unimelb.edu.au
[2]Royal Botanic Gardens, Melbourne, Birdwood Ave, South Yarra, Vic. 3141, Australia
[3]Instituto de Ciencias Naturales, Universidad Nacional de Colombia, A. A. 7495, Bogotá, Colombia

Abstract:
The eucalypt group includes seven genera, including relictual rainforest taxa of restricted distribution and species-rich taxa that are widespread in drier environments. Three of the rainforest taxa, form a well supported clade with *Allosyncarpia* from Arnhem Land the sister taxon to *Eucalyptopsis* of New Guinea and the eastern Indonesian archipelago, and *Stockwellia* from the Atherton Tableland in north-east Queensland. The monotypic *Arillastrum* is endemic to New Caledonia, and based on a vicariance hypothesis and the age of fossil eucalypt pollen, we argue that the eucalypt group extends back to the Late Cretaceous. The more species-rich *Angophora*, *Corymbia* and *Eucalyptus* dominate the sclerophyll vegetation of Australia.

Recent analyses of the largely tropical bloodwood genus *Corymbia* based on ETS and ITS sequences support the monophyly of the genus and identify two major clades, with overlapping biogeographic patterns. The two clades are: (1) the red bloodwoods (sect. *Rufaria* and sect. *Apteria*) and (2) the spotted gums (sect. *Politaria*, Eastern Australia), yellow bloodwoods (sect. *Ochraria*, Eastern Australia) and ghost gums (sect. *Blakearia*, northern Australia & New Guinea), in that phyletic order. Among the red bloodwoods, relictual taxa occur in south-western Australia (clade of 3 species) and eastern Australia (1 species), with all other red bloodwoods (64 species) forming a northern clade in both dry and wetter regions – Pilbara, Western Desert, Kimberley, Arnhem, Queensland and New Guinea. The biogeographic patterns, including the south-west/eastern disjunctions, suggest that differentiation of various bloodwoods lineages pre-dates mid-Miocene aridity.

Phylogeny and diversity of Australian acacias (Leguminosae)

Murphy, Daniel J. (1) Gillian K. Brown (2) & Pauline Y. Ladiges (2)
(1) Royal Botanic Gardens Melbourne, Birdwood Ave, South Yarra, Vic. 3141;
(2)School of Botany, The University of Melbourne, Parkville, Vic. 3010

Acacia (subgenus *Phyllodineae*) in Australia is a diverse plant group with over 950 species, almost all of which are confined to the Australian continent. The majority of species are characterised by the presence of phyllodes, although there are two species groups with bi-pinnate adult foliage. DNA evidence supports the monophyly of Australian *Acacia,* and has revealed the sister taxon to be in the tribe Ingeae. Within the *Acacia* clade relationships are more problematic and have remained largely unresolved. It is now clear that most of the classified sections are not monophyletic; instead there are a large number of informal species groups, falling into three main clades that encompass enormous morphological diversity.

To investigate area relationships within Australia, two divergent clades were compared. The first clade includes groups of species related to *Acacia victoriae*, *A. murrayana* and *A. pyrifolia*, which grow predominantly in the arid zone (Eremea). The second clade was section *Botrycephalae*, which traditionally includes all eastern Australian species with bi-pinnate adult foliage. Notably higher levels of sequence variation were found in the arid zone clade, despite lower taxonomic diversity, than in the comparatively species-rich *Botrycephalae* clade. This is indicative of the older patterns underlying areas of endemism in the Eremean zone in comparison to the more recent radiation of the eastern Australian *Botrycephalae*.

When did the Nullarbor become a barrier? The timing of divergences between south-eastern and south-western Australian plant lineages

Crisp, M. D. and L. G. Cook
School of Botany and Zoology, The Australian National University, Canberra, ACT 0200, Australia.

The temperate floras of south-eastern and south-western Australia share many lineages (genera and species groups) but have few species in common. The Nullarbor Plain, which lies immediately north of the Great Australian Bight, comprises a barrier that divides many allopatric sister taxa. It has a depauperate arid-adapted flora, dominated by chenopods, that also extends across central Australia. The sister taxa must have diverged either when the barrier was formed or when it was subsequently breached. Hypotheses vary about the nature and origin of the barrier and include early-Cenozoic marine incursions, climatic cooling and drying in the Oligocene, elevation of the limestone plateau (an edaphic barrier) and aridification from the late Miocene. We will use a relaxed molecular clock to date east-west divergences in plant taxa and test which, if any, biogeographic events may be ruled out. Taxa will include *Banksia*, Casuarinaceae, Fabaceae and *Xanthorrhoea*. Comparisons will be made with studies on animal taxa.

