Dampier 300

Biodiversity in Australia 1699–1999 and beyond

Changes to lecture program

Thursday 9 December, Fourth Session, Subterranean Biota:

Delete paper by David Slaney

Friday 10 December, First Session, Methodology:

Christine Lambkin & David Yeates: substitute 'Significant incongruence: just when is it significant?' for 'Unordered mutlistate characters: prudent choice or cop-out?' (both in Abstracts)

Friday 10 December, Third Session, Contributed Papers:

Note amended schedule:

1345 Philippa Uwins, Richard Webb, Majid Ghoddusi, Anya Yago, Tom Loy & Kathleen Murphy, Novel nano-organisms (nanobes): living analogues for Martian 'nannobacteria'?

1425 Jane Fromont & Gary Kendrick, Marine sponges (Porifera) of the Dampier Archipelago

1445 Belinda Alvarez, Karen Miller, Chris Battershill & Peter Northcote, Phylogenetic relationships of cryptic species within the sponge genus *Latrunculia* (Porifera: Demospongiae)

Additional posters

John Beard, Alex Chapman and Paul Gioia, Species richness and endemism in the Western Australian flora and the comparison of the South-West with other mediterranean regions

Steve O'Shea, Belinda Alvarez and Malcolm Clark, Benthic biodiversity on seamounts (in Abstracts)

Karin Strehlow, Jenny Davis, Stuart Bradley and Gordon Friend, Short-term impact of timber harvesting on terrestrial spider communities in jarrah forest: preliminary results

Karen Sutcliffe, Conservation status of freshwater insects in south-western Australia

Registrants

Mr Stuart Anstee, Hamersley Iron Pty Ltd, GPO Box A42, Perth, W.A. 6837
stuart.anstee@hi.riotinto.com.au

Dr John Beard, 6 Fraser Rd, Applecross, W.A. 6153

Mr Mark Cowan, Western Australian Museum, Francis St, Perth, W.A. 6000
mark.cowan@museum.wa.gov.au

Dr Jenny Davis, School of Environmental Science, Murdoch University, Murdoch, W.A. 6150
davis@essun1.murdoch.edu.au

Mr Brett Fitzgerald, Department of Conservation, 67 Knight Tce, Denham, W.A. 6537
brettf@calm.denham.wa.gov.au

Dr Jay Gomboso, Department of Conservation, Locked Bag 104, Bentley Delivery Centre, W.A. 6983
jayg@calm.wa.gov.au

Ms Diana Jones, Crustacean Dept, Western Australian Museum, Francis St, Perth, W.A. 6000
jonesd@museum.wa.gov.au

Ms Andrea Jordan, CSIRO Publishing, PO Box 1139, Collingwood, Vic. 3066
andrea.jordan@publish.csiro.au

Dr Peter Kendrick, Department of Conservation, PO Box 835, Karratha, W.A. 6714
peterke@calm.wa.gov.au

Dr Ebbe Nielsen, CSIRO Entomology, GPO Box 1700, Canberra, A.C.T. 2601 ebbe.nielsen@ento.csiro.au

Dr Tony Orchard, Australian Biological Resources Study, GPO Box 787, Canberra, A.C.T. 2601
tony.orchard@dest.gov.au

Mrs Lesley Polomka, Western Australian Herbarium, Locked Bag 104, Bentley Delivery Centre, W.A. 6983
lesleyp@calm.wa.gov.au

Dr Barbara Rye, Western Australian Herbarium, Locked Bag 104, Bentley Delivery Centre, W.A. 6983 barbarar@calm.wa.gov.au

Mrs Shirley Slack-Smith, Western Australian Museum, Francis St, Perth, W.A. 6000 shirley.slack-smith@museum.wa.gov.au

Ms Karin Strehlow, School of Environmental Science, Murdoch University, Murdoch, W.A. 6150 strehlow@central.murdoch.edu.au

Ms Karen Sutcliffe, School of Environmental Science, Murdoch University, Murdoch, W.A. 6150 k.sutcliffe@student.murdoch.edu.au

Mr Paul Van Heurck, 105 Buntine Rd, Wembley Downs, W.A. 6019 paulv@calm.wa.gov.au

Mr Paul West, 629 Newcastle St, Leederville, W.A. 6007 plw@hgm.com.au

Poster abstracts

Domiciliary disputation among thrips in arid-land Australia

David Morris[1] and Laurence Mound[2]

[1]Flinders University, South Australia

[2]CSIRO Entomology, GPO Box 1700, Canberra, Australian Capital Territory 2601

Acacia trees in Australian arid-lands support a highly diverse suite of thrips. This suite includes about 200 phytophagous species, many with a high level of host specificity. Intense insolation and aridity has led to a range of defensive behaviours that are associated with securing the sole occupancy of species-specific domiciles. Some species induce galls, and amongst these several species have evolved a soldier morph to defend the gall from specific kleptoparasitic thrips. Others glue two or more *Acacia* phyllodes together and raise their brood in the space so enclosed, although these domiciles may be usurped by other species of thrips. Yet other species invade old Hymenoptera galls, or establish colonies in cracks in the plant stems. The defensive behaviours can be both physical and chemical, and involve remarkable structural adaptations.

Short-term impact of timber harvesting on terrestrial spider communities in jarrah forest: preliminary results

Karin Strehlow[1], Jenny Davis[2], Stuart Bradley[1] and Gordon Friend[2]

[1]School of Biological Sciences and Biotechnology, Murdoch University, Murdoch, Western Australia 6150

[2]School of Environmental Science, Murdoch University, Murdoch, Western Australia 6150

This study investigated the impacts of timber harvesting on terrestrial spider communities in order to identify those spider species that may be potential indicator species. Twenty sites (control and impact sites) were sampled simultaneously before and after logging over a period of 22 months (May 1994–March 1996). Spiders were collected with pitfall traps. Logging activities (i.e. removal of trees but no post harvest burn) had no impact on overall spider abundance and richness. A small negative impact on density was observed in the most abundant spider species but not in the less common ones. Further statistical analysis of the data is still required to determine whether the sampling design used had sufficient power to detect changes at lower taxonomic levels.

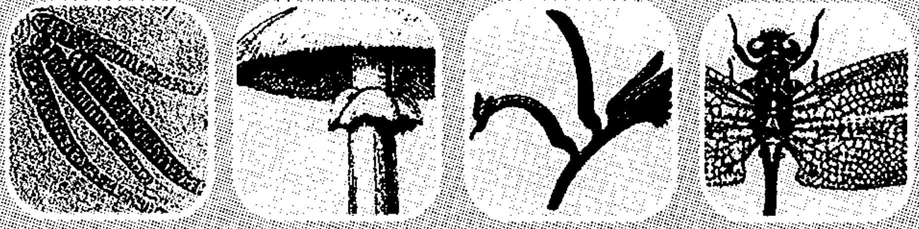
Organising Committee

Mark Harvey, Western Australian Museum; **Jenny Chappill**, University of Western Australia; **Bill Humphreys**, Western Australian Museum; **Di Jones**, Western Australian Museum; **Terry Macfarlane**, Western Australian Herbarium; **Jonathan Majer**, Curtin University; **Alex George**, Kardinya

The Committee acknowledges the assistance of Pierre Horwitz and Brendan Lepschi during the early days of organising the conference, and Andrew Storey until recently. All were unable to continue direct participation due to other duties.

Dampier 300

BIODIVERSITY IN AUSTRALIA



1699-1999 *and beyond*

6 TO 10 DECEMBER 1999

Alexander Library Theatre, Perth Cultural Centre
Francis Street, Perth, Western Australia

◆

PROGRAM AND ABSTRACTS

◆

ORGANISERS

Australian Systematic Botany Society
Society of Australian Systematic Biologists
Invertebrate Biodiversity and Conservation

Associated Society
Royal Society of Western Australia

Published on 5 December 1999 by the Organising Committee for the conference Dampier 300: Biodiversity in Australia 1699–1999 and beyond.

Further copies of this publication may be purchased for $A20.00 (including postage) from the Australian Systematic Botany Society, c/- Alex George, 'Four Gables', 18 Barclay Road, Kardinya, Western Australia 6163.

Printed by the Publications Department, Western Australian Museum, Francis St, Perth, Western Australia 6000

DAMPIER 300

Introduction

This book contains the program, abstracts and list of registrants (current at 15 November). Papers and posters are arranged in separate sections, in alphabetical order of the first author who in most cases is also the presenter. There is an index to authors.

Venues

Except concurrent sessions, all lectures will be in the Alexander Library Lecture Theatre. The first of each concurrent session will be held in this Theatre, and the second in a TAFE lecture theatre directly across Francis Street from the Alexander Library. Signs will be erected to indicate the location of theatres. Entry to the Library should be from Francis Street for the first session each day but later (once the main library opens) may be from the entrance on the city (south) side.

Posters will be set up in the foyer of the Library, just outside the Theatre. There will be two lunch-time poster sessions (Thursday and Friday) when presenters will be available to discuss their work.

Three small rooms are available, one for setting up slides, carousels etc., one for demonstrations, and the third for small meetings as required.

Toilets are directly across the foyer from the Theatre.

The Duty Officer of the Alexander Library will accept incoming emergency phone calls on (08) 9427 3101. The Western Australian Museum, next door to the Library, will also accept emergency calls on (08) 9427 2700 (ask for Anne Nevin).

All-day pay parking is available under the Alexander Library (enter from Francis St on the north side) and under the Art Gallery of Western Australia (enter from Roe St, opposite the Perth Central Railway Station).

Tours

The river cruise on Wednesday afternoon leaves from Pier 4, Barrack Street Jetty. It follows the Swan River upstream to the Swan Valley, includes a visit to Sandalford Winery, and returns to the city. The morning conference session finishes early to allow those going to have lunch beforehand. Tea, coffee and biscuits will be available *gratis* on the boat. Please be aboard by 1.15. It takes about 15 minutes to walk from the Alexander Library to the jetty (follow Francis St, right into Beaufort St, over the railway line and down Barrack St). The cruise finishes at Barrack Street Jetty at 7.30. Tickets may be purchased on the day. The boat is airconditioned.

Those who have booked for the post-conference tour are asked to contact Alex George during the week to arrange being picked up on Saturday morning.

PROGRAM

Sunday 5 December

1600 Registration at Western Australian Museum

1700 Welcoming reception, Western Australian Museum

Monday 6 December

0800 Registration

0900 Welcome

0910 Welcome by Dr Lyn Allen, Chief Executive Officer, Library & Information Service of Western Australia

FIRST SESSION SHARK BAY Convenor: Steve Hopper

0920 Phillip E. Playford, The history and geology of the Shark Bay district

1000 Greg Keighery & Neil Gibson, Vascular flora of the southern Carnarvon Basin

1020 Paul Brown and Brett Fitzgerald, Project Eden—reconstructing mammal diversity on Peron Peninsula, Shark Bay

1040 Morning tea

SECOND SESSION SHARK BAY Convenor: Di Jones

✓ 1110 Allan Burbidge & Ron Johnstone, Historical changes in the bird fauna of the Shark Bay region

✓ 1130 Alison Downing & Serena Marner [presented by Alex George], William Dampier's 'New Holland' moss

1145 Stephen Hopper, From Dampier to DNA: the 300-year-old mystery of *Conostylis stylidioides* (Haemodoraceae)

1205 Norm L. McKenzie, Greg Keighery, Neil Gibson & J Rolfe, Patterns in the southern Carnarvon Basin's terrestrial biodiversity

1230 Lunch

THIRD SESSION ARID ZONE BIODIVERSITY Convenor: Barbara Main

✓ 1400 Tracey Churchill, What we never never knew: the diversity of spiders in the outback

✓ 1440 Andrew Beattie, Ian Oliver & Mark Dangerfield, Arid zone land systems as surrogates for plant, invertebrate and microbial biodiversity

✓ 1500 Stuart Halse, The important contribution of micro-invertebrates to aquatic biodiversity in arid Western Australia

1520 Bronwen Scott, Gondwanan land snails in arid Australia

1600 Afternoon tea

FOURTH SESSION (concurrent) ALGAE Convenor: Alex George

1630 Roberta Cowan, Australian phycology: its influence

1650 John Huisman, Roberta Cowan & Michael Borowitzka, Macroalgal biodiversity in Western Australia

1710 Tim Entwisle, Freshwater algae in Australia: 300 years on

FOURTH SESSION (concurrent) INVERTEBRATE SYSTEMATICS Convenor: Heather Proctor

1630 Claudia Arango, Australian pycnogonids

1650 Christine Hass, Diversity of sphaeromatid isopods in Western Australia

1710 Yuki Konishi, J. Prince & Brenton Knott, The fauna of thrombolitic microbialites, Lake Clifton, Western Australia

1800 Book launch: *Australia 300 years of Botanical Illustration* by Helen Hewson, published by CSIRO Publishing. Alexander Library Theatre; refreshments in foyer.

Tuesday 7 December

0830 Registration

FIRST SESSION CO-EVOLUTION Convenor: Peter Cranston

0900 Laurence Mound and Bernie Crespi, Niche exploitation: multiple radiations of thrips on Australian Acacia trees

0940 Lyn Cook, A scale insect radiation that appears to be tracking eucalypt divergence

1000 Penny Gullan & Lyn Cook, Multiple origins of galling in scale insects

1020 Andy Austin, The co-evolution of antagonistic interactions: parasitoids rule OK!

1040 Morning tea

* SECOND SESSION INFORMATION SYSTEMS Convenor: Terry Macfarlane

✓1110 Alex Chapman, Biodiversity information system trends , Herbarium

✓1130 Paul Gioia, Interpreting specimen data with GIS

✓1150 ~~Barry Conn~~ Bill Barker, Sharing data, the Virtual Australian Herbarium and a distributed Australian Flora

1210 Ian Reid & Steve Shattuck, BioLink: software for managing biological collections

1230 Lunch

1300 Meeting to discuss planning the bicentenary (beginning Dec. 2001) of Matthew Flinders' *Investigator* voyage to New Holland. There will be a paper by David Moore, Some background to Robert Brown's collecting in Western Australia, 9 December 1801 to 17 January 1802: sources and collections. Convenor: John Clarkson

THIRD SESSION INVERTEBRATE BIODIVERSITY Convenor: Jonathan Majer

✓ 1400 Simon Judd, Pierre Horwitz & Diana Jones, Distribution patterns of inland aquatic and terrestrial malacostracan crustaceans in south-western Australia

✓ 1420 Graham Osler, Changes in free-living soil invertebrates under different crops in the Western Australian wheatbelt

✓ 1440 Wonje Lee & David J. Patterson, Diversity and geographic distribution of free-living heterotrophic flagellates — good. (unicellular protozoa).

✓ 1500 Geoff Meggs, Habitat modelling of a threatened species of stag beetle in production forests in Tasmania

1520 Peter McQuillan, Patterns of diversity in the phytophagous insects of southern Australia

1540 Afternoon tea

FOURTH SESSION INFORMATION SYSTEMS Convenor: Barry ~~Conn~~ Alex

✓ 1610 Chris Glasby & Dennis Gordon, Progress toward an aquatic biodiversity information system

• 1630 Roger Bramble, Biotrack: a bioinformatics solution for biodiversity assessment and research

• 1650 Nicholas Lander & Terry Macfarlane, Interactive identification

• 1710 Tom Alford, HORTBASE, a database of horticultural information on the Western Australian flora

1730 ANNUAL GENERAL MEETING, SOCIETY OF AUSTRALIAN SYSTEMATIC BIOLOGISTS

Wednesday 8 December

0830 Registration

FIRST SESSION BIOGEOGRAPHY Convenor: Andy Austin

0900 John Jennings, Systematics and biogeography of hyptiogastrine wasps (Hymenoptera: Gasteruptiidae)

0920 Peter J. Unmack, Biogeography of Australian freshwater fishes

0940 Karen Bell, David Yeates & Craig Moritz, Molecular systematics and biogeography of the Australian dung beetle genus *Temnoplectron* (Coleoptera: Scarabaeidae)

1000 Vicki Funk, Biogeography and floral evolution of the Cichorioideae (Compositae): a southern hemisphere event

1020 Morning tea

SECOND SESSION INVERTEBRATE SYSTEMATICS Convenor: Lyn Cook

1050 Barbara Main, Water tapping and harvesting by trapdoor spiders

1110 Jeff Skevington & David Yeates, Tribal turmoil: systematics of the Eudorylini (Diptera, Pipunculidae)

1130 Faye Christidis, A cladistic analysis of *Austrophlebioides* and related genera (Ephemeroptera: Leptophlebiidae)

1150 Patrice Bouchard & David Yeates, Systematics of Australian Coelometopini (Coleoptera: Tenebrionidae)

1210 Lunch

1315 RIVER CRUISE. Departs from Barrack Street jetty, Swan River (returns 1930)

Thursday 9 December

0830 Registration

FIRST SESSION PLANT SYSTEMATICS Convenor: Judy West

0900 Rogier de Kok, Mike Crisp & Jenny Chappill, An overview of legume systematics in Australia

0920 Bruce Maslin, *Acacia* (Mimosaceae) from Dampier to the 21st Century

0940 Kristina Lemson, Phylogeny of *Andersonia* (Ericaceae)

1000 Murray Henwood, Flannel flower phylogeny: evolution and diversity of *Actinotus* (Apiaceae)

1020 Richard Olmstead, The molecular systematics of the Australian endemic plants in the Chloanthoideae and Prostantheroideae (Lamiaceae)

1040 Morning tea

SECOND SESSION (concurrent) PLANT SYSTEMATICS Convenor: Don Foreman

1110 Bill Barker, Taxonomic discoveries in Australian flowering plants, a continuing process, with particular reference to the Scrophulariaceae

1130 Juliet Wege, Vegetative morphology and anatomy in *Stylidium* (Stylidiaceae)—a systematic approach

1150 Elise Raulings, Morphology, pollination ecology and evolution of the *Stylidium graminifolium* complex

1210 Ryonen Butcher, Taxonomic revision and cladistic analysis of *Sphaerolobium* (Papilionaceae: Mirbelieae)

SECOND SESSION (concurrent) SUBTERRANEAN BIOTA Convenor: Fred Stone

1110 ✓ Andrew Boulton, 'Twixt two worlds: surface water/groundwater interface

1140 George Wilson, Australian groundwater-dependent isopod crustaceans

1200 Brenton Knott & Edyta Jasinska, Insights into the fauna of the Gnangara Mound aquifer, Western Australia—the significance of springs

in Melaleuca Swa
EPP173 contains
one spp fish that
occurs in none
of other SCP
EPP lakes

1220 Bill Humphreys, Groundwater calcrete aquifers in the Australian arid zone: an unfolding plethora of stygal diversity

1240 Lunch

1345 NANCY BURBIDGE MEMORIAL LECTURE

Andrew Burbidge, Conservation of the biota of the South-West Botanical Province of Western Australia

THIRD SESSION (concurrent) FUNGI Convenor: Alex George

✓ 1430 Neale Bougher, Australian fungi: much to learn about their taxonomy and ecology

1450 Mark Brundrett, The diversity of Glomalean mycorrhizal fungi in tropical Australian habitats

1510 Teresa Lebel, Systematics of the truffle-like fungi of Australia: a case study of the Russulales

THIRD SESSION (concurrent) SUBTERRANEAN BIOTA Convenor: Bill Humphreys

1430 Mia Thurgate & Andy Spate, Biodiversity of the invertebrate fauna of caves in New South Wales

1450 Fred Stone & Frank Howarth, Why are there so many cave-adapted species in Australia? Relictual species versus the adaptive shift hypothesis

1510 Elery Hamilton-Smith and Stefan Eberhard, Maintenance of karst biodiversity

1530 Afternoon tea

FOURTH SESSION (concurrent) PLANT SYSTEMATICS Convenor: Neville Marchant

1600 Kerri Clarke, Karen Wilson & Jeremy Bruhl, Assessment of taxonomic limits in *Abilgaardia*, *Crosslandia* and *Fimbristylis spiralis* (Cyperaceae) in Australia

1620 Don Foreman & Lynne Milne, A review of the proteaceous genera *Isopogon* and *Petrophile*

1640 Lina Juswara, Morphology, distribution and taxonomy of the *Hibiscus panduriformis* (Malvaceae) complex in Australia

1700 David J. Coates & Margaret Byrne, Molecular systematic and evolutionary studies in the south-west flora: implications for conservation

FOURTH SESSION (concurrent) SUBTERRANEAN BIOTA Convenor: Andrew Boulton

1600 Hannelore Hoch & Barbara Hosfeld [presented by Fred Stone], Cave-adaptation in Australian planthoppers (Insecta: Hemiptera: Fulgoromorpha: Cixiidae): colonisation of novel habitat or response to climatic change?

1620 David Slaney, Evolution of cave cockroaches in Australia

1640 Edyta Jasinska & Brenton Knott, Origins and ecology of root mat fauna from cave waters, Leeuwin–Naturaliste Ridge, Western Australia

1700 Stefan Eberhard, Managing and monitoring cave fauna in Tasmania

1800 ANNUAL GENERAL MEETING, AUSTRALIAN SYSTEMATIC BOTANY SOCIETY

Friday 10 December

0830 Registration

FIRST SESSION METHODOLOGY Convenor: Vicki Funk

0900 Christine Hass & Brenton Knott, Taxonomy, a discipline of great significance

0920 David Yeates & Christine Lambkin, Taxon sampling

0940 Christine Lambkin & David Yeates, Unordered multistate characters: prudent choice or cop-out?

1000 Morning tea

SECOND SESSION INVERTEBRATE CONSERVATION Convenor: Penny Gullan

1030 David Walter, Endemism and invasions: mites and world heritage

1050 Mark Harvey & Paul West, Small bugs in a big land: the biogeographic and conservation significance of some terrestrial taxa displaying high endemicity

1110 Heather Proctor, Aquatic mites in surveys of stream macroinvertebrate diversity: is neglect of a subphylum justified?

1130 Graham Lewis, Andy Austin, Hugh Possingham, Paul Dangerfield & M.Brownlow, Development of a protocol for sampling arthropod diversity in areas of native vegetation

1200 Launch of ABRS web site

1230 Lunch

THIRD SESSION CONTRIBUTED PAPERS Convenor: Loisette Marsh

1345 Philippa Uwins, Richard Webb, Majid Ghoddusi, Anya Yago, Tom Loy & Kathleen Murphy, Novel nano-organisms (nanobes): living analogues for Martian 'nannobacteria'?

1405 Jane Fromont & Gary Kendrick, Marine sponges (Porifera) of the Dampier Archipelago

1425 Belinda Alvarez, Karen Miller, Chris Battershill & Peter Northcote, Phylogenetic relationships of cryptic species within the sponge genus *Latrunculia* (Porifera: Demospongiae)

1505 Afternoon tea

FOURTH SESSION RESEARCH PRIORITIES AND FUNDING Convenor: Tim Entwisle

1530 Eleanor Bennett & Bob Anderson, Biodiversity and large scale agricultural development

1550 Max Whitten & William H. Settle, The role of the small-scale farmer in preserving the link between biodiversity and sustainable agriculture

1610 Jay Gomboso, Biodiversity in Western Australia: developing a State strategy

1630 Ian Mansergh & David Parkes, Biodiversity conservation and management in Victoria

1650 Hugh Possingham, Funding biodiversity research: manipulation, money, media and morals

CLOSE OF CONFERENCE

1900 CONFERENCE DINNER

Harry's Seafood Grill & Garden Restaurant, 94 Aberdeen St, Northbridge

POSTERS

Honi Adolphson, Soil mite (acarine) diversity under *Eucalyptus globulus* plantations

Michael Borowitzka, Marine sponge symbioses: diversity within diversity

Mark Brundrett & Neale Bougher, World-wide diversity of eucalypt-compatible ectomycorrhizal fungi

Ainsley Calladine, Investigating the evolution of the mistletoe family Loranthaceae using a molecular phylogenetic approach

Jason Cody, The species abundance and diversity of invertebrates in mound springs and bore drains

Niall Doran, Ian Houshold & Mike Driessen, Tasmanian cave guides: an under-used resource?

Travis Gotch, Spiders of the South Australian mound springs and bore drains

Jennifer Hart, A phylogenetic analysis of the Xanthosiinae (Apiaceae) based on morphological data

My-My Huynh, The effect of broom invasion on arthropod diversity in open eucalypt woodland in South Australia

Claudette Kellar, Megan Short & Josephine Milne, Epiphytes and invertebrates in cool-temperate rainforest

Chris Reid, Ian Reid & Peter Cranston, Dung beetles and Far North Queensland biogeography—deep history?

Donovan Sharp, Bryan Simon & Derek Clayton, Interactive keys to the grasses of Australia

David Slaney, Evolution of cave cockroaches in Australia

Andy Spate, Jane Gough & Mia Thurgate, Karstic groundwater ecosystems in the Murray Darling and Otway groundwater basins

Claire Stephens, Grasshopper assemblages in natural temperate grasslands of differing native plant diversities

Nicholas Stevens, Systematics and distribution of micro-flea wasps: *Baeus* spp. (Hymenoptera: Scelionidae) in Australia

Fred Stone, Distribution of surface and cave-adapted cockroaches in the family Nocticolidae in Australia: evidence for evolution of tropical troglobites

Gary Taylor, Diversity associated with fly (Diptera: Fergusoninidae) and nematode (Tylenchida: Sphaerulariidae) galls on Myrtaceae

Mia Thurgate, Stromatolite biodiversity in the South-East of South Australia

Michael Whyms, Tertiary plant fossils at Stuart Creek South Australia

Ian Wyndham & Megan Short, The impact of the Argentine Ant, *Linepithema humile*, on surface-active invertebrates in urban parkland

DEMONSTRATIONS

Tuesday 7 December

W. (Bill) R. Barker, The Electronic Flora of South Australia: demonstration of a working prototype

John Doolan, KE Software, KE Emu: software for museum collections management

Alex Chapman, FloraBase a botanical information system for Western Australia

Ian Reid & Steve Shattuck, BioLink: software for managing biological collections

Registrants

Miss Honi Adolphson, 33 Woodville St, North Perth, W.A. 6006 honimelita@hotmail

Dr Belinda Alvarez de Glasby, National Institute for Water & Atmospheric Research, PO Box 14-901, Kilbirnie, Wellington, New Zealand b.glasby@niwa.cri.nz

Ms Claudia Arango, Department of Zoology & Tropical Ecology, James Cook University, Townsville, Qld 4811 Claudia.Arango@jcu.edu.au

Mrs Siti Ariati, School of Botany, The University of Melbourne, Parkville, Vic. 3010 s.ariati@pgrad.unimelb.edu.au

Dr Andy Austin, Department of Applied & Molecular Ecology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, S.A. 5064 aaustin@waite.adelaide.edu.au

Mrs Robyn Barker, Plant Biodiversity Centre, Hackney Rd, Hackney, S.A. 5069 rbarker@dehaa.sa.gov.au

Dr Bill Barker, Plant Biodiversity Centre, Hackney Rd, Hackney, S.A. 5069 bbarker@dehaa.sa.gov.au

Dr Alex Baynes, Western Australian Museum, Francis St, Perth, W.A. 6000 baynesa@museum.wa.gov.au

Prof. Andy Beattie, Key Centre for Biodiversity & Bioresources, Dept of Biological Sciences, Macquarie University, N.S.W. 2109 abeattie@rna.bio.mq.edu.au

Ms Karen Bell, Department of Zoology and Entomology, University of Queensland, St Lucia, Qld 4072 s006981@student.uq.edu.au

Dr Eleanor Bennett, c/- Kinhill Pty Ltd, 47 Burswood Rd, Victoria Park, W.A. 6100 eleanor.bennett@halliburton.com

Dr Michael Borowitzka, School of Biological Sciences and Biotechnology, Murdoch University, Murdoch, Western Australia 6150 borowitz@possum.murdoch.edu.au

Mr Patrice Bouchard, Department of Zoology and Entomology, University of Queensland, St Lucia, Qld 4072 p.bouchard@ento.uq.edu.au

Dr Neale Bougher, CSIRO Forestry & Forest Products, Private Bag, P.O., Wembley, W.A. 6014 n.bougher@ccmar.csiro.au

Dr Andrew Boulton, Ecosystem Management, University of New England, Armidale, N.S.W. 2350 aboulton@metz.une.edu.au

Mr Roger Bramble, Key Centre for Biodiversity and Bioresources, Department of Biological Sciences, Macquarie University, N.S.W. 2109 rbramble@rna.bio.mq.edu.au

Mr Paul Brown, Department of CALM, 67 Knight Tce, Denham, W.A. 6537 paulb@calm-denham.wa.gov.au

Dr Mark Brundrett, CSIRO Forestry & Forest Products, Private Bag, Post Office, Wembley, W.A. 6014 mark.brundrett@ccmar.csiro.au

Dr Allan Burbidge, Department of CALM, PO Box 51, Wanneroo, W.A 6065 allanb@calm.wa.gov.au

Ms Ryonen Butcher, Department of Botany, University of Western Australia, Nedlands, W.A. 6907 ryonen@cyllene.uwa.edu.au

Dr Margaret Byrne, CALM Science, Western Australian Herbarium, Locked Bag 104, Bentley Delivery Centre, W.A. 6983 margaretb@calm.wa.gov.au

Mr Ainslie Calladine, TESAG, James Cook University, Townsville, Qld 4811 Ainsley.Calladine@jcu.edu.au

Dr Jenny Chappill, Department of Botany, University of Western Australia, Nedlands, W.A. 6907 chappill@cyllene.uwa.edu.au

Mr Alex Chapman, CALM Science, Western Australian Herbarium, Locked Bag 104, Bentley Delivery Centre, W.A. 6983 alexc@calm.wa.gov.au

Ms Faye Christidis, Department of Zoology and Tropical Ecology, James Cook University, Townsville, Qld 4811 faye.christidis@jcu.edu.au

Dr Tracey Churchill, CSIRO Wildlife & Ecology, PMB 44, Winnellie, N.T. 0822 tracey.churchill@terc.csiro.au

Ms Kerri Clarke, Botany, School of Rural Science & Natural Resources, University of New England, Armidale, N.S.W. 2351 ksmith@metz.une.edu.au

Mr John Clarkson, Centre for Tropical Agriculture, PO Box 1054, Mareeba, Qld 4880 john.clarkson@dnr.qld.gov.au

Dr David Coates, CALM Science, Western Australian Herbarium, Locked Bag 104, Bentley Delivery Centre, W.A. 6983 davidc@calm.wa.gov.au

Mr Jason Cody, 8 Eyre St, Seaview Downs, S.A. 5049 jason.cody@student.adelaide.edu.au

Dr Barry Conn, Royal Botanic Gardens, Mrs Macquaries Road, Sydney, N.S.W. 2000 barry@rbgsyd.gov.au

Ms Lyn Cook, Division of Botany & Zoology, Australian National University, Canberra, A.C.T. 0200 Lyn.Cook@anu.edu.au

Dr Roberta Cowan, SBSB/DSE, Murdoch University, Murdoch, W.A. 6150 cowan@possum.murdoch.edu.au

Professor Peter Cranston, CSIRO Entomology, GPO Box 1700, Canberra, A.C.T. 2601 petercr@ento.csiro.au

Dr Michael Crisp, Department of Botany & Zoology, Australian National University, Canberra, A.C.T. 0200 mike.crisp@anu.edu.au

Dr Rogier de Kok, Centre for Plant Biodiversity Research, CSIRO, GPO Box 1600, Canberra, A.C.T. 2601 Rogier.deKok@pi.csiro.au

Dr Niall Doran, Threatened Species Unit, Tasmanian Parks & Wildlife Service, GPO Box 44A, Hobart, Tas. 7001 NE_Doran@tassie.net.au

Dr Andrew Drinnan, School of Botany, The University of Melbourne, Parkville, Vic. 3010 drinnan@botany.unimelb.edu.au

Dr Marco Duretto, National Herbarium of Victoria, Royal Botanic Gardens, Birdwood Ave, South Yarra, Vic. 3141 duretto@rbgmelb.org.au

Mr Stefan Eberhard, Caveworks, PO Witchcliffe, W.A. 6286 smecwork@netserv.net.au

Dr Tim Entwisle, Royal Botanic Gardens, Mrs Macquaries Rd, Sydney, N.S.W. 2000 tim_entwisle@rbgsyd.gov.au

Dr Ross Field, Museum Victoria, GPO Box 666E, Melbourne, Vic. 3001 rfield@mov.vic.gov.au

Dr Don Foreman, ABRS, GPO Box 787, Canberra, A.C.T. 2601 Don.Foreman@ea.gov.au

Dr Jane Fromont, Museum of Natural Science, Western Australian Museum, Francis St, Perth, W.A. 6000 jane.fromont@museum.wa.gov.au

Dr Vicki Funk, Department of Botany MRC 166, Smithsonian Institution, Washington DC 20560, USA funkv@nmnh.si.edu

Mr Alex George, 'Four Gables', 18 Barclay Rd, Kardinya, W.A. 6163 alextris@iinet.net.au

Mrs Elizabeth George, 18 Halwest Way, Alexander Heights, W.A. 6064

Dr Neil Gibson, Wildlife Research Centre, P.O. Box 51, Wanneroo, W.A. 6065 neilg@calm.wa.gov.au

Mr Paul Gioia, Western Australian Herbarium, CALM, Locked Bag 104, Bentley Delivery Centre, W.A. 6983 paulg@calm.wa.gov.au

Dr Chris Glasby, National Institute for Water & Atmospheric Research, PO Box 14-901, Kilbirnie, Wellington, New Zealand c.glasby@niwa.cri.nz

Mr Travis Gotch, 6 Locke Drive, Fairview Park, S.A. 5126 t-gotch@roseworthy.adelaide.edu.au

Dr Penny Gullan, Division of Botany & Zoology, Australian National University, Canberra, A.C.T. 0200 Penny.Gullan@anu.edu.au

Dr Stuart Halse, CALM, PO Box 51, Wanneroo, W.A. 6946 stuarth@calm.wa.gov.au

Dr Jenny Hart, School of Biological Sciences, Macleay Bldg A12, The University of Sydney. N.S.W 2006 jmh@bio.usyd.edu.au

Ms Judith Harvey, CALM, PO Box 51, Wanneroo, W.A. 6946 judithh@calm.wa.gov.au

Dr Mark Harvey, WA Museum, Francis St, Perth, W.A. 6000 mark.harvey@museum.wa.gov.au

Dr Christine Hass, Department of Zoology, University of Western Australia, W.A. 6907 chass@cyllene.uwa.edu.au

Dr Murray Henwood, School of Biological Sciences, Macleay Bldg A12, University of Sydney, N.S.W. 2006 murray@bio.usyd.edu.au

Ms Melissa Hewitt, Museum of Natural Science, WA Museum, Francis St, Perth, W.A. 6000 melissa.hewitt@museum.wa.gov.au

Dr Helen Hewson, PO Box 11, Gunning, N.S.W. 2581 helen.hewson@ea.gov.au

Prof. Bob Hill, Department of Environmental Biology, University of Adelaide, S.A. 5005 bob.hill@adelaide.edu.au

Dr Steve Hopper, Kings Park & Botanic Garden, West Perth, W.A. 6005 steveh@kpbg.wa.gov.au

Dr Pierre Horwitz, Centre for Ecosystem Management, Edith Cowan University, Joondalup, W.A. 6027 p.horwitz@cowan.edu.au

Dr Keith Houston, Australian Biological Resources Study, GPO Box 787, Canberra, A.C.T. 2601 keith.houston@ea.gov.au

Dr John Huisman, SBSB/DSE, Murdoch University, Murdoch, W.A. 6150 huisman@possum.murdoch.edu.au

Dr Bill Humphreys, Western Australian Museum, Francis St, Perth, W.A. 6000 humphw@museum.wa.gov.au

Miss My-My Huynh, Department of Applied & Molecular Ecology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, S.A. 5064 huynh.my-my@saugov.sa.gov.au

Dr Muhammad Iqbal, Department of Applied & Molecular Ecology, Waite Campus, Adelaide University, P.O., Glen Osmond, S.A. 5064 a.austin@waite.adelaide.edu.au

Dr Edyta Jasinska, Centre for Ecosystem Management, Edith Cowan University, Joondalup, W.A. 6027 edytajj@hotmail.com

Mr John Jennings, Department of Applied & Molecular Ecology, Waite Campus, University of Adelaide, Glen Osmond, S.A. 5064 J_Jennings@onaustralia.com.au

Dr Simon Judd, Department of Aquatic Zoology, Western Australian Museum. Francis St, Perth, W.A. 6000 s.judd@cowan.edu.au

Ms Lina Juswara, Burton & Garran Hall, Australian National University, GPO Box 813, Canberra, A.C.T. 2601 lina.juswara@pi.csiro.au

Mr Greg Keighery, Wildlife Research, CALM, PO Box 51, Wanneroo, W.A. 6065 gregk@calm.wa.gov.au

Mrs Bronwyn Keighery, Department of Environmental Protection, Westralia Square, 141 St Georges Tce, Perth, W.A. 6000 bronwen_keighery@environ.wa.gov.au

Ms Claudette Kellar, Deakin University, Rusden Campus, 662 Blackburn Rd, Clayton, Vic. 3168 kellar@deakin.edu.au

Mr George Kendrick, Western Australian Museum, Francis St, Perth, W.A. 6000

A/Professor Adrianne Kinnear, School of Natural Sciences, Edith Cowan University, 2 Bradford St, Mount Lawley, W.A. 6050 a.kinnear@cowan.edu.au

Dr Brenton Knott, Department of Zoology, University of Western Australia, W.A. 6907 bknott@cyllene.uwa.edu.au

Ms Yuki Konishi, Department of Zoology, University of Western Australia, Nedlands, W.A. 6907 ykonishi@cyllene.uwa.edu.au

Ms Chris Lambkin, Department of Zoology and Entomology, University of Queensland, Brisbane, Qld 4072 s357711@student.uq.edu.au

Mr Nicholas Lander, Western Australian Herbarium, CALM, Locked Bag 104, Bentley Delivery Centre, W.A. 6983 nickl@calm.wa.gov.au

Dr Teresa Lebel, Royal Botanic Gardens, Birdwood Ave, South Yarra, Vic. 3141 tlebel@rbgmelb.org.au

Mr Wonje Lee, Protsville, School of Biological Sciences, University of Sydney, N.S.W. 2006 wonje@bio.usyd.edu.au

Ms Kristina Lemson, Department of Botany, University of Western Australia, Nedlands, W.A. 6907 lemson@networx.net.au

Mr Graham Lewis, 1/77 North Valley Rd, Highton, Vic. 3216 g.lewis@pgrad.unimelb.edu.au

Dr Terry Macfarlane, Western Australian Herbarium, CALM, Manjimup Research, Brain St, Manjimup, W.A. 6258 terrym@calm.wa.gov.au

Dr Barbara Main, Department of Zoology, University of Western Australia, Nedlands, W.A. 6907 bymain@cyllene.uwa.edu.au

Prof. Bert Main, Department of Zoology, University of Western Australia, Nedlands, W.A. 6907

Dr Ian Mansergh, Flora and Fauna Directorate, Department of Natural Resources and Environment, Nicholson St, East Melbourne, Vic. 3002 Ian.Mansergh@nre.vic.gov.au

Dr Neville Marchant, Western Australian Herbarium, CALM, Locked Bag 104, Bentley Delivery Centre, W.A. 6983 nevillem@calm.wa.gov.au

Mrs Loisette Marsh, 6 Lillian St, Cottesloe, W.A. 6011

Dr Alison McCusker, PO Box 793, Woden, A.C.T. 2606 alisonmc@ozemail.com.au

Mr Norm McKenzie, CALM, PO Box 51, Wanneroo, W.A. 6065 normm@calm.wa.gov.au

Dr Peter McQuillan, Centre for Environmental Studies, University of Tasmania, GPO Box 252-78, Hobart, Tas. 7001 P.B.McQuillan@utas.edu.au

Dr Jeff Meggs, School of Forestry, University of Tasmania, GPO Box 252, Hobart, Tas. 7001 jeffrey.meggs@forestrytas.com.au

Ms Nicole Middleton, School of Botany, The University of Melbourne, Parkville, Vic. 3010 n.middleton@botany.unimelb.edu.au

Dr Lynne Milne, Department of Geography, University of Western Australia, W.A. 6907 lmilne@geog.uwa.edu.au

Mr David Moore, 52 Cranmore Lane, Aldershot, Hants GU11 3AT, United Kingdom

Dr David A. Morrison, Department of Environmental Sciences, University of Technology, Sydney, Westbourne St, Gore Hill, N.S.W. 2065 David.Morrison@uts.edu.au

Dr Laurence Mound, CSIRO Entomology, GPO Box 1700, Canberra, A.C.T. 2601 laurence@ento.csiro.au

Dr Richard Olmstead, Department of Botany, Campus Box 355325, University of Washington, Seattle, WA 98195, USA olmstead@u.washington.edu

Dr Graham Osler, Soil Science & Plant Nutrition, Faculty of Agriculture, University of Western Australia, Nedlands, W.A. 6907 gosler@agric.uwa.edu.au

Professor Simon Owens, The Herbarium, Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AE, England S.Owens@rbgkew.org.uk

Mrs Sue Patrick, Western Australian Herbarium, CALM, Locked Bag 104, Bentley Delivery Centre, W.A. 6983 suep@calm.wa.gov.au

Prof. David J. Patterson, School of Biological Sciences, University of Sydney, N.S.W. 2006 djp@bio.usyd.edu.au

Mr Bernard Pfiel, Centre for Plant Biodiversity Research, CSIRO, GPO Box 1600, Canberra, A.C.T. 2601 bpfeil@pi.csiro.au

Dr Winston Ponder, Australian Museum, 6 College St, Sydney, N.S.W. 2010 winstonp@amsg.austmus.gov.au

Prof. Hugh Possingham, Department of Applied & Molecular Ecology, University of Adelaide, S.A. 5005 hpossing@maths.adelaide.edu.au

Dr Heather Proctor, A.E.S, Griffith University, Nathan, Qld 4111 h.proctor@mailbox.gu.edu.au

Ms Elisa Raulings, School of Botany, The University of Melbourne, Parkville, Vic. 3010 e.raulings@pgrad.unimelb.edu.au

Dr Chris Reid, CSIRO Entomology, GPO Box 1700, Canberra, A.C.T. 2601 semelvillea@yahoo.com

Mr Ian Reid, CSIRO Entomology, GPO Box 1700, Canberra, A.C.T. 2601 ianr@ento.csiro.au

Dr Jim Ross, Royal Botanic Gardens, Birdwood Ave, South Yarra, Vic. 3141 jross@rbgmelb.org.au

Dr Andrew Rozefelds, Tasmanian Herbarium, GPO Box 252-04, Hobart, Tas. 7001 arozefelds@tmag.tas.gov.au

Dr Barry Russell, Museum & Art Gallery of NT, PO Box 4646, Darwin, N.T. 0801 barry.russell@nt.gov.au

Miss Alison Sampey, 300 Weller Rd, Hovea, W.A. 6071 sampeya@hotmail.com

Dr Bronwen Scott, School of Life Sciences, Victoria University - S008, PO Box 14428, Melbourne City MC, Vic. 8001 Bronwen.Scott@vu.edu.au

Ms Kelly Shepherd, Plant Sciences, Faculty of Agriculture, University of Western Australia, Nedlands, W.A. 6907 kshepher@agric.uwa.edu.au

Ms Megan Short, Deakin University, Rusden Campus, 662 Blackburn Rd, Clayton, Vic. 3168 mshort@deakin.edu.au

Dr Dany Simon, Department of Zoology, Tel-Aviv University, Tel-Aviv, 69978, Israel dysimon@post.tau.ac.il

Mr Jeff Skevington, Department of Zoology & Entomology, University of Queensland, St Lucia, Qld 4072 j.skevington@ento.uq.edu.au

Mr David Slaney, Department of Zoology, James Cook University, Townsville, Qld 4811 david.slaney@jcu.edu.au

Ms Claire Stephens, Department of Applied & Molecular Ecology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, S.A. 5064

Mr Nicholas Stevens, 39 Churinga Rd, Aldgate, S.A. 5154 stevensnb@yahoo.com

Dr Fred Stone, PO Box 1430, Kurtistown, Hawaii 96760, USA fred@hawaii.edu

Mr Derek Swarts, School of Natural Sciences, Edith Cowan University, 2 Bradford St, Mt Lawley, W.A. 6050 d.swarts@ecu.edu.au

Dr Gary Taylor, Department of Applied & Molecular Ecology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, S.A. 5064 Gary.Taylor@adelaide.edu.au

Ms Mia Thurgate, Jenolan Caves Reserve Trust, P.O. Box 1495, Bathurst, N.S.W. 2795 karst@jenolan.org.au

Mr Peter Unmack, Biology Department, Arizona State University, Tempe, Arizona 85287-1501, USA peter.unmack@asu.edu

Dr Philippa Uwins, Centre for Microscopy & Microanalysis, University of Queensland, St Lucia, Qld 4072
j.kassan.whistler@uq.net.au

Dr Stephen van Leeuwen, Department of Conservation and Land Management, Karratha, W.A. 6714
stephenv@calm.wa.gov.au

Mr Erich Volschenk, Environmental Biology, Curtin University, GPO Box U1987, Perth, W.A. 6845
pvolschenke@cc.curtin.edu.au

Ms Julianne Waldock, Department of Terrestrial Invertebrates, Western Australian Museum, Francis St,
Perth, W.A. 6000 waldockj@museum.wa.gov.au

Dr David Walter, Department of Zoology & Entomology, University of Queensland, St Lucia, Qld 4072
D.Walter@mailbox.uq.edu.au

Dr Deborah Ward, PO Box 918, Kurtistown, Hawaii 96760, USA dward@hawaii.edu

A/Professor Lesley Warner, School of Biological & Environmental Science, Central Queensland
University, Rockhampton, Qld 4702 l.warner@cqu.edu.au

Ms Juliet Wege, Department of Botany, University of Western Australia, Nedlands, W.A. 6907
jawege@cyllene.uwa.edu.au

Dr Alice Wells, ABRS, GPO Box 787, Canberra, A.C.T. 2601 alice.wells@ea.gov.au

Dr Judy West, Centre for Plant Biodiversity Research, CSIRO, GPO Box 1600, Canberra, A.C.T. 2601
judy.west@pi.csiro.au

Dr Max Whitten, CSIRO TERC, Darwin, PMB 44, Winnellie, N.T. 0822 maxipm@ibm.net

Mr Michael Whyms, 2 Maxwell Ct, Attwood, Vic. 3049 michael-whyms@students.vu.edu.au

Ms Carol Wilkins, 7 Alexander Rd, Dalkeith, W.A. 6009 cwil@cyllene.uwa.edu.au

Dr George D.F. Wilson, Australian Museum, 6 College St, Sydney, N.S.W. 2010
buzw@amsg.austmus.gov.au

Mr Paul G. Wilson, Western Australian Herbarium, CALM, Locked Bag 104, Bentley Delivery Centre,
W.A. 6983 paulw@calm.wa.gov.au

Dr David Yeates, Department of Zoology and Entomology, University of Queensland, St Lucia, Qld 4072
d.yeates@mailbox.uq.edu.au

PAPERS

HORTBASE, a database of horticultural information on the Western Australian flora

Tom Alford

Wildflower Society of Western Australia, PO Box 64, Nedlands, Western Australia 6909

The Western Australian Native Flora Database is a major project describing the botanic and horticultural aspects of the Western Australian flora. It is a combined initiative of the Western Australian Wildflower Society, Western Australian Herbarium and Kings Park & Botanic Garden and is funded by the Gordon Reid Foundation. The first stage of this database (an important component of Western Australian Herbarium's FLORABASE), containing the botanical descriptions of 12,780 taxa, has been completed. The next stage of the project, now under way, is to develop a database providing the horticultural details for each of the taxa.

The horticultural database (HORTBASE) aims to capture information from primary sources to provide a central database on the propagation and cultivation of the Western Australian flora for use by industry and the community. The database will represent a significant milestone for the consolidation of horticultural information for the Western Australian flora.

Phylogenetic relationships of cryptic species in the sponge genus *Latrunculia* (Porifera: Demospongiae)

Belinda Alvarez[1], Karen Miller[1,2], Chris Battershill[1,3] and Peter Northcote[4]

[1]National Institute of Water and Atmosphere, PO Box 14-901, Kilbirnie, Wellington, New Zealand

[2]Department of Biological Sciences, University of Wollongong, Wollongong, New South Wales 2522

[3]Australian Institute of Marine Science, PMB 3, Townsville, Queensland 4811

[4]Department of Chemistry, Victoria University of Wellington, Wellington, New Zealand

The genus *Latrunculia* Bocagei, allocated to the sponge family Latrunculiidae, is represented by 15 species with a wide distribution (Arctic, Atlantic Ocean, Caribbean, Mediterranean, Red Sea, Indian Ocean, Indo-Malayan region, Australia, New Zealand). Species of the genus are generally massive, with special pore areas (papillae, sieve-plates) and oscules encircled with elevated rims. The skeleton is formed of siliceous spicules (styles with strongylote modifications) arranged in an irregular reticulation of poorly defined tracts or bundles, supporting a thick crust of discorhabds, a distinctive microsclere of the genus.

The discovery of different profiles of bioactive compounds (discorhabdins) with anti-tumour and cytotoxic activity, associated with populations of *Latrunculia* from New Zealand (NZ), has focused attention on the genus. It was thought that the genus was represented by at least two species: *L. brevis* Ridley & Dendy and an undescribed species. Populations of these putative species have a patchy distribution around NZ and are represented by two colour morphotypes (green and brown). Studies have been undertaken to examine whether the production of discorhabdins is genetically or environmentally determined and to delimit, based on phylogenetic principles, the species of *Latrunculia* present in NZ.

Allozyme electrophoresis at 9 polymorphic loci of approximately 30 individuals collected from 8 sites in 4 locations around NZ (Wellington (W), Tutukaka (T), Doubtful Sound (DS) and Kaikoura (K) where the brown and green morphs coexist), indicated that sponges from each geographical location are genetically distinct, and that they display genetic differences of the magnitude usually associated with reproductively isolated species (Nei's D between locations = 1.047–2.174). Additionally, the comparisons revealed that the green (KG) and brown morphs (KB) found at Kaikoura are distinct and that there are two genetic groups within the green morph in Doubtful Sound (DS1, DS2).

A preliminary phylogenetic analysis was carried out using morphological (qualitative) and morphometric (continuous) characters. Morphological characters used were related to skeletal features, such as organisation of the choanosome, spicule composition and geometry and coded as presence or absence. Morphometric characters such as width of styles, length and width of dischorhabds, distance between the apical end and the dischorhabd whorls (2 or 3), were coded using the gap-weighting procedure described by Thiele (1993) and treated as ordered. A previous multivariate analysis (MANOVA and CDA) showed significant variation of these characters among the genetic groups (Pillai's Trace = 1.74, F = 31.25, P < 0.001). *Latrunculia apicalis* Ridley & Dendy, a species found in Antarctica, was used as outgroup.

One most parsimonious tree (length = 226, CI = 0.801, RI = 0.632) with a polytomy at the base, separates two major lineages, one including the groups of DS1 and KB and the other with the remaining groups [DS2 (KG {T, W})]. The number of whorls present in the discorhabds (2 or 3) is the synapomorphic character that defines these two major groups. The topology of the ingroup also agrees with the dendrogram based on allozyme data [(DS1, KB), (DS2 (KG, W) T)] but differing in the position of the T group. Within these clades the frequency distributions of the morphometric characters overlap among the groups and, in practice, they could not be used as diagnostic features to separate species. Despite the data overlap, to a certain extent there is enough phylogenetic signal to delimit the genetic groups under study.

Comparisons of chemical extracts from *Latrunculia* also showed diagnostic variation in the amount of five different bioactive compounds (discorhabdins) among sponges collected in the four localities. Chemical variation matched exactly the genetic and morphological relationships in the genus, with each genetic/ morphological species having a different compliment of the five major discorhabdin types.

We conclude that the genus *Latrunculia* in NZ contains at least six cryptic species separated in two groups that can be distinguished on the basis of dischorhabd types; the phylogenetic position of these two groups in relation to the outgroup remains unresolved at this stage. We suggest that species coexisting in the same locality (i.e. DS1 and DS2; KB and KG) represent relict populations that were once more widely distributed through New Zealand, and that geographical isolation has led to allopatric speciation in the genus and the present disjunct and patchy distribution of species. The life history of these species is not well known and the mechanisms involved in the speciation process cannot be explained yet. We also suggest that chemical variation in *Latrunculia*, previously thought to be intra-specific and associated with environmental variability, is more likely to reflect the presence of cryptic species. Our results highlight the need for a thorough taxonomic revision of the genus in NZ to formally describe the species that were detected here using genetic and phylogenetic methods.

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Australian sea spiders (Pycnogonida): state of knowledge and a phylogenetic perspective

Claudia Arango

Department of Zoology and Tropical Ecology, James Cook University, Townsville, Queensland 4811

The pycnogonids are marine arthropods recently grouped within Chelicerata and often referred to as sea spiders because of their superficial resemblance to true spiders. They have a wide geographical and bathymetric range, being represented from polar regions to tropical seas and from the intertidal to the abyssal depths. Australian pycnogonids have not been well studied. Approximately 115 species are known from Australian waters, most of them collected before the 1970's. The collections have been very discontinuous, leaving many areas where pycnogonid are unknown. Despite this setback, interesting suggestions (with zoobiogeographical implications) have been made in the past 30 years. The Australian region appears to be characterised by an abundance of genera and species of Callipallenidae, many of which are endemic or appear to have their centre of distribution in the Australian region or the Austro-Malayan region. On the other hand, the few contributions to the pycnogonid fauna from Western Australia have suggested that the sea spiders from Western Australia have their closest affinities with the fauna of eastern Australia, rather than the warm waters of the Indian Ocean. The whole picture of pycnogonid distribution should be considered under the idea that this group does not have planktonic larvae, so they rely on passive dispersion mechanisms, and for the same reason it is believed that high rates of speciation are commonly occurring. According to the preliminary results and collections made in the present project, intertidal and reef habitats sampled in the North Queensland area have not shown a high abundance of Callipallenids as expected. Meanwhile, the genus *Anoplodactylus* is quite frequent and diverse with groups of closely related species which, on further examination, could indicate a high chance of speciation in the relatively enclosed, isolated shallow water areas at least for this genus. At present, there is little more to be said on this matter until more material is collected.

There is virtually no information available on the biology or ecology of pycnogonids, especially from tropical regions. Although they are not usually highly abundant, some specific 'associations' with coelenterates, sponges, molluscs and algae have been reported but in few cases have these findings given any insight on their ecological function. The sampling of certain shallow water habitats in tropical Australia where pycnogonids occur in reasonable numbers could provide knowledge on the ecology of these critters, since the few complete reports have dealt with temperate and polar species.

The evolutionary history of the group is as interesting as obscure. The uniqueness of pycnogonid morphology and the scarceness of fossil records have made the group difficult to relate to any other arthropods. The within-group phylogenetic relationships have not been well studied, and an intuitively based hypothesis has been raised suggesting a reduction series of the appendages (palps, chelifores and ovigers) as an evolutionary trend. In the present work, approximately 30 species have been found in rocky intertidal zones and different coral reef habitats, mainly from the central section of the Great Barrier Reef and Townsville area. These collections have given an indication of the high diversity of forms and taxa representing most of the main lineages of sea spiders in tropical Australian waters. This has allowed start on collecting morphological information for a range of taxa to be included in a phylogenetic analysis of the higher-level relationships. This is expected to give insight on the evolutionary history and confront the conventional classification of the group. The research is expected to provide a testable phylogenetic hypothesis using both morphological and molecular data that will contribute significantly to our knowledge of the Pycnogonida.

The co-evolution of antagonistic interactions: parasitoids rule OK!

Andrew Austin

Department of Applied & Molecular Ecology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, South Australia 5064

The parasitic wasps represent one of the truly mega-diverse groups of organisms, numbering several hundred thousand species world-wide. They use other arthropods as hosts for their parasitic larvae which develop either internally or externally, eventually killing the host. The evolutionary 'arms race' that has occurred between wasps and their hosts has yielded some of the most intriguing and complex relationships known among the insects. These have resulted in a bewildering array of adaptations recognisable at the morphological to molecular level. This arms race has led to the evolution of high levels of host specificity and, consequently, strict co-phylogenetic relationships among wasps and hosts for some groups. In others, however, substantial host switching has occurred, and co-phylogenetic patterns are less clear. Using examples from recent research on particular wasp families, I will briefly review parasitoid host relationships, their involvement in mimicry complexes, the role played by their association with specific mutualistic viruses, and their application as model systems in biodiversity and evolutionary studies.

Taxonomic discoveries in Australian flowering plants, with particular reference to the Scrophulariaceae: a continuing process

W.R. (Bill) Barker

State Herbarium of South Australia, Plant Biodiversity Centre, Department for Environment, Heritage & Aboriginal Affairs, Hackney Road, Hackney, South Australia 5069

Inventories of flowering plant species, particularly of rare and threatened species, are important components in biodiversity data for today's conservation decision-making. There is a view that knowledge of Australia's flowering plant families is largely complete with production of State and national Floras. However, classifications change at all levels. From a conservation viewpoint, many new flowering plant species continue to be discovered, a significant number rarities. Many result from changes in circumscription of known populations, less commonly from newly discovered ones. The extent to which outcomes of systematic studies depart from current knowledge depends on many factors, including personal and collective goals, time, resources, general and specialised taxonomic expertise, experience in the group, appropriate selection of analytical techniques, and the adequacy of sampling in collections and observations. Flora treatments performed in minimal time in general consolidate existing knowledge and bring to light only the obvious novelties. Generally, in-depth revisionary studies, provided with adequate resources, fieldwork or special techniques, are the basis for major advances in existing floristic knowledge.

In four generic groups of the Scrophulariaceae revisionary studies continue to realise new taxa in high numbers which bring to light previously unknown major global centres of diversity in their tribes. These groups had received little attention for a century until the author's involvement in the 1970s. Outcomes of these studies have already impacted on conservation with communication of rare species, often by informal phrase names. A fifth group revised over this period by Barbara Briggs and associates, (with input by Phil Garnock-Jones concentrating on New Zealand taxa) is the Veroniceae. Many species have been designated and major generic redefinition has resulted from cladistic appraisal.

Euphrasia, despite clarification by in-depth study some years ago going from about 12 taxa to nearly 60 (many of conservation significance) is still realising new taxa; up to 9 new taxa await description. In the subtribe Mimulinae, recent fieldwork in good seasons has produced an unexpected doubling of species, while seed and pollen studies point to generic redefinition. *Stemodia s. lat.*, already with new species evident, needs field study in some parts of its range.

Attention will be given to *Lindernia*. As a tropical parallel to *Euphrasia*, *Lindernia* has shown a spectacular four-fold increase in species, many of conservation significance, arising from microscopic examination of flowers, and fieldwork in various seasons. *Lindernia* in Australia has been poorly understood to this time. A revision being undertaken by the author will increase the representation of species from ten known by the 1980s (Hnatiuk, 1990) to over 40 (W.R.Barker, in preparation). Four subgenera occur in Australia. Of these *Lindernia*, *Tittomannia* and *Bonnaya* are widespread and more diverse in other parts of the world, but they are represented in Australia not only by widespread Malesian or wider-ranging species, but also by endemics.

The recently recognised subgenus *Didymadenia*, defined by the synapomorphy of large 2-celled epidermal glands and a characteristic seed surface, encompasses most of the species diversity in Australia. A preliminary cladistic study summarises its remarkable evolutionary diversification. Character transformations include: development variously of a sub-scapose, scandent, prostrate or pendent habit, reduction of stem leaves to subulate, development of a capitate inflorescence, reduction and loss of the upper corolla lip, reduction or elongation of the corolla tube, great variation in coloration, loss of the upper anthers, loss of the lower anther pair, loss or fusion of anthers cells, varying fruit shape and presentation, and development of striking foliar scents. These are paralleled by: occupation of different ecological niches (e.g. herbfield, shallow water, pavements, caverns never exposed to sun, exposed rock faces); flowering in differing seasons; and a likely instance of pollination by large moths. *Lindernia* joins other plant groups with highest diversity on the Arnhem Land escarpments, the north-east having about 15 species in the subgenus, many endemic in the region. Speciation in clades tends to be allopatric, even in clades confined to Arnhem Land. However, *L. plantaginea* and an unnamed relative are often found sympatrically. They diverge in scent of the foliage and at each site in the intensity of the blue in flowers, and limited collections indicate that they may have different native bee pollinators.

Environmental decision-makers must to allow for incompleteness of biodiversity data and their potential to mislead. Floristic and spatial inventories of 'known components' of biodiversity, which form a basis for modelling and particularly directed at rare and threatened taxa, must account for this advancing knowledge base. While support for the traditionally poorly funded, more diverse but little-known lower plants, algae, invertebrates and fungi should be expanded, resourcing of taxonomic revisional study for the less known groups of flowering plants must continue to be actively promoted.

Arid Zone land systems as surrogates for plant, invertebrate and microbial biodiversity

Andrew Beattie, Ian Oliver and Mark Dangerfield

Key Centre for Biodiversity & Bioresources, Department of Biological Sciences, Macquarie University, New South Wales 2109

This research sampled the vegetation, selected invertebrates and fungal DNA in four land systems in Sturt National Park in north-western NSW. Over 3000 samples, located as close as 1 m and as distant as 100 km, were arranged in a nested spatial design and revealed 187 vascular plant, 304 fly, 208 ant species and 48 fungal taxa. The specimens and the data derived from them were managed and analysed using a new biodiversity data management system developed at the Key Centre called BioTrack.

Few differences were observed in the numbers of taxa recorded from different land systems on the same geology. However, each land system harboured significantly different vascular plant, fly and ant species assemblages. There were few difference in the fungal taxa among land systems. Overall, land systems contained significantly different assemblages of organisms although the overlap was large.

Distance was an important variable in the spatial arrangement of species diversity. Thus, although land systems may be reasonable surrogates for much biodiversity, reserve selection based on land system diversity should sample the geographical space occupied by each one.

Hierarchical spatial sampling of multi-species components of biodiversity such as vascular plants and selected invertebrate and microbial groups provides a powerful tool for landscape-scale analysis and reserve selection.

Molecular systematics and biogeography of the Australian dung beetle genus *Temnoplectron* (Coleoptera: Scarabaeidae)

Karen Bell, David K. Yeates and Craig Moritz

Department of Zoology and Entomology, University of Queensland, St Lucia, Queensland 4072

Previous studies of the biogeography of the tropical rainforests of north-east Queensland have emphasised vertebrates and plants. However, invertebrate phylogenies tend to be biogeographically informative on a much finer scale. The few available phylogenies of Australian tropical rainforest vertebrate species strongly suggest refugial isolation and allopatric divergence between populations. A common historical barrier has already been shown in the Wet Tropics for vertebrates, named the Black Mountain Boundary. This barrier is just one of the many revealed by assessments of scarabaeine sister-species vicariance patterns across the Wet Tropics and surrounding forest. Molecular studies of the genus *Temnoplectron*, particularly the wingless species, using the mitochondrial gene cytochrome oxidase I (COI), may be useful for the study of speciation mechanisms in the Wet Tropics. Other work planned includes a molecular phylogeny and population genetics of another scarab genus, *Amphistomus*. We will compare the responses to refugial isolation in tropical versus temperate regions using examples from this genus.

Biodiversity and large scale agricultural development

Eleanor Bennett and Bob Anderson

Kinhill Pty Ltd, 47 Burswood Rd, Victoria Park, Western Australia 6100

With any proposed development it is important that the National Strategy for the Conservation of Australia's Biological Diversity guidelines for biodiversity are met. This is even more important for large scale developments in biologically unknown or unusual environments. In addition the Environmental Protection Agency of Western Australia and the Parks and Wildlife Commission of the Northern Territory require that no known vegetation community, plant species, faunal habitat or fauna species be 'lost' as a result of proposed developments. These requirements are part of current planning for facing the proposed Ord Stage 2, a horticultural development (32,000 ha) for the Kimberley region of Western Australia and the north west of the Northern Territory.

Three plains are to be developed, the Knox Creek Plain, predominantly in Western Australia, Weaber Plain represented in both Western Australia and the Northern Territory, and the Keep River Plain in the Northern Territory. Each plain has a natural boundary—hills, creeks or rivers. The cracking clay soil plains (Cununurra and aquitaine phase) are proposed for the development.

A biological study of the total proposed development area, including the rocky outcrops, creeks, rivers and lagoons (October 1996) and a wet season survey (February 1997) identified priority flora and fauna species, restricted faunal habitats and restricted vegetation units. A limited survey was undertaken of the cracking clay plains. A further survey of the plains only was undertaken in June 1999. From all three surveys, together with aerial photographs, a vegetation map was produced for the whole area.

Input on the significance of the plains for the traditional owners (Miriuwung and Gajerrong families) was sought. As part of the project planning, a decision was made to conserve all rock outcrops, riparian zones along creeks and rivers, and lagoons. This satisfied many environmental and traditional owner requirements. In addition, the northern area of the Weaber Plains is adjacent to the Point Springs Nature Reserve, which contains a significant area of remnant rainforest. The surveys identified that most significant plant species and habitat types occurred in the area proposed for conservation. Two poorly reserved vegetation types were identified in the Northern Territory, one—*Melaleuca minutifolia* woodland—occurred in some areas proposed for conservation. A second—*Xerochloa* sp. grassland—was recorded to the north of the proposed development in the area intended for conservation.

Currently some areas are used for fishing and picnicking but access is restricted due to pastoral activities. These restrictions will be removed once development occurs making many areas more accessible, such as the Keep River for fishing and Milligans Lagoon for picnicking. With such a large area proposed for development, plus the expected increased pressure of tourism in this sensitive environment, many environmental management guidelines must be in place. An overview of these will be presented.

This paper will present information on the extent and methods of the monitoring undertaken. It will also demonstrate how it is intended to conserve the biodiversity of the area prior to and during development, and later, i.e. once the land is purchased and farmed. Factors to be considered will be the conservation of protected flora and fauna, vegetation communities, habitats, and aquatic environments. A brief outline of the innovative management prescriptions will be discussed.

Systematics of the Australasian and Pacific Coelometopini (Coleoptera; Tenebrionidae)

Patrice Bouchard[1] and David K. Yeates

[1]Department of Zoology and Entomology, University of Queensland, Brisbane, Queensland 4072

Adult and immature tenebrionids are known to feed mostly on dead or decaying plant matter. The family is one of the largest in the order Coleoptera with over 16 000 described species worldwide. Lacordaire's classification of the world Tenebrionidae (1859) remained almost unchanged until about 20 years ago, when internal as well as larval characters were investigated thoroughly throughout the family. This resulted in a new classification of the world tenebrionids, with one of the better supported higher clades (subfamily Coelometopinae) comprising a diverse group of both winged and flightless beetles. Members of the tribe Coelometopini, one of three tribes in the Coelometopinae, mostly occupy forests and woodlands in the subtropical and tropical regions of the world. The adults browse at night on fungal and algal growths on the outer surface of dead and live trees, and the larvae can be found in dead and decaying wood, both in and under bark. Approximately 100 species in the tribe Coelometopini are known to occur in Australia. A large number of these species were described during the late 1800's or early this century and only isolated and sporadic papers have concentrated on this fauna since the 1930's. Although adults of the tribe are typically scarce in collections, careful, intensive sampling of north Queensland's rainforests by Queensland Museum staff has yielded a large number of specimens over the past two decades. About 45 flightless species of Coelometopini, represented by over 3000 specimens, have been identified in this sampling. In this presentation, data on a morphological phylogenetic analysis of the Australian, Papuan and Pacific Coelometopini will be presented. Being the first phylogenetic analysis of this tribe, we hope to find useful characters which will help in the generic classification in the region and, most importantly, find the closest relatives of the northern Queensland wet tropics Coelometopini.

Australian fungi: much to learn about their taxonomy and ecology

Neale L. Bougher and Inez C. Tommerup

CSIRO Forestry and Forest Products, Private Bag, PO Wembley, Western Australia 6014

Fungi are neither plants nor animals but constitute the separate Kingdom Fungi (Eumycota). Fungi are an ancient component of the Australian biota. Fungi are a healthy sign for ecosystems, and have significant roles in ecology, conservation and habitat restoration.

Australian ecosystems have a naturally evolved, high level of fungal diversity, and the presence of fungal fruit bodies is a healthy sign that a robust, sustainable soil nutrient cycling system is operating. Many Australian ecosystems have nutrient-poor soils, and nutrient cycling is a key aspect of their functioning (O'Connell & Grove, 1996). Key ecosystem processes that underpin productivity, maintenance of ecosystem values and their recovery after disturbance occurs below-ground, and nutrient cycling is an important aspect of their functioning and sustainability. Soil micro-organisms largely maintain the fertility of soil. Fungi are crucial components contributing to the biodiversity, health and natural processes of ecosystems as they transport, store, release and recycle nutrients. For example, fungi decompose many types of organic matter, and have unique abilities to decompose recalcitrant lignin and cellulose plant components. Fungi bind soil and improve organic matter development, and interact with other soil organisms to improve soil quality.

There are many times more fungi than plants in Australia. A large proportion of the species are unique to Australia, as they have co-evolved with our unique plants and animals. Perhaps only 5–10% of Australian fungi have been named and another 10% are known but not named. Hence the total number can only be estimated—there may be 250,000 species of fungi (microscopic and larger fungi) in Australia, including about 5,000 mushrooms and similar types (Pascoe, 1991). There is less knowledge about Australian fungi than about higher plants because less scientific attention has been given to them, probably because of their inconspicuous nature and a lack of mycologists. 'Fungi-phobia' has also been a factor in Australia—the peculiarly English attitude regarding fungi with suspicion and perhaps overstating the risk of illness or death from eating fungi. There has been ignorance about the effects of ecological disturbance on fungi, and efforts to nominate potentially rare and endangered fungi have been hampered by the low level of knowledge and exploration—there is a need for more extensive collections and better distribution maps. Recently, the Australian Biological Resources Study launched a concerted effort to improve the level of knowledge by releasing the first volumes of the *Fungi of Australia* series.

Large areas of the Australian continent remain poorly explored for fungal diversity, including urban bushlands which are important refuges for great numbers of fungi. In Western Australia, most records of fungi are from the south-west forest region, and few are from the large botanical provinces to the north, e.g. the Northern and Eremean Provinces occupy the majority of WA (12.5% and 70.2% of land area) but have the least known fungi. The Wheatbelt region of WA has a range of geographically fragmented vegetation types including eucalypt woodland dominated by species such as *Eucalyptus wandoo* and *E. salmonophloia*. Few fungi of this region had been documented prior to our recent studies on the fungi of remnant patches of indigenous woodland. The studies have yielded a large spectrum of mycorrhizal and saprotrophic species, indicating that fungal diversity in the Wheatbelt vegetation may equal that of wetter eucalypt forests in Australia. Like many other parts of Australia, soils of Wheatbelt woodlands are nutrient-poor. Diversity among mycorrhizal and saprotrophic fungi which are involved in crucial nutrient cycling processes is likely to have contributed to sustainability of the woodlands in the past. Although many Wheatbelt fungal species also occur outside the region, some putatively ectomycorrhizal fungi such as two recently discovered new species of *Torrendia* are currently known only from a few remnant patches of Wheatbelt woodland. The discovery of such potentially rare, endangered fungi adds to the conservation significance of the remnant woodland. Data so far show that badly degraded patches have comparatively few sequestrate fungi, and farmlands revegetated with woody shrubs and trees have none. Potential implications of reduced or eliminated fungal biodiversity in such situations include loss of a biodiverse component of the soil, run-down in soil and nutrient cycling processes undertaken by the fungi, and ineffective re-introduction of mycophagous mammals. In areas such as the WA woodlands, there is a need to actively assist re-introduction of sequestrate fungi in revegetation/reconstruction programs which aim to restore ecosystem biodiversity and soil processes (Tommerup & Bougher, 1999).

Many taxonomic groups of Australian fungi remain virtually unknown, or are in need of thorough, modern taxonomic treatments. The use of European names for Australian fungi has been common, but most local taxa differ from their Northern Hemisphere relatives. Taxonomic schemes based on Northern hemisphere fungi have not always been adequate to accommodate Australian taxa. For example, intensive collecting expeditions and taxonomic studies since the early 1980's throughout Australia have yielded more than 500 species of previously unknown sequestrate (truffle-like) fungi. The findings have altered and expanded taxonomic schemes for fungi, e.g. elucidation of novel systematic relationships between epigeous (above-ground fruiting) fungi and sequestrate fungi. The ecological significance of sequestrate fungi in Australia has also been studied. They are central to three-way mutually beneficial relationships involving plants and some mycophagous (fungus-eating) native animals (Claridge *et al.*, 1996). Small mammals such as the Woylie and Potoroo are lured by irresistible aromas to dig up and eat the spore-bearing fruit bodies. The truffle spores pass unharmed through the mammalian gut and are deposited in dung potentially far from the site of consumption. The fungus benefits by dispersal of its spores. The mammal benefits from the nutrition value of the fruit body. Sequestrate fungi are the dominant diet of Gilbert's Potoroo—one of Australia's most critically endangered mammals. Significant to the proposed translocation of potoroos to new areas is evidence that much of the diet of Gilbert's Potoroo is truffle-like fungi having mycorrhizal associations, particularly with N-fixing *Gastrolobium bilobum* shrubs in main potoroo habitats.

Many other specific ecological types of Australian fungi have remained unknown until recently: For example, the 'ghoul fungus' (*Hebeloma aminophilum*) is a so-called 'ammonia fungus'—a group of fungi with greatly enhanced activity in the presence of ammonium nitrogen compounds. Under natural conditions ammonia fungi occur only in specialised ecological circumstances such as near animal corpses or other NH_4 nitrogen depositions. Our experiments have induced a succession of various ammonia fungi to appear in eucalypt forests by applying ammonium nitrogen in the form of urea. Certain Deuteromycetes (e.g. *Ambylosporium botrytis*) are stimulated shortly after application of ammonium, followed in turn by various Ascomycetes (e.g. *Ascobolus denudatus*) and Basidiomycetes (e.g. *Hebeloma spoliatum*). Ammonia fungi include decomposer and mycorrhizal species and are therefore important components of microbial nutrient cycling in forest ecosystems.

There are many conservation and protection issues for fungi such as the effect of fire and other ecological disturbances. Maintenance of fungal biodiversity requires management for diversity of habitats (habitat-based conservation approach, Scott *et al.*, 1997), to take account of large-scale vegetation and soil types, and microhabitats. Names, identity and detailed characterisation of fungal taxa are crucial to tracking their recovery following disturbance. Morphospecies should be assessed in conjunction with molecular analysis to assess accurately below-ground activity in order to deal with intermittent, unpredictable fruiting patterns. CSIRO Forestry and Forest Products is investigating the effects of fire history on mycorrhizal fungi in eucalypt forests. Results so far suggest that, as with plants and animals, some fungi are favoured by fire whereas other are less so.

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'Twixt two worlds: surface water/groundwater interface

Andrew Boulton

Ecosystem Management, University of New England, Armidale, New South Wales 2350

Most of us are familiar with the taxonomic and functional biodiversity associated with the ecotones between two habitats, often resulting from an overlap of the biota and ecological processes that typify the two 'worlds that collide'. Two such worlds are the dark 'underworld' of groundwater and the well-lit surface environment of streams and rivers. 'Twixt these two contrasting worlds lies the hyporheic zone—the saturated sediments below the channel and extending out beneath the banks of many streams and rivers throughout the world. Surface stream water downwells into the hyporheic zone at the heads of riffles or the leading edges of central and lateral bars, and may travel underground for long distances (up to several kilometres) before emerging. Such upwelling water is usually altered chemically during its travels, and capable of influencing the composition of surface communities near its outflow. For example, in some streams, upwelling water may be enriched in nutrients that otherwise limit algal growth in the surface stream so that the upwelling zones are 'hotspots' for benthic algal production.

The hyporheic zone first attracted scientists' attention in European rivers during the early part of this century. Extraordinary creatures, many of them never seen in the surface waters, were described, often typified by morphological features interpreted as adaptations to a subterranean (stygal) existence: blind, unpigmented, elongate appendages, long sensory setae or antennae. This specialised fauna, termed the hyporheos, has now been found worldwide, living below nearly all rivers with a well-developed hyporheic zone. Diverse hyporheic assemblages occur from the unstable sandbeds of intermittent desert streams to the extensive glacial sediments of large lowland temperate rivers. Hyporheic invertebrates have been collected several kilometres from the main channel, and the magnitude of the hyporheic zone is sometimes an order of magnitude greater than the surface stream. Often, surface invertebrates temporarily occupy the hyporheic zone, apparently seeking refuge from droughts, floods or pollutants in the surface stream. Others, usually as small instars, may avoid predators or be actively entering the hyporheic zone to graze microbial biofilms on the sediment particles. Meanwhile, denizens typical of the saturated interstices of the deeper sediments near true groundwater are sometimes found quite close to the surface, carried there by upwelling water or perhaps actively migrating for some unknown reason.

In Australia, the hyporheos has been sampled in relatively few rivers. Biodiversity seems to be related to sediment particle size, water quality, and possibly food availability. In some places, the diversity of some groups (e.g. water mites) seems surprisingly high but as there are so few regional data, it is difficult to judge whether this is typical or not. Human activities, such as uncontrolled land clearance and consequent siltation, probably impact on the diversity of the hyporheos. It is likely that the 'health' of the hyporheic zone may be measured by hyporheic invertebrate biodiversity in similar ways to our assessment of river health using surface macro-invertebrate assemblage composition.

Trophic biodiversity in the hyporheic zone is biased towards detritivory and carnivory as the dark conditions minimise the amount of subterranean photosynthesis. In downwelling zones, some green plant material may be transported, but the main food and energy source appears to be derived from dead organic matter imported from the surface. Recent efforts to classify hyporheic invertebrates into 'functional groups' based on their diet and typical habitat have provided tools to predict responses to changes in physical features of the hyporheic zone or to hypothesise about the likely assemblages to be found in habitats of different particle size and hyporheic water residence time.