Taxic to community level adaptations to aridification in the Australian terrestrial mammal fauna

Aplin, K.P.
(1) Australian National Wildlife Collection, CSIRO Sustainable Ecosystems, Australian Capital Territory, 2601

Abstract: Progressive aridification of the Australian continent through the late Tertiary had profound and sweeping impacts on the nature of the Australian terrestrial mammal fauna. Within the allochthonous groups (Marsupialia and Monotremata), many of the genera that dominate the contemporary mammal fauna of the drier, more open habitats of Australia arose during the latest Miocene to Early Pliocene, often with novel morphological adaptations to life in open habitats. At a community level, the same period witnessed a rise to dominance of three families of terrestrial mammals–Dasyuridae, Macropodidae and Diprotodontidae–with simultaneous declines or extinctions of other, formerly important lineages. From late Pliocene times there is little evidence for any directional change within the mammal fauna but much evidence of local adjustments in response to glacial cycles. The few mammal lineages that remained confined to closed forest habitats through this period show little evidence of diversification or morphological specialisation. Many lineages were presumably lost from isolated forest blocks such as southwestern Australia and the Lofty Ranges in South Australia. A possible autochthonous ‘New Guinean’ component to the mammal fauna is present in fossils faunas of early Pliocene age in eastern Australia, presumably derived from a latest Miocene period of faunal interchange across an exposed Torresian plain. Contraction and fragmentation of rainforest habitats since that time led to a contraction of this fauna to small regions of northeast Queensland where some, but not all, of these New Guinean lineages survive today. Rats and mice (family Muridae, of Asian origin) also arrived in Australia during the latest Miocene or earliest Pliocene. Much of the contemporary generic diversity in this family probably arose during a phase of rapid taxic and morphological differentiation, much of it occurring in more xeric habitats. The genus *Rattus* arrived even more recently and radiated into every habitat.

Lineage-specific effects of aridification on agamid lizard diversification

D. Rabosky[1], A.F. Hugall[2] and M.S.Y. Lee[2*]

[1]Department of Ecology and Evolutionary Biology, 237 Corson Hall, Cornell University, Ithaca, NY14853-2701 USA
[2]Earth and Environmental Sciences, University of Adelaide, Adelaide SA 5005.
*Presenter

A maximum-likelihood approach for evaluating shifts in diversification rates was applied to a nearly-complete, dated phylogeny of Australian agamid lizards constructed from nuclear and mitochondrial genes. The core Australian radiation consists of two clades, the *Amphibolurus* group occupying a range of habitats, and the *Ctenophorus* group found almost exclusively in arid areas. There is no evidence for abrupt shifts in net speciation rate within the *Amphibolurus* group. However, the *Ctenophorus* group shows two periods of increased net speciation rate, from 20 to 10 mya, and again from 5 mya to the present; these pulses might be linked to phases of rapid aridification. The contrasting diversification profiles exhibited by these sister-groups could be a consequence of their contrasting ecologies, with aridification only increasing diversification rates in the arid-adapted Ctenophorus group. Lineage-through-time analyses on heterogenous clades might miss patterns manifested in ecologically distinct subsets of species.

Spatial Distribution of Phylogenetic Diversity in Camaenid Land Snails of Eastern Australia

A. F. Hugall

Centre for Evolutionary Biology and Biodiversity, School of Earth and Environmental Sciences, University of Adelaide.

A species complete molecular phylogeny combined with fine scale distribution dataset can provide a geographical picture of biodiversity in terms of diversification rate, historical refugia and biogeographical boundaries. I have done this for the Camaenid Land Snails of Eastern Australia using a 327 taxa phylogeny and 10,000 point distribution dataset, giving a fairly continuous map at 50km scale for a transect from Cape York to the Victorian Border. Major rainforest regions, such as the Wet Tropics, are areas of accumulation and retention of historical diversity, with most recent local diversification occurring in areas peripheral to these domains and adjacent to major ecogeographical boundaries.

Coevolution, Host-Use Pattern, and Radiation in the *Fergusonina-Fergusobia* (fly-worm) galling mutualism on Australasian Myrtaceae.