We have known of the existence of the hyporheos for nearly 80 years. The functional significance of the hyporheic zone has only become clear in the last 20 years or so. As we enter a new millenium with a clearer understanding of the linkages among streams, their catchments, their airsheds and the groundwater, we have a growing appreciation of the fundamental importance of the ecotones between these ecosystem compartments, and their taxonomic and trophic biodiversity. We need to preserve this biodiversity, already threatened by many of our activities but also at risk from our ignorance of its existence. As we change the conditions on either side of the hyporheic zone, what happens 'twixt the two worlds? And if we alter the exchanges of water, nutrients, energy, and fauna across this dynamic ecotone, what will be the ultimate fate of the two worlds that depend on the maintenance of this pathway?

BioTrack: a bioinformatics solution for biodiversity assessment and research

R.A. Bramble, J.M. Dangerfield, A. Pik, D.A. Nipperess and A.J. Beattie

Key Centre for Biodiversity and Bioresources, Macquarie University, Sydney, New South Wales 2109

Current understanding of biodiversity is limited largely to information on vertebrates and plants. Sampling constraints, taxonomic impediments and the sheer volume of material have constrained our use of the organismal diversity in other taxa. However, the fact remains that invertebrates and microbes account for 99% of extant biodiversity. Past efforts to include these groups in biodiversity research have been hampered by the effort and costs required to sample, assess and then analyse such abundant and poorly known groups. Here we describe BioTrack, a system that integrates para-taxonomy, sampling protocols, a powerful relational database, bar-code technology and the use of high-quality digital images into a complete solution for assessing and monitoring biodiversity. Informatics solutions like BioTrack will allow the inclusion of invertebrates in surveys and help us to understand more of biodiversity.

Project Eden—reconstructing mammal biodiversity on Peron Peninsula, Shark Bay in semi-arid Western Australia

Paul Brown and Brett Fitzgerald

Department of Conservation and Land Management, 67 Knight Tce, Denham, Western Australia 6537

In Western Australia seventeen species of mammals in the size range 35–5,000 g have become extinct and another 25 are known to have declined significantly since European settlement. The IUCN *Red List of Threatened Mammals* (1988) lists 26 species of Australian mammals. Shark Bay has the only or major populations of 5 of the 26 species, all of which were formerly widespread. Found on Bernier and Dorre Islands, these are the Banded Hare-wallaby, Western Barred Bandicoot, Shark Bay Mouse or Djoongari, the Mala or Rufous Hare-wallaby and the Boodie or Burrowing Bettong. Thirty-two terrestrial mammal species are known to have occurred on the Shark Bay islands and peninsulas (Baynes, 1990; McKenzie, in prep).

Peron Peninsula once supported 18 species of ground mammal, but only six now persist (Euro, Echidna, Spinifex Hopping Mouse, Little Long-tailed Dunnart, Hairy-footed Dunnart and Sandy Inland Mouse). All the Critical Weight Range (CWR) mammals (35–5,000 g) except the Echidna have disappeared. The Crescent Nailtail Wallaby and the Lesser Stick-nest Rat are extinct. Other mammals that once occurred on Peron are Mulgara, Chuditch, Red-tailed Phascogale, Greater Stick-nest Rat, Djoongari, Djini, Western Barred Bandicoot, Banded Hare-wallaby and Mala. Woylie were also part of the pre-European fauna of Peron and this species has now been reintroduced to the Peninsula.

The only mammal George (1999, pp 130–132) recorded from William Dampier's journal during his visit to Shark Bay in 1699 was 'a sort of Raccoons' thought to be either the now-threatened Banded Hare-wallaby or Burrowing Bettong.

Project Eden

Project Eden aims to reconstruct the ground mammal fauna biodiversity of Peron Peninsula as a large scale (105,000 ha.) case study for arid Australia and as a resource for education through eco-tourism. Focus of the project has been on control of threatening processes (foxes, feral cats, grazing), captive breeding of threatened mammals, and reintroducing terrestrial mammals to Peron.

Phase I: Control of threatening processes

Predation by foxes and feral cats

Over the last 20 years, it has been demonstrated that the fox has been a primary factor in the decline of Australia's CWR mammals and other fauna, particularly in the southern half of Australia (Kinnear *et al.*, 1988; Friend, 1990; Morris *et al.*, 1995).

It was estimated that about 2,500 foxes were on Peron Peninsula in early 1995, one of the highest densities recorded in WA. Broadscale baiting with 1080 meat baits occurred in 1995 and it was estimated that 98% of foxes were eliminated from the Peninsula. The barrier fence and associated deterrents at Taillefer Isthmus has prevented reinvasion from pastoral lands to the south. Annual aerial baiting for feral cats over the project area, and fox baiting on adjoining pastoral lands to the south of the study site by the local Landcare District Committee, have eliminated foxes from the Peninsula and reduced the likelihood of immigration.

More recently the feral cat has been implicated in the decline of native mammals up to 2 000 g in weight (Dickman, 1996) and in particular native rodents that did not construct deep burrow systems (Morris, 1997). Feral cats have also been implicated in the extinction of some island populations of mammals (Taylor, 1979) and the failure or limited success of programs to reintroduce endangered mammals to arid Australia (Christensen and Burrows, 1994).

Feral cat control requires a new set of techniques, to date untried on a broadscale mainland site in Australia. Project Eden has been field testing the new baiting and trapping techniques developed by the Department of Conservation and Land Management over the past 4 years. A cat-specific 1080 meat bait has been used during broadscale aerial baiting, selective ground baiting, and to monitor bait uptake by feral cats on Peron Peninsula. A comprehensive trapping program for feral cats using Victor soft-jawed leg-hold traps has resulted in 1659 feral cats being destroyed between 1 May 1996 and 30 September 1999. All cats have been autopsied and Project Eden now has one of the most extensive databases on feral cats in the world. Town cats are also being registered and monitored, and stray cats controlled.

Grazing and habitat degradation (goats/sheep and rabbits)

Feral goats and sheep compete with both native animals and domestic stock for food, water and shelter and have had a major effect on native vegetation. Since the purchase of the Peron pastoral station in 1990, 25,000 goats and sheep have been removed from the Peninsula. Rabbits compete for food with native mammals, and their high numbers help maintain high fox and feral cat numbers year round. Rabbit control has been patchy, the Rabbit Calici Virus not successfully establishing.

Phase II: Reconstruction of mammal biodiversity

Extant fauna recovery

Since the first fox baiting took place in 1995, the populations of all extant ground mammals have increased significantly. Other studies on Peron Peninsula have indicated significant increases in reptiles and birds.

Captive breeding

In 1997, a captive-breeding centre was established in François Peron National Park to breed threatened mammals for release onto Peron. The Centre currently holds Banded-hare Wallabies and Western Barred Bandicoots from Bernier Island, and Bilbies from arid Western Australia and the Northern Territory. To date 22 bilbies, 6 Banded-hare Wallabies and 27 Western Barred Bandicoots had been bred. Mala are due to arrive at the breeding centre from the Great Sandy Desert in November 1999.

Reintroduction

During the last three years, Woylies have been introduced in late winter directly from wild populations. Monitoring using cage traps and radio-collared animals has shown no predation. Once established, animals appear to be surviving well and breeding. In mid-1999, six independent juvenile Woylies were captured. 67 Malleefowl have been raised from wild-collected eggs and released onto Peron. They are now well established. Plans are being put in place for the release of a number of other CWR mammals in 2000–2001.

Phase III: Eco-tourism

The science of Project Eden has been combined with a major education program for the Shark Bay community and the 100,000 tourists visiting the area each year. Inclusion of the local community in the day to day management and vision for Project Eden has been a significant factor in the success of this project.

Understanding the diversity of Glomalean fungi in tropical Australian habitats

Mark Brundrett

CSIRO Forestry and Forest Products, Private Bag, PO, Wembley, Western Australia 6014

The diversity and distribution of Glomalean fungi forming arbuscular mycorrhizal associations were examined throughout a region of tropical Australia which includes Kakadu National Park. Topsoil was collected from 32 sites, including natural habitats (eucalypt savanna, rocky hillsides, wetlands & rainforest) and highly disturbed minesite habitats. Methods used to examine fungal populations in soils included (a) spore numbers (b) spore biovolumes (c) identification of fungi by colonisation patterns in bioassay plant roots and (d) isolation of fungi in pot cultures. 16 species of VAM fungi were identified from spores found in these samples, but 7 additional fungi were recovered from the same soils using 4 complimentary pot culturing methods. Different methods of detecting fungi produced different answers about which fungi were most important in soils. Undisturbed sites contained between 5 and 13 species of VAM fungi and disturbed sites had a much lower diversity. Most species were widespread, but some only occurred in disturbed habitats or waterlogged soils, suggesting that their distribution was influenced by habitat conditions. Fungi were restricted to patches of vegetation in highly disturbed habitats and the abundance of their spores and other propagules increased with plant cover, eventually reaching levels well above those found in undisturbed plant communities. Spore occurrence data provided good information about most species in the genera *Scutellospora*, *Acaulospora* and *Gigaspora* but greatly underestimated the importance of *Glomus* species in soils, as these were more dominant in bioassay plant roots and trap cultures. Differences in propagule strategies suggest that fungi had different life history categories, corresponding with genera or groups within genera. Observations of fungi in pot cultures provided valuable new information about their biology.

Historical changes in the bird fauna of the Shark Bay region

Allan H. Burbidge[1] and Ron Johnstone[2]

[1]Department of Conservation and Land Management, PO Box 51, Wanneroo, Western Australia 6065

[2]Western Australian Museum, Francis Street, Perth, Western Australia 6000

As part of a joint Conservation and Land Management/Western Australian Museum survey of the Carnarvon Basin, Western Australia, we documented geographical range and status for the 278 bird species known to occur in the region. Most of the historical bird records came from the Storr-Johnstone database of birds in Western Australia. Bird records in the Shark Bay area extend from the 17th Century to the present, but very few records are from before 1900. The 163 breeding species known from the Carnarvon Basin were mapped, and each was assessed for possible changes in abundance during the last century. No species is known to have become extinct. For about 75% of breeding species we could not detect a change, but about 13% have increased in abundance, and 10–15% have decreased in abundance. These changes are comparable to those reported for a nearby arid area (the Murchison catchment), but are less than those reported for an eastern Australian arid area (western New South Wales).

A taxonomic revision of *Sphaerolobium* Sm. (Papilionaceae: Mirbelieae)

Ryonen Butcher

Department of Botany, The University of Western Australia, Nedlands, Western Australia 6907

Sphaerolobium was described by Smith in 1805 from a single specimen of *S. vimineum* Sm. collected from New South Wales. The genus is commonly known as 'leafless globe pea' and is characterised by its small, usually caducous leaves and small, stipitate, more-or-less globose pods. The most diagnostic features of the genus are the presence of a sub-stigmatic membranous wing formed from a laterally flattened portion of the style and/or a ring of long hairs surrounding the stigma. Other features considered diagnostic include bracts and bracteoles which are usually caducous, a glabrous ovary with two broadly funiculate ovules and a bi-labiate, usually glabrous calyx with strongly fused upper lobes. Exceptions exist to most of these diagnostic characters, however, as *S. linophyllum* (Hügel) Benth., *S. gracile* Benth. and *S. nudiflorum* (Meisn.) Benth. all have persistent leaves, *S. linophyllum* has persistent bracts and bracteoles, *S. medium* R. Br. lacks any stylar appendages and *S. pubescens* R. Butcher has spreading hairs on its calyx, bracts, bracteoles and pedicels.

Sphaerolobium is endemic in Australia and is found in all States except the Northern Territory, with the greatest concentration of species in the south-west of Western Australia. Of the taxa found in the eastern States, *S. vimineum* also grows in WA, but *S. minus* Labill. is endemic in New South Wales, Victoria, Tasmania, Queensland and the ACT, and *S. acanthos* Crisp is restricted to The Grampians in Victoria. The remainder of the species are endemic to the South-west Botanical Province of Western Australia, between Kalbarri and Cape Arid National Parks. Within this region, the highest level of species diversity and endemism occurs in the Albany district, where seven species occur in seasonally wet habitats between D'Entrecasteaux National Park and the Green Range. Comparatively, the kwongan (heath) north of Perth has two endemic taxa, the southern kwongan two, and the Swan Coastal Plain one. Three species are widespread between Busselton and Esperance, with a further four species being widespread across the entire South-West Botanical Province.

Prior to this study, 14 species were recognised following the reinstatement of *S. minus* and the description of *S. acanthos* by M.D.Crisp in 1993 and 1994 respectively. Following a taxonomic revision and cladistic analysis of *Sphaerolobium* undertaken in 1996, the number of species in the genus now stands at 18, with two or three more taxa yet to be formally recognised. The increase in recognised species from 1994 to the present reflects the lack of taxonomic research into the Western Australian members of this genus since Bentham's 1864 revision of *Sphaerolobium* in *Flora Australiensis*.

In his revision Bentham made a number of significant changes to the taxonomy of *Sphaerolobium*, including the incorporation of *Roea* Hügel, a genus defined by the presence of a narrow-turbinate calyx tube which is longer than the lobes, persistent leaves and a ring of long hairs around the stigma, into

Sphaerolobium as sect. *Roea*. His decision to merge these two genera was based on *S. racemulosum* Benth., a species with both a broad sub-stigmatic 'wing' and a 'beard' of long hairs, and calyx lobes and tube of almost equal-length. A cladistic analysis of *Sphaerolobium* confirms that the genus is monophyletic, and supports Bentham's placement of the foliose *S. linophyllum*, *S. gracile* and *S. nudiflorum* into sect. *Roea*, but suggests that *S. alatum* Benth. and S. racemulosum also be included into this section. Characters shared by these taxa include a racemose inflorescence, crumpled rather than flat petals, wing petals which envelop the keel and, with the exception of *S. alatum*, long hairs surrounding the stigma. The cladistic analysis also suggests the placement of *S. scabriusculum* Meisn. into a monospecific section based on its large, pendulous flowers arranged in a terminal raceme. The remainder of the species in *Sphaerolobium* fall within Bentham's section *Eusphaerolobium*, which is defined by leafless flowering stems and a style which is either naked or with a longitudinal wing under the stigma. All these taxa also share an inflorescence type consisting of flowers which are paired in the leaf axils on a very short peduncle.

Another area of interest in this revision and analysis concerned the 'S. macranthum complex'; the end result of Bentham placing *S. drummondii* Turcz. and *S. crassirameum* Meisn. in synonymy with *S. macranthum* Meisn., reducing *S. pulchellum* Meisn. to a variety of *S. macranthum* and describing a new taxon, *S. macranthum* var. *parviflorum* on the basis of its having 'Flowers smaller, all yellow'. This action caused a number of taxonomic headaches in *Sphaerolobium* until my recent revision reinstated the names *S. drummondii* and *S. pulchellum* and elevated *S. parviflorum* (Benth.) R.Butcher to species status. In addition to investigating this complex, recent work on the genus has seen the description (Butcher 1998) of two new species, *S. pubescens* and *S. rostratum* R.Butcher, from the Albany district as well as the recognition of a further two new species with affinities to *S. grandiflorum* and *S. parviflorum* respectively which have not yet been formally named.

Reference

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Biological Information Systems

Alex R. Chapman

Western Australian Herbarium, Department of Conservation and Land Management, Locked Bag 104, Bentley Delivery Centre, Western Australia 6983

Scientific electronic information systems have become embedded into the fundamental operations of museums, herbaria and university departments over the last 25 years. In general, they take the form of either centralised, indeterminate databases of core taxonomic information (such as taxon names, voucher specimens, species distributions and descriptions) or specific, often finite, research datasets focused on special-interest groups or regions.

As institutional processes are streamlined with these information systems at their centre, and as the volume of quality data increases, more sophisticated data analysis can be performed. For example, spatial modelling of biological datasets has offered support to biodiversity planning and conservation management decisions.

While there are some fully functional examples of integrated information systems from a single institution where different types of taxonomic information are amalgamated into a truly online resource, there are a number of major examples of multi-institution data integration.

Combining data of varying types within a single institution, or integrating data of a similar type from multiple institutions, both require developed and widely supported data standards. As information delivery mechanisms progress, such standards must be reviewed, refined and improved. The presence of global networks will demand the adoption of global metadata standards in order to facilitate the development of large-scale biodiversity information systems.

A cladistic analysis of *Austrophlebioides* and related genera (Ephemeroptera: Leptophlebiidae)

Faye Christidis

Department of Zoology and Tropical Ecology, James Cook University, Townsville, Queensland 4811

The Leptophlebiidae is the largest mayfly family in Australia, comprising 65 described species in 16 genera. All Australian genera belong to the subfamily Atalophlebiinae and are members of a Gondwanan lineage which is distributed throughout the Southern Hemisphere. A phylogeny for this Gondwanan group was proposed by Pescador and Peters (1980) in which they recognised five main monophyletic lineages, the Hapsiphlebia, Penaphlebia, Nousia, Dactylophlebia and Meridialaris lineages. In this study a cladistic analysis based on morphological characters was used to investigate the phylogenetic relationships of the Australian genera and species of the Meridialaris lineage and test the monophyly of this group. Secondly, I compared the results from parsimony analysis of the Australian genera with the phylogeny derived by Pescador and Peters (1980) using traditional Hennigian methods. The findings of this study strongly support the monophyly of a clade containing the three Australian genera of the Meridialaris lineage: *Austrophlebioides* Campbell & Suter, *Kirrara* Harker, and *Tillyardophlebia* Dean. The cladistic analysis also supports the tentative placement of several undescribed species into *Austrophlebioides*. The placement of several other undescribed taxa is discussed. The outcomes from the parsimony analysis of the Australian genera agree in part with the higher level relationships proposed by Pescador and Peters (1980).

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What we never knew : the diversity of spiders in the outback

Tracey B. Churchill

CRC for Tropical Savannas & CSIRO Wildlife & Ecology, CSIRO Tropical Ecosystems Research Centre, PMB 44 Winnellie, N.T. 0822

Our understanding of spider communities across Australia has been characterised by surveys from eastern coastal habitats (where taxonomists are more abundant), the western wheatbelt (where Barbara York Main works), and rainforests or mountain summits (where it's cool, lush and rich in endemics). Even forays into the hot, sweaty interior have tended to focus on biogeographical oases such as the beautiful gorges of central Australia or the amazing caves of the Nullarbor.

The fauna of the 'typical outback' is clearly less well known, and the north, in particular, represents an arachnological frontier. Our work over recent years has revealed some patterns in the distribution and abundance of dominant groups across a major rainfall gradient and three soil types. In conjunction with other surveys, it is becoming evident that the outback nurtures a rich, unique spider fauna that includes species-level radiations in families such as the Zodariidae. Its evolutionary history is yet to be fully appreciated.

In terms of conservation, grazing is the most widespread land use and its impact on biodiversity is now the subject of a number of studies throughout Australia. In collaboration, our project has been investigating the responses of several invertebrate taxa to grazing intensity. Preliminary results show differential responses across foliage-dwelling and ground-active spider taxa for different regions or soil types. The relationships between such responses and landscape processes are being explored with more detailed studies in the Victoria River District of the N.T. These results are helping to direct future research within our larger multidisciplinary project.

Assessment of taxonomic limits in *Abildgaardia*, *Crosslandia* and *Fimbristylis spiralis* (Cyperaceae) in Australia

Kerri Clarke[1], Karen L. Wilson[2] and Jeremy J. Bruhl[1]

[1]Botany Department, University of New England, Armidale, New South Wales 2351

[2]National Herbarium of New South Wales, Royal Botanic Gardens, Sydney, New South Wales 2000

Correspondence: Kerri Clarke (ksmith@metz.une.edu.au)

Progress in a study of the tribe Abildgaardieae worldwide is here reported.

Acceptance of *Abildgaardia*, *Bulbostylis* and *Fimbristylis* as separate genera is still contentious. Goetghebeur delimited the genus *Abildgaardia* on the basis of distichous glumes that are always glabrous, stipitate fruit, *Abildgaardia*-type embryo, absence of pilose hairs at the leaf sheath orifice, and dehiscent style base. Of the c. 17 species of *Abildgaardia*, seven occur in Australia, six being endemic.

Crosslandia is a monotypic genus restricted to Northern Territory and northern Western Australia. It was separated from *Abildgaardia* and *Fimbristylis* by the spikelets being monoecious and the presence of basal female spikelets. The variation in inflorescence structure and breeding system for *Crosslandia* is such that Goetghebeur introduced a tentative name for a second species with an anthelate rather than capitate inflorescence, and bisexual florets in the aerial spikelets. A study of species limits in *Crosslandia* has so far revealed much variability in the breeding system. Aerial spikelets can have a mix of bisexual florets, male and female florets, only male florets; and basal spikelets possess female only or, more rarely, bisexual florets. Similarity exists between *Fimbristylis spiralis* and *C. setifolia*. *Fimbristylis spiralis* is the only member of *Fimbristylis* that bears basal spikelets with female florets. Limits and relationships of *F. spiralis* and *C. setifolia* are being assessed.

The results of phenetic analyses presented are based on 41 characters taken from plant morphology, leaf and culm anatomy, and embryo morphology. These analyses allow the assessment of the entities in the genera *Crosslandia* (including *F. spiralis*) and *Abildgaardia*. Representative samples from *Bulbostylis* and *Fimbristylis* provide comparative data for these and subsequent cladistic analyses of the tribe.

Molecular systematic and evolutionary studies in the south-western Australian flora: implications for conservation

David J. Coates and Margaret Byrne

Western Australian Herbarium, CALMScience, Department of Conservation and Land Management, Locked Bag 104, Bentley Delivery Centre, Western Australia 6983

The south-western Australian flora of shows a diverse array of evolutionary patterns and exceptionally high species richness. Examples of this evolutionary diversity are presented in studies on a number of species complexes in *Acacia*, *Eucalyptus*, *Eremaea*, *Lambertia* and *Stylidium*. Comparative studies of phylogenetic patterns revealed by molecular markers such as allozymes, nuclear DNA RFLPs, chloroplast DNA RFLPs, and chromosomes have been particularly informative in resolving the complex evolutionary relationships observed between taxa and between populations within taxa. In a number of cases, phytogeographical patterns indicate that historical fragmentation associated with past climatic events, and the retention of relatively ancient and genetically divergent population remnants are features of many species. These patterns are particularly evident in rare, geographically restricted species such as *Acacia anomala*, *Banksia cuneata*, *Dryandra mimica*, *Lambertia orbifolia*, *Lambertia echinata* and *Stylidium coroniforme*. They also appear to be characteristic of more widespread species in the *Stylidium caricifolium* species complex. In contrast, studies on other, geographically more widespread species in the *Acacia acuminata*, *Eucalyptus kochii* and *Eucalyptus loxophleba* groups and the genus *Eremaea* indicate relatively recent population divergence and a more reticulate pattern of evolution associated with hybridisation.

These complex evolutionary patterns at both the population and species levels present a significant challenge to the development of appropriate conservation strategies for this flora. To be effective, these strategies should aim not only to preserve current levels of species diversity but also to consider intraspecific variation and the evolutionary and ecological processes associated with the generation and maintenance of that variation. The identification and characterisation of conservation units, based on population genetic structure and phytogeographical patterns within species, provide a useful basis upon which more general conservation principles can be developed for the maintenance of these processes. Determining conservation units within species defines not only suitable units for conservation but also the appropriate geographical scale for management.

Sharing data, the Virtual Australian Herbarium, and a distributed electronic Australian Flora

Barry J. Conn

Royal Botanic Gardens, Mrs Macquaries Road, Sydney, New South Wales 2000

The major Australian herbaria have played a key role in the development of database standards for botanical information. They have also developed HISPID, an internationally recognised data interchange standard. This standard is currently being implemented throughout Australia. During 1999, the Herbarium Information Systems Committee (HISCOM), a subcommittee of the Council of Heads of Australian Herbaria (CHAH), developed the 'Virtual Australian Herbarium' (VAH). The VAH is a prototype distributed database system that is searchable over the Internet. Currently, the prototype presents Australian distributional information (as dot maps) of *Acacia* species. This major collaborative project simultaneously searches locally held State and Territory herbarium databases. The results of the query are collated and presented as distribution maps. The major benefit of the VAH is that the information remains current because the data are drawn directly from institutional databases. The natural extension of this project will be to link the State and Territory Plant Censuses, through the Internet, in a distributed model. This will enable a list of Australian plants to be built up from the various State and Territory lists. Most importantly, however, this information can be presented collectively, through a single Internet 'window'. Since descriptive plant information together with identification tools are being stored electronically (e.g. FloraBase, PlantNET), a distributed electronic Australian Flora may be possible in the very near future.

A phylogeny of the eucalypts—as told by scale insects

Lyn Cook

Division of Botany and Zoology, The Australian National University, Canberra, Australian Capital Territory 0200

Australia has a diverse, gall-inducing scale insect fauna, many members of which are restricted to eucalypts. *Cystococcus* and *Ascelis* occur only on species of *Corymbia*, and *Maskellia*, *Lachnodius*, *Opisthoscelis* and *Apiomorpha* occur only on *Eucalyptus sens. str.* Host specificity in *Apiomorpha*, the most speciose gall-inducing scale insect genus, occurs at five levels of the host classification:

1. *Apiomorpha* occurs only on species of *Eucalyptus sens. str.*

2. Species-groups are each confined to only one subgenus of *Eucalyptus.*

3. Some species-groups or species are confined to eucalypt species of only one or a few sections.

4. Some species or chromosomal forms appear to be restricted to eucalypt species of only one or a few series.

5. Some species or chromosomal forms appear to be restricted to only one or a few species of eucalypt.

It is proposed that cladogenesis in *Apiomorpha* has tracked that of its host genus. If so, then phylogenetic estimates of relationships within *Apiomorpha* may be construed as mirroring those of the host eucalypt species and therefore provide surrogate hypotheses of eucalypt evolution.

Australian phycology—its influence

Roberta A. Cowan

School of Biological Sciences and Biotechnology, Division of Science and Engineering, Murdoch University, Murdoch, Western Australia 6150

William Dampier was the first European to return home with a collection of an Australian alga. It took until the nineteenth century for Australian specimens to appear regularly among the descriptions of marine and freshwater plants. A number of cosmopolitan species found in Australia were described from Europe and the near East, in the mid-eighteenth century including the plant Dampier collected, *Cystoseira trinodis* (Forsskål) C.Agardh. Plants such as *Dictyota prolifera* Lamouroux, *Amphibolis antarctica* (Labillardière) Sonder & Ascherson were described, in the early nineteenth century, from collections made on the French expeditions sent to Australia during the late eighteenth century, or from collections made at Sydney Cove and sent to England by Governor Hunter, as in the case of *Microdictyon umbilicatum* (Velley) Zanardini.

The number of known taxa increased over the first 40 years of the nineteenth century, mainly through the study of European collections of Australian plants. Although Robert Brown described a number of freshwater taxa in his *Prodromus*, his equivalent in the Australian marine and freshwater flora, in terms of number of protologues, is William Harvey. Harvey collected in Australia during the mid-nineteenth century but had already described many plants in association with J.D.Hooker. Mueller's influence impacted this flora, as it did the terrestrial flora. Along with a band of dedicated collectors he was able to supply many European botanists with plants. Other collectors sent plants directly to Europe and so the number of described taxa peaked once again towards the end of the nineteenth century through the publications of J.G.Agardh, Ascherson, Braun, Grunow, Kuetzing and Watts.

Publications by Australian resident botanists on the marine and freshwater plants began to appear at the end of the century. They appeared as floral lists, e.g., Watts, Wilson, Bastow. A period of consolidation followed which culminated in publications such as the *Seaweeds of South Australia* by Lucas & Perrin, *The Plankton of Australian Coastal Waters off N.S.W.* by W.Dakin & A.Colefax. A new phase in flora treatments began in the 1950's when botanists such as H.B.S.Womersley , S.C.Ducker and A.B.Cribb began publishing regional floras. As the students trained by these scientists also began to publish, the number of taxa again rose with a peak in the 1980's. This latest peak is of interest since it reflects the financial support provided by the grants schemes of the Australian Government such as the Marine Science and Technologies grant scheme of the late 1970's and early 1980's.

Dampier's pea, and the radiation of Fabaceae in Australia

Rogier de Kok[1], Mike Crisp[2], and Jenny Chappill[3]

[1]Centre for Plant Biodiversity Research, CSIRO, GPO Box 1600, Canberra, Australian Capital Territory 2601

[2]Division of Botany and Zoology, Australian National University, Canberra, Australian Capital Territory 0200

[3]Dept of Botany, The University of Western Australia, Nedlands, Western Australia 6907

Among the first plants to be collected by western botanists is one of Australia's most recognisable icons, the Sturt Desert Pea (or Dampier Pea). This plant was collected by William Dampier in Western Australia, 300 years ago. The number of species and genera grew rapidly following further exploration and especially after the establishment of the colonies both in eastern and Western Australia. James Edward Smith and Robert Brown described a number of species and genera including some of the most diverse ones such as *Daviesia* and *Pultenaea*. Bentham had a great influence on the classification of Australian Fabaceae. He divided the 'genistoid' genera, on the basis of the amount of fusion in the stamens, into two tribes: the Podalyrieae and the Genisteae. This classification was accepted until Polhill's revision in 1981. Early workers such as Bentham used a Linnaean framework based on sex and number of stamens. On the basis of these selected characters they established two tribes and shoehorned everything into them. Polhill started a new broad approach in using the widest range of evidence and so breaking the old mould. Furthermore he synthesised the characters within a phylogenetic framework. The result was seven new tribes, including those that are so characteristic for Australia: the Mirbelieae and Bossiaeeae (but he expressed his doubt about the distinctness of the latter two).

Most of the work done on the Australian Fabaceae since Polhill has been centred around two themes: first, revisions for the *Flora of Australia* and second, an increasing amount of work on the phylogeny of the groups. Both themes have benefited positively from each other. Jenny Chappill based her phylogeny of the legumes of the world on morphological characters. Her tree shows the placement of a number of important Australian groups (*Acacia*, *Senna*, *Tephrosia*, *Indigofera*, *Crotalaria* and *Castanospermum*). In this talk we concentrate on only a few groups. The Galegeae/Carmichaelieae clade (Wagstaff *et al.*) is of interest because it shows the position of the Sturt Desert Pea, which is clearly placed within the genus *Swainsona*. Also, the Mirbelieae/Bossiaeeae and Brongniartieae clades are emphasised because of their ecological importance and their problems in generic and tribal delimitation. In the cladogram based on ITS DNA sequences, the Brongniartieae form a near-basal group. The 'core' genistoids also form a monophyletic group with little Australian representation, except for Crotalarieae. The Mirbelieae and Bossiaeeae form a clade nested in the major radiation of the Papilionoideae, close to major groups such as the Millettieae, Phaseoleae, Indigofereae and Galegeae. The Bossiaeeae are nested within the basal group of genera of the Mirbelieae (*Daviesia* group), with which they share giant antipodal cells in the embryo sac. Most of the problems in the Mirbelieae and Bossiaeeae are about generic delimitation in the so-called multiple embryo sacs group (*Pultenaea*, *Callistachys* and *Oxylobium* groups). Plans to tackle these problems were developed at a recent workshop where further sampling of the problem genera, new DNA markers and re-evaluation of morphological characters will hopefully result in a more resolved and robust phylogeny. Also, a collaboration was established to develop an interactive key to all the species of Papilionoideae in Australia before the Legumes IV Conference in 2001.

William Dampier's 'New Holland' moss

Alison Downing[1] and Serena Marner[2]

[1]Department of Biological Sciences, Macquarie University, New South Wales 2109

[2]Oxford University Herbaria, Department of Plant Sciences, South Parks Road, Oxford OX1 3RB, United Kingdom

In 1699, William Dampier collected plants at two or three locations on the north-west coast of Australia, viz. Shark Bay, the Dampier Archipelago and Lagrange Bay. Dampier's collection is now housed in the Fielding-Druce Herbarium at Oxford University. It includes a specimen of the moss *Leucobryum candidum* (P.Beauv.) Wils. The location given for this moss is 'New Holland' which implies that it was collected by Dampier at one of the above locations, making it the first bryological record for Australia.

After Dampier's return to England, the moss specimen appears to have had an unusual history. Our investigations have shown an intriguing insight into the way in which collections were managed, and raided in a fashion which now might be viewed as less than ethical. Most notably, Dillenius appears to have removed a portion of the moss (the fertile portion) from the Dampier collection in the Sherardian Herbarium and placed it in his own collection (also at Oxford) where it was described in his *Historia Muscorum* as 'Bryum candidum fragile, foliis recurvis'.

The moss appears to have been overlooked in Australia. Ferdinand Mueller knew of Dampier's plant collection from New Holland, but the moss is not mentioned in his 1883 *Catalogue of Australian Mosses*. *Leucobryum candidum* commonly occurs in moist forests of eastern and northern Australia, New Zealand and South East Asia. It was not included in the 1993 census of mosses of Western Australia and references elsewhere to its presence in the forests of the south-west of Western Australia can probably be attributed to *Leucobryum subchlorophyllosum* Hampe. Dampier's specimen is labelled 'New Holland', but its presence at Shark Bay, in the Dampier Archipelago or Lagrange Bay seems unlikely. Species recorded for the regions that include these localities are typical of arid and semi-arid areas of southern Australia, and are very different from the species found in the closed forests and woodlands of high rainfall areas of south-western and south-eastern Australia. Although it is possible that *Leucobryum candidum* may occur in the Mitchell Plateau area of the north Kimberley, it now seems more probable that the specimen was collected by Dampier in Timor or New Guinea later on the voyage.

Although it is unlikely that the specimen was collected in Australia, it is still probably the oldest bryological record for South-East Asia, and is thus of great scientific and historical interest.

Managing and monitoring cave fauna in Tasmania

Stefan Eberhard

Caveworks, PO Witchcliffe, Western Australia 6286

In Tasmania, cave management plans and monitoring programs recognise the significance of cave fauna, which is among the richest and most spectacular in temperate Australia. Conservation management of cave fauna has involved: (i) legislative protection of rare and threatened species; (ii) protection of sensitive habitats in caves by marking routes or no-go (sanctuary) areas; (iii) educating cave users, including minimum-impact caving techniques. Monitoring cave fauna has been undertaken for the purposes of: (i) gathering baseline ecological information for research, visitor management, and interpretation; (ii) measuring the ecological impacts of limestone quarrying and subsequent recovery during rehabilitation efforts.

In Kubla Khan Cave at Mole Creek, Tas., habitat degradation caused by cave visitors has been halted by installing a steel stairway. In Exit Cave at Ida Bay, certain representative or key habitat areas have been protected with string-line pathways, or else designated as no-go fauna sanctuary areas. The fauna sanctuaries include, *inter alia*, optimum habitat of the extremely rare blind cave beetle *Goedetrechus mendumae*. Although currently listed as vulnerable, this species is not considered threatened by trampling. A number of Tasmanian cave species are listed as rare or vulnerable, whilst others are wholly protected. The integrity of cave ecosystems at Mole Creek is most under threat from farm development on the karst, which affects the surface vegetation, water quality, flow regimes, nutrient and sediment inputs. Public awareness of cave fauna has been addressed by producing illustrated fact sheets which describe Tasmanian cave species, their vulnerable habitats, and minimum impact caving techniques.

The Little Trimmer Cave monitoring program was established by the Forestry Commission in 1991, to gather baseline environmental data. The biological monitoring, which has been continued by the University of Tasmania, has provided very useful life history and behavioural information on cave spiders, crickets and amphipods. Monitoring the abundance of stream-dwelling snails, as a potential indicator of quarrying impacts, commenced in Exit Cave in 1992. This monitoring is being continued in an attempt to gauge the effectiveness of rehabilitation efforts. The same quarrying operation caused extinction of the aquatic fauna in Bradley Chesterman Cave, but recovery of the fauna occurred within five years of quarry closure, after intensive rehabilitation measures.

Monitoring of glow-worms, cave crickets and cave spiders has been initiated in Exit Cave and Mystery Creek Cave to: (i) expand knowledge of the caves' biological resources; (ii) to identify environmental seasons, cycles, changes and trends; (iii) to provide a baseline upon which to assess the impact of human activity in the caves. However, obtaining statistical validity may be difficult when attempting to detect human impacts to cave fauna.

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Freshwater algae in Australia: 300 years on

Tim Entwisle

Royal Botanic Gardens, Mrs Macquaries Road, Sydney, New South Wales 2000

The *Census of Freshwater Algae in Australia* is now online (at http://www.rbgsyd.gov.au). Although the *Census* is currently based on published records (many of them unvouchered and poorly documented), it allows us for the first time to make some sweeping generalisations about the diversity of freshwater algae in Australia.

History: William Dampier collected a marine alga during his second visit to Australia, but no freshwater algae were documented until Robert Brown in 1810. Brown collected some charophytes and one red alga from freshwater. The first local product was that of H.Watts in 1865; this was also the first checklist to be produced, reporting 45 species from Victoria. By 1906, A.D.Hardy had expanded that list to 316 species for the State. In 1913, F.M.Bailey reported 550 species from Queensland, and in 1917, G.I.Playfair listed 569 species from New South Wales (see T.J.Entwisle 1990, *History of Systematic Botany in Australasia*, pp. 239–246, for references).

Diversity: There has been a slow but steady increase in the number of species reported from Australia. The *Census* now includes:

Rank	Current names	Synonyms
Genus	573	5
Species	3404	755
Subspecies	13	28
Variety	1555	409
Form	343	96

These figures undoubtedly include many misidentifications and misunderstandings, but they give a whiff of the true diversity. As elsewhere, most species of freshwater water algae in Australia are desmids (Chlorophyta, Zygnematophyceae) or diatoms (Heterokontophyta, Bacillariophyceae). Most records are from N.S.W., Qld, Victoria and N.T. W.A. and S.A. are drier States and may contain fewer algae, but they have also been less thoroughly sampled.

Conservation status: We have made a brave attempt at calculating conservation status.

Preliminary conservation codes of accepted species

State	Rare	Vulnerable	Endangered	Total
Western Australia	2	16	0	183
Northern Territory	34	298	0	999
South Australia	1	32	0	283
Queensland	22	160	1	1323
New South Wales	24	284	0	1569
Aust. Capital Territory	1	3	0	35
Victoria	11	166	0	1293
Tasmania	45	73	0	615
Australia-wide	135	1024	1	3404

A sizeable proportion (1024 species, 2027 taxa) could be considered vulnerable. We adapted the standard codes and used vulnerable for 'any taxon reported from a single locality (e.g. the type locality), or from two or three collections in the same (smallish) catchment, or from two or three localities where the taxon is described as rare or under threat'. Of course, as with most algae and fungi, undercollecting will be responsible for some or most of the vulnerable taxa. However, a precautionary approach should be used (particularly given that many restricted taxa are likely to be obscured by misapplied Northern Hemisphere names).

Endemism: The degree of endemism in published references is about 10% for species and a third for infraspecies. However, our assessment of endemism was based on Australian literature, and many species will have been found subsequently elsewhere. Equally, endemism is likely to be under-scored because so many Northern Hemisphere names have been slapped on as best fits. No species has been reported from every State and Territory, but if we remove A.C.T. we find 14 species in common. Only 25% of species are shared by N.T. and Tasmania (both areas have been sampled by the same research team looking at similar taxonomic groups, so there is some commensurability). The data no doubt reflect the lack of systematic collecting as much as restricted distributions, but algae are not the same everywhere.

If we look at a group that has been reasonably well collected, the Batrachospermales, we see how taxonomic study has a huge impact on endemism. Endemism has risen from the pre-taxonomic revision stage in 1929 of maybe 10% (similar to that based on our literature database) to more than half in 1997. Of the 573 genera of freshwater algae reported from Australia, I would estimate less than 5% have been revised with any degree of taxonomic rigour (and even those groups require further collecting and study to bring them to the level of most groups of vascular plants). Endemism is likely to vary from group to group but it likely to be much higher than currently documented. Work on the Batrachospermales indicates that the freshwater algae will be useful for biogeographical studies of the Australian region once we better understand taxic diversity and relationships.

Commensurability: A big issue in sorting out endemism is commensurability of taxa. If we look again at the Batrachospermales, molecular sequencing data has confirmed a high degree of endemism and a distinct Australasian clade. Although many new species have been described, we may need to 'split' further: for at least one taxon referred to a cosmopolitan species, the Australian sample is distantly related to the Northern Hemisphere representatives. In this case we will describe a new species. On the other hand there are cosmopolitan taxa that are supported by the molecular data, so we can't generalise about the results.

Historical changes: We have little idea of changes to our freshwater algal flora since the arrival of Europeans or before. Certainly habitats have been destroyed and particular environments have few pristine lakes or streams. There are, however, interesting rediscoveries of micro- and macro-algae. In 1989, Peter Tyler and colleagues (*Brit. Phycol. J.* **24**: 329–37) reported the rediscovery of an endemic monotypic genus of microalgae, *Tessellaria*. *Tessellaria* was first reported in 1905 and described (by Playfair) as 'distinctly rare', found only in lagoons around Lismore, N.S.W. It is still considered rare, but widespread and disjunct in occurrence across Australia. I have rediscovered algae first collected by Ferdinand Mueller, Robert Brown and Arthur Lucas, some in the inner suburbs of Sydney. In other cases a species has apparently retracted upstream as the lower reaches have become polluted.

Collecting freshwater algae in Australia still holds the same thrills that I presume vascular plant collecting held for Dampier, Banks, Solander, Brown and Mueller. After 300 years we have a mud map of what freshwater algae occur in Australia. We still lack the connecting trails, and most names are too faint to read.

Acknowledgments: The development of the Census was supported by the Australian Biological Resources Study, Royal Botanic Gardens Melbourne, Deakin University and Royal Botanic Gardens Sydney. Data entry was by Rosemaree Wickham, Sandra Day and Lucy Nairn. Peter Tyler and Tim Entwisle provided coordination and expertise in the earlier version (*Bibliographic Checklist of Non-marine Algae in Australia*, 1995, ABRS), and Tim Entwisle has overseen the project throughout. All publications recording freshwater algae from Australia should be sent to Tim Entwisle, and a voucher for each record deposited in the relevant State herbarium.

A multidisciplinary review of the proteaceous genera *Isopogon* and *Petrophile*

Don Foreman[1] and Lynne A. Milne[2]

[1]Australian Biological Resources Study, G.P.O. Box 787, Canberra, Australian Capital Territory 2601

[2]Department of Geography, The University of Western Australia, Nedlands, Western Australia 6907

The genera *Isopogon* R.Br. ex Knight and *Petrophile* R.Br. ex Knight have been linked since they were first described, such that it is unusual for the name of one to be uttered without the other being far behind. Both genera reach their maximum diversification in the sandy and lateritic heathlands of south-west Western Australia, with just a few species from each genus occurring in eastern Australia. In Western Australia, *Isopogon* and *Petrophile* extend from north of Geraldton (but not reaching Shark Bay) to east of Esperance, forming a conspicuous part of the landscape at their peak flowering from August to December.

In the past there has been some confusion about the generic limits of these two genera, with taxa often being wrongly assigned. This is understandable, given that they exhibit a wide range of similar micro- and macro- morphologies. Although a number of new species in *Isopogon* and *Petrophile* have recently been described, the infrageneric classification of both genera have not been reviewed since Bentham's account was published in *Flora Australiensis* in 1870. However, alliances of various groups of species have been suggested in more recent times (e.g. Foreman 1995a, 1995b).

Belonging to the subfamily Proteoideae, the flowers of *Isopogon* and *Petrophile* are borne singly in the axil of a bract and are clustered together to form dense cone-like inflorescences which give rise to the common names coneflowers, drumsticks and cone sticks. The persistence and woodiness of the subtending bracts combined with features of the fruits, such as shape and the distribution of hairs, is generally enough to satisfactorily separate *Isopogon* from *Petrophile*. The variously modified pollen presenters are less useful, in that a significant number of species in both genera only show a slight swelling of the style tip. The position of some species such as *Petrophile circinata* Kippist ex Meisn. and *Isopogon buxifolius* R.Br. and its four varieties, however, remains unclear. The specific limits of variable taxa such as *Isopogon anemonifolius* (Salisb.) Knight, *I. trilobus* R.Br., *I. formosus* R.Br., *Petrophile serruriae* R.Br., and *P. squamata* R.Br. also remain unresolved, as does the significance of variation in flower colour in a number of species.

Plant taxonomy traditionally relies on macro-morphology. However, micro-morphology (e.g. of pollen) is also species specific in many families. A detailed study of *Petrophile* pollen, and resultant classification on pollen morphology, has shown a remarkable correlation between the methods of micro- and macro- morphological classifications. Continuing comparison of results from these two methods is intended to aid resolution of the problematic groups within *Isopogon* and *Petrophile*, and revise the infrageneric classification.

Within Conospermeae, each species and genus has a distinct set of pollen morphological characters (Milne and Martin 1998). Sculptural type is consistent within species, genera, and often subtribes. Aperture type is consistent within species, but within a genus it may be diverse and has little suprageneric taxonomic significance. *Petrophile* and *Isopogon* pollen have in common a reticulate surface pattern. The muri that form the reticulum are stranded in the majority of species, but may also be partially stranded or smooth. Within Proteaceae, *Isopogon* and *Petrophile* share this reticulum feature with *Symphionema* R.Br. and some Proteeae genera including *Sorocephalus* R.Br., *Paranomus* Salisb., *Leucospermum* R.Br. and *Serruria* Brum. ex Salisb.

Petrophile pollen morphology is exceptionally diverse, with a wide range of grain size, aperture types, and sculptural detail. Using a combination of morphological characters, and with no reference to known parent plant relationships, *Petrophile* pollen has been grouped into pollen types. Although the pollen types do not directly correlate with Bentham's sections, there are marked similarities. Several of Bentham's sections coincide with only one pollen type, while others predominantly contain two pollen types. With rare exceptions, the pollen types correlate very well with more recently noted parent plant alliances. Rare species for which pollen and parent plant indicated relationships do not concur (e.g. *P. acicularis* R.Br.) have borderline pollen type characters, possessing some features in common with another pollen type. Species with curious macro-morphology, such as *Petrophile circinata* with its unusual leathery bracts, have similarly interesting pollen morphology.

Pollen of *Isopogon* so far examined falls into two groups that do not correspond to the two series recognised by Bentham; the small amb-circular aperture type characterised by *I. fletcheri* F.Muell. and I anethifolius (Salisb.) Knight, and the massive amb-lalongate aperture type represented by *I. petiolaris* A. Cunn. ex R.Br. and *I. villosus* Meisn. The small-grained *Isopogon* pollen is broadly similar to eastern Australian *Petrophile* species (pollen type 1A), a group with allies in the Tertiary of Australia and New Zealand (Milne 1998).

Molecular studies by Hoot and Douglas (1998) do not support the very close relationship between *Isopogon* and *Petrophile* that are suggested by both micro- and macro-morphology. However, their work does support fairly strong links with some members of the South African Proteeae that have also been indicated by pollen morphology. Further study of *Isopogon* and *Petrophile* pollen and the morphological relationships in the two genera may shed more light on their joint history.

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Marine sponges (Porifera) of the Dampier Archipelago

Jane Fromont[1] and Gary Kendrick[2]

[1]Department of Aquatic Zoology, Western Australian Museum, Francis St, Perth, Western Australia 6000

[2]Department of Botany, The University of Western Australia, Nedlands, Western Australia 6907

Marine sponges of the Dampier Archipelago, north-western Australia, are poorly known (14 species described to date). This lack of knowledge prompted their inclusion in a major study of the marine biodiversity of the Archipelago presently being undertaken by the Western Australian Museum, funded by Woodside Petroleum Ltd. Results of sponge diversity from the first diving expedition by the Museum will be presented.

The term 'biodiversity' is generally equated with species richness or number of species. Some authors also incorporate an abundance estimate which provides a proportional representation of each species in an area, and thus allow comparison with other areas for which the same data are known. This additional component is incorporated into the sampling program for marine sponges, with the aim of determining whether relative abundance or 'evenness' is a useful component in studies of marine sponge diversity.

More than 250 species of sponge were found from 34 sites in the northern half of the Archipelago, a 17-fold increase in the number so far recorded from the area. The results are analysed both as a presence/absence matrix and as a quantitative data set. The advantages and disadvantages of the methodology will be discussed, and the implications for future marine surveys examined.

Biogeography and floral evolution of the Cichorioideae (Compositae): a southern hemisphere event

Vicki A. Funk

Department of Botany, MRC166, Smithsonian Institution, Washington, DC 20560, USA

The Compositae (or Asteraceae) is the largest family of flowering plants in the world with ca. 25,000 species and over 1100 genera. They have long been recognised as a monophyletic group and are divided into a number of tribes (see Heywood *et al.*, 1977, for a review). For many years there were 13 tribes, but more recently many smaller tribes have been described and there are now around 22 tribes. Recent molecular and morphological studies have altered our way of thinking about the family and the relationships among the tribes. For instance, the Mutisieae were once thought to be a tribe with many highly specialised characters and they were believed to occupy one of the terminal branches of the family; now we know that the Mutisieae are a basal, probably paraphyletic group (Bremer, 1994; Kim & Jansen, 1995). The family is broken up into 3 subfamilies: the Barnadesioideae, the basal branch of the phylogeny (< 1% of the species in the family), the Cichorioideae, unresolved in the center of the phylogeny (c. 35 %), and the largest, the Asteroideae, the terminal branch (c. 65%). The Barnadesioideae and the Asteroideae are well-defined using both morphological and molecular characters (Bremer, 1994; Kim & Jansen, 1995) and in between the two are the members of the Cichorioideae which vary in their morphological and molecular characters. The subfamily consistently appears to be paraphyletic but the branches of the cladograms are weakly supported and the relationships among some of the groups of genera are different on alternative, equally parsimonious trees. The focus of my current research is the systematics of the Cichorioideae. The tribes of this subfamily are the Mutisieae, Cardueae, Lactuceae, Vernonieae, Liabeae, and Arctoteae.

Australia has a large number of Compositae, c. 200 genera and c. 1000 species (Brown *et al.*, 1992). Most of the diversity and nearly all of the really interesting evolutionary questions are in the Asterioideae, not in the Cichorioideae.

MUTISIEAE. The members are grouped into 76 genera, found mainly in Central and South America. The greatest South American concentration is along the southern Andes, in Brazil and on the Guiana Shield. There are also 11 genera in Africa and Madagascar, 12 genera in Asia, and one South American genus, *Trichocline* Cass., that has one endemic species in Western Australia.

CARDUEAE (thistles). This tribe has 83 genera that are found primarily in the northern African and Eurasian area. A few genera have extended their distribution to North America, tropical Africa and into Australia where many are successful weeds.

LACTUCEAE (lettuce, dandelion). This tribe has 98 genera of mostly annuals from the Northern Hemisphere. There are concentrations of genera and species in the Mediterranean, Central Asia, and south-western North America. Many Lactuceae are widespread, successful, and noxious weeds. In Australia there are many species in 22 genera but only five genera are believed to be native.

VERNONIEAE (ironweeds). A pantropical tribe of 98 genera with a large amount of its diversity in Brazil and a lesser amount in tropical Africa. The tribe is poorly represented in Australia and few have been introduced.

LIABEAE. A small tribe of 15 genera found primarily in Peru and Ecuador but also in the northern Andes, Central America, Mexico and the Caribbean. There are no known species from this tribe in Australia.

ARCTOTEAE (gerbera daisy). A small group of 16 genera found mostly in Southern Africa with two outlying genera, one in Turkey and the Middle East and the second, *Cymbonotus* Cass. endemic in Australia.

While we have a good idea of what many of the groups are within the Cichorioideae, we do not have conclusive evidence of how they all fit together. The ndhF molecular data have given some insight into the relationships, the most recent cladogram indicating that all tribes except the Mutisieae are probably monophyletic. These cladograms show the Mutisieae containing several monophyletic groups of genera but the relationships among these groups are weakly supported. The members of the Cardueae have a number of unique morphological characters and have always been considered to be a 'good group' and while the molecular data agree that this is monophyletic, it is tentatively placed inside a group of Mutisieae genera from Asia and Africa. The tribes Lactuceae and Vernonieae are each considered a natural group but they are rather poorly sampled. The Liabeae and Arctoteae appear to be monophyletic. No single resolution of the relationships among the non-Mutisieae tribes (Lactuceae, Arctoteae, Liabeae, Vernonieae) is well supported but certain trends are present in all diagrams.

The biogeography and floral evolution of the Cichorioideae are very interesting. The basal branches, including the first outgroup, are neotropical, mainly from southern South America, except a small group of Asian and African Mutisieae with bilabiate corollas. The next group contains most of the Asian and African Mutisieae, those that have only actinomorphic disk corollas. Nested in this group is the primarily Eurasian tribe Cardueae. The next area on the cladogram contains the other tribes of the Cichorioideae with only actinomorphic disk corollas, the Vernonieae and Moquineae. This area is followed by the remaining four tribes of the Cichorioideae which occur in different areas of the world. The Arctoteae and Liabeae have the typical Compositae 'true ray' and disk florets and Lactuceae have only their unique ligulate florets. These tribes are followed by the Asteroideae with the bulk of the species in the family, most of which have 'true ray' and disk florets. This seems to indicate that the origin of the extant members of the Compositae was in southern South America with two independent radiations into Asia and Africa. It further indicates that bilabiate corollas were characteristic of the basal members, followed by an absence of ray florets, followed by the development of true rays. The traditional concept of the Compositae florets with actinomorphic, heterogamous disk florets surrounded by zygomorphic, female, ray florets does not hold with most of the Cichorioideae and is not characteristic of the basal branches of the family. However, as explained above, the resolution of some critical nodes is not strong, and additional data are needed to try and resolve these nodes.

Mapping the future of the herbarium

The role of Geographic Information Systems in enhancing the value of our vouchered science

Paul Gioia

Western Australian Herbarium, Department of Conservation and Land Management, Locked Bag 104, Bentley Delivery Centre, Western Australia 6983

Today's herbaria are at a crossroad. Many institutions have faced a repeated downturn in available funding, to the point where difficult decisions must be made regarding resource allocation. Despite possessing a huge potential for documenting our plant biodiversity and promoting conservation, herbaria face diminishing staff, a reduced taxonomic effort and, in some cases, insufficient resources to maintain the integrity of their collections or keep their doors open.

In this light, it is essential that herbaria promote the value of their collections to conservation and land management agencies, to researchers and land managers. One of the most effective ways this can be done is to utilise more effectively the spatial component of the specimen record with the assistance of geographic information systems (GIS) and spatial analysis techniques.

The provision of species distribution maps is a basic function that immediately provides a statement of the current extent of our recorded knowledge of a species. At the Western Australian Herbarium, GIS is used to generate maps which are displayed over the Internet to a wide variety of users. By providing a spatial view of herbarium data in such a forum, specialists are more able to identify gaps in knowledge. Outliers are more easily located and corrected and, in so doing, enhance the value of the collection.

Herbarium collections suffer, however, from notable biases which become evident when data are viewed spatially. Broad-scale mapping quickly shows the clustering of points around roads, towns or monitoring sites. However, more subtle biases exist. Because of the opportunistic manner in which much science is vouchered, some groups of taxa receive disproportionate levels of representation in collections. GIS can be used to identify and address these biases.

At the Western Australian Herbarium, recent work using GIS technology has shown that ubiquitous species are often under-represented in collections. A spatial analysis of taxa in the forested area of Western Australia has suggested that annuals may also be under-represented (Gioia & Pigott, 1999, in prep.).

GIS has also been used to fill gaps in plant distributions. Statistical models can be employed within a GIS environment to predict the distribution of plant species. Such techniques have been employed to generate models for a large number of taxa in south-western Australia.

By applying GIS technology in the herbarium, gaps in the collection can be identified and addressed, thus increasing its conservation and scientific value and providing a more secure future for our vouchered science.

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Progress toward an aquatic biodiversity information system

Chris Glasby and Dennis Gordon

National Institute for Water & Atmospheric Research (NIWA), Wellington, New Zealand

Considerable time and effort are being invested by several countries in developing biodiversity information systems and distributing the information via computer networks. Biodiversity information systems having a global scope include Species 2001[1], which aims to index and produce lists of validated names to all described species, and the Ocean Biogeographic Information System (OBIS)[2] which, through mapping marine species distributions, aims to describe biodiversity patterns in the oceans. In addition, both information systems provide links to a variety of associated biological and ecological data pertaining to each species.

In order for these global initiatives to succeed, an equal or greater effort should be given to databasing biodiversity at the regional level, and the data made available to the broad-brush global initiatives. Regional initiatives, which will be more attuned to national priorities, are also likely to have more diverse user requirements and clients, ranging from local councils to international agencies. Several regionally-focused projects have been under way for some time, for example, the North American project ITIS (Integrated Taxonomic Information System)[3] and Australia's Environmental Resources Information Network (ERIN)[4]. In New Zealand, we are developing a regionally-based information system focussing on the aquatic environment—a National Aquatic Biodiversity Information System (NABIS)[5]. Developers of NABIS are committed to contributing to both Species 2000 and OBIS through lists of validated taxon names and associated environmental data, as well as serving the national community. NABIS will facilitate a better understanding of ecological and biogeographical processes in aquatic environments, and therefore enable improved management opportunities. Also, through the integration of a diverse range of aquatic databases, identification of gaps in our data will be made easier.

The NABIS project will incorporate various aquatic databases including those of NIWA, and partner organisations potentially including other Crown Research Institutes, museums, universities and the private sector. We have identified partnerships as the most crucial element in the success of NABIS[5]. At the national level, partnerships are necessary in order to facilitate data sharing and understand end-user requirements, and internationally they are important in order to adopt global standards, contribute to higher level 'megascience' projects, and fulfil international obligations.

A model for NABIS is presented, involving a series of interlinked databases holding a variety of data types, including specimen data, taxonomic data, and environmental and survey data. Aquatic taxonomic data will be based primarily on checklists prepared for the forthcoming Species 2000: NZ Symposium[6]. Examples will be given of the potential of the system when coupled to a Geographic Information System (GIS) to: 1) map species distributions; 2) map environmental data; and 3) overlay environmental data with distributions. Other exciting possibilities include access of data and maps over the Web, modelling ecological parameters to predict 'what if' scenarios on species distributions; and assessing areas for conservation/marine reserve potential.

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Biodiversity in Western Australia: developing a State strategy

Jay Gomboso

Nature Conservation Division, Department of Conservation and Land Management, Locked Bag 104, Bentley Delivery Centre, Bentley, Western Australia 6983

In line with the National Strategy for the Conservation of Australia's Biodiversity, the Department of Conservation and Land Management is beginning the development of a Western Australian Biological Diversity Conservation Strategy, for completion in 2000. This will complement the proposed WA Biodiversity Conservation Act that is intended to repeal and replace the Wildlife Conservation Act 1950.

The Strategy, which will be developed with input from the community and Government agencies, will provide a framework for coordinating and integrating government and community efforts to conserve and sustainably use and manage Western Australia's biodiversity.

In line with the national goal to protect biological diversity and maintain ecological processes and systems, the Western Australian Biodiversity Conservation Strategy will aim to:

- establish a vision for nature conservation in Western Australia in which ecologically sustainable management across all lands and waters can ensure that the State's biological diversity is maintained;
- review conservation objectives to ensure that strategies for the maintenance of the State's biodiversity are in place;
- review the major issues involved in nature conservation in Western Australia, the scientific and social bases upon which it is managed and the constraints within which it is conducted; and
- act as a resource document for government agencies, private sector and the community.

The paper will describe the suggested framework for Western Australia's biodiversity conservation strategy. In particular, the paper and presentation will also address the proposed communication and reporting process required for strategy development.

Multiple origins of galling in scale insects

Penny J. Gullan and Lyn G. Cook

Division of Botany and Zoology, The Australian National University, Canberra, Australian Capital Territory 0200

Insect galls are abnormal plant growths elicited by the feeding or ovipositing activities of a range of insects. Gall structure ranges from simple (e.g. shallow depressions in leaves or stems) to highly complex fruit-like or bract-covered outgrowths. The Australian gall fauna is unusual in comprising many taxa of scale insects (Hemiptera: Coccoidea). Australia has more species of gall-inducing coccoids than the whole of the rest of the world. There are about 85 described species of Australian gall-inducing scale insects, unevenly distributed among 18 genera in five families. The vast majority of species belong to the Eriococcidae and at least another 50 species of gall-inducing eriococcids remain to be described. Furthermore, the galls of many of our eriococcids are sexually dimorphic and/or of unusual shape. The vast majority of coccoid species induce galls on *Eucalyptus* (Myrtaceae), and only about 20 species on other plant genera (*Acacia*, *Agathis*, *Araucaria*, *Banksia*, *Allocasuarina*, *Casuarina*, *Leptospermum* and *Melaleuca*). Usually each genus of scale insect elicits galls on only one genus of host plant. It is not known whether the gall-inducing genera within each coccoid family are closely related and, in particular, whether those taxa galling eucalypts form a clade.

We used nucleotide sequence data from the 5' region of the nuclear gene 18S rRNA to reconstruct a gene tree for over 100 scale insect species belonging to 15 families, including many Australian eriococcid genera. The data set included 14 gall-inducing species (11 Australian and 3 foreign) representing six families. We found good support for monophyly of many higher taxa (tribes, subfamilies and families) of Coccoidea, although there was little support for others. Although support for most nodes was weak (very short branches), the composition of many clades was constant under different tree construction models. Eriococcid gallers of eucalypts belonged to two separate clades—the speciose genus *Apiomorpha* was not closely related to *Ascelis*, *Cystococcus*, *Lachnodius* and *Opisthoscelis*. Three *Melaleuca*-galling species of uncertain taxonomic placement formed a weakly-supported clade in the analysis and are clearly eriococcids. The sheoak-galling genus *Cylindrococcus* grouped (with strong support) with a gall-inducing Beesoniidae and two other non-galling taxa. The ability to induce galls is most likely to be a derived condition within the Eriococcidae, although we cannot exclude the possibility that the galling habit evolved once and was lost several times. If galling is the derived condition, then there appears to have been a minimum of four independent origins of the galling habit among the Australian eriococcids and at least eight origins among all Australian scale insect families (a minimum of one origin per family but four for the Eriococcidae).

The important contribution of micro-invertebrates to aquatic biodiversity in arid Western Australia

Stuart A. Halse and R.J. Shiel

Department of Conservation and Land Management, PO Box 51, Wanneroo, Western Australia 6946

At least 491 species of aquatic invertebrate were collected during a biological survey in 1994 and 1995 of the semi-arid and arid southern Carnarvon Basin, on the mid-west coast of Western Australia. Fifty-seven sites on wetlands and rivers were surveyed, mostly in both winter and summer, although some sites contained water only one occasion. The invertebrate fauna was characterised by high turnover between sites (a third of the species were collected at a single site on only one occasion), aseasonality, and a high proportion of micro-invertebrates. Although many species could not be identified to species level, we are confident that at least 35 undescribed species were found. In addition, many major range extensions were recorded, reflecting lack of previous aquatic invertebrate work in the region.

In the past, the biogeographical and conservation values of arid zone wetlands and rivers in Western Australia have been largely overlooked in favour of waterbodies in the wetter south-west corner of the State. Furthermore, previous studies have focused largely on macro-invertebrates and underestimated the richness of micro-invertebrates. Half the species collected in the southern Carnarvon Basin were micro-invertebrates, as were 32 of the 35 undescribed species, most apparently local endemics and species with Gondwanan links. Micro-invertebrates constitute at least half the species in all areas of Western Australia where they have been studied. The State is a major region of micro-invertebrate radiation and this is particularly evident in seasonal and ephemeral waterbodies of the arid zone. Micro-invertebrates warrant far more scientific study throughout Western Australia than they currently receive.

Maintenance of karst biodiversity

Elery Hamilton-Smith[1] and Stefan Eberhard[2]

[1]IUCN/WCPA Working Group on Cave and Karst Protection

[2]Caveworks, PO Witchcliffe, W.A. 6286

Biospeleology—the study of cave-dwelling organisms—has long been recognised as making a major contribution to the understanding of both evolutionary and adaptive processes and community ecology. A focus on the broader concept of the karst environment as a whole leads to consideration of a much wider range of inter-dependent organisms, ranging from microbiota, through a wide range of terrestrial, freshwater and anchialine invertebrates, various vertebrates, and karst-dependent plant associations adapted to life on alkaline soils, often with cyclic aridity.

This paper will review the Australian fauna, identify the major threats to its continuing biodiversity and discuss the importance of, and potential strategies for, protection. It will conclude by identifying major priorities for research and protective action.

Small bugs in a big land: the biogeographical and conservation significance of some terrestrial taxa displaying high endemicity

Mark S. Harvey[1] and Paul L.J. West[2]

[1]Department of Terrestrial Invertebrates, Western Australian Museum, Francis Street, Perth, Western Australia 6000

[2]Halpern Glick & Maunsell Pty Ltd, John Tonkin Centre, 629 Newcastle St, Leederville, Western Australia 6007

Many biogeographical studies concentrate on taxa that possess at least one mobile life stage (e.g. winged adults, cursorial nymphs and/or adults, dispersive seed). We have recently conducted taxonomic studies on two different groups of terrestrial organisms which share a significant feature—the lack of any obvious dispersal mechanism—and here report on the biogeographical patterns evident in these taxa, and highlight their conservation status.

The first is the arachnid order Schizomida—a small group of terrestrial arachnids which have recently been shown to be relatively diverse in tropical Australia, especially in rainforest, vine thickets and caves. The cave-dwelling fauna is, not surprisingly, highly endemic, with some cave systems possessing sister-taxa only a few kilometres apart. Similar endemic patterns can be found in the rainforest patches of eastern Queensland, with over 20 species currently recognised—each apparently allopatric, as no two species have been collected at a single site.

The second group is the millipede genus *Antichiropus* which is endemic in south-western Australia and east to South Australia. These large, black millipedes are represented by over 40 species, mostly undescribed, and all are restricted to relatively small geographical areas. These species appear to be incapable of any form of long-range dispersal, and *in situ* speciation events appear to have occurred within the diverse habitats and geological settings of the region.

Both these taxa include species that appear restricted to seasonally moist biotypes—in the case of *Antichiropus* it appears that individuals are active for only a short period during times of high winter rainfall.

The conservation significance of such highly-restricted, non-vagile species is discussed, and is considered to be analogous to species that are restricted to caves or islands. Many may be susceptible to land degradation and clearing, but definitive taxonomic and ecological studies are currently lacking to determine their full ranges or any threatening processes.

Species richness of Western Australian coastal waters: a biodiversity study on free living marine isopods (Sphaeromatidae)

Christine Hass

Department of Zoology, The University of Western Australia, Nedlands, Western Australia 6907

Sphaeromatids occur in a wide range of habitats. In Western Australia they have been collected from the shallow intertidal zone to depths as great as 450 m, colonising both soft and hard substrates. Some occur only in defined habitat niches. Species of the genera *Oxinasphsera* and *Cilicaea*, for example, live exclusively on and in sponges. Others are found on algae, seagrass, soft corals, tunicates and in empty barnacle tests. Tolerance to salinity changes allows some species to inhabit estuaries, rivers and lakes.

As members of fouling communities on ship hulls they can travel long distances, leading to dispersal far beyond their natural distribution. Three species, *Paracerceis sculpta* (Holmes, 1904), *Paradella dianae* (Menzies, 1962) and *Sphaeroma serratum* Fabricius, 1787, have been introduced to Western Australia in this way.

This study, based on my own collection, published data and the extensive isopod collection of the Western Australian Museum, shows that at least 89 species from 31 genera inhabit Western Australian waters, with many still to be described.

Taxonomy, a discipline of great relevance

Christine Hass and Brenton Knott

Department of Zoology, The University of Western Australia, Nedlands, Western Australia 6907.

Sound knowledge of the fauna is essential in many fields of zoological research, yet taxonomic expertise particularly in the area of invertebrate studies is often not available to researchers in ecology and conservation, resulting in these studies being of only limited use. Despite this situation, students are not encouraged to pursue taxonomic studies which are often seen as not suitable for postgraduate research.

This paper examines critically the problems that arise from the neglect of taxonomy and predicts the likely consequences of the failure to give adequate support to postgraduate taxonomic research in Western Australia.

Flannel flower phylogeny: the evolution and diversity of *Actinotus* (Apiaceae)

Murray J. Henwood[1], Greg J. Keighery[2] & J.M. Hart[1]

[1]School of Biological Sciences, Macleay Building A12, University of Sydney, New South Wales 2006

[2]Department of Conservation and Land Management, Wildlife Research Centre, Woodvale, PO Box 51, Wanneroo, Western Australia 6065

Actinotus (flannel flowers) comprises 21 species, 20 of which are endemic to Australia and one restricted to New Zealand. Of the Australian species, ten are endemic in eastern Australia (one in central Australia) with the remainder occurring only in Western Australia. There are no species shared between eastern and western Australia.

The genus is easily recognisable by its more or less compressed uniloculate ovary and often showy involucral bracts that form pseudanthial umbels or capitula. Within Apiaceae, the derivation of the uniloculate ovary of *Actinotus* seems to be unique. Rather than the suppression of one of a pair of monocarps, *Actinotus* appears to have lost the commissural septum that separates each of the locules of the more typical apiaceous gynoecium. This derivation is indicated by the regular production of two ovules within a single locule, with subsequent suppression of one of the ovules.

Placement of the genus within Apiaceae is, like much of the suprageneric classification of the family, somewhat equivocal. Currently it is accommodated within the Xanthosiinae of the Hydrocotyleae (*sensu*

Drude, 1898), but at various times it has been placed in the Saniculae (Endlicher, 1836) or in the Hydrocotylinae (Rompel, 1895). Based on a study of gynoecial anatomy, Magin (1977) went as far as to suggest that *Actinotus* was, in fact, more closely allied to a broadly defined Cornales than to Apiaceae. This hypothesis remains to be tested. The infrageneric classification of *Actinotus* is no clearer than its generic affinities. Thus one of our aims is to place *Actinotus* in Apiales and to resolve the phylogenetic relationships within the genus.

Whilst the genus is moderately small, it exhibits a range of life-histories and habitat preferences. Species occur in alpine, scopulicolous and semi-arid habitats and, whereas most species are perennial, some are annual, biennial or ephemeral. Furthermore, there is a range of floral biology involving inflorescence structure (cymose or simple aggregations of umbels or capitula) and sexual systems (gynodioecy, multiple duodichogamy, multiple protandry and synchronous protandry) in the genus. All functionally hermaphrodite flowers are protandrous. Our second aim, therefore, is to investigate the evolution of these life-history and reproductive attributes.

An analysis of morphological and anatomical data of Apiales indicated the Xanthosiinae as currently circumscribed is paraphyletic. *Actinotus* is monophyletic and sister to *Trachymene* (Hydrocotylinae), but neither genus is nested in Xanthosiinae. Analysis of a more inclusive sample of *Actinotus* and selected outgroups revealed a clade comprising the Western Australian endemics *A. laxus*, *A. omnifertilis*, *A. rhomboideus* and *A.* 'sp. walpole' (cymose inflorescence and multiple protandry) to be basal. The four alpine taxa (*A. bellidioides*, *A. moorei*, *A. suffocatus* and *A. novaezelandae*), previously comprising *Hemiphues*, are monophyletic. This clade is characterised by capitula and synchronous protandry. The Western Australian endemic *A. glomeratus* (andromonoecious capitula) is sister to the clade of alpine species. *Actinotus schwarzii*, *A. periculosus* and *A. helianthi* (cymose inflorescence of umbels, multiple dichogamy) likewise form a clade, with the geographically more widespread *A helianthi* being basal to the two narrow endemics. A number of east/west sister relationships were also revealed. These included *A. minor* and *A. whicherae* plus *A. paddisonii* and *A.* 'sp. cometvale'.

Cave-adaptation in Australian planthoppers (Insecta: Hemiptera: Fulgoromorpha: Cixiidae): colonisation of novel habitat or response to climatic change?

Hannelore Hoch and Barbara Hosfeld

Presented by Fred Stone

Museum für Naturkunde, Humboldt-Universitet, Institut für Systematische Zoologie, Invalidenstr. 43, D - 10115 Berlin, Germany

The evolution of obligately cavernicolous (troglobitic) terrestrial organisms has been controversially discussed (relict versus adaptive shift hypotheses). The monophyletic cixiid genus *Solonaima* Kirkaldy, endemic in Australia (Queensland, New South Wales) provides an excellent model to test these hypotheses. At present, the monophylum contains 8 epigean species (Queensland, New South Wales) and 6 cavernicolous species (Queensland). Epigean *Solonaima* species, which are largely known from museum collections only, have so far been recorded from localities along the continental divide, while cavernicolous species appear to be restricted to areas farther inland (Chillagoe Karst, Undara lava tubes) characterised by greater aridity. The cavernicolous species feed on tree roots (presumably *Ficus* spp.) which penetrate the cavernous rock. These roots provide a rich food resource for those organisms able to cope with high humidity, permanent darkness, and potentially high carbon dioxide concentrations. The cavernicolous *Solonaima* species represent several evolutionary lineages that have invaded caves in Queensland ranging from 5–10 m.y. old limestone caves to 190,000 year young lava tubes. The different lineages display varying degrees of troglomorphy, ranging from only slightly modified, troglophilic taxa to completely blind, flight- and pigment-less troglobitic species. Their geographical distribution (areas with arid climate) indicates that climatic factors may have been the driving force for the evolution of cave-adapted taxa in *Solonaima*. It is conceivable that the desertification of the Australian continent during the Miocene has triggered a shift in behavioural or ecological strategies (e.g. food preference, choice of oviposition sites, larval development) that eventually resulted in cave-adaptation. In contrast, the degree of troglomorphy in the cavernicolous *Solonaima* species correlates strongly with the physical parameters (e.g. light availability, relative humidity, carbon dioxide concentration) of the cave environment where they are found rather than with the age of the caves or the availability of suitable food resource. These observations suggest that evolution of cave species in *Solonaima* may as well be an active adaptation to novel habitats.

Objectives of our present study are:

1. to reconstruct the phylogenetic relationships within the monophylum *Solonaima*
2. to find a genetic marker that will allow us to calibrate speciation events against geological time.

In our analysis, we include previously uninvestigated character sets such as the ultrastructure of sensory organs, especially those located on the antennae and mouthparts, as well as configuration of leg spinulation and tarsal structure. These characters are expected to be of adaptive value during the colonisation of subterranean environments, as they may facilitate the insects' search for food and mating partners as well as enhance mobility on wet, rocky surfaces.

The results of our study are expected to contribute to better understand not only the evolutionary history of *Solonaima* but to the general processes underlying adaptation to high-stress environments.

From Dampier to DNA: the 300-year-old mystery of *Conostylis stylidioides* (Haemodoraceae)

Stephen D. Hopper and Siegfried L. Krauss

Botanic Gardens and Parks Authority, Kings Park and Botanic Garden, West Perth, Western Australia 6005

The application of DNA sequence and marker analysis in plants is currently providing revolutionary new insights into evolution and ecology. The revised ordinal classification of flowering plants published by the Angiosperm Phylogeny Group in 1998 is a notable example. Here, we explore another relating to Dampier's *Conostylis*.

One of the plants surviving as a herbarium specimen in the collection made by William Dampier from Dirk Hartog Island in Shark Bay in 1699 proved difficult to identify then and has remained problematic since. In his journal, Dampier remarked 'whether this plant be a Scabious, Thrift or Helichrysum is hard to judge from the imperfect flower from the dry'd specimen.' This revolved around encountering a completely new plant family (Haemodoraceae) with no European representatives.

Until the 1930's, the identity of Dampier's *Conostylis* remained utterly confused. Charles Gardner, when Australian Botanical Liaison Officer at Kew in 1939, correctly determined the specimen as a *Conostylis*, placing it in *C. candicans* var. *leptophylla* Benth. In 1960, J.W. Green countered Gardner's determination, correctly placing specimens matching Dampier's *Conostylis* in the species *C. stylidioides*, which was named by Victoria's government botanist Baron von Mueller in 1873 from a collection made by Augustus Oldfield near the Murchison River. However, Green had a very broad concept for the species *C. stylidioides*, including within it as a synonym the widespread *C. prolifera* Benth.

After extensive field and herbarium studies, Hopper (1978) proposed that *C. stylidioides* and *C. prolifera* were distinct diploid (n = 8) taxa, differing by several characters. Furthermore, he proposed that '*C. stylidioides* has affinities with both *C. candicans* and *C. prolifera*. It bears a very close resemblance to diploid hybrids of these species and is most probably a stabilised allotetraploid hybrid derivative.' Subsequently, he established that the type of *C. candicans* var. *leptophylla* matches diploid hybrids of *C. candicans* and *C. prolifera*.

We are testing the hypothesis that *C. stylidioides* is a stabilised allotetraploid hybrid between *C. candicans* and *C. prolifera*, using the powerful new PCR-based multi-locus DNA-fingerprinting technique Amplified Fragment Length Polymorphism (AFLP). Six plants from each of two populations from each of these three taxa, as well as plants from putative outgroups *C. aculeata* and *C. robusta*, have been genotyped. Preliminary results indicate a very high level of polymorphism within and among these taxa, with in excess of 100 polymorphic loci. Results from ordination and phylogenetic analyses will be presented and discussed in the light of recent research that suggests that most polyploid species have formed recurrently from different populations of their progenitors and are therefore polyphyletic.

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Macroalgal biodiversity in Western Australia

John Huisman, Roberta Cowan and Michael Borowitzka

Algae Research Group. School of Biological Sciences and Biotechnology, Murdoch University, Murdoch, Western Australia 6150

Our knowledge of the biodiversity of marine macroalgae is quite variable and reflects, in part, the research and collecting effort in the different regions. In Western Australia there is a rich temperate flora with some 750 species recorded in the Flindersian Province. This compares well with the number of species recorded in South Australia and Victoria. In the tropical Dampierian Province of W.A., only 209 species are recorded and, although a reduction in species diversity in the tropics is expected, the number recorded in tropical WA is less than 30% of that recorded in tropical Queensland. Our work in tropical WA, especially in the Dampier Archipelago, shows that the WA tropical macroalgal flora is at least as diverse as that of tropical Qld, and that further detailed study will increase the number significantly. Furthermore, comparison with the floras of Indonesia and the Philippines strongly suggests that one can expect an even higher diversity in north-western Australia. Our results indicate clearly that more systematic effort is needed to obtain a reasonable understanding of the marine macroalgal biodiversity of tropical WA and Australia in general.