Scheffer , S. (1), R. Giblin-Davis (2), G.Taylor (3), K. Davies (3), M. Purcell (4), M. Lewis (1), W. Ye (2), W. Thomas (5)
(1) Systematic Entomology Laboratory, USDA, 10300 Baltimore Av., Beltsville, MD, 20705 USA
(2) University of Florida Institute of Food and Agricultural Sciences, Davie, FL USA
(3) Adelaide University, Glen Osmond, South Australia, Australia
(4) USDA Australian Biological Control Laboratory, Indooroopilly, Queensland, Australia
(5) University of New Hampshire, Durham, NH USA

Fergusonina (Diptera: Fergusoninidae) flies and *Fergusobia* (Tylenchida: Neotylenchidae) nematodes together form galls on plants in the Myrtaceae in what appears to be a unique and obligate mutualism. *Fergusobia* nematodes are carried within the abdomens of all female fergusoninid flies. Fly oviposition into suitable host plant tissue includes the simultaneous deposition of juvenile nematodes, which are believed to be responsible for initial gall formation. Within the developed gall, both fly larvae and nematodes are phytophagous, feeding on gall tissue. At the completion of the fly larval stage, mated adult female nematodes enter the fly larva and persist through fly metamorphosis. The emerging female flies carry nematodes as they proceed to new host plant oviposition sites.

Fergusoninid flies and their associated nematodes are almost exclusively Australasian, with the vast majority being known from Australia. Plant hosts of the >65 species pairs collected so far are restricted to six genera within the Myrtaceae -- *Eucalyptus, Melaleuca, Corymbia*, *Syzygium, Metrosideros,* and *Angophora* -- with most species pairs appearing to be highly host-specific. Phylogenetic analysis of DNA sequence data from multiple genes from both *Fergusonina* flies and their associated *Fergusobia* worms will be used to address questions of cospeciation, host-use evolution, and the timing of radiations and other evolutionary events.

Radiation of gall-inducing scale insects on Myrtaceae through the Cenozoic

Cook, L. G. (1) and P. J. Gullan (2)
(1) School of Botany and Zoology, ANU, Canberra, ACT 0200
(2) Dept of Entomology, UCDavis, Davis, California, USA

There have been two large (> 100 species) radiations of gall-inducing scale insects on Myrtaceae in Australia. One of these, *Apiomorpha*, is restricted to eucalypts but the other clade comprises radiations on several speciose myrtaceous groups such as *Eucalypteae*, *Melaleuceae* and *Leptospermeae*. Phylogenies indicate that the gall-inducing scale insects form host-specific clades. In this presentation we will discuss the species radiation of the gall-inducing scale insects in respect of host-specificity, biogeography and timing of divergence events. We will also draw comparisons with the diversification and evolution of their hosts.

Speciation modes of diving beetles in the arid zone of Australia

R. Leijs (1,2), S.J.B. Cooper (2), C.H.S. Watts (2) & W.F. Humphreys (3).
(1) Department of Earth and Environmental Sciences, Adelaide University, SA 5000;
(2) South Australian Museum, Adelaide, SA 5000;
(3) Western Australian Museum, Perth, WA 6000.

Numerous isolated aquifers in arid Australia contain a rich invertebrate subterranean fauna, comprising various crustacean groups as well as the world's most diverse assemblage of subterranean diving beetle species. More than 100 new species have been recognised and this number is increasing with the sampling of new aquifers. Molecular phylogenetic research has shown that the subterranean beetles originated from a small number of surface species that independently made the transition from the surface to the subterranean environment *circa* 5 million years ago. Each aquifer is now home to 1 to 3 endemic species, which significantly differ in size and morphology.
Here we show that different speciation modes shaped the present diversity of the subterranean diving beetles: besides numerous cases of allopatric speciation, caused by isolation of a few ancestral species in widely distributed isolated aquifers, approximately 33 % of the aquifers contain pairs of species that are phylogenetic sister species. We investigate the mode of speciation for these sympatric sister species pairs by applying a simple model that simulates random occupation of niches by ancestral surface species during colonisation of the subterranean environments. We show that the number of observed sister pairs is better explained by a drive to occupy empty niches by species within the aquifer than by repeated colonisation of the aquifers by the same ancestral surface species, suggesting the that sister species evolved through sympatric speciation.
We also show that the body sizes of beetle species in single aquifers are significantly non-overlapping and are larger than expected by chance. This pattern is remarkably consistent over all aquifers that have been sampled to date (>46 aquifers). However, size differentiation in individual aquifers appears to be irrespective of ancestry. We will discuss potential general underlying ecological processes that resulted in the repeated pattern of size differentiation in the aquifers.