Groundwater calcrete aquifers in the Australian arid zone: an unfolding plethora of stygal diversity

W.F. Humphreys

Museum of Natural Science, Western Australian Museum, Francis Street, Perth, Western Australia 6000

Present land that has ever been covered by the sea, even as far back as the Mesozoic, often supports communities of obligate subterranean aquatic species of marine lineages 'stranded' inland by marine recession, particularly in karstic areas. Large parts of Australia have not been inundated by the sea since at least the Palaeozoic, including the Pilbara and Yilgarn Cratons of Western Australia and their associated orogens, collectively referred to as the Western Shield. These Precambrian rocks covered by a thin regolith seem to be a poor prospect for the exploration of stygal biodiversity.

The Western Shield is incised by palaeodrainage systems dating from at least the Late Cretaceous, and with elements possibly dating from the Permian. A central watershed now separates the westerly drainages, some still active, from the largely inactive and disorganised inland drainages.

It was hypothesised that aquatic fauna associated with the palaeodrainage channels, with the onset of regional aridity, would progressively have become constrained to subterranean habitats and that the increasing salinity of the groundwater ultimately would have constrained the stygofauna to the still fresh headwaters of the palaeodrainage channels. As such, these isolated stygal communities should each contain a distinct fauna and thus contain substantial hidden biodiversity. Together these communities should provide information as to the history of these isolating events.

Sampling from the palaeodrainage systems has shown that the isolated freshwater bodies in the palaeodrainage systems contain distinct, even diverse, stygal communities and that they are isolated from others by intervening hypersaline water. The presumption that these isolated communities would be at the fresh headwaters of minor palaeodrainage channels was naive and the fauna is found within isolated groundwater calcrete bodies. It is not yet known whether the process by which this vicariance has occurred conforms with the hypothesis, but the stygofauna in these aquifers does represent substantial biodiversity. In addition, it has extended the salinity range of stygal habitat in continental groundwaters from oligohaline-limnic (< 5 g L-1) to polyhaline (18-30 g L-1), possibly for the first time globally.

In the Australian arid zone, groundwater calcretes form within these palaeodrainage channels as a result of carbonate deposition due to evaporation from near surface groundwaters. They form in a particular part of a hydrogeological cycle that repeats itself along the length of the palaeodrainage lines, especially on the Western Shield. As a result, discrete calcrete bodies have formed along the length of the palaeodrainage channels, and some contain aquifers variously of fresh to hypersaline water. In places, karst processes within these calcretes have formed open conduit systems, thus providing habitat most suitable for subterranean fauna, both terrestrial and aquatic, while at the same time having properties ideal for water abstraction for human use, both attributes being sparse in the arid zone.

The calcrete aquifers contain subterranean aquatic faunas (stygofauna) that are both very diverse and often of a relictual nature. They include higher taxa new to Australia, amongst them Spelaeogriphacea, a Pangean lineage now restricted to the hypogean zone of Gondwanan fragments and an order new to Australia, the genus *Tiramideopsis* (Acarina: Hydracarina) previously known from India, and Phreodrilidae (Oligochaeta). In addition, numerous species, largely in new genera, occur in the Bathynellidae (Syncarida), Copepoda (Cyclopoidea, Harpacticoidea, Calanoidea), Ostracoda (Candoninae), Amphipoda (Melitidae, Ceinidae, crangonyctoid), Isopoda (Phreatoicidea, Flabellifera and Oniscoidea) and Dytiscidae (Coleoptera).

Origins and ecology of root mat faunas from cave waters, Leeuwin–Naturaliste Ridge, Western Australia

Edyta J. Jasinska[1,2] and Brenton Knott[1]

[1]Department of Zoology, The University of Western Australia, Nedlands, Western Australia 6970

[2]present address: Department of Ecosystem Management, Edith Cowan University, Joondalup, Western Australia 6027

Food limitation is one of the principal factors restricting the development of abundant, diverse faunal communities in caves. Due to the lack of photosynthetic production in dark subterranean environments, substantial, nutritious and reliable sources of food are uncommon in cave waters. In recent years, aquatic root mats have been shown to support some of the most diverse, abundant aquatic communities in caves. In the Leeuwin–Naturaliste region of Western Australia, extensive aquatic root mats are known from five caves between Augusta and Yallingup. These root mat environments vary in terms of tree species which produce the roots (*Agonis flexuosa*, *Corymbia calophylla* and *Eucalyptus diversicolor*), water quality, hydrology, accessibility from the epigean environment, and past history. The five aquatic cave communities were investigated to elucidate the main factors controlling the development of rich animal communities in caves. Two species of aquatic crustaceans with highly restricted distributions were selected to determine whether their absence from certain caves might be due to water quality limitations or their inability to survive and/or reproduce on root mats from different species of trees. The water quality of all five caves was found to be suitable for the survival and reproduction of the two species. Likewise, all three species of trees were found to produce root mats that could sustain breeding populations of these crustaceans. However, the density, species richness and conservation value of cavernicoles varied vastly between the five aquatic root mat communities. It was found that the main factors controlling the development of aquatic cave faunas in the presence of suitable water quality and

reliable food resources are (1) the degree of isolation of these habitats from potential sources of colonisers, and (2) the continual maintenance of adequate water quality (including presence of permanent water) for survival of the animals.

Systematics and biogeography of hyptiogastrine wasps (Hymenoptera: Evanioidea; Gasteruptiidae)

John T. Jennings and Andy Austin

Department of Applied & Molecular Ecology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, South Australia 5064

The Hyptiogastrinae are a Gondwanan subfamily of small to medium-sized wasps that are predator-inquilines of solitary ground-nesting bees that provision their nests with pollen. Along with the Gasteruptiinae they comprise the family Gasteruptiidae. Whereas *Gasteruption* L. (Gasteruptiinae) is almost cosmopolitan, the Hyptiogastrinae occur mostly in Australia but also in South America, New Zealand, New Guinea and on several south-west Pacific islands. Before this study, the latter subfamily comprised c. 37 species in five genera: *Aulacofoenus*, *Crassifoenus*, *Eufoenus*, *Hyptiogaster* and *Pseudofoenus*. Recent extensive collecting using techniques such as malaise traps has greatly increased the number of specimens which have provided the basis for the present study. Overall, the project aimed to investigate the phylogenetic relationships among genera and species of Hyptiogastrinae, examine whether the current distribution of taxa can be explained by vicariance events, and revise the taxonomy of species.

A number of important outcomes were evident. The genera *Crassifoenus*, *Hyptiogaster* and *Pseudofoenus s. str.* were shown to be monophyletic and well supported by a number of characters. However, *Crassifoenus* and *Pseudofoenus s. str.* were contained within larger clades which encompass *Aulacofoenus* and *Eufoenus*, the latter genera being polyphyletic. A new phylogenetically-based classification is proposed for the Hyptiogastrinae, reflecting the results of a successively weighted analysis. In brief, the subfamily is divided into two monophyletic genera— *Hyptiogaster* Crosskey (10 spp.) and *Pseudofoenus s. l.* which contains all other members of the subfamily (58 spp.).

The results of the phylogenetic analyses were also used to examine the biogeography of the Hyptiogastrinae, in particular whether their current distribution can be explained by vicariance events alone. If the present hyptiogastrine distribution is determined by geographical barriers (i.e. continental drift), then the New Zealand and South American taxa would be expected to occur basally in the phylogeny. However, this is not the case: they occur separately and in apical positions in the most parsimonious trees. Further, the presence of several hyptiogastrine species on oceanic islands in the south-west Pacific shows that the group is capable of dispersal over intermediate distances. Finally, the lack of any significant speciation in South America and New Zealand compared with Australia, together with the results of the phylogenetic analysis, suggests that the Gondwanan distribution of the subfamily is best explained by having an Australian centre of origin and radiation, and that the group has reached New Zealand and South America by dispersal more recently than the break-up of the Australian–Antarctic–South American connection. As far is known, this is the first time a vicariance hypothesis has been rejected convincingly for any group of animals that show such a restricted Gondwanan distribution.

Distribution patterns of inland aquatic and terrestrial malacostracan crustaceans in south-western Australia

Simon Judd[1, 2], Pierre Horwitz[1] and Diana Jones[2]

[1]Centre for Ecosystem Management, Edith Cowan University, Joondalup, Western Australia 6207

[2]Western Australian Museum, Francis St, Perth, Western Australia 6000

Funding made available through the Comprehensive Regional Assessment for the forests of south-western Australia enabled the preparation of a database of records of inland aquatic and terrestrial Crustacea from the Swan Coastal Plain, Warren and Jarrah Forest bioregions. This paper reports on distribution patterns discernible by examining the data available for malacostracan crustaceans. Records were assembled from the collection in the Western Australian Museum, from published literature, and from personal collections of particular groups. The malacostracan data comprised 2459 records in 34 data fields. Fields included taxonomic, location, date, and collector data. Each record was then assessed for its taxonomic and locational reliability and, where available, habitat information was also included.

While some taxa were found to be distributed broadly throughout the bioregions, others were distributed broadly within a single region, in inland areas or along the coast. Other taxa were restricted to one or relatively few locations, together signifying patches of local endemism. Commonly occurring patterns of restricted species include those found along the Cape Leeuwin–Cape Naturaliste ridge, or on the extreme south coast, or both, in which case they reflected accurately the Warren Bioregion. Two forms of disjunction were detected: taxa found in the Warren Bioregion and north of Perth, but not in between, and those broadly distributed species that have not been collected from the Collie Basin.

Explanations for these broad, restricted and disjunct distributions in south-western Australia are sought from climate, vegetation patterns, geological history, salt, fire and European disturbance over the last 170 years.

A taxonomic study of the *Hibiscus panduriformis* complex (Malvaceae) in Australia

Lina S. Juswara[1, 2] and Lyn A. Craven[3]

[1]Herbarium Bogoriense, Bogor, Indonesia

[2]Present address: Department of Botany and Zoology, Australian National University and Centre for Plant Biodiversity Research, CSIRO, GPO Box 1600, Canberra, Australian Capital Territory 0200

[3]Centre for Plant Biodiversity Research, CSIRO, GPO Box 1600, Canberra, Australian Capital Territory 0200

The *Hibiscus panduriformis* Burm. f. species complex in Australia is revised. Nine morphs were hypothesised and tested using ordination and cluster analysis of gross morphological data from leaves, flowers and indumentum, taken from dried herbarium specimens. The phenetic analyses indicated that six more or less discrete morphs are present in the complex together with a seventh that could not be clearly separated with the data at hand. It is concluded that six species of the complex occur in Australia. One, *H. panduriformis* Burm. f. *s. str.*, occurs widely outside Australia and the remaining five described as new are endemic in northern Australia.

Vascular flora of the southern Carnarvon Basin, Western Australia

Greg Keighery and Neil Gibson

Department of Conservation and Land Management, Wildlife Research Centre, Woodvale, PO Box 51, Wanneroo, Western Australia 6065

Recently a regional biogeographical survey of the biota of the southern Carnarvon Basin was undertaken by Conservation and Land Management and the Western Australian Museum. This study included vascular plants of both terrestrial and wetland habitats, collected in a quadrat based study with additional survey of conservation reserves and the Shark Bay World Heritage Area.

The vascular flora of the southern Carnarvon Basin comprises over 2133 taxa from 122 families. These consisted of 9 ferns, 2 Gymnosperms and 2122 flowering plants. The largest families are the Myrtaceae (231 taxa), Asteraceae (181 taxa) and Poaceae (168 taxa). The broad composition of the flora reflects the major climatic influences of the region—a southern coastal winter rainfall zone and an inland and northern arid zone, although still in the winter rainfall influence.

There are 8 major conservation reserves in the area, which together contain 1559 taxa. Kalbarri National Park, with 1,071 taxa recorded within its boundaries of which 223 are at their northern range limit, was confirmed as an area of major botanical significance comparable to the Stirling Range and the Fitzgerald River Biosphere reserve.

Some 574 (37%) taxa were not recorded in any conservation reserve. These unreserved taxa are mainly taxa from the *Acacia*-dominated red sandplains, wetlands, tropical taxa at their range ends, and taxa endemic in the Shark Bay area. Proposed changes in reserved areas are currently addressing these gaps. The area also contains 13 species of declared rare flora and 158 taxa of CALM Priority flora.

Much of the southern section is in the Shark Bay World Heritage Area, a major value of which is the change over zone between the South-West Botanical Province and the Eremean Botanical Province. This region has a rich, varied flora of over 850 taxa in the World Heritage Area, of which 53 are endemic in the area, 229 are at their northern limit and 56 at their southern limit. Detailed studies on the floristics of Bernier and Dorre Island have added numerous new records for these islands. An ongoing program of floristic survey is also under way on the mainland.

Eighty-eight species of weed were recorded for the southern Carnarvon Basin. The areas severely impacted by weeds are the riverine margins where, along the Gascoyne and Wooramel Rivers, Buffel Grass (*Cenchrus ciliaris*) now often dominates, or along the Irwin River in Kalbarri Cape Weed (*Arctotheca calendula*) dominates. Parts of the World Heritage Area have been invaded extensively by Prickly Turnip (*Brassica tournefortii*). In all cases native herbfields have been displaced.

Epiphytes and invertebrates in cool temperate rainforest

Claudette Kellar[1], Megan Short[1] and Josephine Milne[2]

[1]Deakin University, Rusden campus, 662 Blackburn Rd., Clayton, Victoria 3168

[2]The National Herbarium of Victoria, Birdwood Ave, South Yarra, Victoria 3141

Epiphytes are a distinctive feature of cool temperate rainforests and provide a habitat for a diversity of invertebrates. This study looked at the epiphytic communities on *Nothofagus cunninghamii* and *Eucalyptus regnans* in a pocket of cool temperate rainforest at Cement Creek, Yarra Ranges National Park, Victoria. The epiphytic cryptogams were identified together with the invertebrates inhabiting these epiphytes. This was done by sampling the vertical distribution of both epiphytes and invertebrates. The invertebrate fauna of the litter layer beneath the trees was also sampled to determine if the epiphytes were inhabited by a distinct invertebrate fauna.

Twenty-two species of epiphytes were identified, comprising 7 liverworts, 6 mosses, 4 ferns, 4 lichens and 1 fungus. Of these, 20 species occurred on *N. cunninghamii*, and only 9 species were identified growing on *E. regnans*.

A total of 11850 invertebrates was collected from 96 epiphyte samples and a further 5199 invertebrates were found in 32 litter layer samples. The most abundant taxon in both habitats was the Acari (72% of total fauna in epiphytes, 61% in litter layer) followed by the Collembola. Epiphytes lower on the tree trunks contained greater numbers of invertebrates.

This study has shown that epiphytic growth is a favourable habitat for invertebrates and illustrates the importance of sampling epiphytes in studies of invertebrate diversity in rainforests.

Insights into the fauna of the Gnangara Mound aquifer, Western Australia – the significance of springs

Brenton Knott[1] and Edyta J. Jasinska[1, 2]

[1]Department of Zoology, The University of Western Australia, Nedlands, Western Australia 6907

[2]present address: Department of Ecosystem Management, Edith Cowan University, Joondalup, Western Australia 6027

Subterranean animals such as the interstitial faunas of aquifers are difficult to study due to problems associated with accessing their environment. An exploratory study of the fauna of the Gnangara Mound—an extensive groundwater aquifer between the Swan and Moore Rivers on the Swan Coastal Plain—identified some interstitial inhabitants of the aquifer from points of active groundwater discharge on the western and eastern sides of the Mound. These springs, where the subterranean intersects the surface, provide a window into the aquifer through which its interstitial fauna can be investigated. Particularly valuable insights were gained through the comparisons of groundwater animals living in cave streams on the western side of the Gnangara Mound and those found in springs on its eastern side.

This paper focuses on spring habitats located on the eastern side of the Gnangara Mound. These points of discharge are valuable both as points of access to the aquifer fauna and as providing mesic oasis in an otherwise arid environment. Due to their long-term, moist micro-environments, some of the springs have a mound-like structure, produced by the accumulation of peat about their boils. These peat mound springs harbour some relictual Gondwanan fauna that was unable to survive elsewhere in the increasingly arid Australian continent. The spatial heterogeneity of the Gnangara Mound groundwater fauna is discussed in this paper as well as the wider biogeographical significance of the springs.

The fauna of thrombolitic microbialites, Lake Clifton, Western Australia

Yuki Konishi, J. Prince and Brenton Knott

Department of Zoology, The University of Western Australia, Nedlands, Western Australia 6907

Lake Clifton is a shallow (< 3 m), elongate (28 km N–S; 1 km E–W) swalar lake subject to seasonal changes in water level. Water level changes reflect a balance between rainfall and groundwater inputs, and evaporation; there is very little surface drainage. Aquifer inflow from the Yanget Mound occurs predominantly along the northern half of the eastern margin of the lake. The restricted microbialite reef associated with the aquifer outflow was core sampled in May (autumn) and November (spring), 1997, to quantify the associated fauna with these organo-sedimentary structures. Thirty microbialites were sampled with respect to site (two sites, 1.5 km apart in the northern part of the reef), season (autumn = low lake water level, spring = high lake water level) and submergence (i.e. permanent, seasonal).

In all, 25 species of aquatic fauna were recorded from the microbialite cores, comprising 20 species of metazoan, predominantly Crustacea (including *Melita kauerti* (Amphipoda), *Exosphaeroma* cf. *serventii* (Isopoda); and *Cyprideis westralensis* (Ostracoda); Polychaeta (*Capitella* cf. *capitata*); nematodes; and five species of Foraminifera (Protista).

Multivariate analysis (MDS) of the five numerically most abundant taxa (amphipods, isopods, ostracods, polychaetes, nematodes) separated microbialites by season and submergence. Numbers of all taxa, particularly polychaetes and amphipods, were much higher in spring than in autumn, and in permanently-inundated compared with seasonally-inundated microbialites. The exception was higher numbers of juvenile polychaetes in seasonally-inundated microbialites at the northern site in spring. The study indicates that strong microbialite growth can be achieved in the presence of a diverse, abundant fauna.

Significant incongruence: just when is it significant?

Christine L. Lambkin and David K. Yeates

Systematic Entomology Laboratory, Department of Zoology and Entomology, University of Queensland, Brisbane 4072

Almost half of the 4,000 described bee flies (Bombyliidae: Diptera) in the world belong to the subfamily Anthracinae. Most of the world diversity in the Anthracinae is in three cosmopolitan tribes: Villini, Anthracini, and Exoprosopini. 830 bp of the 16S mtDNA were sequenced from 35 specimens of 18 species-groups that were recognised in the Australian Anthracinae, together with a lomatiine as outgroup. Over 300 morphological characters have been scored for the same exemplars. Cladistic analysis produces two most parsimonious trees, whose consensus differs only slightly from the consensus of the two trees from the molecular data set. Analysis of the combined molecular and morphological data matrices produces a single tree, containing groupings from both molecular and morphological cladograms. Use of the PAUP*4.0b2a Partition Homogeneity Test indicates that the different data sources are significantly incongruent. Significant character incongruence occurs when groups well supported by one data partition conflict with groups well supported by the other; when data partitions strongly support conflicting nodes. The nodes at which disagreement occurs may not be significant to the questions being addressed via the analysis. If terminal nodes disagree but the questions being asked are in a higher level phylogenetic analysis, then significant incongruence may be insignificant. Significant incongruence may not be significant! However, significant incongruence is always important because its presence should lead to questions about our character analysis, taxon sampling, and evolutionary processes. Why did it happen?

Unordered multistate characters: prudent choice or cop-out?

Christine L. Lambkin and David K. Yeates

Systematic Entomology Laboratory, Department of Zoology and Entomology, University of Queensland, Brisbane, Queensland 4072

The use of unordered (non-additive) multistate characters in phylogenetic analyses has increased over the past decade, especially with the explosive increase in molecular datasets. Many morphologists use unordered multistate characters since they are unsure of the character state ordering, and feel it is more valid to allow the order of transformation to be determined during analysis. Mickevich developed Transformation Series Analysis (TSA) in the 1980's to determine ordering for multistate characters in which a priori ordering was unclear, but this method is rarely used today. Studies comparing ordered (additive) and unordered character state coding have found that unordered analyses produce tree lengths as short or shorter than ordered analyses. On this criterion alone, unordered character coding would be preferred over ordered coding. However, these comparisons have ignored other attributes of unordered multistate characters. Most attempts to recode an unordered multistate character as an ordered character underestimate the number of equally plausible ordered recodings for an unordered character. Ordering fails since it cannot faithfully reproduce the transformation cost matrix between the states implied by the unordered coding. However, the transformation cost matrix implied by an unordered character contradicts the initial assumptions about homology between the states of a character. In other words, unordered character coding provides too much flexibility in character state transformations calculated during the analysis.

Identifying organisms by computer — some current developments

Nicholas Lander[1] and Terry Macfarlane[2]

[1]Western Australian Herbarium, Department of Conservation and Land Management, Locked Bag 104, Bentley Delivery Centre, Western Australia 6983

[2]Western Australian Herbarium, c/o Department of Conservation and Land Management, Brain Street, Manjimup, Western Australia 6258

Computers have been applied to the identification of organisms for over 30 years. During that period there have been major developments in technology which have influenced the design of systems and affected the degree to which computer systems have gained acceptability. Technological changes are still an important influence, and it is not clear what methods will be in common use in another decade.

Different models have been explored for identification systems, including full expert systems, simultaneous models, and non-rule based systems, of which there are more than twenty. Software and data (including images) can be installed on the user's computer, downloaded as required from a network, or the whole system can be used remotely over a network, especially in web-based systems. Publication methods for data sets are still developing, since this differs from traditional publishing, but it currently includes CD-ROM, and formal and informal channels on the Internet. The integration of identification systems with other information types will be discussed. Identification systems may be of individual, institutional, national and international scope, and the relative importance of each is currently undergoing change. Glimpses of some of the various flavours of identification systems will be shown.

Systematics of truffle-like fungi from Australia: a case study of the Russulales

Teresa Lebel

National Herbarium of Victoria, Royal Botanic Gardens, Birdwood Avenue, South Yarra, Victoria 3141

The first truffle-like fungi named from Australia, *Secotium coarctatum* and *S. melanosporum*, were collected by J.Drummond in Western Australia in 1843 and sent to M.J.Berkeley in England who described them in 1845. By 1932 approximately 60 species of truffle-like fungi had been recorded from Australia, most of which were described by foreign mycologists such as the C.Kalchbrenner, E.M.Fries, M.C.Cooke, G.E.Massee and C.G.Lloyd. Some of these fungi were first described as exotics introduced to the northern hemisphere with *Eucalyptus* and only later found in Australia, e.g. *Hydnangium carneum* was described by Klotzsch in 1839 from collections made in a botanic garden in Germany and was recorded from England and Ecuador before L. Rodway provided the first record for Tasmania in 1898. Many collections were small, often single, and in poor condition by the time they were received by taxonomists, whose experience and literature was based upon European taxa. Most Australian taxa were 'forced' into northern hemisphere genera and families, a trend that that continued into the 1950's.

From the 1960's to 1980's a large number of truffle-like taxa (c. 83 species) were described from regional studies in New Zealand, Victoria and Queensland. With this increased knowledge came the recognition of the difficulty of fitting many Australian taxa into the European-based taxonomic framework; several new genera were described and others revised. Recent intensive collecting efforts by Australian and overseas mycologists have again increased our knowledge of the diversity of truffle-like fungi considerably. 24 families, 69 genera and over 280 spp. of truffle-like fungi have now been described from Australia—a recent study by Claridge *et al.* (1999), collecting twice from a 14 ha. area in south-eastern Australia, produced 208 species of truffle fungi, of which 153 were undescribed. This one study nearly doubled the number of known species. Trappe *et al.* (1999) estimated that there may be well over 600 species of truffle fungi in Australia.

Case study

The truffle-like genera *Macowanites*, *Elasmomyces*, *Martellia*, *Cystangium*, *Gymnomyces*, *Arcangeliella* and *Zelleromyces* have long been recognised as related more closely to *Russula* and *Lactarius* than to other truffle-like fungi on the basis of similarities in spore ornamentation, tissue anatomy and overall sporocarp morphology. In 1960, R.Singer & A.H.Smith described about 60 species of truffle-like Russulales from North and South America and Australia and defined generic limits. The type species of both *Cystangium* and *Gymnomyces* are Australian, though the genera were defined on a much broader taxon sampling. Later workers have used their concepts with few changes, as only a few new species have since been described by authors such as McNabb and Bougher.

Prior to 1997, only 12 truffle-like relatives of *Russula* and 8 of *Lactarius* had been described from Australia. Recent revision of this group has expanded the diversity considerably with some 65–70 new species related to *Russula* and 3–8 to *Lactarius*. A re-examination of morphological characters used by Singer & Smith to define genera has found several to be of limited use at this level. In particular, peridiopellis structure was found to be more stable than other characters used previously. Generic limits were revised and five genera are now recognised instead of seven: *Gymnomyces* is restricted to those species lacking an epithelial pellis and a stipe; *Cystangium* is expanded to include all species (astipitate and stipitate) which have an epithelial pellis; *Macowanites* is relatively unchanged and includes species which are stipitate and lack an epithelial pellis; the boundaries of *Arcangeliella* and *Zelleromyces* require further study.

Recent molecular work supports the relationship of *Macowanites*, *Gymnomyces* and *Cystangium* to *Russula*, and *Arcangeliella* and *Zelleromyces* to *Lactarius*. Preliminary data show that the truffle-like form arose several times within *Russula* and *Lactarius*. Currently not enough taxa from Australia or South America have been sampled to show whether they will fall into clades different from northern hemisphere taxa; it may be that genera with truffle-like forms will be reduced to synonymy with *Russula* and *Lactarius*, and the lineages with truffle-like forms will be better defined.

Many recent changes in our understanding of the taxonomy and systematics of the Russulales are applicable to other groups with truffle-like forms such as the Cortinariales and Boletales. The high diversity of these groups in Australia and re-examination of generic boundaries will certainly bring many changes. A considerable gap in presenting taxonomic information to the general public and the scientific community is also apparent. The only key to the Australian truffle-like fungi is that of Cunningham (1944), which is out of date as the taxonomic placement of taxa has changed, as well as a number of new genera described. Revised keys, both fixed and interactive, descriptions of the genera of truffle-like fungi, and keys to the spores of genera of use and interest to a broad audience is being developed.

Diversity and geographical distribution of free-living heterotrophic flagellates

Wonje Lee and David J. Patterson

School of Biological Sciences, University of Sydney, New South Wales 2006

Free-living heterotrophic flagellates are the primary consumers in aquatic ecosystems. The biodiversity of this group is not well understood, nor are the factors that determine the distribution of species. We have sought to establish patterns of geographical distribution and global diversity. A survey of the literature on the distribution of flagellates from marine zones reveals that more than half the species have been reported from a single location. This suggests that these organisms are commonly endemic. In our series of surveys, we have described the distribution of approximately 370 species of heterotrophic flagellates in 35 communities. The studies are from sites around the world—inclusive of marine and freshwater habitats, water column and benthic habitats, and 'extreme' (i.e. anoxic and hypersaline) habitats—have been reported by our group. About 40% of the species were reported from a single location, again suggestive of endemism. When the communities from these surveys are compared using the clustering algorithm in the PRIMER package, there is, in contrast, no evidence of endemism because the communities from geographical regions do not cluster together. Communities cluster on the type of habitat from which they were drawn (i.e., water column communities group together, as do benthic communities, or freshwater and marine communities). This suggests that geographical location may play no part in the makeup of communities. The conflict between insights from information on species and information on communities creates uncertainty over the geographical distribution of flagellates. This is probably because the actual distribution of these organisms is obscured by factors extrinsic to their distribution. The most likely factors are under-reporting of communities and arguable species concepts. Our interpretation of available data is constrained by the morphological species concepts. Our interpretation is that there are not many species of heterotrophic flagellates (perhaps no more than 3000) and most have a cosmopolitan distribution. High intensity sampling reveals that there are assemblages of flagellates with distinctive taxonomic compositions, but we are unable to describe these more precisely until the impact of factors external to the biology of the organisms, but which influence our understanding of the structure of communities of heterotrophic flagellates, is reduced.

Phylogeny of *Andersonia* R.Br. (Ericaceae)

Kristina L. Lemson

Department of Botany, The University of Western Australia, Nedlands, Western Australia 6907

A taxonomic revision and cladistic analysis of *Andersonia* R.Br. was undertaken. The genus, of 45 species, is endemic in the south-west of Western Australia. Its two closest relatives are *Cosmelia* R.Br. (a monotypic WA endemic) and *Sprengelia* Sm. (4 spp.) from eastern Australia and within which *Andersonia* was once included. The most recent revision was made in 1962 (L.Watson, *Kew Bulletin* 16: 108–122), and recognised 22 species which were arranged in two sections: *Multibracteatae* (7 spp.), with terminal flowers preceded by a series of modified leaves; and *Bibracteatae* (15 spp.), with axillary flowers each subtended by a pair of prophylls only. The current study identified seventeen previously undescribed species amongst the large volume of material collected in the past 30 years, and identified several problems with recognised species. In particular, *A. lehmanniana* Sond., *A. sprengelioides* R.Br., *A. simplex* (Stschegl.) Druce and *A. caerulea* R.Br. required close study, as all included a range of divergent morphologies.

The cladistic analysis aimed to test the monophyly of *Andersonia* in relation to *Sprengelia* and Watson's (1962) subgeneric groupings. The analysis considered 67 taxa, using species of *Lysinema* R.Br., *Richea* R.Br., *Dracophyllum* Labill. and *Sphenotoma* Sweet as outgroups and breaking several species into putatively monophyletic subgroups. Ninety morphological and anatomical characters were scored. The results of the cladistic analysis and taxonomic conclusions will be presented.

Development of a protocol for sampling arthropod diversity in areas of native vegetation

G.A. Lewis[1], A.D. Austin[2], H. Possingham[2], P. Dangerfield[2] and M.D. Brownlow[3]

[1]Department of Zoology, The University of Melbourne, Victoria 3012

[2]Department of Applied and Molecular Ecology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, South Australia 5064

[3]WorkCover Corporation, Adelaide, South Australia 5000

This study attempted to determine the most effective and efficient means of obtaining a representative sample of arthropod diversity in areas of native vegetation. A range of sampling techniques was used to collect Formicidae, Coleoptera and Araneae in two adjacent habitats in Cox Scrub Conservation Park, South Australia. Net sweeping collected the greatest number of species, followed by visual searching, pitfall trap 4 (diameter 126 mm), pitfall trap 3 (diameter 84 mm) and Malaise traps. Pitfall trap 1 (18 mm), pitfall trap 2 (42 mm), and yellow pans consistently collected fewer species. There were also differences in the suitability of techniques for each target group. The number of species collected in pitfall traps was proportional to diameter size, with larger traps collecting more.

Compositional analysis revealed a distinctive fauna within each technique. This confirmed the proposition that any technique will undersample the arthropod community when used in isolation. The concept of sampling complementarity also found support, with the need for a range of sampling techniques to obtain a comprehensive census of arthropod diversity. Family level analyses of Coleoptera and Araneae enabled comparisons of preferred habitat location of certain taxa, and the choice of appropriate sampling techniques. Greenslade's (1978) functional classification for Formicidae, and Anderson's (1995) predictive model of ant community composition and vegetation type also proved very useful. Anderson's

(1995) model predicted correctly that in a 'cold-adapted heathland', which suitably describes Cox Scrub, neither 'Generalised Myrmicinae' nor 'Opportunists' would dominate. Instead, there appeared to be a formicid community in which all functional groups were present in relatively equal proportions.

Due to lack of site replication, few comments can be made regarding the level of interaction between habitat type and sampling technique. Preliminary results suggested that the degree of undersampling by a single technique was not greater in closed habitats. Significant interaction levels were found for Coleoptera, however, suggesting that interaction levels should be interpreted cautiously, and that this issue requires further investigation. A linear relationship was discovered between cost and the number of species collected. This relationship also requires further analysis using optimisation equations, to determine the most cost-effective technique combination.

While researchers should implement their own range of sampling techniques, standardisation should be encouraged in the areas of equipment design, duration and timing of sampling period, spacing between traps and transects, and identification procedures. A sampling protocol could be applied in the areas of environmental health, academic research, and assessment of conservation value. This will be accomplished, however, only if the inclusion of arthropods is seen as informative, cost-effective, and a worthwhile adjunct to existing plant and vertebrate surveys.

Water tapping and harvesting by trapdoor spiders

Barbara York Main

Department of Zoology, University of Western Australia, Nedlands, Western Australia 6907

Spiders, along with many other arthropods, are relatively abundant in the Australian arid zone. However, very few can cope with the stringent conditions of extremes of temperature and lack of moisture. Nevertheless, many species display remarkable behaviours whereby they avoid rather than confront or overcome demands of desert conditions. Mygalomorphs (trapdoor spiders), an ancient group of spiders, are peculiar in that the aridity, in an historical sense, has developed around or been imposed on them, rather than the spiders having invaded the arid zone. Many are relictual (Main 1996, 1997). As a consequence trapdoor spiders have evolved behavioural tactics of:

(a) avoidance, which minimises the imposition of arid conditions, and

(b) opportunism, whereby behavioural (and perhaps physiological) advantages are taken of infrequent water availability.

This talk, firstly gives examples of avoidance tactics mainly related to burrowing behaviour, and secondly presents for the first time a selection of natural history data on (i) water harvesting and (ii) water tapping by trapdoor spiders.

(i) Water harvesting

Many species through burrow siting take advantage of water harvesting by physical features (e.g. rocks) and by plants that direct or funnel rain water into potential habitats of spiders. For example (a) granite rock outcrops as natural catchments direct water into soil meadows and aprons; (b) rock piles similarly capture water from rain, fog and mist and hold it in soil filled interstices; (c) tree trunks channel rain water as beads or streams which form a froth at the base that later seeps into the soil. All these 'catchments' are favoured spider habitats. Some species are able to counter (behaviourally) flooding (a characteristic result of intermittent downpours in arid areas) and conversely at other seasons actively harvest water with silk contrivances.

(ii) Water tapping

During dry seasons spiders are able to utilise deep moisture storages (from earlier rain) in soil. Firstly, the high humidity provided in deep burrows prevents desiccation, but it is also postulated that spiders suck moisture from soil at the base of burrows. Additionally, soil moisture (which spiders take advantage of) is augmented through root transpiration of plants. Many desert trapdoor spiders form aggregations between the radiating root spokes of Acacias and other shrubs and in the dense litter under hummock-shaped tree/shrub crowns which spread at ground level.

Burrow siting of trapdoor spiders in habitat associations with plant occurrences and plant biology, whether related to the above examples or simply in relation to shade and litter cover is vital to the survival of many species in arid habitats.

Specific examples of trapdoor spiders exhibiting the above tactics will be discussed and illustrated.

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Biodiversity conservation and management in Victoria

Ian Mansergh and David Parkes

Flora and Fauna Directorate, Department of Natural Resources and Environment, Victoria

Biodiversity conservation encompasses more than the associated scientific, ecological and biological questions. Improvement will be most likely within a clear, transparent and accountable framework. In Victoria, through the Department of Natural Resources and Environment (DNRE),* an overall framework for biodiversity conservation and management has been developed. Such a framework is important in the strategic progression of better conservation outcomes across both land and waterscapes. One expression of this is the Flora and Fauna Guarantee Strategy, Victoria's Biodiversity (December, 1997). The status of this strategy under the recently elected Labor Government is yet to be determined. The broad policy, technical and scientific framework of biodiversity conservation and management in Victoria is outlined.

Relevant characteristics of the framework are:

Comprehensive:

- Includes the entire land, water and marine scapes, with particular emphasis on the latter;
- Management approaches and key directions are set for the broad environments (largely Natural Land and Seacapes, Rural Landscapes and Urban–Urban Fringe areas.
- Consolidates all international, national and state obligations;
- Relevant to all agencies and activities with effect or potential to affect natural resources across the state.
- Data sets are provided for each bioregion (e.g. percentage of Broad Vegetation Types (BVTs), area no longer present, and area extant by tenure, number and status of species) with specific directions.

Innovation:

- Provides a State-wide system of bioregions which can be used in planning implementation and monitoring which are complementary to the national IBRA and IMCRA;
- Provides a 20-year vision as to the landscape in which biodiversity outcomes are improved and industries can express a tangible trend toward ecologically sustainable development;
- Encompasses the whole community government, business, public and community – biodiversity is an important component of what has become known as 'triple-bottom-line reporting';
- Promotes and highlights an adaptive management cycle for biodiversity monitoring and reporting;

- Provides specific policy goals, for example 'no net loss of extent and condition of native vegetation' as a prelude to net gain after 2001. This has initiated development of concepts such as the 'habitat hectare'.

The implementation consists of three broad areas:

- Establishment of actions for agencies and other groups under the established directions in management (risk assessment and management). As an example, this has led to Water Authorities being required to report on biodiversity within their planning and annual reporting (i.e. Financial, Service Delivery, and now, Environment with emphasis on biodiversity). The action list also directs the finalisation and development of key biodiversity data sets and facilitates their accessibility into the planning and monitoring processes.
- Establishment of new bioregional networks (asset monitoring). In the first year, a comprehensive assessment of threatened species was derived.
- Continuation of dissemination and community involvement.

* DNRE is a broadly based resource management department incorporating a variety of agencies; agriculture, catchment management, forestry, flora and fauna and parks etc.

Patterns in the southern Carnarvon Basin's terrestrial biodiversity

Norm L. McKenzie, Greg J. Keighery, Neil Gibson and J.K. Rolfe

Western Australian Department of Conservation and Land Management, PO Box 51, Wanneroo, Western Australia 6065

Sixty-three quadrats each of 16 ha. were chosen to represent the geographical extent and diversity of terrestrial environments in a 75 000 km^2 area of the Carnarvon Basin, Western Australia. A total of 625 plant and 458 animal species were recorded from the quadrats, an average of 120 (s.d. = 22.1) species per quadrat. These comprised frogs, lizards, small ground mammals birds, scorpions, centipedes, ground-dwelling spiders and plants.

The data were compiled into a single matrix. When the species were classified according to their co-occurrences, thirteen assemblages were distinguished in terms of the Australia-wide habitat preferences of its component species. Also, quadrat similarity matrices were generated for each of the seven types of organism sampled, and the differences in their biodiversity patterns were quantified.

Analyses revealed that:

(1) Patterns in species composition correlated with processes operating at both biogeographical and ecological scales: the compositional structure of each assemblage related to gradients in a different set of climatic plus soil and/or topographic attributes. Poisson error models with logarithmic links fitted the gradient in species richness of each assemblage across the study area. Similar environmental attributes emerged whether an assemblage's composition or its richness was analysed.

(2) Each of the seven ecologically different types of organism had a distinct influence on the biodiversity model.

To be representative, a Carnarvon Basin reserve system should sample the geographical range of the various climatic, soil and topographic gradients identified by the analyses. It should also be designed using a biodiversity model that incorporates a wide range of organisms.

Patterns of diversity in the phytophagous insects of southern Australia

Peter B. McQuillan

Centre for Environmental Studies, University of Tasmania, GPO Box 252-78, Hobart Tasmania 7001

Geometrid moths comprise one of the largest families of insects with c. 3,000 species in Australia. They are an old group and include both Gondwanan and globally distributed higher taxa (many tribes, some genera). A key synapomorphy is paired anterior tympanal organs on the abdomen, but the distinctive larvae of most species have lost 3 pairs of abdominal prolegs, leaving a functional pair on segments 6 and 10. This has resulted in a peculiar form of locomotion (looping), and has facilitated novel forms of crypsis, especially of twigs and petioles, since the larva can hold itself rigid at an angle from a substrate. Since a full complement of prolegs is plesiomorphic in the Lepidoptera, reduction in their number is an apomorphy. Australia is notably rich in geometrid genera with the plesiomorphic proleg condition but pathways to more derived taxa remain uncertain. Unlike the tropics where another family of moths, the Noctuidae, are conspicuous foliage feeders, geometrids in southern Australia are important herbivores on native plants. Recent recognition of various monophyletic clades in the Australian geometrids is beginning to enlighten our understanding of their association with the flora.

Associations with the palaeoflora

Gondwanan elements in the flora may preserve elements of a more widespread old insect fauna. Unfortunately, the accumulation of insects expected from the long history of some plants is largely offset by the limited contemporary range of their hosts. Nevertheless, remnants of a richer fauna on the formerly more diverse and widespread Australian conifers may be evident in the Archiearinae (4 spp.) on Cupressaceae and Taxodiaceae, *Corula* on *Callitris* and *Milionia* on Araucariaceae and Podocarpaceae. *Nothofagus* is now relictual in Australia and supports a low diversity of geometrids (4 genera), in contrast to southern South America and, to a lesser extent, New Zealand. However, larval associations with the more primitive plant families are not necessarily evidence of long coevolution. Some Trichopterygini eat Podocarpaceae in Australia and eastern Asia but not in New Zealand and are unreported on this host from South America: *Archephanes* on Winteraceae in Australia is not obviously basal in the Nacophorini.

Proteaceae, especially the widespread genera *Hakea* and *Grevillea*, support the 'heavy-bodied oenochromines' amongst others, but many of the small isolated genera (e.g. *Bellendena, Agastachys*), are devoid of geometrids. *Austrocidaria* and *Acodia* feed on *Coprosma* which is widespread in the Pacific Basin.

Associations with Myrtaceae and Mimosaceae

The most favoured plant families are generally also the most widespread. Myrtaceae and Mimosaceae commonly dominate plant communities over large areas and *Eucalyptus* (supporting at least 34 genera) and *Acacia* (16 genera) commonly occur together. The Geometridae–Eucalyptus interface is of long standing, but the contemporary outcomes seem to be geographically specific, especially at species level. Tasmania, one of 5 hotspots for eucalypt endemism, has considerable speciation in a few dependent moth genera, e.g. *Paralaea* with 6 species, half of which are endemic; but in SW Australia, another eucalypt hotspot, only 2 *Paralaea* are known. There appears to be no parallel in the family to the very extensive speciation seen in some other eucalypt herbivores such as chrysomelid beetles (*Paropsis/Chrysoptharta*), or psyllids. Evidence so far is that the Symphyomyrtus/Monocalyptus divide is only weakly influential in patterning communities of geometrids. However, local dominance of one subgenus may be predisposing to occasional outbreaks in some moth species (e.g. *Mnesampela privata* in Symphyomyrtus, *M. heliochrysa* in Monocalyptus), as increasingly manifest in plantation monocultures.

Although some *Eucalyptus* feeders also exploit *Corymbia* and *Angophora* (e.g. *Niceteria*), none of these is reported from *Leptospermum* or *Callistemon*, and moths dependent on the latter two genera (e.g. *Euphronarcha, Syneora*) are not known to attack *Eucalyptus* or its close relatives. The cosmopolitan tribe Boarmiini has a strong association with *Acacia* (*Ectropis, Parathemis*) but also extends to *Eucalyptus* (*Gastrinodes, Heteroptila*), *Callitris* (*Symmetroctena*), *Nothofagus* (*Boarmia s.l.*), and *Exocarpos* (*Boarmia s.l.*). The tribe Macariini is associated with *Acacia* in Africa, southern Asia and

Australia (2 genera including *Dissomorphia*). In contrast to Africa, its low diversity in the vast *Acacia* shrublands and woodlands of Australia would seem to be an under-utilised opportunity.

Associations with other elements in the flora

It is clear that Geometridae have generally not speciated in proportion to food plant opportunities as measured by abundance or species diversification. There are no grass feeders, no sedge feeders, no dead leaf feeders and no bryophyte feeders known from Australia. Casuarinaceae supports only 2 genera: the monophagous *Rhynchopsota* (2 spp.) and the polyphagous *Horisme*. Caberini (*Casbia* and relatives) have an association with Rhamnaceae that extends to Asia. Feeding on forbs is strongly entrenched in some lineages, notably Xanthorhoini, but novel adaptations to it include the ennomine genus *Ciampa*, derived from arboreal *Chlenias*. Fern-feeding is a specialisation exhibited by several genera in Australia, and is also reported from New Zealand and temperate South America. The widespread tribe Lithinini is largely associated with ferns wherever it occurs. Although most geometrid larvae are external feeders, many Eupitheciini specialise on the reproductive parts of plants, especially the flowers and developing seeds. Feeding within the inflorescence offers advantages in predator avoidance, protection from environmental extremes, and less energy is devoted to locomotion and food searching.

Polyphagy

Feeding on more than one plant family is an uncommon derived condition in some geometrid clades in temperate Australia, although opportunities for it are probably limited by the low diversity in generic makeup of the forest canopy. Of the arboreal taxa, *Capusa*, *Chlenias*, *Ectropis* and *Androchela* are some of the few examples. In New Zealand, however, where multi-genus forest canopies are typical, polyphagy is proportionally more common in the larger genera such as *Declana* and *Pseudocoremia*. There is a tendency to aposematic colouration in some larvae (*Chlenias* and *Nisista*), but not all (*Ectropis*), although evidence that such larvae are distasteful to predators is lacking. The cosmopolitan tribe Boarmiini has a few species (e.g. *Ectropis excursaria*, *Pholodes sinistraria*, *Zermizinga* sp.) which disperse aerially by the first larval instar and feed on a range of shrub and tree families.

Conclusions

Food plant associations in the southern Australian Geometridae are generally conservative, with various clades commonly specific to a particular order or family of plants, or sometimes a plant life form (e.g. some genera in the tribe Xanthorhoini on forbs). Such patterns of association may have a geographical basis, or reflect possible coevolution. However, hypotheses of coevolution may be confounded with responses to high plant apparency given the hyperdominance of *Eucalyptus* biomass in forest canopies and the ubiquitous presence of Myrtaceae in shrublands. Moreover, examples of novel host capture exist. Archiearines in Tasmania form a monophyletic group associated with montane/alpine Taxodiaceae and Cupressaceae except for one species which feeds on *Epacris serpyllifolia*.

Large gaps remain in our knowledge and accumulation of information has been slow. Better resolution of the relationships within and between plant genera is critical in understanding the evolutionary trajectories and patterns of adaptation by the large Australian moth fauna. The ongoing publication of plant phylogenies will assist strategic larval collecting to occur. For example the demonstration that New Caledonia is rich in Myrtaceae basal to *Eucalyptus* makes larval prospecting there a priority.

Habitat modelling of a threatened species of stag beetle in production forests in Tasmania

Jeff M. Meggs[1] and S.A. Munks[2]

[1]Forestry School, University of Tasmania, GPO Box 252, Hobart, Tasmania, 7001

[2]Forest Practices Board, 30 Patrick St, Hobart, Tasmania 7000

The characteristics of habitat utilised by *Hoplogonus simsoni* (Coleoptera: Lucanidae) were investigated using a combination of intensive field sampling and generalised linear modelling. *H. simsoni* is listed as a vulnerable species under the Tasmanian Threatened Species Protection Act 1995 due to its restricted distribution in north-east Tasmania, low population densities and the perceived threat of modern forestry practices. Various GLMs identified a range of habitat variables that appeared to influence the occurrence and/or abundance of the beetle. From these models the following subset of variables was identified as constituting optimal habitat for *H. simsoni* in wet eucalypt forest: < 300 m altitude; deep litter layer; gentle slopes and flat areas, but not in the floodplain of streams; easterly and south-easterly aspects; and a particular forest structure with a well-developed canopy and an open understorey. These habitat characteristics appear to relate to a requirement of the species for a cool, moist, stable microclimate and the absence of wildfire for some time.

To assess more accurately the conservation status of the species and to provide forest managers with a tool for targeting conservation measures, further modelling was conducted to produce a predictive distribution map of beetle abundance across its 240 km^2 range. The relationship between the frequence of occurrence of *H. simsoni* and those habitat variables for which spatial information was available from Forestry Tasmania's GIS database was examined using GLM. Models for both of the broad forest types in which the species was known to occur (wet eucalypt forest and mixed/rainforest) were constructed. Hence, the models consist of a sub-set of the habitat variables important to the species. The wet eucalypt model is based on a relationship between altitude aspect and slope, whilst the mixed/rainforest model is based on altitude alone. These models were coupled with GIS data for each 100 m grid square resulting in predictions of abundance over an area of potential forest habitat of 174 km^2. For mapping purposes the predictions were categorised into high, medium and low abundance; analogous to optimal, sub-optimal and marginal habitat for the species.

The map indicated that the beetle was not evenly distributed over its range, with moderate to high density populations occurring in a narrow band along the eastern edge, and apparently-isolated, low density populations in the west and north. Both optimal and sub-optimal habitat for the species was poorly reserved across its range. The majority of its habitat is managed as production forest and there was a strong correlation between quality beetle habitat and forest proposed for conversion to pine plantation. The establishment of pine plantation was shown to result in the local extinction of the species.

The results of the study supported the classification of *H. simsoni* as a vulnerable taxon according to IUCN threatened species criteria and led to the development of a proposed landscape management strategy for conservation of the beetle's habitat throughout its range. This strategy aimed to reserve areas of high-density populations and/or optimal habitat, maintain connections of unlogged forest between areas of high-quality habitat, and to limit the extent of plantation development throughout its range. This latter recommendation led a sceptical forest industry to insist on ground-truthing of the predictive map.

Hence, surveys of beetle abundance and habitat characteristics were conducted at a further 68 sites, encompassing 31 proposed coupes. For management purposes sites were selected in coupes (~ 50 ha scale) predicted to contain at least 30% optimal and sub-optimal habitat. These two categories were amalgamated due to the very low occurrence of predicted optimal habitat over the beetle's range. At the coupe scale, the predictive map was shown to have an accuracy of 71%, with 29% of coupes having a lower than expected abundance. The predictive map now forms the basis of a 10-year species management plan as part of a Public Authority Management Agreement between the Department of Primary Industries, Water and Environment and Forestry Tasmania for the conservation of the species' habitat on public land. This agreement, which is in the final stages of negotiation, proposes to conditionally reserve 480 ha of quality beetle habitat and to exclude plantation development over 7,150 ha of production native forest.

Further interrogation of the accuracy of the predictive map and models is required. At the 100 m grid square scale, 69% of sites were accurately predicted to contain high beetle abundance, but only 6% accuracy was obtained for sites predicted to contain medium beetle abundance. The majority of these sites were found to contain a higher than predicted occurrence of beetles. Predictions of low abundance will be ground-truthed this summer, allowing a more comprehensive analysis of the accuracy of the map predictions. It is also anticipated that the habitat variables collected in these surveys will be used to refine the models.

This study is one of the few to attempt to model the habitat requirements of an invertebrate, let alone a threatened species. It is significant in that the species is not closely associated with a particular component of its habitat such as a specific food plant, but appears to be dependent on an undetermined microclimate. Thus, the accuracy of the predictive map at a scale appropriate to the conservation management of the species is remarkable. This study illustrates the importance of 'off-reserve' conservation for threatened species, especially invertebrates, which are often poorly represented in or absent from formal reserves due to their restricted distributions. It also illustrates the role that threatened invertebrates can play as 'umbrella' taxa, resulting in the conservation of biodiversity in an area subject to large-scale disturbance.

Some background to Robert Brown's collecting in Western Australia (9 December 1801 – 17 January 1802): sources and collections

David T. Moore

52 Cranmore Lane, Aldershot, Hampshire GU11 3AT, United Kingdom

Matthew Flinders made a rather free interpretation of his orders for the investigation the south coast of Australia and it was, perhaps, as well for botany that he did. If the original orders had been followed to the letter, the ship being in the state it was, the naturalists might not have got to King George Sound. And Brown was later to comment in a letter to Banks that the south-western Australian flora was the most interesting he saw.

Investigator was at King George Sound/Princess Royal Harbour from 8 December 1801 to 5 January 1802. Sailing eastward from there she was in Archipelago of the Recherche on 6 January 1802. There followed an interlude at Lucky Bay from 9 to 14 January while Flinders examined and mapped the Archipelago from high land there. They sailed off again on 14 January into the dangerous waters of the Archipelago, making the relatively short journey to Middle Island where they anchored and remained until 16 January 1802. We should remember that the naturalists were again at Middle Island (17 to 21 May 1803) on the return trip from Timor to Sydney and plants were collected and sketches made. Consequently it is not safe to conclude that the localities 'Bay II', 'Middle Island' or 'Goose Island Bay' imply collecting in January 1802.

Many botanical, ethnographic, geological and zoological observations were made, and specimens collected, during these landings in Western Australia and even at sea. It appears that upward of 674 dried plant specimens still exist in London (BM) from the Western Australia collecting of Robert Brown and Peter Good (and there are duplicates at Kew (K) and in Australia). Surviving dried plant material and field sketches resulting from Ferdinand Bauer's activities are also extant in Vienna (W). We know that some of Peter Good's seeds from his collecting here were grown at Kew and had an effect on Bauer's drawings. Sixty-one superb completed watercolour plant drawings by Bauer and numerous landscape sketches by William Westall exist in London and Canberra. There are also at least four completed drawings of Western Australian fauna by Bauer in London. However, the geological specimens from the same area fared less well. The surviving artwork and botanical, geological and zoological sources/manuscripts of the *Investigator* expedition will be outlined as well as previous published work on the natural history of the voyage, namely that of Flinders (1814), Bauer (1813–16/17) and (1989), Endlicher (1833, 1833–35, 1837–41), Bentham & Mueller (1863–78), Britten (1909), Willis (1959), Perry & Simpson (1962), Blunt & Stearn (1976), Edwards (1981), Vallance & Moore (1982), Mabberley (1985), Groves & Moore (1989), Vallance (1990), Wheeler & Moore (1994), Moore & Beasley (1997), Watts *et al.* (1997) and Mabberley & Moore (1999).

Niche exploitation: multiple radiations of thrips on Australian *Acacia* trees

Laurence A. Mound[1] & Bernard J. Crespi[2]

[1]CSIRO Entomology, GPO Box 1700, Canberra, Australia

[2]Simon Fraser University, Burnaby, British Columbia V5A 1S6, Canada

Thrips are insects of the order Thysanoptera, an hemipteroid group that shares a common ancestor with the Hemiptera, Psocoptera and Phthiraptera. Adults and larvae have suctorial mouthparts formed from a pair of needle-like laciniae that enclose a single median feeding channel. Uniquely amongst insects they have only a single mandible—that on the right hand side of the head not developing beyond the embryonic stage. Worldwide there are rather more than 5000 described species, but the Australian fauna is predicted to include about 1000 species. More than 50% of thrips species are placed in the single family Phlaeothripidae, the members of which show a wide range of biologies. About 50% of phlaeothripid species feed on fungal hyphae or fungal spores, 10% on flowers, and 40% on green tissues. Our studies on Australian *Acacia* thrips are concerned solely with this last group.

The plant genus *Acacia* in Australia is estimated to include more than 1000 species, of which only about 150 retain the plesiotypic bipinnate leaf form. The vast majority of Australian *Acacia* species bear phyllodes—extensions of the stems that range in form from slender cylindrical structures or small flattened thorns to medium or large leaves. Phyllodinous *Acacia* species are arrayed into three major groupings: section Phyllodineae (almost 50% of the species), and sections Juliflorae and Plurinerves. There are few authentic records of thrips associated with members of the first of these, most being associated with the second and third sections.

With 1000 species of thrips in Australia, it is interesting to consider the range of vascular plant host associations, bearing in mind that half of the species can be expected to be associated with fungi. *Eucalyptus*, with about 800 species, does not support a single leaf-feeding member of the Phlaeothripinae, although a few species are associated with other Myrtaceae including *Callistemon* and *Melaleuca*. The Proteaceae seem to be ignored by all Phlaeothripinae, and alone among the Rutaceae the small genus *Geijera* supports at least 10 species. *Casuarina*, but not apparently *Allocasuarina*, supports at least a dozen leaf feeding species of phlaeothripines, and *Ficus* also supports an array of species. In contrast, the 450 species in the *Acacia* sections Juliflorae and Plurinerves support between them about 200 species of Phlaeothripinae, and it is this asymmetry of host associations that is the focus of our research. Have these *Acacia* species attracted several lineages of phlaeothripine thrips, or are the species of thrips on *Acacia* trees closely related to each other? Current evidence indicates that most of the genera recognised, several of which remain undescribed, form a single clade restricted to *Acacia*.

The diversity of thrips on *Acacia* in Australia is bewildering, and is apparently associated with the production, adoption, or usurpation of domiciles. The aridity and insolation, together with the ubiquity of predatory ants, has led to these thrips species seeking appropriate protection for themselves and their brood. Firstly there is a suite of species that induce bubble-galls on young phyllodes. A total of 21 species in three genera is described, some of which are host-specific but others appear to be polyphagous. This, however, is probably an over-simplification because, from molecular biological data, some of the polyphages now appear to comprise sets of sibling species, and the genera as distinguished are not single lineages. Some of these species produce a small first generation that comprises specially adapted wingless adults that function as soldiers that defend their gall, followed by a second generation of dispersing winged forms.

A second suite of species creates domiciles by using an anal secretion to glue or sew together two or more phyllodes to enclose a space within which to feed and breed. The range of such structures is considerable, from pairs of phyllodes glued cross-wise by a single female, to simple tents woven on the surface of a phyllode by a singe female, to more complex groups of apical phyllodes loosely sewn together with a fine webbing and either founded by, or progressively extended by, groups of adults. A third suite of species invades these domiciles, but this suite exhibits a range of behaviours. Some species expel the domicile producer, whereas a few species appear to be tolerated within the domicile and thus function as inquilines rather than as kleptoparasites. A fourth suite comprises a single genus that attacks and usually destroys one of the gall inducing species, and then raises its brood within the gall. These are kleptoparasites that feed on the gall tissue, they are not predators.

A fifth suite of species is associated with old, abandoned Hymenoptera galls, and many of these species have bizarre defensive adaptations to the front legs. Further suites of species, whose biology remains largely conjectural, are found in abandoned lepidopterous leaf-ties, or leaf-mines created by both moths and weevils. These thrips are often very small and thus difficult to study under field conditions, but have remarkable defensive adaptations at the posterior end of the abdomen, including tubercles that are sometimes developed as claspers, as well as powerful chemical deterrents.

Each of these multiple radiations of phlaeothripinae thrips is restricted to the phyllodinous *Acacia* groups. However, evidence of strict co-speciation remains weak. This is not surprising, because the driving force for the radiations seems to be the ownership of a suitable domicile, and in such a hostile and unpredictable environment this is best achieved through opportunism.

A molecular systematic study of the Prostantheroideae (Lamiaceae), including Chloantheae (formerly Verbenaceae)

Richard Olmstead[1], Philip Cantino[2], Brendan Lepschi[3] and Patrick Reeves[1]

[1]Department of Botany, University of Washington, Seattle, Washington 98195, USA

[2]Department of Environmental and Plant Biology, Ohio University, Athens, Ohio 45701, USA

[3]Australian National Herbarium, GPO Box 1600, Canberra, Australian Capital Territory 2601

As part of our ongoing molecular systematic research into the phylogeny of the Lamiales, we have conducted an investigation of the hypothesis put forward by Cantino that the Australian endemic labiate tribe Westringieae (= Prostanthereae) and the Australian endemic verbenaceous tribe Chloantheae together form a monophyletic group, which also include *Tectona* (Verbenaceae/Viticoideae *sensu* Briquet). The evidence for this postulated relationship comes from a cladistic analysis of morphological and anatomical characters, in which members of these two groups come out adjacent to each other in an unrooted tree. Prior to Cantino's suggestion, these groups generally had been assigned to separate families. However, Junell included Chloantheae and much of the rest of the Verbenaceae in the Lamiaceae. In contrast, Hutchinson elevated the Chloantheae to Chloanthaceae, a move accepted in a series of papers on the group by Munir.

Based on the study cited above, Cantino *et al.* suggested a provisional classification for the Labiatae that included Westringieae and *Tectona* in subfamily Prostantheroideae (= Chloanthoideae, *sensu* Cantino *et al.*), but excluded the Australian endemic *Spartothamnella* from the subfamily. *Spartothamnella* is included in Chloantheae in some treatments. This study builds upon previous studies, using chloroplast DNA (cpDNA) sequences of the gene ndhF for phylogenetic inference in the Lamiales. Twenty-four species, including all recognised genera in both tribes, were sampled. Sampling was accomplished through a combination of field-collected material preserved on silica gel and tissue samples removed from herbarium specimens. Sequences of ndhF were determined for the region encompassing the first 2135 nucleotides (nt) of tobacco ndhF (2086 nt excluding PCR primers at each end), followed by either manual or automated sequencing. A total of 58 sequences was analysed, including the 24 sequences representing Chloantheae and Westringieae, along with 33 sequences representing species from throughout the Lamiaceae (including *Spartothamnella*) and related families. Parsimony analyses were done using PAUP* vers. 4.0, with bootstrap analysis to confirm the strength of support for individual clades on the resulting tree.

The results provide strong support for monophyletic groups comprising Chloantheae, Westringieae, and those two clades combined (Prostantheroideae). *Tectona* is found not to belong to this group and *Callicarpa* is inferred to be the sister group to Prostantheroideae, albeit with weak support. A test of trees in which *Tectona* is sister to Prostantheroideae could not reject the possibility that it is the sister group, instead of *Callicarpa*. A probable synapomorphy for the Prostantheroideae is the persistence of the style after corolla abscission. This trait also characterises *Tectona*, but not *Callicarpa*.

Chloantheae is characterised by branched trichomes, although, once again, this character occurs in *Tectona*, where it might be homologous if *Tectona* were sister to Prostantheroideae. Traditional groups in this clade are not supported by cpDNA, and *Pityrodia* is paraphyletic with respect to all other genera of Chloantheae, in agreement with the inference based on morphology in Cantino's study.

Westringieae (Prostanthereae) is characterised by a lobed ovary and racemose inflorescence and consists of two well-defined clades, Prostantherinae (*Cryphia, Eichlerago, Prostanthera, Wrixonia*) and Westringiinae (*Hemiandra, Hemigenia, Microcorys, Westringia*). *Spartothamnella* is found to belong not with the Prostantheroideae but in Teucrioideae. It is sister to another Australian endemic, *Oncinocalyx*, and together they are sister to the New Zealand endemic *Teucridium*. These three taxa, all formerly assigned to Verbenaceae, are most closely related to *Teucrium*, traditionally assigned to Lamiaceae. Sampling the widespread *Teucrium* is not sufficient to tell whether the Australian and New Zealand endemics are its sister or are derived from ancestors in *Teucrium*.

Changes in free-living soil invertebrate communities under different crops in the Western Australian wheatbelt

Graham Osler, Petra van Vliet, Craig Gauci and Lyn Abbott

Soil Science and Plant Nutrition, Faculty of Agriculture, University of Western Australia, Nedlands, Western Australia 6907

Knowledge of the community structure and species composition of soil invertebrate communities in Western Australia is very limited. We have been describing some of these communities and examining the effects of different crop species on the free-living soil fauna in the Western Australian wheatbelt. Two important crops there are canola and lupins which may both improve the growth of following wheat. Improved growth of wheat following canola may be the consequence of biofumigation, and lupins may increase nitrogen availability. We examined free-living soil fauna in canola–wheat–lupin rotation near Moora to determine the effects of these crops on the soil fauna. Each crop in the rotation was sampled in June, August and October 1998. Prostigmatid mites were the dominant arthropod group and were sorted into morphospecies. Twenty-four nominal prostigmatid species were identified. An active, abundant faunal community was present under all crops, demonstrating that the canola variety in this study, Pinnacle TT, did not eliminate the free-living fauna, including nematodes and protozoans. The structure of the mite communities changed through the year, and the changes were different under the three crops. At the end of the growing season, the soil arthropod communities under lupin were distinctly different in two ways. First, five times more animals were present under lupin than under wheat or canola, primarily an increase in the number of a tydeid and a tarsonemid mite species. Second, the tarsonemid species was always the second most abundant species under lupin but was infrequently the second-ranked species under the two other crops. The soil arthropod communities were also different at the start of the growing season, when the prostigmatid community under canola was dominated by a rhagidiid species, whereas under lupin and wheat a caligonellid and a eupodid species dominated. The canola followed a lupin crop, and thus the difference in June may be attributed to the preceding lupins. Mite data from the lupin plots were consistent with a previously described succession from another environment.

In May 1999 we conducted an experiment to determine whether mite community structure was similar to that found at Moora at other sites through the wheatbelt. The three study sites were at Cadoux, Avondale and Newdegate which are several hundred kilometres distant from each other. One field each of canola and another crop were sampled at each site. Preliminary results indicate that there are differences in the mite communities following different crops, but there is little consistency between sites in the structure. Implications of these similarities and differences will be discussed.

Shark Bay geology and history

Phillip E Playford

c/- Geological Survey of Western Australia, Department of Minerals and Energy, 100 Plain St, East Perth, Western Australia 6004.

Shark Bay is renowned for its geology and biology and for its remarkable human history, which extends back almost 400 years for Europeans and many thousands of years for Aborigines.

Peron and Edel Land peninsulas, and Dirk Hartog, Dorre, and Bernier Islands, are composed of Quaternary aeolian deposits, which accumulated on Tertiary anticlines. The Zuytdorp Cliffs, marking the western limit of the Shark Bay area, constitute a Quaternary fault scarp, which resulted from up to 300 m of vertical fault displacement during the late Pleistocene or early Holocene, after the calcareous eolianites of the Tamala Limestone had been deposited. This fault scarp is arguably the longest and most prominent in Australia and it testifies to major seismic activity in the area during the recent past, even though the area is seismically quiescent today.

Among the most renowned features of the geology and biology are the Holocene stromatolites and coquinas of Hamelin Pool and Lharidon Bight. Those two basins are hypersaline arms of the sea, barred by a shallow sand and seagrass bank, the Faure Sill, through which interchange with oceanic water of normal salinity is severely restricted. As a result of this high salinity (about double that of normal seawater), most elements of the open marine fauna of Shark Bay are excluded from the two basins. Consequently, in the absence of grazing gastropods, the cyanobacteria that construct stromatolites are able to flourish, building in Hamelin Pool the most abundant and diverse assemblage of living stromatolites known in the world. They mimic life on earth as it existing billions of years ago.

Only one mollusc is able to flourish in the highly saline waters of Hamelin Pool and Lharidon Bight. This is *Fragum erugatum*, a small bivalve that flourishes in the low-nutrient environment through a symbiotic relationship with zooxanthellae, minute algae that live in its tissues, generating food for its use. The shells of *Fragum* accumulate in vast numbers around the shores of these two basins, thrown up as successive coquina beach ridges. Studies have shown that these ridges have been accumulating for some 5,000 years, since the Faure Sill was first formed, and that the major beach ridges result from successive cyclones. Such cyclones have passed over Hamelin Pool with an average frequency of 50 years.

Little is known about the Aboriginal history of the Shark Bay area, but middens dating back more than 4,000 years have been found at a number of localities. When Europeans first settled in the area, during the mid 19th century, several hundred Aborigines of the Malgana Tribe were living there, but that population was soon decimated, largely as a result of introduced diseases. Today there are no full-blood Malgana people remaining, and their language has become extinct.

The first Europeans to visit Shark Bay were crew of the Dutch East India Company ship *Eendracht*, skippered by Dirk Hartog, who landed at Cape Inscription on Dirk Hartog Island on 25 October 1616. As a record of his visit Hartog left an inscribed plate, nailed to an oak post, and fixed in a rock crevice at the top of the cliff. This is the oldest record of a European landing in Australia. As a result of Dirk Hartog's discovery Australia appeared on world maps for the first time as 'The Land of the Eendracht'.

In following years many ships of the Dutch East India Company sailed along the Western Australian coast, and the next people to land at Shark Bay were crew of Willem de Vlamingh's expedition, who went ashore on Dirk Hartog Island in February 1697. They climbed the cliff at Cape Inscription and found Dirk Hartog's plate lying at the foot of a decayed post. Vlamingh took away 'the old dish', replacing it with one of his own, inscribed with the text of the original plate, plus a record of his own visit.

William Dampier, the renowned English adventurer and naturalist, visited Shark Bay in 1699, two years after Vlamingh's landing. He went ashore south of Cape Levillian on Dirk Hartog Island, at a place that I have recently named 'Dampier Landing'. There he assembled the first collection ever made of Australian plants, which is still preserved in the collection of Oxford University, and is currently on display at the Western Australian Museum. Dampier named the great bay into which he had sailed 'Shark's Bay', unknowingly replacing the earlier Dutch name 'Bay of Dirk Hartog'.

In June 1712, the *Zuytdorp*, of the Dutch East India Company, was wrecked at the foot of the cliffs that now bear its name. There is evidence that a few of the 200 people aboard scrambled ashore and lived nearby for some time. Their fate is unknown, but it is likely that some interbred with Aborigines. None returned to civilisation. The fate of the ship remained a mystery until 1957 when I proved, through coinage found at the site, that the *Zuytdorp* had been wrecked there. Most of the 250,000 guilders in silver coins carried on the ship remained on the sea floor until the early 1980s, as a 'carpet of silver'. About 10% of this treasure was recovered by the Western Australian Museum, but most of the rest has been looted.

Fifty years after the loss of the *Zuytdorp*, in 1772, a French explorer appeared in the area for the first time. François de St Allouarn landed at Turtle Bay on Dirk Hartog Island, hoisting the French flag on the cliff top and burying a bottle containing a silver coin and a parchment inscribed with a claim to the west coast of New Holland in the name of the King of France. This bottle, with a well-preserved French coin, was found buried at the cliff top in 1998, but the parchment had by then completely decayed away.

Vlamingh's plate remained untouched from 1697 to 1801, when a sailor from the French vessel *Naturaliste* found it lying beside two weathered posts at Cape Inscription. The skipper of the ship, Emanuel Hamelin, believed it would be sacrilege to remove this historic plate, so he nailed it to a new post, placing it in position beside the remains of Dirk Hartog's and Vlamingh's original posts. However, one of his young lieutenants, Louis de Freycinet, did not share his skipper's lofty view. Seventeen years later, in 1818, he returned in command of the *Uranie*, and had no scruples in removing the plate and placing it in the archives of the French Academy in Paris. It remained there until 1947, when it was presented by France to the Australian government and can now be seen in the Western Australian Maritime Museum in Fremantle.

The next explorer to visit the Shark Bay area was the Australian-born navigator, Phillip Parker King, in 1822. He landed at Cape Inscription, where from the sea he could see two posts standing at the cliff top. He climbed the cliff, following the same route as the early Dutch and French explorers, fully expecting to find the Vlamingh plate still there, as he was unaware of Freycinet's visit four years previously. King was disappointed to find that the plate had gone, but he left his name marked with nails driven into the Hamelin post. That post, together with Vlamingh's post, remained at the site until 1907, when they were removed to Perth by surveyors planning the construction of a lighthouse and quarters at Cape Inscription.

Shark Bay was settled by Europeans in the early 1860s for pastoral and sandalwood-gathering purposes. Pearling began soon afterwards and continued until the 1930s. Today the area supports several sheep and cattle pastoral properties, together with thriving tourism, fishing, culture-pearl, and solar-salt industries.

Recent publications on the history and geology of the Shark Bay area are as follows:

Edwards, H. (1999). *Shark Bay through four centuries, 1616 to 2000.* Shark Bay Shire, Denham.

George, A.S. (1999). *William Dampier in New Holland; Australia's first natural historian.* Bloomings Books, Hawthorn.

Playford, P.E. (1990). Geology of the Shark Bay area. Pp. 13–31 *in* P.F.Berry *et al.* (eds), *Research in Shark Bay.* Western Australian Museum.

Playford, P.E. (1996). *Carpet of Silver; the wreck of the Zuytdorp.* University of Western Australia Press, Nedlands.

Playford, P.E. (1998). *Voyage of discovery to Terra Australis by Willem de Vlamingh in 1696-97.* Western Australian Museum, Perth.

Funding biodiversity research: manipulation, money, media and morals

Hugh Possingham

Department of Applied & Molecular Ecology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, South Australia 5064

In this brief talk I will discuss a few contentious questions regarding the future of taxonomy and systematics in Australia: How much does the discipline need to sell it self to other biologists, industry and the broader community? How can we make the discipline more relevant without detracting from core business? Should we, or indeed can we, present a more unified, proactive face to the community? Are there enough young scientists in the discipline and do they have a career path?

Aquatic mites in assessments of stream invertebrate diversity: is neglect of a subphylum justified?

Heather C. Proctor

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

Introduction In many countries, macro-invertebrate assemblages are used to assess the health of running water. Assessment schemes typically involve either the assignment of an indicator value to each taxon (e.g. BMWP scores in the UK, SIGNAL in Australia), or the use of multivariate statistics to predict sets of taxa that should occur in a site based on that site's abiotic characteristics (e.g. RivPACS in the UK, AusRivAS in Australia). All three extant subphyla of arthropods (Atelocerata, Crustacea, Chelicerata) are present in streams, and together are the dominant group of invertebrates in these indices. Depending on the assessment scheme, recommended taxonomic resolution for insects and for some groups of crustaceans is as fine as family, genus or species. Mites, on the other hand, are either lumped into the relatively uninformative taxon Acari, combined with a variety of small-bodied taxa as 'other', or simply ignored.

This neglect is often justified by the statement that mites are physically too small and difficult to identify. However, with the arrival of Harvey's (1998) key to the genera of Australian water mites, much of the taxonomic impediment has been removed for assessments of mite diversity in Australian streams. Next to the caddisflies (Trichoptera), water mites are the most species-rich group of freshwater arthropods in Australia (416 spp). They also appear sensitive to organic pollution, according to studies in the Northern Hemisphere and in New South Wales. But despite these selling points, there is the pragmatic need for biodiversity surveys that are rapid as well as informative. In order to be identified to genus, mites must first be cleared and, often, mounted for microscopic examination. Both take time and the latter takes considerable skill in micro-dissection. In this paper I report on progress in a two-year study that compares the abundance and diversity of mites with that of other stream invertebrates, with the goal of determining whether the inclusion of mites adds information about stream quality that compensates for the time involved in their processing.

Methods I have sampled six stream-reaches in south-east Queensland. Each stream was sampled twice (winter and summer), but currently only one set of sampling dates has been analysed. Ten stones per reach were thoroughly scrubbed and their contents washed into a 250 µm-mesh net. For each stone-based sample, all invertebrates were counted and identified. Insects were identified to family, and the following taxa are being identified to genus: Ephemeroptera, Plecoptera, Trichoptera, Odonata, Coleoptera. Mites were identified to genus. Crustaceans were identified more coarsely, to family for Decapoda and to ordinal level for microcrustacea.

Current results A total of 7187 invertebrates were extracted and identified from the 60 stone samples (Table 1). Mites were commonly encountered on stones, ranging from 7 of 10 stones for Enoggera Creek, 8 of 10 for Moran's (Cow Pasture), 9 of 10 for Moran's (Wishing Tree) and Canungra Creek, and 10 of 10 for Peter's Creek and Lobster Creek. The percentage of invertebrates that were mites averaged 7.9%, ranging from 1.58% for Canungra Creek to 14.01% for Moran's (Wishing Tree). Mites consistently outnumbered Odonata, and were often more numerous than Plecoptera (stoneflies) and Crustacea.

The three taxa that are most often considered to be important indicators of 'clean' water are the Ephemeroptera (mayflies), Plecoptera (stoneflies) and Trichoptera (caddisflies). At the familial level (the level to which taxa are identified in Chessman's 1995 SIGNAL index), mites at 5–9 families per site were invariably more diverse than Ephemeroptera (2 or 3 families) and Plecoptera (1 or 2 families), and were sometimes more diverse than Trichoptera (2–11 families). At the genus level (Table 2), mites at 6–11 genera per site were always more diverse than Plecoptera (1 or 2 genera), usually more diverse than Ephemeroptera (2–10 genera), and sometimes more diverse than Trichoptera (2–15 genera).

As expected, most of the aquatic mites were Hydracarina, or water mites *sensu stricto*. However, there were often a high number (if low diversity) of oribatid mites, mostly in the genus *Hydrozetes* and *Trimalaconothrus*. Oribatid mites are very rarely mentioned as inhabitants of stream communities, but they were present on 23 of the 60 stones from 5 of the 6 sites. In the Moran's Creek (Cow Pasture) site there were more oribatids (301 individuals) than either mayflies (224) or caddisflies (also 224).

Discussion Mites are ubiquitous and occasionally abundant inhabitants of forested streams in south-east Queensland. They are diverse at both the familial and generic level, and provide as much or more taxonomic information than co-occurring stoneflies and mayflies. Based on data analysed to date, Trichoptera tend to be as or more diverse than mites. Future analyses will involve comparisons of taxon-accumulation curves between mites and other taxa, and multivariate analyses to test whether the inclusion of mite data strongly alters the interpretation of relationships among sites.

Table 1. Taxonomic composition of selected groups of arthropods from sampled streams.

SITES	TOTAL#	Ephem	Plec	Trich	Odonata	Coleo	Dipt	Crust	Acari	%Acari
Peter's Creek	1232	234	11	374	16	240	235	13	55	4.46
Moran's Creek, Wishing Tree	392	86	2	115	1	76	58	4	40	10.20
Moran's Creek, Cow Pasture	2406	224	5	224	19	16	1012	70	337	14.01
Lobster Creek	863	250	0	13	8	57	321	76	67	7.76
Enoggera Creek	586	158	19	31	13	29	51	157	14	2.39
Canungra Creek	1708	259	0	180	14	42	787	3	27	1.58

Table 2. Number of identified genera of EPT taxa and of mites. n/a means that no individuals were mature enough to be identified to genus.