Divergence Time Estimates for the Evolutionary Radiations of Australian Stiletto Flies (Diptera: Therevidae)

C Lambkin[1], DK Yeates[1], BM Wiegmann[2], J Thorne[3], B. Cassel[2] and M Hauser[4]

1. CSIRO Entomology, Canberra ACT 2601 AUSTRALIA
2. Dept of Entomology, North Carolina State University, Raleigh, NC, 27695 USA
3. Dept of Statistical Genetics, North Carolina State University, Raleigh, NC, 27695, USA
4. Dept of Entomology University of Illinois, Urbana, IL 61801, USA

Why are there so many stiletto flies (Therevidae) in Australia? Intensive field and systematic research over the last decade has revealed a fauna we estimate at 700 species, arranged in three independent lineages, the Agapophytinae, the *Taenogera* group of genera, and the *Anabarrhynchus* group of genera. Species diversity is highest in semi-arid and arid regions, and is very low in rainforest. Large numbers of superficially similar species occur in each of the three lineages, and each has a few species in Chile or Argentina. We discuss the latest divergence time estimates for the Australian Therevidae and the implications for studies of evolutionary radiations of Australian fauna. Previous research showed that Australian therevid divergence times correlated with known gondwanan biogeographical events. Recent paleontological research has provided accurate phylogenetic assignments and ages for key fossils required to calibrate the molecular clock. A new dataset comprising intense taxon samples from the three radiations shows that while these lineages arose in the late Cretaceous or early Tertiary, the intense species-level evolutionary diversification did not begin until the mid Tertiary.

Australian gall-thrips on *Acacia* and the formation of xeric biomes

McLeish, M. & T. Chapman
School of Biological Sciences, Flinders University, South Australia 5042.

Australian gall-thrips parasitise *Acacia* species, the richest plant genus on the continent, covering over 70% of the Australian landmass. Preferences for food and life habits are presumed to be evolutionary conservative with strong patterns of host specialisation evident for this group. Gall-thrips/*Acacia* host affiliations likely comprise closely related monophagous and closely related oligophagous species living on closely related *Acacia* species. We use a phylogenetic approach to probe the diversification of gall-thrips in context with the formation of xeric biomes in Australia. The underlying explanation for galling species diversity is strongly correlated with aridity and transitional vegetation gradients. The radiation of gall-inducing thrips on *Acacia* appears to be tightly associated with the aridification of the Australian continent over the last 10 to 15 million years. Gall-thrips are expected to have diversified in parallel with *Acacia* host radiations via a combination of host shifting and cospeciation.

Comparative phylogeography reveals historical fragmentation in the ancient landscape of south-western Australia

Margaret Byrne
Science Division, Department of Conservation and Land Management, Locked Bag 104, Bentley Delivery Centre, WA 6983

The subdued landscape of south-western Australia has had a stable geological history with no major glaciation events, although it did experience climatic oscillations during the Pleistocene. The area has a highly diverse and largely endemic flora characterised by both relictual taxa that have persisted through landscape stability and lack of glaciation, and more recently evolved components resulting from adaptation to a more arid environment. Species with fragmented distributions often show significant levels of population divergence indicating a high degree of natural historical isolation and fragmentation within the flora. Widespread species with continuous distributions would not be expected to harbour significant population divergence. However, studies on three species, *Acacia acuminata* (Jam), *Eucalyptus loxophleba* (York Gum) and *Santalum spicatum* (WA Sandalwood), that all have widespread distributions in southern Western Australia, show congruent phylogeographical patterns in cpDNA variation. All species have two distinct genetic lineages with similar geographical distributions and nucleotide divergence. The similar patterns observed in these species from three different families implies that this is a response to historical events common to all species, and likely to have had similar effects in other currently widespread species. Nested clade analysis inferred past fragmentation as the most likely cause of lineage divergence. This is consistent with biogeographical evidence for climatic oscillations during the Pleistocene due to cyclic contraction and expansion of the mesic and arid zones leading to fragmentation in the transition area between these zones. Phylogeographic analysis of *Eucalyptus marginata* (Jarrah), the common forest tree, also showed divergence between the Coastal Plain lineage and the forest lineage on the Darling Plateau, consistent with fragmentation due to uplifting of the plateau in the late Pliocene. Comparative phylogeography has revealed significant influences of historical processes that would not have been predicted in a geological stable landscape that has not experienced major glaciations.

Comparative phylogeography of stygofauna from calcrete aquifers of central Western Australia: speciation patterns in subterranean islands

Cooper S. (1,2), R. Leys (1,2), J. Bradbury (1,2), K. Saint (1), S. Taiti (3), M. Guzik (2), A. Allford (2), C. Watts (1), A. Austin (2) and W. Humphreys (4)

(1) South Australian Museum, Adelaide, SA 5000;
(2) Centre for Evolutionary Biology and Biodiversity and School of Earth and Environmental Sciences, The University of Adelaide, Adelaide, SA 5005;
(3) Istituto per lo Studio degli Ecosistemi, CNR, Via Madonna del Piano, Sesto Fiorentino, Florence, Italy
(4) Western Australian Museum, Perth WA 6000.