SITES	Ephem	Plec	Trich	Acari
Peter's Creek	7	2	15	9
Moran's Creek, Wishing Tree	4	n/a	10	10
Moran's Creek, Cow Pasture	10	n/a	12	8
Lobster Creek	4	0	4	11
Enoggera Creek	2	1	2	6
Canungra Creek	3	0	10	6

Morphology, pollination ecology and evolution of the *Stylidium graminifolium* complex

Elisa Raulings

School of Botany, University of Melbourne, Grattan St, Carlton, Victoria 3052

Characteristic of triggerplants (*Stylidium*) is the fusion of the style with the stamens to form a column (the gynostemium) which bears male and female reproductive features at its apex. The column is mobile, and when triggered by a foraging insect will rotate rapidly from its set position to land on the insect, where it may deposit or retrieve pollen depending on the reproductive phase of the flower. In Western Australian *Stylidium* species, three column placement positions exist—dorsal, lateral and ventral. If species share pollinators, differences in column placement may be a possible means for coexistence of triggerplants with minimal interspecific exchange of pollen. Alternatively, *Stylidium* species may use different insect pollinators, and column position may be a result of non-adaptive speciation.

In eastern Australia, the most widespread *Stylidium* species is the Grass Triggerplant *S. graminifolium*, a morphologically variable species occurring on a diversity of soil types throughout coastal and montane regions. The plant bears a raceme of white to dark pink flowers which are laterally paired so the column swings from the side when triggered by a foraging insect.

Multivariate analyses using vegetative, floral and anatomical characters identified four groups in the *Stylidium graminifolium* complex which will be described as four new taxa. The position of pollen placement on insects was investigated by comparing morphometric measurements and pollinator observations at sites of sympatry and allopatry. In order to determine whether taxa were competing for pollinators, the number of visits to male and female flowers and the number of triggering incidents were recorded for species under conditions of allopatry and sympatry.

A number of insects were observed to visit each taxon, and at sympatric sites pollinators were shared between taxa. In co-existing *Stylidium graminifolium* taxa, gamete transfer was partitioned on the pollinator's body. A shift in pollen placement position may be the result of competitive interactions between *Stylidium graminifolium* taxa, and may enforce genetic isolation under conditions of sympatry. A shift in column position in Western Australian *Stylidium* may have been the result of competition for limited pollination resources, which may partially account for the diversity of species in that region.

BioLink: Software for managing biodiversity information

Ian Reid and Steve Shattuck

CSIRO Entomology, GPO Box 1700, Canberra, Australian Capital Territory 2601

BioLink is a computer system used to collect, maintain, analyse, apply and disseminate taxonomic, biodiversity and environmental information. The system provides an easy to use set of tools for researchers in a range of fields who work with taxonomic information and field-collected specimens. Central to the BioLink system are Explorers. Explorers are used to graphically manage hierarchical information for taxon names and collection material. These Explorers make managing large amounts of data with complex relationships quick and easy. BioLink also includes a number of tools. For example, generating a distribution map is as easy as selecting a taxon from the Checklist Explorer and choosing the Distribution Map command. This will automatically retrieve all material for the taxon, open the Mapping Assistant and display all records on a customisable map. There is no need to generate intermediate files or use a stand-alone GIS or mapping tool. Another commonly used tool is eGaz, the Electronic Gazetteer. eGaz provides access to latitude/longitude information for over 250,000 Australian place names as well as several hundred thousand places overseas. eGaz will also calculate the coordinates for collecting sites a known distance and direction from a named place (for example, '10 km NE of Perth') and the distance between two places. Details concerning BioLink are available at http://www.ento.csiro.au/biolink/home.htm or by contacting biolink@ento.csiro.au.

Gondwanan land snails in arid Australia

Bronwen Scott

School of Life Sciences, Victoria University of Technology, McKechnie Street, St Albans, Victoria 3021

Biogeographical studies of land snails in Australia have identified two major faunal assemblages: southern relict (Gondwanan) and palaeo-oriental (Laurasian) (Solem, 1959; Bishop, 1981). The disjunct distribution of southern relict families such as Rhytididae in Australia, New Zealand and southern Africa, and Bulimulidae in Australia, New Zealand and South America can be explained most simply as the result of their occurrence in Gondwana (van Bruggen, 1980). The origin of the palaeo-oriental families is less clear. Previous studies have interpreted their distribution as the product of southward dispersal from northern centres of origin (Solem, 1959; Bishop, 1981). If this is so, then it involves one or more post-Miocene invasions following the collision of the Australian and Asia plates (Solem, 1985). However, this north-to-south dispersal scenario, which has become axiomatic, fails to consider the Gondwanan origin of many Asian terranes.

Ov [illegible]

Although the origins of the two assemblages differ, rainforest is regarded as the ancestral habitat for both. Rainforest was widespread in Australia during and immediately after the break up of Gondwana. Increasing aridity in the late Miocene/early Pliocene pushed this rainforest to the margins of the continent, creating 'new' habitats in the interior. Consequently, arid-adapted land snails are regarded as the descendants of ancestors that either dispersed to the centre as pre-adapted pioneers or were stranded there when the rainforests retreated (Solem, 1997).

Relatively few of Australia's land snail families have representatives in arid Australia. This pattern corroborates the ancestral rainforest scenario. There are no operculate snails, and most of the pulmonate families in the arid zone are each represented by only one or two species (Scott, 1997). The remaining families (Bulimulidae, Camaenidae and Pupillidae) also occur in both arid and humid habitats, but for each the diversity in arid habitats exceeds that in humid ones. Evidence from these groups suggests that arid habitats were well-established in Gondwana and persisted in post-Gondwana Australia.

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Tribal turmoil: Systematics of the Eudorylini (Diptera, Pipunculidae)

Jeff H. Skevington and David K. Yeates

Department of Zoology and Entomology, Hartley Teakle Building, University of Queensland, St Lucia, Queensland 4072

Key words: Diptera, Pipunculidae, Eudorylini, *Eudorylas*, *Claraeola*, systematics, morphology, revision, Australia.

The Eudorylini are the largest tribe of big-headed flies (Diptera, Pipunculidae) and include 492 described species. Until recently, one huge genus (*Eudorylas* Aczél) and a small genus of five species (*Claraeola* Aczél) represented the tribe. New species have typically been added without reference to other species, no keys are available, and the group is at a taxonomic impasse. Several new genera have recently been erected to accommodate small groups of species with a few synapomorphies. This will allow for the creation of keys for subsets of the tribe, but has left an unmanageable paraphyletic mass of species. Even a concept for the type genus has remained elusive. We have attempted to place the Australian Eudorylini into a World context. Analysis of 70 exemplars using 194 morphological characters has led to a new hypothesis of relationships in the group. Exemplars were selected from all recognised species groups in all biogeographical regions. We propose two new genera based on cladistic analysis and provide a key to all genera of Eudorylini. The Australian pipunculid fauna, always considered depauperate, is actually a diverse assemblage of mostly endemic species. Only 16 Australian species of Eudorylini from one genus are currently described. Our revision recognises 97 species in 4 genera. Recent collection efforts have increased the Australian pipunculid holdings in collections by a factor of ten to over 7000 specimens. Despite this, many new species are represented by single specimens, suggesting that considerable collecting is still necessary before the Australian Pipunculidae are well known.

Evolutionary origins of cave cockroaches in the genus *Paratemnopteryx* Saussure (Blattodea: Blattellidae)

David Slaney

Department of Zoology and Tropical Ecology, James Cook University, Townsville, Queensland 4811

For over 150 years scientists have debated the origins of cave-dwelling organisms. To investigate the origin of cavernicolous fauna in North Queensland, I selected the cockroach genus *Paratemnopteryx* Saussure (Blattaria, Blattellidae) to test alternative hypotheses for the evolution of cave-dwelling species within the genus. The genus contains 13 described species, 11 of which are endemic in Australia, and five of which are cave-dwelling. Three species found during this study are new to science and are described herein. One new surface-dwelling species, *P. rosensis*, was collected from south-east Queensland, and two new cavernicolous species, *P. kookabinnensis* and *P. weinsteini*, were collected from central Western Australia and north-east Queensland respectively. My initial hypothesis was that some surface-dwelling species in this genus gave rise to cavernicolous species as a result of increasing aridity in Australia during the late Cenozoic. To test this, I used a combined morphological and molecular approach.

To reconstruct the phylogeny of *Paratemnopteryx* using a traditional morphological approach, 30 morphological characters were chosen, 11 binary and 19 multistate. The most informative sources of taxonomic characters were the male tergal glands, and the genitalia and associated structures for both sexes. The resulting most parsimonious trees were consistent with previously proposed relationships within the genus. In using a molecular approach to investigate relationships in *Paratemnopteryx*, I sequenced the second internal transcribed spacer (ITS2) region of nuclear ribosomal DNA, and the entire mitochondrial cytochrome oxidase II gene (COII). In total, sequence data were obtained for nine *Paratemnopteryx* species and from several populations of some of those species. The size of the ITS2 gene region was 458–970 base pairs, with a GC content of 50–58%. The ITS2 data were useful for taxonomic discrimination at the population level but the ITS2 region was too variable to be phylogenetically informative at the species level in *Paratemnopteryx*. Analyses of the COII sequences from the same nine species revealed a high AT bias (71–72%). The majority of variable sites (80%) occurred in the 3rd codon position, which contained most of the phylogenetic structure. The tree derived from maximum likelihood analysis of all sites in the COII gene was more similar to the morphological derived tree than the parsimony-based one.

Cave colonisation events were traced on to the reconstructed phylogeny for *Paratemnopteryx* to determine whether a single, or multiple, colonisations have occurred. Results from this analysis indicate that cave colonisation has occurred independently on at least three occasions, once in Western Australia and twice in North Queensland.

In placing *Paratemnopteryx* species into seven main geographical regions covering continental Australia, two traceable vicariance events were identified—one between species distributed in north-west Western Australia, a second in North Queensland. On a finer geographical scale, most species have restricted distributions with no overlap, and on this basis seven additional vicariance events may be identified. These events involve mainly comparisons of cave-dwelling species distributions, where specimens have been found only in certain karst regions. Investigation of the mode of speciation in *Paratemnopteryx* supports allopatric speciation, with little or no subsequent range changes. Analyses indicate recent allopatric speciation between the cave-dwelling species in North Queensland.

Currently I am investigating the possible timing and mechanisms for the evolution of cave-dwelling species in *Paratemnopteryx* in relation to known past climatic events, using the maximum likelihood tree derived from the molecular data.

Biodiversity of New South Wales subterranean fauna

Mia Thurgate[1] and Andy Spate[2]

[1]Jenolan Caves Trust, PO Box 1495, Bathurst, New South Wales 2795

[2]NSW National Parks and Wildlife Service, P O Box 2115, Queanbeyan, New South Wales 2620

New South Wales has some 450 carbonate rock outcrops of which 95 are known to be cavernous. Well over 2200 individual caves are known in these karst environments. In 1994/95, Eberhard and Spate (1995) completed a major survey of cave macro-invertebrate fauna from over 130 caves. More than 1200 specimens from at least 172 taxa were collected. The results of this survey significantly increased the known subterranean fauna of NSW. Compared with the state of knowledge published prior to 1993, the number of orders increased by nearly a third (from 21 to 30), and the number of families recorded was almost doubled (from 61 to 115). An increase in richness was evident amongst cave-limited genera as well. Before 1993, 11 troglobitic species had been recorded, and this has since increased to between 17 and 32 genera. The survey also revealed a previously unsuspected diversity of aquatic taxa.

At the level of individual karst areas, the overall richness of NSW areas is typically 10–25 species, considerably lower than for karst areas in Tasmania and Western Australia. However, several karst areas in NSW have a much higher level of richness. Some of the most notable sites include Jenolan (67 taxa), Wombeyan (58 taxa) and Wee Jasper (54 taxa). These sites also contain the highest number of troglobitic taxa in the State, including a diverse aquatic crustacean fauna. The richness of these sites may be due in part to their large size, topographic relief, and highly cavernous structure containing a wide variety of habitats. They have probably been maintained as stable, moist refugia (especially the permanent aquifers) over a geologically significant period, facilitating the survival of relictual populations.

Since the initial reporting of results of the Eberhard and Spate survey, several other locations have been flagged as important centres of biodiversity for subterranean biota. The Macleay Valley (west of Kempsey), includes a number of scattered karst localities with high species richness including Stockyard Creek (74 taxa) and Willi Willi (61 taxa). The Valley is also particularly important for its highly diverse terrestrial calciophilic gastropod assemblages. The Wellington karst aquifer and possibly the Bell River alluvial aquifers have also proved to be particularly important for their diverse, endemic aquatic invertebrate fauna. One taxonomic group, the division Syncarida, is particularly well represented in the Wellington/Bell River aquifer systems and across New South Wales generally, with a new family and two new genera represented by eight new species, currently being described.

As custodians of Jenolan, Wombeyan, Abercrombie and Borenore Karst Conservation Reserves, the Jenolan Caves Reserve Trust responsible for the conservation of several of the more significant subterranean biota sites in NSW. Jenolan Caves receive one of the highest cave visitations in the State, and there is concern that potentially high levels of impacts may occur in the show cave systems, in the more popular wild caves, and in the karst aquifer. In response to these potential threats, the Trust has formed a Visitor Impact Management system, which is overseen by the Social and Environmental Monitoring Committee. This Committee has given high priority to the maintenance of subterranean fauna populations and their habitats. Currently the Committee, along with the Trust's Karst Resources Department, is developing suitable survey methods for subterranean fauna collection, with a view to developing a long-term monitoring program.

This paper provides an overview of the current knowledge of the diversity of the subterranean biota of New South Wales. The more important karst regions and their taxa are described in detail, updating the Eberhard and Spate report (1995). The paper highlights several of the more important taxonomic groups including the amphipod, syncarid and gastropod faunas. Gaps in the current knowledge and suggestions for further research are outlined. Management implications for NSW karst areas, focusing on the Jenolan Caves Reserve Trust sites and Wellington Caves, are discussed.

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Biogeography of Australian freshwater fishes

Peter J. Unmack

Biology Department, Arizona State University, Tempe, Arizona 85287-1501, USA

Biogeographical patterns of obligate freshwater fishes of Australia were investigated. Similarity indices, parsimony analysis, and drainage-based plots of species' ranges were used to identify patterns. Relationships among regions were deduced largely by concordance between methodologies, then summarised into a proposed series of faunal provinces. The most striking pattern was in the incidence of endemism across the continent. Provinces in southern, central, and western Australia have high numbers of endemic fishes, presumably resulting from isolation by aridity and drainage divides. With exception of one region, northern and eastern Australia provinces have few endemics, likely explained in the north by high drainage connectivity during times of lowered sea level. This does not account for low endemism in the east, since drainages appear to have remained isolated during lowered sea levels and patterns suggest an absence of distinct barriers of other kinds. By default, climate again seems the most likely cause of species' distributional limits. Whatever the case, most patterns were almost certainly established in the distant past, perhaps as early as Miocene. Influences of Plio-Pleistocene events on broad patterns of freshwater fish distributions seem minimal.

Novel nano-organisms (nanobes): living analogues for Martian 'nannobacteria'?

Philippa J.R. Uwins[1], * Richard I. Webb[1,2], Majid Ghoddusi[1], Anya J.E. Yago[1], Tom Loy[3,4] and Kathleen Murphy[3,5]

[1]Centre for Microscopy and Microanalysis, [2]Department of Microbiology and Parasitology, [3]Centre for Molecular and Cell Biology, [4]Department of Anthropology and Sociology, [5]Queensland Agricultural Biotechnology Centre,

The University of Queensland, St Lucia, Queensland 4072

On August 7 1996, NASA announced that they had found evidence that a Martian meteorite (ALH84001) contained evidence for past life on Mars (McKay *et al.* 1996). At the centre of their thesis, and perhaps the most controversial of their findings, were the fossil remnants of sub-bacteria sized 'cells' called nannobacteria. Whilst the findings were of great scientific interest they fuelled a fierce, highly contentious debate concerning the minimum size of autonomous life on earth.

The identification and existence of nannobacteria and nanobacteria was not new and had been proposed previously by a number of workers (Folk, 1993; Sillitoe *et al.*, 1996; Pedone & Folk, 1996; Vasconcelos & Mckenzie, 1997; Folk & Lynch, 1997; Kajander *et al.*, 1994; Kajander *et al.*, 1998). The existence of nan(n)obacteria, however, has been fiercely questioned, since it is argued that the minimum size of autonomous life is 200 nm in diameter for a spherical cell (Vogel, 1998). It is thought that any organism smaller than 200 nm in diameter would have insufficient volume to conduct the metabolic and reproductive processes essential to live (Maniloff, 1997; Nealson, 1997; Psenner & Loferer, 1997; Vogel, 1998). It therefore remained unresolved whether 'nannobacteria' are fossilised remnants of autonomous life-forms, artefacts of sample preparation or unusual mineral deposits.

More recently, novel nano-organisms (nanobes) have been described growing on Triassic and Jurassic sandstones collected from petroleum exploration boreholes off the Western Australian coast (Uwins *et al.*, 1998). These cells (20–150 nm in diameter) provide further evidence in strong support of nano-scopic life. For example, analysis of these growths shows that nanobes are communicable and grow; are composed predominantly of carbon, oxygen and nitrogen; contain DNA and RNA; and are membrane-bound structures surrounding a dense cytoplasm and nuclear area. The morphology of these growths closely resemble Actinomycetes and fungi, only on a much reduced scale. It is difficult to explain what these organic features are if they are not living cells, given that they are not composed of mineral compounds (silicates, sulphides or metal oxides), or carbonaceous compounds (e.g. fullerenes, carbon nanotubes or carbonates), nor can they be explained as non-living polymers.

The morphology, elemental composition, and ultrastructural detail of nanobes will be described, illustrated and discussed in the context of the nan(n)obacterial debate. It is our thesis that nanobes are living biological organisms in the same size range as the controversial nan(n)obacteria found in a range of different rock types, in biological tissues and in Martian Meteorite ALH84001.

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Endemism and invasions: mites and World Heritage

David Evans Walter

Department of Zoology and Entomology, The University of Queensland, St Lucia, Queensland 4072

http://www.uq.edu.au/entomology/david.evans.walter.html

After insects, mites (Acari) are the most diverse group of animals, but our knowledge of the Australian acarofauna is extremely limited. For example, Halliday's checklist (*Mites of Australia*, 1998) contains fewer than 3,000 species. Yet, nonparametric diversity estimators predict that a minimum of 2,000 species of mites inhabit the Green Mountains Section of Lamington National Park (hereafter, Lamington) in the Border Ranges of south-east Queensland. These mites inhabit every conceivable ecological niche, usually in extraordinary numbers, but most species and many higher level taxa at Lamington are undescribed. For example, my inventory of the acarine order Parasitiformes at Lamington is now at 202 species representing 30 families. Although this order includes the most intensively studied Australian mites (e.g.

ticks, phytoseiid biocontrol agents, vertebrate and insect symbiotes), only 35 species (17%) were described, at least 3 families and 7 genera are new to science, and 2 family records are new for Australia.

Similar investigations of the most diverse acarine order, the Acariformes (c. 80% of described species worldwide), have only recently begun, but the results for two targeted families, Cunaxidae and Labidostommatidae, are highly suggestive. Halliday (1998) listed only one genus (2 species) of Labidostommatidae and 3 genera (5 species) of Cunaxidae known from all of Australia. From Lamington I have on hand 2 genera (*Sellnickiella*, *Labidostomma* [new record]) and 3 undescribed species of Labidostommatidae. At least 8 genera of Cunaxidae are present at Lamington, including at least 5 new Australian records: *Dactyloscirus* [new record], *Neocunaxoides*, *Neoscirula* [new record], *Parabonzia* [new record], *Pulaeus* [new record], *Pseudobonzia* [new record], *Rubroscirus*, and *Scutopalus*. Some species in these families reflect relationships to the New Zealand fauna, e.g. a species of *Neoscirula* near *proctorae* (Smiley, 1992), and of *Sellnickiella* near *circinus* (Atyeo & Crossley, 1961) and others to the South African fauna, e.g. a species of *Parabonzia* near *maranthae* (Den Heyer).

Overlain on this extraordinary diversity of endemic species is a fauna of introduced mites that are invading this World Heritage-listed site and a group of taxa whose origins are obscure (cryptogenic). Except on islands, exotics tend to be associated with human disturbance and are rare in habitats where humans have made relatively little impact. Although there are numerous weedy exceptions (e.g. the honeybee), the tendency of introduced species to remain within areas of high human disturbance has often been attributed to 'biotic resistance' on the part of endemic communities. However, at least three ecological classes of mites appear to be evading biotic resistance: plant-parasites that are co-invading on introduced weeds; blood-feeding parasites of birds, reptiles and small mammals; and predators of invertebrates living in soil-litter habitats. This last group includes a number of cryptogenic species with cosmopolitan distributions that reproduce by all-female parthenogenesis (thelytoky).

Vegetative morphology and anatomy in *Stylidium* (Stylidiaceae)—a systematic perspective

Juliet Wege

Department of Botany, The University of Western Australia, Nedlands, Western Australia 6907

Stylidiaceae comprise five genera of Gondwanan distribution that are clearly distinguished from related families in the Asterales by the presence of a central floral column which bears both the anthers and stigma at its apex. *Stylidium*, the largest genus, is characterised by a unique pollination system whereby column movement is triggered by an external stimulus. *Stylidium* has undergone extensive radiative speciation, particularly in the south-west of Western Australia, and exhibits a remarkable range in morphology. Life forms represented by the genus include annual herbs, cormous perennials, basally-rosetted perennials, erect leafy-stemmed sub-shrubs and plants with laterally-spreading stoloniferous stems. A feature unifying the majority of species is the presence of a leaf rosette but the relative position of the rosette and the arrangement of any additional leaves are variable between species.

Corresponding to this morphological diversity is a high degree of anatomical variation. *Stylidium* leaves are especially diverse in structure, particularly with regard to the form of the epidermal cells and the distribution of stomata. Elongate, obliquely oriented, thickened leaf epidermal cells are characteristic of a variety of species and are a feature unique to the family. Flowering scape anatomy is relatively uniform across the genus, with the exception of section Junceae which is unique in possessing specialised palisade cells in the cortex. Stem anatomy is more varied, with many stylidia possessing either 'determinate' or 'indeterminate' pericyclic cambial activity. The anatomical differences between the stems and scapes are shown to be important in identifying homologous vegetative features. The variation in vegetative morphology and anatomy in *Stylidium* is discussed in relation to other genera in Stylidiaceae and a phylogeny of the family is presented.

The role of the small-scale farmer in preserving the link between biodiversity and sustainable agriculture

Max Whitten and William H Settle

Food and Agriculture Organisation of the UN, Manila, the Philippines

Convincing evidence is emerging in tropical Asia to demonstrate that economically and ecologically sustainable agriculture depends on a diverse array of plants, animals (especially invertebrates) and micro-organisms in the agro-ecosystem. For example, the emergence of secondary pests in many crops that are exposed to pesticides has revealed that large guilds of natural enemies play a stabilising role in regulating numbers of plant herbivores. In the tropics, two recent surveys of invertebrates in rice paddies in Indonesia and Lao PDR demonstrate a very high abundance of insects in an agro-ecosystem that biologists from temperate regions might assume to be depauperate. Soil fertility and the availability of nutrients to crop plants also depends on a network of organisms, fungi, nematodes, annelids, insects, mites, bacteria, viruses and protozoans. Clearly more work needs to be done to define the complex links between biodiversity and sustainable agricultural production. However, caution would recommend we err on the side of conservation and management of the biodiversity in agro-ecosystems until we establish whether any of these biological riches are ecologically redundant and can be sacrificed as we intensify production.

How are these considerations linked to small-scale farming and food security? One third of the world's population consists of Asian farming households, and the region's food security relies on their economic and ecological survival. It follows that small-scale farmers are dependent on the preservation of bio-diversity for theirs and mankind's continued well being. They must be the custodians of much of the earth's biodiversity. Small-scale farmers, therefore, are the ones who need to be literate in conserving, managing and exploiting the local biodiversity of their agro-ecosystems. In this context, the Green Revolution has been a grand diversion from the main game plan. It has temporarily increased the carrying capacity for human populations by raising yields considerably. But it has done so in a non-sustainable manner with its high input/high output philosophy without regard to the negative economic, social and biological externalities. Perhaps of greatest significance, its technological thrust has disempowered small-scale farmers; they have tended to lose much of their traditional knowledge; and, in many senses, they have ceased to be true experts at growing a healthy crop. The challenge is to enable farmers once again to become experts at growing a healthy crop in an economically and ecologically sustainable manner.

A novel approach to this challenge, called Farmer Field Schools (FFSs), has emerged in Southeast Asia; it offers a real prospect that farmers can enjoy the gains from higher-yielding varieties but, at the same time, keep a responsible eye on broader and long term issues—among them conserving the biodiversity of their local paddies and gardens. Thousands of FFSs have been run successfully in a number of Southeast Asian countries, especially Indonesia, Vietnam and the Philippines which promise to put the farmer back in the driver's seat. This approach to farmer empowerment relies on farmer discovery, by experimentation where the farmer's field is the class room, and where trainers are there to facilitate, not to instruct. IPM is often the entry point for discovery but a graduate from the FFS is more expert at making informed decisions on most aspects of plant production and protection. Preserving local biodiversity is one of the genuinely surprising objectives to emerge for these 'IPM' farmers. Such literate farmers make better working colleagues for trainers, researchers and those industries who are not dependent of selling farmers unnecessary inputs. Thus, this successful approach to farmer empowerment is a win for all legitimate players; and it strengthens the link between biodiversity and sustainable agriculture.

The Miocene macroflora of Stuart Creek, South Australia

Michael R. Whyms[1], David R. Greenwood[1] and Andrew I. Rowett[2]

[1]School of Life Sciences and Technology (S008), Victoria University of Technology, PO Box 14428, MCMC, Melbourne, Victoria 8001

[2]Geological Survey Branch, Mineral Resources Group, Primary Industry and Resources, GPO Box 1671, Adelaide, South Australia 5001

The interior of the Australian continent today is characterised by an arid climate with highly variable mean annual rainfall, averaging below 200 mm/yr over much of the region around Lake Eyre. Vegetation in the interior today is sparse, with species of *Acacia* and *Casuarina* the dominant trees, and *Eucalyptus* in riparian stands. Tertiary age macrofloras in the continental interior, however, document vegetation types indicative of much wetter climates than today. A discontinuous sedimentary sequence is present in the Lake Eyre region, including Middle Eocene and younger floras in the Poole Creek Palaeochannel, and Miocene floras at Stuart Creek and to the south near Woomera. Additional Tertiary macrofloras are reported from near Broken Hill and Alice Springs. The Lake Eyre region macrofloras indicate gallery rainforests with more sclerophyllous hinterland vegetation with rainfall around 800–1400 mm/yr for both the Middle Eocene and Miocene, but indicate a shift towards more sclerophyllous vegetation by the Miocene. The Late Miocene Stuart Creek flora contains some 'rainforest' elements, and a wet-dry deciduous element (*Brachychiton* and *Cochlospermum*), but is overwhelmingly dominated by sclerophyllous forms, including *Banksia*, *Eucalyptus*, *Casuarina*, and *Grevillea* and other sclerophyllous Proteaceae.

Table 1. Tertiary macrofloras from the interior of Australia. Data from various sources, as indicated in the table.

macroflora	stratigraphic unit	stratigraphic age	pollen zone or other age	significant taxa	sources
Mt Eba/Jacks Hill	Munjena Fm equivalent	Paleocene - Middle Eocene	lithological correlation	*Araucaria*, *Papuacedrus*	Offler, 1969; Lange, 1982
Mt Eba/Haggard Hill	Munjena Fm equivalent	Paleocene - Middle Eocene	lithological correlation	*Arauacria*, *Papuacerdrus*	Offler, 1969; Lange, 1982
Mt Margaret Mine	?Eyre Formation	Paleocene - Miocene	lithological correlation	*Banksia*, RF Myrtaceae	Chapman, 1936
Marree	Eyre Fm or equiv.	Paleogene, poss. Eocene	lithological correlation	*Brachychiton*	Alley & Rowett, unpubl. data
Nelly Creek	Eyre Fm	Middle Eocene	Lower Nothofagidites asperus	*Agathis*, *Gymnostoma*, *Brachychiton*, cf. *Syzygium*, legumes, RF Proteaceae	Christophel *et al.*, 1992
Poole Creek	Eyre Fm	Middle Eocene/Oligocene?	lithological correlation	*Gymnostoma*, cf. *Syzygium*, legumes, RF Proteaceae	Greenwood, 1996
Mt Alford	Eyre Fm	Middle Eocene	lithological correlation	*Gymnostoma*, cf. *Eucalyptus*, *Brachychiton*	unpubl. data
Fowlers Gap	Eyre Fm equiv.	Paleogene	lithological correlation	no recognisable forms	Greenwood & S. Hill, work in progress
Bottle Hill/Woomera	Willalinchina eq	Miocene	lithological correlation		Chapman, 1936
Island Lagoon	?Eyre Fm	Miocene	lithological correlation	*Eucalyptus*, *Leptospermum* & other woody capsulate Myrtaceae	Lange, 1978 & 1982
Poole Creek South	Etadunna Fm	Miocene	lithological correlation	*Casuarina*	unpubl. data
Morris Creek	?Willalinchina Ss	late Early to Late Miocene	equiv. to Willalinchina Sandstone	*Banksia*, *Brachychiton*	Greenwood, 1996
Stuart Creek	Willalinchina Sandstone	late Early to Late Miocene	lithological; above Watchie Sandstone	*Banksia*, *Brachychiton*, *Cochlospermum*, *Gymnostoma*, *Grevillea* and other Scl Proteaceae	Greenwood, 1996 & Alley & Rowett, unpubl. data
Lake Ngapakaldi	Wipajiri Formation	Late Miocene	Upper Triporopollenites bellus	*Eucalyptus*	Stirton & Tedford, 1966

Australian groundwater-dependent isopod crustaceans

George D.F. Wilson

Centre for Evolutionary Research, Australian Museum, 6 College Street, Sydney, New South Wales 2000

This paper reviews the phylogenetic history, biogeography and diversity of isopod crustaceans that depend on Australian groundwater resources (AGDI). These isopods belong to two suborders, Phreatoicidea and Asellota. Other, more recently evolved isopods are present in Australian groundwaters (e.g. Cirolanidae), but in much lower frequencies.

1. Phylogenetically, AGDI are ancient, with either fossils or indirect phylogenetic information leading to presumptive ages from the late Palaeozoic to the early Mesozoic Eras. Palaeozoic marine fossils and Triassic freshwater Australian fossils establish the antiquity of Phreatoicidea. Peracaridan crustacean cladograms show the Phreatoicidea to be the earliest-derived group of all isopods. In these same cladograms, the Asellota are either a sister group of the Phreatoicidea, or derived one branch later. Although Asellota do not fossilise, this phylogenetic pattern is consistent with a Palaeozoic origin of this suborder. This conclusion is also supported by a Gondwanan biogeographical pattern for both suborders. Sister taxa (related genera) of Australian genera are found in other Gondwanan fragments, providing a minimum age of approximately 180 million years for these taxa. A recent Northern Territory discovery of species belonging to the asellotan family Protojaniridae, known previously from South Africa and Sri Lanka, establishes another Gondwanan pattern. A much later-derived asellotan genus, *Heterias*, is also found in South America, providing another ancient Gondwanan connection. *Heterias*, however, belongs to a poorly defined family that includes marine, brackish and freshwater taxa, so a marine origin for Australian *Heterias* cannot be discounted.

2. AGDI may be classified into three ecotypes: surface-cryptic, surface-burrower, and groundwater forms. The phylogenetic distribution of these ecotypes in phreatoicidean isopods provides evidence for at least two separate colonisations of groundwater habitats. One colonisation event may be older than the rifting of the Indian subcontinent and the other is dated approximately by the separation of New Zealand from East Gondwana. Although phylogenetic results are not available for the Asellota, both surface-cryptic and groundwater ecotypes are common. Freshwater Asellota do not burrow, but live either interstitially or in the burrows of other animals (pholeteros).

3. Species and genera of AGDI are highly endemic. Single distinctive genera of Phreatoicidea occur in small areas of Australia. For example, the distinctive genus *Phreatomerus* occurs only in artesian mound springs of South Australia. Several new genera found recently are restricted to extremely small sites such as single groundwater-fed streams in the north-west Kimberley. In some cases, the regions have been sampled extensively, so the tiny distributions are not artifactual. We can say little about the Protojaniridae species, since only one Australian site is known and its taxonomic affinities have not been established. According to recent genetic studies, *Heterias* may be highly endemic at the species level.

4. Some regions in Australia harbour flocks of AGDI species. The currently monotypic genus *Eophreatoicus* Nicholls, 1943, found in Kakadu National Park and Arnhem Land (Northern Territory), contains 14+ undescribed species. *Crenoicus* has two or three undescribed species in each large watershed region in New South Wales above 1000 m (e.g. Kosciusko Plateau, Boyd Plateau, Barrington Tops), possibly reaching a total of 14–16 species in this State alone. Tasmania is replete with species flocks in several genera, especially in *Colubotelson*. The prevalence of species flocks of AGDI means that these taxa may add considerably to regional groundwater biodiversity assessments.

Taken together, these observations confer a high conservation value on AGDI, especially when using phylogenetic diversity models. Detailed systematics, phylogenies and biogeographical patterns thus have important roles in assisting informed decisions on the conservation of these and other invertebrate taxa.

Taxon sampling

David Yeates and Chris Lambkin

Department of Zoology and Entomology, The University of Queensland, St Lucia, Queensland 4072

All systematists sample taxa and characters in order to conduct phylogenetic analyses. Taxon sampling has become critically important in the design of phylogenetic analyses. It has been treated sparely in the literature, leading to the commonsense notion that, in general, more taxa are better than fewer taxa, and that some taxa are more useful than others in a taxon sample. This contribution assesses those ideas. Taxon sampling depends on the hypothesis under test, and this is a critical first step in choosing an appropriate sample. For many interesting questions in phylogeny reconstruction, sampling all species is not necessary and is logistically impossible. Statistical theory suggests that sampling should be designed so that samples are replicated below the level of inference. For example, if the question asked of a phylogenetic analysis is 'What are the relationships of subfamilies within family Xidae?' then more than one representative of each subfamily should be used in the taxon sample. In this case, taxon sampling relies on the classification of the group. The limits of our current system of classification in a phylogenetic context should be taken into consideration. A new approach that quantifies the quality of taxon sampling for comparative purposes will be discussed.

POSTERS

Soil mite (Acari) abundance and diversity under *Eucalyptus globulus* plantations

Honi Adolphson

School of Natural Sciences, Edith Cowan University, 2 Bradford St, Mount Lawley, Western Australia 6050

Keywords: soil and litter mites, Acari, *Eucalyptus globulus*, jarrah forest

This study was designed to investigate the impact of *Eucalyptus globulus* subsp. *globulus* (Tasmanian Bluegum) monocultures on the diversity and abundance of the soil and litter acarine (mite) fauna. Soil mites form the dominant group of mesofauna in the soil environment, playing important roles in decomposition and nutrient cycling processes.

Limited studies by various workers have shown mesofaunal populations in monoculture plantations to decrease in species diversity in comparison to native ecosystems (Ahern & Yen, 1977; di Castri & Vitali-di Castri, 1981; Serrelheiro & Madeira, 1990; Springett, 1976). With the increased planting of *E. globulus* monoculture plantations in the 21st Century, concerns surround the impact these mass plantings will have not only on the soil environment, but on the wider ecosystem in general. Despite the importance of mites, no investigations of litter and soil communities of these plantations in Australia, particularly Western Australia, have been performed.

In this present study, the soil and litter mite communities of an 8-year-old *E. globulus* plantation sited on reclaimed pasture land were compared with an adjacent native *E. marginata* (Jarrah) forest and grazed pasture in the mediterranean-type region of south-west Western Australia.

As expected, there were strong seasonal variations in mean abundance and diversity between the sampling periods of spring 1997 and autumn 1998, influenced considerably by soil moisture. Abundances in the litter were greater in the native forest, and soil abundances were slightly higher in the *E. globulus* plantation. Mean abundances varied between 35 and 2193 individuals kg-1 of dry litter, and between 351 × 10–3 and 4668 × 10–3 m-2 in the soil.

Species richness was consistently higher in both the soil and litter layers of the native forest. The *E. globulus* plantation was intermediate to the native forest (< 50%) and the pasture (> 30%). A total of 130 mite species were recognised—23 Mesostigmata, 56 Prostigmata, 50 Cryptostigmata and 1 Astigmata. Of the total mite species, 49 were recorded in soil, 39 in surface litter, and 42 in both surface litter and soil.

Species diversity was considerably higher in the native forest litter than the *E. globulus* plantation. In the soil, species diversity was similar for the native forest and *E. globulus* plantation, despite the considerable differences in species richness. Species diversity of the pasture was very poor in comparison to the two forest systems.

Classification and ordination analyses further illustrated seasonal separation on the basis of species composition. The *E. globulus* plantation and native forest shared 25% of the total number of species recorded in both the soil and litter habitats. Litter species shared included *Tectocepheus*, Oppiinae, Oppiellinae, Bdellidae, Cheyletidae, Stigmaeidae, and several Mesostigmata. Soil species included *Tegeozetes*, Haplochthoniidae, Oppiidae, Bdellidae, and Mesostigmata. The pasture sites shared < 9% of the total number of species with both the native forest and plantation sites. These were predominantly Mesostigmata and several Prostigmata (Bdellidae, Rhagidiidae and Penthalodidae).

Although having a lower species diversity than the native forest, the monoculture supports a diverse group of mites found in considerable abundance, particularly Cryptostigmatid species. This suggests that these species are able to colonise an available ecological niche in the monoculture ecosystem.

Phylogeny of *Acacia* section *Botrycephalae* (subgenus *Phyllodineae*)

Siti Roosita Ariati

School of Botany, University of Melbourne, Grattan St, Parkville, Victoria 3052

Acacia sect. *Botrycephalae* (Mimosaceae) comprises approximately 40 species that are confined to eastern Australia. They occur from south-eastern Queensland to Tasmania and South Australia, with the greatest diversity in the Central Coast region of New South Wales. The section is readily distinguished by the bipinnate leaves and capitulate inflorescences arranged in racemes. In a few cases species are difficult to delimit.

A preliminary study of inflorescence development indicates that the group is monophyletic, but the relationships of the *Botrycephalae* to the remainder of subgenus *Phyllodineae* are unresolved. There have been a few studies of the infrasectional classification of the *Botrycephalae* which have provided partly congruent results, although they all examined only a few taxa and each a different group. Thus, the results are not comparable. Early studies on the phylogeny of *Acacia* indicate that the *Botrycephalae* is closely related to sect. *Phyllodineae*.

Cladistic parsimony analyses are based on morphological and anatomical characters, including adult and seedling plants. All specific and infraspecific taxa were investigated from both herbarium and spirit material. Three species of sect. *Phyllodineae* (*A. podalyriaefolia*, *A. calamifolia*, *A. ligulata*) were chosen as outgroups. Using this morphological data set, the relationships of sect. *Botrycephalae* will be discussed.

Marine sponge symbioses: diversity within diversity

Michael Borowitzka

Algae Research Group, School of Biological Sciences and Biotechnology, Murdoch University, Murdoch, Western Australia 6150

Sponges are very common and very diverse benthic marine invertebrates throughout the world's oceans. They are a popular phylum for bioprospecting, due to the high proportion of novel compounds that they produce.