Groundwater calcrete aquifers of the Yilgarn region of central Western Australia have been shown to contain a diverse subterranean invertebrate fauna (stygofauna), including the world's most diverse collection of subterranean dytiscid diving beetles. Each of about 100 dytiscid species described to date are endemic to an individual calcrete aquifer, with between one and four species per aquifer. Considerable diversity also is present in a number of crustacean groups, including Amphipoda, Isopoda and Bathynellacea. The aim of our research is to document the diversity of stygofauna present in the Yilgarn region and investigate the factors that have led to their evolution. With this aim in mind we have explored the evolutionary history of stygofauna using a comparative phylogeographic approach in combination with detailed morphological analyses. Mitochondrial DNA phylogeographies of dytiscids, crangonyctoid amphipods and isopods (*Haloniscus*) reveal long-term isolation of populations within individual calcrete aquifers. Molecular clock analyses suggest that populations have been isolated at least since the Late Miocene/ Pliocene, coinciding with a major period of aridification of the Australian continent. Morphological analyses further support the existence of unique species within calcrete aquifers and, together with the molecular data, lend support to the hypothesis that calcrete aquifers are equivalent to "subterranean islands", each with a highly endemic stygofauna. Speciation in allopatry appears to be the principle mode driving diversification, but there is evidence that sympatric speciation may also have operated to drive ecological diversification of the dytiscid fauna within aquifers. We are exploring this latter possibility using a combination of different approaches, including population genetic analyses of dytiscids and comparative phylogeographic analyses of species within aquifers. Some preliminary results will be discussed.

Fine scale comparative phylogeography and speciation: the view from fallen timber in temperate montane Australia

Sunnucks, P. (1), R. Garrick (2), C. J. Sands (2), J.M. Taylor (1), M.J. Blacket (3), A. Beavis (4), N. N. Tait (5) and D.M. Rowell (4)

(1) School of Biological Sciences and Australian Centre for Biodiversity Analysis Policy and Management, Monash University, Victoria 3800.
(2) Department of Genetics, La Trobe University, Bundoora, Vic, 3086.
(3) CESAR, University of Melbourne, Parkville, Vic, 3010
(4) Division of Botany & Zoology, Australian National University, ACT, 0200.
(5) Department of Biological Sciences, Macquarie University, Sydney, NSW, 2109.

The maturation of molecular population genetics in the last decade has produced a vast wealth of sophisticated studies on the relationship between fine scale phylogeographic patterns and the emergence of novel species. The great majority of this research in terrestrial organisms has been in northern hemisphere or tropical ecosystems, which have their distinct characters. We have been working on a fine scale model system in temperate montane Australia, which acts as an interesting counterpoint to the large body of work elsewhere. Specifically we have chosen a habitat dominated by species of low mobility and/or high habitat specificity – organisms dependent on decaying fallen timber. Our study organisms include paired exemplars of velvet worms (Onychophora), log-adapted Collembola, terrestrial flatworms (Terricola, Platyhelminthes) and funnel-web spiders (Mygalomorphae). As well as representing major taxonomic differences, each pair of organisms has different microhabitat preferences. We have used molecular population genetic approaches coupled with field ecology to examine their responses to palaeoecological changes in a system of 5 adjacent drainages with very different characteristics. Landscape-scale environmental changes and individual life history traits interact to produce an array of patterns of biodiversity and modes of diversification. Despite species-specific responses to repeated palaeoecological impacts owing to different impacts of history, habitat and life history, the essential physical stability of the study area appears to have promoted patterns of endemism that are strongly concordant while differing temporally. Physical and genetic analyses through contact zones between adjacent areas can reveal the extent to which repeated cycles of contraction and expansion refuge areas have resulted in populations that no longer freely interbreed.

Grasshopper speciation in semi-arid New Zealand.

Trewick, S. A.
Allan Wilson Centre for Molecular Ecology and Evolution,
Massey University, Palmerston North
New Zealand 5301

Semi-arid environments are rare in New Zealand and are largely overlooked by ecologists and evolutionists. Prior to the arrival of humans the dominant vegetation type was wet forest, although the tree line in NZ is relatively low and an extensive alpine zone exists throughout the Southern Alps of South Island, and on the volcanic mountains of North Island. Acridid grasshoppers are, compared to many other invertebrate groups, relatively speciose in New Zealand and almost all are primarily associated with the alpine or subalpine zone. Their phylogeography indicates prolonged (Plio-Pleistocene) population subdivision on mountain ranges, presumably limited by the absence of open habitat below the tree line. However, two species of grasshopper, belonging to two genera (*Sigaus*, *Brachaspis*), are specific to lowland environments in central South Island that have climates described as semi-arid and even continental. I present molecular data on these grasshoppers and their relatives that indicate very fine scale speciation and contrast patterns of speciation and genetic diversity with alpine and forest insects across New Zealand.

Conservation and hybrid origins of a cryptic mountain species are impacted by changing thermal landscapes.

Prof. J. M. Scriber, R. Mercader, and G. J. Ording
DEPARTMANT OF ENTOMOLOGY, MICHIGAN STATE UNIVERSITY, EAST LANSING, MI 48824, USA scriber@msu.edu

Hybrid animals may harbor significant genetic novelties, and provide valuable genotypes needed for rapidly changing environments. Recently (and probably directly related to extensive regional global warming in the region since 1998) considerable northward and rapid interspecific introgression (150-350 km in 6 years) into historical *Papilio canadensis* populations has been observed for several autosomal species-diagnostic traits of *P. glaucus.* These include detoxification of tulip tree leaves, several morphological wing traits, and *Hk*-100 allozymes. In addition, some X-linked traits such as *Pgd*-100 alleles and tulip tree oviposition preference behavior have also moved extensively northward. However, there has been little introgression of certain other sex-linked *P. glaucus* traits (such as facultative diapause, dark morph females, and *Ldh*-100 allozymes). We have determined that recombination and strong selection on *Ldh*-100 alleles (or an unknown trait with very close linkage) seem to limit gene flow North of the hybrid zone wherever fewer than 2700 degree-days accrue. We have created backcross hybrids (exhibiting recombined X-chromosome traits) that largely match the morphological and delayed post-diapause emergences of the new mountain swallowtail species, *P. appalachiensis* (Pavulaan & Wright 2002). The new species expresses an extensive introgressed mix of both *glaucus* and *canadensis* diagnostic traits and may represent the high altitude version of our high latitude northern "false second generation" hybrid swarm populations. It may also represent a recombinnt "hybrid species" (Scriber & Ording 2005). Detailed GIS mapping of thermal accumulations allows prediction of the geographic location of the purportedly new mountain species in West Virginia as well as for Georgia in the southern Appalachian Mts. The exceptionally warm seasons since 2002 may be leading to extirpation of the new species as genetic swamping from *P. glaucus* may occur from lower elevations.

Proposed for Program Symposia #13 (David Rowell; "Fine scale phylogeography and speciation")

The geographic ranges of Tasmanian crayfish: extent and pattern

Richardson, A. (1), N. Doran (2) & B. Hansen (1)

(1) School of Zoology, University of Tasmania, Private Bag 05, Hobart, Tasmania 7001
(2) Nature Conservation Branch, Department of Primary Industry, Water and Environment, GPO Box 44A, Hobart, Tasmania 7001

The geographic ranges of the 34 native species of freshwater crayfish known from Tasmania are mapped and described from extensive museum collections. Extents of occurrence range from over 30,000 to about 5 km^{-2} and species in the open water genus *Astacopsis* have significantly greater ranges than the burrowing species in one of two undescribed genera within *Parastacoides*. Species living in Type 1 burrows associated with open water have significantly larger ranges than those found in Type 2, water table, burrows. Many species show mosaic distributions with either parapatric boundaries, or narrow zones of geographic overlap, or sympatric contact zones. In most cases, closely related species are also geographically close; exceptions to this trend may represent older clades, some members of which have suffered range contractions. Freshwater crayfish, especially burrowing species, present a useful opportunity to examine questions about geographic ranges.

Many legs… tiny distances – A study of Speciation and Biogeography of a Gondwanan millipede genus within Southwestern Australia.

Karen L. Edward (1), Mark Harvey (1), and Mike Johnson (2)
(1) Department of Terrestrial Invertebrates, Western Australian Museum, Locked Bag 49, Welshpool DC, Western Australia 6986.
(2) School of Animal Biology, University of Western Australia, Crawley, Western Australia 6009.