Many sponges, especially tropical ones, contain symbionts including bacteria, cyanobacteria, red algae, green algae, diatoms and dinoflagellates, even fungi. Some contain several symbionts simultaneously. The biomass of the symbionts can equal or even exceed that of the sponge tissue. Sponges also contain other organisms such as polychaetes in their aquiferous system. A sponge can thus be its own diverse mini-ecosystem

The degree of association between a sponge and its symbionts varies. Most data are limited to ultra-structural studies, and almost nothing is known of the degree of metabolic, biochemical or possible genetic integration. Structurally, symbionts may be (a) intracellular, in either a cell or cytoplasm; (b) intercellular in the sponge mesohyl; or (c) extracellular, where the sponge grows over the symbiont, often changing the latter's growth form. No other symbiontic system shows such diversity in structural integration. It is likely that similar diversity exists in the level of metabolic integration.

One difficulty that this presents is what to call an organism. Is it correct to call it a sponge when much of the biomass may not be sponge? At least one analogous symbiotic system—lichens, with a symbiosis between fungi and algae—has its own classification. Do we need a separate classification for 'symbio-sponges'?

Another problem involves monitoring and conserving these organisms. Do we consider those with photosynthetic symbionts as animals or plants? This question is not trivial, as our approach to the study of organisms, their biology and ecology, and ultimately their conservation, is often different as we deal with animals and plants.

The chemistry of sponges reflects both the diversity of the phylum and probably that of the symbionts. In recent years a major question in sponge chemistry has been 'What is the role of the symbionts in the biochemical diversity of sponges?' The biosynthetic origin of most 'sponge' secondary metabolites is unknown, although several recent studies have shown that at least some are synthesised by the symbiont and not the sponge.

World-wide diversity of eucalypt-compatible ectomycorrhizal fungi.

Mark Brundrett and Neale Bougher

CSIRO Forestry and Forest Products, Private Bag, PO, Wembley, Western Australia 6014

This poster summarises knowledge about ectomycorrhizal fungus diversity in eucalypt stands in exotic locations throughout the world. This information was complied from published papers, unpublished information generously provided by the acknowledged people and our own collections. An annotated list of species which are considered to be mycorrhizal with eucalypts from 15 countries in Australasia, Africa, Europe, South America and North America is provided. This information is contrasted with our knowledge of fungal diversity in natural stands and plantations in Australia. A list of fungi we have shown to be compatible with eucalypts in synthesis experiments under controlled conditions is also provided. Problems with fungal identification and the inclusion of fungi which are probably saprophytes, or those not compatible with eucalypts in survey lists are discussed. The information provided should help researchers to designate mycorrhizal species in the future. Accurate information about the diversity of indigenous and exotic eucalypt-compatible fungi which are already present in different regions is required before the potential benefits of introducing new fungi can be considered. Updated lists of eucalypt ectomycorrhizal associates are available on the web (http://www.ffp.csiro.au/research/mycorrhiza/).

Investigating the evolution of the mistletoe family Loranthaceae using a molecular phylogenetic approach

Ainsley Calladine

Tropical Plant Sciences and Tropical Environment Studies and Geography, James Cook University, Townsville, Queensland 4811

The Loranthaceae is a large family of mostly woody perennials which occur as aerial parasites known as mistletoes and three putatively primitive species which are terrestrial root parasites. Believed to be of ancient Gondwanan origin, well established before the rifting of the southern continents, this family is widely distributed throughout the tropics but with representatives in southern temperate regions.

Mistletoes are a prominent feature of the Australian flora which is recognised as comprising both Gondwanan and intrusive elements. There are two Gondwanan sub-elements, one relictual, the other, a derived autochthonous group, rich in endemics and believed to have been evolving in Australia for a long period. The intrusive element is comprised of plants that arrived during the mid-Miocene to early Pliocene when there were suitable continuous land surfaces to the north with Malesia. Consequently, the derived Australian lineages, which are predominantly tropical or arid radiations, may be derived from these two distinct origins.

Some Australian genera may be easily recognised as ancestral, possibly remnants of a former paleoaustral flora, for example *Atkinsonia* and *Nuytsia* which exhibit plesiomorphic character states including the terrestrial habit. Determining the status of other Australian taxa is more problematic. Although the taxonomy of Australian mistletoes is well developed our phylogenetic understanding, based largely on cytological data and presumed patterns of flower, inflorescence and haustorial biology evolution, is not so advanced. There appears to have been significant karyological differentiation prior to Gondwanan fragmentation leading to complex patterns of chromosome number reduction in widespread groups; floral and inflorescence morphology has been well studied but the determination of ancestral character states remains very problematic; and the evolution of the mode of parasitism and haustorial structure remains contentious.

A molecular systematic approach can provide an independent view of evolutionary trends and can be used to determine which features are ancestral and which are derived. When used in conjunction with these other data and distributional information molecular sequence data are proving to be a useful tool in reconstructing biogeographical histories as well as providing insight into the evolution of these characters.

Here evolutionary and biogeographical trends among the Australian members of the Loranthaceae are examined using inferred phylogenetic relationships generated with 18S rDNA and trnL cpDNA sequence data. My study includes phylogenetic analyses incorporating GenBank data of ribosomal 18S sequence for taxa from South and Central America, New Zealand and Africa and my Australian contributions. There is evidence of two groups among the Australian mistletoes, one an apparently derived group including Amyema and *Dendrophthoe* which are associated with the group of African taxa with the ancestral genus *Muellerina* at the base. The remaining Australian genera are associated with American and New Zealand taxa. The putatively primitive terrestrial *Atkinsonia* and *Nuytsia* appear to be allied with the only other terrestrial mistletoe *Gaiadendron* from South and Central America. Phylogenies inferred from trnL data have begun to resolve inter- and intrageneric relationships of Australian Loranthaceae including evidence of the paraphyly of *Amyema* and its affinity with *Diplatia*. Preliminary data also add evidence that *Amyema sanguinea* should be reinstated in *Pilostigma* Tieghem.

This molecular phylogenetic approach is resolving the complex evolutionary relationships in this important family which has been used to model biogeographical trends in the evolution of the Australian flora.

Species abundance and diversity of aquatic invertebrates in South Australian mound springs and bore drains

Jason Cody, Andy Austin, John Jennings and Hugh Possingham

Department of Applied & Molecular Ecology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, South Australia 5064

The artesian mound springs found in the north-east of South Australia are of special ecological interest because they are the only source of relatively fresh, permanent free-water. Until recently, these were used extensively as water points for cattle, although some now have stock excluded. Since European settlement bores have also been sunk in the area to provide water for both humans and stock. Mound springs and bore drains provide a habitat for a number of invertebrate species in an otherwise arid environment. Some invertebrates (e.g. the isopod *Phreatomerus latipes*, the ostracod *Ngarawa dirga*, a phreatic amphipod *Phreatochiltonia anophthalma*, and amphipods of the genus *Austrochiltonia*.) appear to be endemic to the mound springs, whilst other non-endemic invertebrates (e.g. chironomids and aquatic beetles) make use of the free-water from bores. The species diversity of both mound springs and bores appears to be affected by the stocking rate imposed upon them. As well, a difference in the species composition between mound springs and bores is apparent. These apparent differences will be examined by comparing the species diversity of a number of springs and bores with similar stocking histories. Initial results suggest there is a general decline in the species diversity of mound springs after de-stocking, although the endemic species diversity appears unaffected. There also appears to be differences in the species composition between the mound springs and bores.

Tasmanian cave guides: an under-used resource?

Niall Doran, Ian Houshold & Mike Driessen

Nature Conservation Branch, Tasmanian Parks & Wildlife Service, GPO Box 44A, Hobart, Tasmania 7001

The enthusiasm of cave guides and Parks & Wildlife field staff in Tasmania potentially offers new opportunities in the ongoing study of invertebrate cave fauna in the State. These opportunities may augment the wealth of taxonomic information gained through cave surveys and fauna collections conducted across Tasmania in the past, as well as the steadily building ecological database produced via established and new long-term monitoring programs (addressing both research and conservation management issues). While such surveys and programs have provided us with a great deal of information on Tasmanian cave fauna, they are commonly restricted to single or few collecting events or to surveys spaced a month (or more!) apart.

Guides employed by the Tasmanian Parks & Wildlife Service make multiple visits, totalling several hours per day, to tourist caves every day. These visits promote an intimate understanding of the caves in which they work and offer monitoring opportunities at a frequency that most scientific programs would envy. At the same time, the field guides are increasingly interested in information on cave fauna and the latest research developments in the subterranean world. At their instigation, we are currently helping to develop monitoring protocols that can be readily incorporated into the regular every day schedules of cave tours without adding significantly to their workload.

We are able to provide the guides with background information on cave fauna and physical karst processes (including, importantly, what is not known or recorded) and, with help in the design and analysis of monitoring programs and data, to ensure that it is in a form valuable to the science. In turn, the guides are able to return quantitative and qualitative data from both observations and surveys, covering events and behaviours that have otherwise only rarely been seen, and providing information that may fill the gaps in larger scale survey programs. It is hoped that this information will not only be of general interest, but may be incorporated in planned studies of the effect of different levels of disturbance on cave environments and invertebrate fauna. Involving the cave guides in this process will hopefully also benefit their ability to relate information directly to a public which itself shows a growing appreciation for the scientific and ecological aspects of cave formation and life. In future, it is hoped that the guides will not only continue relaying the latest information on cave fauna to the public, but will also relay increasing amounts of information that they themselves have been involved in collecting.

Spiders of the South Australian mound springs and bore drains

Travis Gotch, Andy Austin, Hugh Possingham, John Jennings and Drew Tyre

Department of Applied & Molecular Ecology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, South Australia 5064

The region to the south of Lake Eyre is one of the driest areas in Australia. The only natural permanent potable water in this region is from a series of discontinuous mound springs and pastoral bores that are clustered around the south-western edge of the Great Artesian Basin, giving them an importance that is out of proportion to the area they actually cover. The springs and bore drains can be considered to be analogous to islands as they are wetlands isolated by desert, effectively limiting the dispersal of some species. Recent research has identified 10 undescribed species of spider that depend on water. Some of these spiders are putatively endemic to the Lake Eyre complex of mound springs, possibly even to individual springs. The Lycosidae make up half of these spiders, the other five species are members of four other families, the Pisauridae, Hahniidae, Clubionidae, and Linyphiidae (two species). This poster outlines research currently under way to 1) identify which of the spider species are restricted to mound springs and which have successfully dispersed into bore drains and 2) identify the micro-habitats of the springs and bore drains that are being utilised by the spiders.

A LucID guide to aquatic macro-invertebrates

Ben Gunn, John W.H. Trueman, Sophia Dimitriadis and Peter Cranston

with the aid of the Australian aquatic invertebrate community

CSIRO Entomology, GPO Box 1700, Australian Capital Territory 2601; now dispersed widely

In 1994, at the outset of a national scheme to monitor the biological health of Australia's rivers (the Monitoring River Health Initiative [MRHI] of the Federal Government), it was realised that the decline in training personnel was one of several possible impediments to the project. Skills once acknowledged and routine in graduate biologists, such as the use of dichotomous keys and understanding of morphology and nomenclature, could no longer be taken for granted. Furthermore, with likely adoption amongst the voluntary community (Waterwatch, Ribbons of Blue etc.), a new group of users of taxonomic information was identified for the scheme, and 'user-friendliness' became of even greater concern.

Options for delivery of information on the full range of Australian macro-invertebrates (i.e. those retained by a 250 m mesh net) were assessed, and we chose an interactive system then under development by the CRC for Tropical Pest Management—the software now known as LucID[1]. The requirements of the MRHI were for identifications predominantly to family level, which at the outset involved 350 terminal taxa. A range of personnel assisted in the construction of character matrices and the search for line drawings to illustrate taxa and character states. A CD-ROM was produced in 1996 after much testing of the software and the compliers' patience. Feedback after dissemination of the CD led us to realise that understanding and interpreting line drawings is an acquired skill that taxonomists take for granted, but causes the untrained or inexpert much difficulty.

Undeterred by the previous experience, in late 1998 we were engaged once again by Land and Water Resources Research and Development Corporation (LWRRDC) and Environment Australia (EA) to use a near commercial release version of LucID and to upgrade it, particularly to include photographs of as many character states and terminal taxa as possible. Photography involved a digital camera and recently developed software to compile automatically in-focus images from several focal planes (Automontage[2]). Several subkeys were produced by consultants to the project, including Heather Proctor and Mark Harvey, Penny Greenslade, Ros St Clair, Phil Suter, John Dean, Keith Walker and Russ Sheil—resulting in the inclusion of 414 terminal taxa, many below family level, and illustrated by over 2,200 images.

In keeping with our views on dissemination of this type of information, distribution of the CD-ROM is free, thanks to additional funding provided by CSIRO Land and Water sector. We acknowledge this funding, as well as that from LWRRDC/ EA and CSIRO Entomology. It is also a pleasure to acknowledge the willingness with which many of the aquatic taxonomy community in Australia provided us with information, and loaned us specimens and scarce images.

[1] http://www.publish.csiro.au/lucid/

[2] http://www.syncroscopy.com/syncroscopy/am.sp

A phylogenetic analysis of the Xanthosiinae (Apiaceae) based on morphological data

Jenny Hart and Murray J. Henwood

John Ray Herbarium, School of Biological Sciences, Macleay Building A12, The University of Sydney, New South Wales 2006

Drude's 1898 classification of the Apiaceae (Umbelliferae), still the most commonly followed, recognises two subtribes within Hydrocotyleae (Hydrocotyloideae). Hydrocotylinae accommodates genera including *Hydrocotyle*, *Trachymene*, *Platysace*, *Centella* and *Chlaenosciadium*, whereas Xanthosiinae comprises *Xanthosia*, *Pentapeltis*, *Schoenolaena* and *Actinotus*. Xanthosiinae is based on the shared possession of a well-developed, often petaloid calyx, whereas Hydrocotylinae have an absent or poorly developed calyx. *Xanthosia*, together with *Pentapeltis* and *Schoenolaena* (the latter two are sometimes been treated as congeneric with *Xanthosia*), are distinguished from other genera in the Apiaceae by their conspicuous petaloid sepals, laterally compressed fruit with 5–11 longitudinal ribs, and an unusual inflorescence—an irregular compound umbel with two or three peripherally inserted bracteoles on each umbellule. The inflorescence can be a simple umbel or reduced to one or a few flowers in some species. *Actinotus*, in contrast, commonly has flowers in dense, bracteate capitula, and other features unusual in the Apiaceae, such as a solitary mericarp and reduced petals (sometimes absent for some species).

The circumscription of the Xanthosiinae excludes several potential sister genera which share inflorescence structure, flower and fruit characteristics with *Xanthosia*, but which lack a calyx. One of these is *Centella* which has traditionally been considered closely allied to *Hydrocotyle*, within which it was sometimes treated as a section. The two genera share superficial similarity in fruit shape. *Centella*, however, is distinct from *Hydrocotyle*, possessing 7–13 longitudinal ribs and transverse ribs in the fruit. *Xanthosia* is the only other genus in Hydrocotyloideae known to have more than five ribs and transverse ribs in the fruit. The inflorescence structure in some species of *Centella* is similar to that found in *Xanthosia*. However, the bracteoles in *Centella* are not as conspicuous, nor asymmetrical as is the case in *Xanthosia*. A second genus with inflorescence structure and petal morphology similar to *Xanthosia* is *Chlaenosciadium*, which has rugose fruit, also reported to have transverse ribs. Furthermore, a recently described, monotypic genus endemic to south-west Western Australia, *Brachyscias*, has similar inflorescence and floral characteristics to *Xanthosia*, adding to the general confusion of the subtribal classification.

Thus a phylogenetic analysis of *Xanthosia* and its allied genera was undertaken for two purposes; firstly, to determine if *Xanthosia* is a monophyletic group of species separable from *Pentapeltis* and *Schoenolaena*, and secondly, to examine the integrity of the subtribe Xanthosiinae as defined by Drude.

A total of 53 morphological characters covering inflorescence, floral, fruit and vegetative characteristics was used in a phylogenetic analysis of 33 terminal taxa. A heuristic search found 1716 equally parsimonious trees of 210 steps (re-scaled consistency index 0.342, retention index 0.678, homoplasy index 0.648) distributed on a single island. Regions of conflicting topology between the most parsimonious trees are restricted to the clade containing *Xanthosia* species, with the exception of a trichotomy at the base of the ingroup.

The results of the analysis do not support the monophyly of *Xanthosia* inclusive of *Pentapeltis* and *Schoenolaena*. With *Schoenolaena* excluded, *Pentapeltis* and *Xanthosia* together form a monophyletic group within which they are monophyletic sister taxa. *Xanthosia* could be recognised as either separate or congeneric with *Pentapeltis* within a monophyletic classification, but as there are a trichome, petal, nectary and style features clearly separating them, they would be most appropriately treated as separate genera.

The placement of *Centella* and *Xanthosia* in separate subtribes by Drude is contradicted by the results of the phylogenetic analysis, in which *Centella*, *Chlaenosciadium* and *Brachyscias* are positioned between the clade containing *Xanthosia* and *Pentapeltis* and the more basal branches containing *Actinotus* and *Schoenolaena*. *Centella*, and the sister taxa *Chlaenosciadium* and *Brachyscias*, lack sepals—the single characteristic excluding them from the Xanthosiinae. These genera, however, share inflorescence, flower and fruit characteristics with *Xanthosia*, *Pentapeltis* and *Schoenolaena*. Thus there is a need for an alternate classification to Drude's presently recognised subtribes within the Hydrocotyleae.

It is uncertain whether *Actinotus* should be considered allied to *Xanthosia*, or if it has more similarities to some other genera. The position of *Actinotus* in this study, situated at the base of the ingroup close to *Trachymene* but also *Schoenolaena*, makes its inclusion or exclusion in the Xanthosiinae ambiguous. *Actinotus* shares clawed petals and petaloid sepals with *Xanthosia*, and has petaloid bracts which may possibly be homologous to the petaloid bracts/bracteoles found in *Xanthosia*. *Actinotus* has some unusual characteristics: a solitary mericarp, flowers in dense, bracteate capitula, styles fused at their base, sometimes forming a column above the base of which the nectaries are attached, and a connate whorl of sepals forming a 'skirt' in some species. These features isolate it from other genera in the Hydrocotyleae, and thus *Actinotus* may warrant separate subtribal or tribal classification.

The effect of broom invasion on arthropod diversity in open eucalypt woodland in South Australia

My-my Huynh and Andy Austin

Department of Applied & Molecular Ecology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, South Australia 5064

Several species of the plants commonly known as broom are environmental weeds in South Australia. A familiar sight in the Adelaide region is hillsides thick with dense stands of *Cytisus scoparius* (L.) Link and *Genista monspessulana* (L.) L.A.S. Johnson in areas where there was once only native vegetation. The native vegetation in the Adelaide Hills is typically open eucalypt woodland with a dense understorey of native shrubs. The dominant eucalypt species in these nutrient poor environments include *Eucalyptus obliqua*, *E. baxteri* and *E. cladocalyx*. Understorey species are dominated by sclerophyllous shrubs, native grasses and wildflowers. Broom often forms a monoculture within native woodland, and therefore directly affects the diversity of plants. However, the effects on the invertebrate fauna in these areas is less visible. Terrestrial arthropods are particularly well suited as target organisms to assess such environmental impacts because they: 1) are easily sampled by cost effective means 2) occur in great abundance in almost every type of habitat 3) have high species richness 4) have differing responses to environmental impacts 5) are vital in ecosystem function by filling a diverse array of niches.

The arthropod communities in stands of broom were compared with those in adjacent areas of native vegetation. These communities were represented by the target groups Formicidae (ants), Coleoptera (beetles) and Araneae (spiders) which were collected by netsweeping, visual searching and pitfall trapping in standardised sampling plots at Cleland National Park and Deep Creek Conservation Park from September to October 1998.

Overall, there were no obvious differences in abundance and species richness of the three target groups between broom and native habitats. However, compositional analysis of the ant, beetle and spider communities revealed highly distinctive communities were present at each site. More 'rare' species existed in the native habitats, compared with the broom stands. The foliage arthropod community showed greater overlap between broom and native plots than for ground-living species, particularly for the spider communities where there were more unique species in native habitat. Functional group analysis of the three target groups revealed similarities in spider community structure and distinctive ant and beetle community structure between broom and native.

The results from this study suggest that open woodland arthropod communities are affected by the invasive weed broom. This project also highlights the importance of looking beyond numerical measures such as species richness and abundance to assess and compare diversity in contrasting habitats.

Benthic biodiversity on seamounts

Steve O'Shea, Belinda Alvarez and Malcolm Clark

National Institute of Water and Atmospheric Research (NIWA), PO Box 14-901, Kilbirnie, New Zealand

Seamounts are volcanic features that rise steeply from the sea floor to below sea level, with relief of over 1000m. 'Knolls', 'pinnacles' and 'hills' are similarly steep but of lesser magnitude. Collectively these features here are referred to as seamounts, and are recognised as being highly productive features often supporting unusual and unique faunas. They are also the focus of intense fishing effort.

With about 800 such structures currently recognised, seamounts are common submarine features around New Zealand. Their variable size, age and origin reflects their long and complex geological history. Of primary concern is the extent of fishing effort on these features * an activity that potentially, detrimentally impacts the associated benthic communities which in general are characterised by large sessile, long-lived species.

Here we report preliminary findings on species richness, composition and biogeography of invertebrate assemblages associated with these features around New Zealand. The data is based on faunas retained from 108 commercial trawls on 21 seamount features with relief greater than 100 m. To date 169 macro-epifaunal invertebrate taxa have been recognised, comprising: antipatharians (black corals, 18 spp.); gorgonians (sea fans, 37 spp); scleractinians (hard corals, 6 spp); crustaceans (30 spp.), including anomurans, barnacles and brachyurans; molluscs (18 spp.) including cephalopods, gastropods and chitons; and echinoderms, including echinoids (sea egg, 9 spp.), asteroids (starfish, 15 spp.), holothurians (sea cucumber, 4 spp.), crinoids (sea lily, 6 spp.), and ophiuroids (brittle starfish, 29 spp.). At least 8 species of less common groups including sponges, bryozoans and zooanthids were also present.

Many of these species represent new records for New Zealand and/or science, with many also appearing endemic to seamount environments. However, as the level of taxonomic expertise required for identification to species is in many instances limited, conclusions regarding the full level of endemism cannot presently be drawn. Moreover, the present samples consist entirely of commercial-fisheries trawl bycatch, a sampling regime biased towards megabenthos retention. It is likely that recognised levels of endemism are underestimated, especially if smaller-bodied taxa are taken into consideration.

Presence/absence species data were analysed using hierarchical agglomerative clustering, with group-average sorting of Bray-Curtis similarity coefficients. Species occurring on one seamount or station only have been excluded from the analysis. The results indicate low (< 50%) levels of species similarity amongst the surveyed seamounts, suggesting they host very distinct assemblages of benthic invertebrates.

The results obtained from this preliminary study indicate that seamount communities around New Zealand support a high diversity of taxa and levels of endemism, in addition to distinct assemblages of taxa. Their biogeography and ecology need to be studied in more detail to enable sound management strategies to be formulated to ensure appropriate levels of protection are afforded to these environments from commercial activities such as deep-sea bottom trawling.

Dung beetles and Far North Queensland biogeography—deep history ?

Chris Reid, Ian Reid and Peter Cranston

CSIRO Entomology, GPO Box 1700, Canberra, Australian Capital Territory 2601

Invertebrates are numerically dominant organisms in rainforest. Although the exact diversity may be unknown (perhaps unknowable), study of speciose and taxonomically well-known invertebrate taxa in rainforest can provide clues for origin, history and maintenance of rainforest assemblages. The scarabaeine dung beetles fulfil the criteria of diversity and taxonomic tractability, with the endemic / Austro-Papuan genera *Coptodactyla*, *Amphistomus* and *Temnoplectron* providing a large data set for predominantly rainforest species.

Morphological phylogenies of these produced by Chris Reid postulate both radiations from dry sclerophyll forest into rainforest (*Amphistomus*) and from rainforest into drier forest (*Coptodactyla*). Within the three genera almost three quarters of all sister-species pairs have separate non-overlapping ranges. Many species are narrow endemics, including cases where close relatives occur on isolated high altitude areas, often associated with loss of wings. Other species pairs are of widespread but non-overlapping taxa.

Predictive modelling (using the program DOMAIN) of the distribution of suitable (bioclimatically matching) environments of these sister-species pairs revealed two patterns:

1. each species fills its potential distribution, and the conditions for one sister are unsuitable for the other;
2. each species is predicted to occupy much of the observed range of its sister.

These different patterns allow discrimination between different models of speciation (allopatric *vs* other): thus when the boundary between sisters coincides with a known range disruption—a postulated vicariance event—type 2 appears likely to be due to allopatric speciation, without subsequent ecological divergence.

The most obvious types of disruptions are gaps of dry habitat between rainforest, although these may not be obvious in the current landscape because the rainforest is more extensive and continuous than in earlier, more arid periods. In some scarabaeine sister-species the ecological or geographical barrier has disappeared, yet the species remain allopatric but adjacent to within 5 kilometres, retaining the historic signal. No hybrids have been identified from morphology for any of the sister-species. For type 1 modelled distributions, ecological speciation cannot be discounted, with each component subsequently tracking its different, most-favoured climate around the landscape as it changes with time.

Interactive keys to the grasses of Australia

Donovan Sharp[1], Bryan Simon[1] and Derek Clayton[2]

with contributions by Peter Bostock[1], Will Smith[1] and Mike Dallwitz[3]

[1]Queensland Herbarium, Toowong, Queensland 4066 (Donovan.Sharp@env.qld.gov.au)

[2]Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AB, England

[3]CSIRO Division of Entomology, Canberra, Australian Capital Territory 2601

Grass identification is notoriously difficult. Our aim is to produce an interactive key to Australian grasses that is reliable and easy to use by the non-specialist. The interactive key will be available in the LuCID format as well as in INTKEY. An Australian subset of the Clayton world grass database scored for morphological data in DELTA format was created. From this initial set quality control of the data has been undertaken by a check of the Clayton characters against those from other sources, including manuscripts for the *Flora of Australia* grass volumes. Extra characters considered more easily interpreted by non-specialists have been inserted in addition to those based on classification and geography. All genera and 80% of species are represented by scanned images of published illustrations, herbarium specimens, habit and habitat photos and distribution maps. The Australian grass database presently comprises 1307 species and 238 characters. Examples of outputs from both packages are shown in the poster.

Karstic groundwater ecosystems in the Murray Darling and Otway Groundwater Basins

Andy Spate[1], Jane Gough[1] and Mia Thurgate[2]

[1]NSW National Parks and Wildlife Service, P O Box 2115, Queanbeyan , New South Wales 2620

[2]Jenolan Caves Trust, PO Box 1495, Bathurst, New South Wales 2795

Small, impounded, karstic aquifers are found widely on the western fall of the Eastern Highlands. Many of the aquifers support highly significant, but little studied, invertebrate faunas. Based on geological considerations, the Otway Groundwater Basin is part of the Murray Darling Groundwater Basin. In the Otway Basin, around Mount Gambier and to the southern coast, there are very many groundwater dependent ecosystems evident. Nothing is known about possible ecosystems in the Murray Group limestones underlying the Late Miocene to Quaternary sediments in the lower parts of the Basin.

This poster discusses aquatic karst ecosystems within the impounded karsts of the NSW portion of the Murray Darling Basin and the major karst province of the Otway Basin. These ecosystems are significant as centres of biodiversity for extant stromatolite communities and for subterranean fauna. Freshwater amphipod and syncarid faunas are particularly diverse within the karst groundwaters of these ecosystems. The Wellington Caves aquifer in particular has many values including a significant and diverse, endemic aquatic invertebrate fauna and is considered worthy of recognition as a RAMSAR site. Some potential threats to these important ecosystems are identified in this poster, and some potential research directions are canvassed. The poster also briefly discusses the presence of hyporheic systems.

Grasshopper assemblages in natural temperate grasslands of differing native plant diversities

Claire Stephens

Division of Botany and Zoology, Australian National University, Canberra, Australian Capital Territory 0200

Current address: Department of Applied & Molecular Ecology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, South Australia 5064

Natural temperate grasslands form an endangered ecological community in the Australian Capital Territory (ACT). The grassland sub-communities found in the region have different conservation values based on native and exotic plant diversity. It is not known, however, if invertebrate biodiversity can be compared with the conservation value of grassland sub-communities based on floristic diversity and, as little is known about most invertebrate species in these grasslands, management often occurs without detailed knowledge of the species present or their specific habitat requirements. This poster outlines research which identified and compared the grasshopper (Orthoptera: Acrididae) assemblage composition of grassland sub-communities with differing native plant diversities and investigated the relationship between food plant preference and grasshopper occurrence.

Sixteen grasshopper species from three subfamilies were identified from *Danthonia* (high native plant diversity) and *Stipa* (low native plant diversity) grasslands. Grasshopper species richness did not differ between grassland types and there were no correlations evident between native plant diversity and grasshopper diversity. However, two different grasshoppers assemblages, characterised by the abundance of different species, could be identified from *Danthonia* and *Stipa* grasslands. Grasshopper dietary preference was related to subfamily membership and there is evidence that subfamily dietary preference for forbs or grasses may be correlated with the subfamily species composition in the natural temperate grasslands studied. In general, however, the abundance of most grasshopper species did not correlate with the abundance of potential food-plants (forbs or grasses), suggesting selectivity for particular plant species rather than general foraging for either forb or grass species. As there were no direct correlations between native plant diversity and grasshopper diversity, further investigation is required to determine food-plant species and other microhabitat factors effecting grasshopper abundance. This study highlights the difficulty in using plant species richness and associated conservation values as a surrogate for invertebrate biodiversity, particularly if invertebrate abundance and community composition are not considered.

Systematics and distribution of micro-flea wasps: *Baeus* spp. (Insecta: Hymenoptera: Scelionidae) in Australia

Nicholas Stevens and Andy Austin

Department of Applied and Molecular Ecology, The University of Adelaide, Waite Campus, Glen Osmond, South Australia 5064

The cosmopolitan genus *Baeus* Haliday are a monophyletic group of obligate endoparasitoids of spider eggs. *Baeus* exhibits extreme levels of sexual dimorphism which has hampered recognition at the species level of male and female conspecifics. Because of this, most taxonomic work has concentrated on females. This study revised the taxonomy of Australian *Baeus*, investigated the evolutionary relationships among species using parsimony methods, and documented and assessed their distribution patterns.

Because members of *Baeus* are very small (approximately 0.5-1.0 mm), scanning electron microscopy was extensively employed to elucidate micro-characters important at the species level. Prior to this study only 20 species had been described world-wide, including three from Australia. This study recognised 17 new Australian species. Forty-four morphological characters were used to investigate the phylogenetic relationships among species. Although the level of homoplasy in the data set was high, the derived strict consensus tree showed unequivocal support for a number of clades.

Australian *Baeus* species were found to be distributed mainly within the peripheral mesic environments of the continent, a pattern also exhibited by their hosts. Only two species were recorded from the semi-arid interior. The eastern seaboard of Australia, from northern Queensland to southern New South Wales, exhibited the greatest species richness. The Kosciuskan and Tasmanian biogeographical subregions had the highest levels of endemism, 42% and 40% of species, respectively.

This study has shown that *Baeus* is more speciose than was previously estimated. There is no doubt that further collection and examination of material will yield additional species given that numerous species are known from only a single or a few specimens, and that many parts of the continent have been inadequately surveyed.

Diversity associated with fly (Diptera: Fergusoninidae) and nematode (Nematoda: Sphaerulariidae) galls on Myrtaceae

Gary Taylor, Andy Austin and Kerrie Davies

Department of Applied & Molecular Biology, Waite Campus, The University of Adelaide, PMB 1, Glen Osmond, South Australia 5064

In a unique symbiotic association, flies of the genus *Fergusonina* (Diptera: Fergusoninidae) and nematodes of the genus *Fergusobia* (Tylenchida: Sphaerulariidae) lead to the formation of galls on various species of Myrtaceae. Galls have been recorded from *Eucalyptus*, *Angophora*, *Corymbia*, *Melaleuca*, *Leptospermum* and *Syzygium*. On *Eucalyptus*, gall morphology is species-specific and can vary from unilocular spherical, axial leaf bud or leaf-tip pea galls to multilocular axial or terminal leaf bud galls, or multilocular flat leaf or flower bud galls.

At oviposition, which is invariably into meristematic tissue, the female fly also deposits juvenile nematodes. Galls develop rapidly, apparently in response to nematode secretions. Fly eggs hatch later and larvae burrow into gall tissue and form cavities within the developing gall. Nematodes then migrate to, and pass through several generations within the cavity of the gall. At or near pupariation, a number of female nematodes enter female flies, migrate to the fly's ovaries, and produce large numbers of eggs. These hatch and juvenile nematodes are again deposited into fresh leaf tissue when the adult fly emerges from the gall and disperses. The essence of the fly/nematode symbiosis is that the fly is dependant on the nematode for gall induction and the nematode is reliant on the fly for dispersal. Fly larvae are unusual in that they have a curiously shaped sclerotised structure termed the dorsal shield which, depending upon species, varies from a series of raised ridges or spicules to a broad plate with prominent, forward projecting spines. The purpose of this structure is unclear but may be used as a scraper to enlarge the gall cavity, perhaps to provide a pelletised food source for the nematodes, or to anchor the fly larva in the gall while feeding. In leaf bud galls the adult fly generally emerges from a tunnel cut from the gall cavity to just under the outer surface. In flower bud galls, fly emergence is apparently synchronised with the dehiscence of the operculum.

Fly/nematode galls are utilised by a complex guild of associated insects. In this study parasitoids and inquilines from galls on *Eucalyptus* were reared from field collected material. Galls were dissected in an attempt to elucidate the biology of gall inhabitants, and specimens associated with *Fergusonina* galls held in various collections were examined. Of the phytophagous inquilines, a total of three species of Coleoptera and two Lepidoptera were recorded. One species of *Thysanoptera* (thrips) was found sheltering in vacated fly cavities. By far the most abundant assemblages were the Hymenoptera with 21 species of parasitoids and commensals recorded. Emergence times of parasitoids and inquilines varied in comparison to emergence of the primary gall former, and larger galls tended to support more diverse assemblages.

Of the beetles, *Corticaria* sp. (Lanthridiidae) feeds on fungal spores in old galls, *Dryophilodes* sp. (Anobiidae) tunnels in dried woody galls reducing them to a brittle shell, and the weevil, *Haplonyx spencei* forms external crypts in which they feed. The moths *Palaeotoma styphelana* and *Strepsicrates macropetana* form tunnels in fresh galls, and undoubtedly reduce the viable fly population of the gall.

The biology of gall-associated Hymenoptera is fundamentally complex and often it is extremely difficult to elucidate the true relationships of species. Galls may contain a range of biologically different Hymenoptera, i.e. primary parasitoids, facultative and obligate hyperparasitoids, cecidogenic commensals and inquilines of which the biology is particularly difficult to unravel. For example, cavities containing parasitoid larvae which contain the sclerotised dorsal remains of *Fergusonina* fly larvae may indicate primary parasitism, or perhaps hyperparasitism where the primary parasite has been completely consumed.

Despite belonging to a family which is almost invariably parasitic, but on the basis of the structure of the larval mandible, *Poecilocryptus galliphagus* and *P. nigromaculatus* (Ichneumonidae) are clearly phytophagous. The Braconidae are represented by *Bracon fergusoninus* (a primary ectoparasitoid of the fly), and five undetermined species in at least three subfamilies (Agathidinae, Braconinae and Doryctinae). *Eurytoma* sp. (Eurytomidae), *Bootanelleus* sp., two species of *Megastigmus* sp. (Torymidae), *Ditropinotella* sp., *Coelocyba nigrocincta*, an undetermined pteromalid (Pteromalidae), *Cirrospilus* sp., *Euderus* sp. and an undetermined eulophid (Eulophidae) are all likely to be primary parasitoids or obligate or facultative hyperparasitoids of species of *Fergusonina*. The biology of *Ceraphron* sp. (Ceraphronidae) and an undetermined species of Encrytidae could not be confirmed. A single species in an undetermined genus (Bethylidae) is a probable parasitoid of the beetle, *Dryophilodes* sp.

Cavities containing parasitoids were almost always close to the surface of the gall. Fly larvae deep within the gall were generally free of parasitism, but were presumably more likely to be affected by the four species of phytophagous inquilines (*Poecilocryptus* spp., or the two tortricids) which tunnel deep within live galls. Undoubtedly, their feeding creates enlarged cavities within the gall, but it is uncertain whether they feed indiscriminately on gall tissue and fly larvae. Certainly they would reduce gall biomass and therefore indirectly reduce the carrying capacity of the gall. Large galls could contain up to c. 200 individual flies and up to ca. 140 hymenopteran parasitoid inquilines. Data from this study indicate that, following emergence of flies and parasitoids, galls are able to support perhaps up to two generations of *Dryophilodes* sp., with up to ca. 70 individuals from larger galls belonging to the same generation. These figures indicate it is possible for larger galls (up to c. 50 mm in length by 20 mm in diameter), to support in excess of 400 individual insects.

This study summarises our current knowledge of the guild of parasitoids and inquilines associated with *Fergusonina* galls on *Eucalyptus*, and discusses similarity with other complex biological systems.

The impact of the Argentine ant (*Linepithema humile*) on surface-active invertebrates in urban parkland

Ian Wyndham and Megan Short

Deakin University, Rusden campus, 662 Blackburn Rd, Clayton, Victoria 3168

The Argentine ant (*Linepithema humile*) was first recorded in Melbourne, Victoria, over 60 years ago and is now widespread throughout the urban area. Its presence in urban parkland appears to be patchy with a study in the suburb of Blackburn showing that while *L. humile* was not recorded in 13 months of pitfall sampling at a number of sites in one park, it was found in abundance at sites in a park nearby.

Pitfall traps were used to investigate the impact of *L. humile* on surface-active invertebrates in an urban park partially infested with the introduced ants. Invertebrates collected from traps in infested areas were compared with those collected from traps placed in uninfested areas. A marked reduction in the number of ant species was found wherever *L. humile* was present. In particular the two opportunistic species *Rhytidoponera victoriae* and *Rhytidoponera tasmaniensis* were absent despite being common elsewhere in the areas of the park where there was no infestation of *L. humile*. Other ant species were severely reduced in abundance in infested areas including the Dolichoderine genera *Iridomyrmex*, *Doleromyrma* and *Ochtellus*.

In contrast, non-ant invertebrate species captured in the pitfall traps did not appear to be adversely affected by the presence of *L. humile*, indicating that they interact with introduced ant species in a similar fashion to native ant species.

This study confirms that *L. humile* is likely to have a devastating effect on the native ant fauna wherever it has successfully established. The impact of this introduced species on overall ecosystem function requires further study, especially in the light of attempts being made to maintain local biodiversity by restoring remnants of indigenous vegetation in many of our urban parks.

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