Allozyme electrophoresis and genital morphometrics were used to examine speciation and biogeographical patterns within the Gondwanan native millipede genus *Atelomastix* from southwestern Australia. Morphometric analysis of adult male gonopods was undertaken to quantitatively distinguish morphological groups among the populations examined. These results were compared with the relationships estimated from allozyme electrophoresis to assess whether the morphospecies actually represented genetic species, and to identify cryptic speciation. Patterns of genetic divergence and genital morphology were largely concordant. However, some inconsistencies were found among populations of one morphospecies, which showed genetic divergence without marked differences in the genitalia (gonopods). Based upon the habitat data analysed in this study, no evidence for adaptive radiation was found in *Atelomastix*. A number of other Gondwanan taxa within southwestern Australia exhibit similar biogeographical patterns. Consequently, it is likely that vicariance events were responsible for the present biogeographic patterns and divergence within *Atelomastix*, in essentially similar niches, with morphological evolution playing only a secondary rather than a central role. The existence of marine, edaphic, and climatic barriers within southwestern Australia since the Eocene, may have influenced the current distribution patterns of *Atelomastix,* and may have been responsible for the high specific endemism in the region. It is possible that all species of the genus *Atelomastix* could be considered short-range endemics that exhibit low vagility, small-ranges, and inhabit restricted Gondwanan habitats. Knowledge of such organisms will provide crucial information in maximising both representation and persistence of diversity and assist in the prioritising of "hot-spots" or areas that have a concentration of short-range endemics for conservation.

Identifying mechanisms of speciation in subterranean cave organisms

Michelle T. Guzik[1, 2], Steven J.B. Cooper[2], William F. Humphreys[3], Chris H.S. Watts[4] and Andrew D. Austin[1]

[1] Centre for Evolutionary Biology and Biodiversity and School of Earth and Environmental Sciences, The University of Adelaide, Adelaide, South Australia, 5005

[2] Evolutionary Biology Unit (and Centre for Evolutionary Biology and Biodiversity) South Australian Museum, North Terrace, Adelaide, South Australia 5000.

[3] Western Australian Museum, Francis Street, Perth, Western Australia, 6000.

[4] Department of Entomology, South Australian Museum, North Terrace, Adelaide, South Australia 5000.

Closed ecosystems offer a unique opportunity to investigate mechanisms of speciation. In such systems, confounding factors like dispersal and many stochastic variables are naturally excluded, such that extrinsic variables can be measured and assessed as factors leading to genetic isolation and potential speciation within the system. A diverse aquatic invertebrate fauna was recently discovered in calcrete aquifers of the Yilgarn region, Western Australia. Individual calcretes are thought to comprise unique 'subterranean islands' in which high numbers of endemic fauna are observed. Dytiscid water beetles are a dominant component of the calcrete fauna, with 80 species now described from 34 isolated calcretes. Many subterranean dytisticid species share epigean ancestors but appear to have evolved and diversified independently of taxa in other calcretes. Interestingly, three distinct size classes of dytiscid species are a common feature within calcretes. Many of these have been identified as sister taxa but the modes of speciation within individual calcretes governing their evolution is yet to be identified. To explore whether allopatric or sympatric processes are operating on present day taxa we use mitochondrial DNA sequences and newly developed microsatellite markers to investigate the population genetic structure of dytiscid species within calcretes. The aim is to determine whether individual calcretes contain panmictic populations of dytiscids or show genetic substructuring strong enough to indicate isolating processes that could lead to allopatric speciation of dytiscids within calcretes. Here, we present our experimental design and preliminary results regarding levels of gene flow and population genetic structure in stygobitic dytiscid species within a single calcrete aquifer.

A comparative phylogeographic study of two niche differentiated funnel web spider species

Beavis, A. S. (1), D.M. Rowell (1) & P. Sunnucks (2)
(1) Division of Botany & Zoology, Australian National University, ACT, 0200, Australia
(2) School of Biological Sciences and Australian Centre for Biodiversity Analysis, Policy and Management, Monash University, Melbourne, Victoria, 3800 Australia

The forest floor provides multiple habitat niches for a diverse range of invertebrate taxa. As part of a broad-scale comparative phylogeography project examining population structure amongst saproxylic (dependent upon decomposing wood) invertebrates, this study compares the phylogeography of funnel web spider species from disparate habitats. The two species of interest share similar ecological characteristics, geographic ranges and are closely related, however each occupies a distinct habitat niche: *Hadronyche* sp. 1 burrows within decomposing logs, while *Atrax* sp. 1 burrows in soil on the forest floor. The niche partitioning of these species allows this study to separate species and habitat as contributing factors to the survival of resident populations through the glacial-interglacial cycles that characterised the Quaternary (1.8 Mybp). Phylogeography was investigated using the mitochondrial gene COI and analysed using distance methods, maximum likelihood and statistical parsimony. *Atrax* sp. 1 displayed high levels of sequence divergence (average = 0.075), and deep phylogeographic structuring of haplotypes while *Hadronyche* sp. 1 showed evidence of a recent colonisation event and a subsequent explosive radiation (average sequence divergence = 0.011). These findings suggest differential responses to historical climate change.

A tale of two flatties: different responses of two terrestrial flatworms to past environmental climatic fluctuations at Tallaganda in south-eastern Australia.

Taylor, JM. (1), M. Blacket (2), SA. Ciavaglia (3) & P. Sunnucks (1).
(1) Australian Centre for Biodiversity: Analysis, Policy and Management. School of Biological Sciences, Monash University, Victoria, 3800.
(2) Centre for Environmental Stress and Adaptation Research (CESAR), University of Melbourne, Parkville, Victoria, 3010.
(3) Department of Genetics, La Trobe University, Victoria, 3086.

Abstract: Phylogeography can be highly informative about the historical and contemporary processes that have shaped the current spatial distribution of genetic variation. DNA sequences from the mitochondrial Cytochrome Oxidase I (COI) gene of two terrestrial flatworm species (Platyhelminthes, Tricladida, Terricola), *Artioposthia lucasi* and *Caenoplana coerulea*, were examined as part of a collaborative investigation into the phylogeography of several saproxylic invertebrates within Tallaganda, southeast New South Wales. Nested Clade Analysis and coalescent demographic estimators indicated recent population growth, yet strong regional localisation of groups of closely- related haplotypes to four *a priori* defined microbiogeographic regions. For both species, there were indications of range expansion within regions and allopatric fragmentation between regions. The Eastern Slopes Region, which was predicted to have provided the highest quality refuges from cool, dry conditions, was indicated to have been the most important long-term refuge for *C. coerulea*, but while important in *A. lucasi*, was not unambiguously the key refuge. Despite the striking similarities in the distribution of genetic lineages across Tallaganda for the two species, the two flatworms show extremely different temporal patterns (assuming a standard evolution rate for mtDNA). Whereas regional divergences appear to have occurred within the Pleistocene for *C. coerulea, A. lucasi* regional divergences correspond to the dry, cool conditions of the Pliocene, with intra-regional fragmentation during the long cycles of wet-dry of the early-mid Pleistocene. This suggests that *A. lucasi* has had a longer continuous occupation within Tallaganda than *C. coerulea*, which may suggest the ability to withstand intense cool, dry periods.

Phylogeography of *Apiomorpha munita*: interplay between host-specificity, chromosomes and geography?

Cook, L. G.
School of Botany and Zoology, ANU, Canberra, ACT, 0200

The *Apiomorpha munita* species-complex is a group of gall-inducing scale insects restricted to *Eucalyptus* subgenus *Symphyomyrtus*. Despite apparently low vagility (adult females are sessile), the two taxa restricted to the SE temperate biome each appear to exhibit local population structuring but no isolation by distance across ranges of more than 1500 km. In contrast, *A. m. malleensis* exhibits population structuring at both local and broad scales. This structuring appears to be due to both host-specificity and multiple E-W divergences among lineages that occur in the mallee regions of both the SE and SW temperate biomes. Phylogeography of this taxon will be discussed, including the possibility of host-tracking.

Chromosomal Phylogeography of *Delena cancerides.*

Sharp, H & Rowell, D
Department of Botany and Zoology, Australian National University, ACT 0200.

The Australian social huntsman spider, *Delena cancerides,* encompasses a number of chromosomally distinct races. These include an ancestral population with an entirely telocentric genome, a metacentric bivalent-forming population saturated for Robertsonian fusions, and a number of races with monobrachial homology, which leads to the formation of sex-linked, alternately segregating chains at male meiosis.
Spiders from throughout southeastern Australia were examined, and eight new karyomorphs identified, possibly representing as many as eleven new races. These occupy clearly delineated geographic ranges within a continuous distribution. Three of the new forms have single sex-linked meiotic chains, similar to those previously reported, and five carry pairs of chains. Stable systems involving more than one chain of chromosomes have not previously been observed in any organism.
A very different sort of chromosomal diversity has also been found in the Victorian high country. Within a very small area, four different forms have been identified that have rings of chromosomes, as well as two types with pairs of rings. These populations all have a diversity of ring types present, intermixed with metacentric bivalent forming individuals. This means *Delena* undoubtedly has the most structurally diverse karyotype known.