ENTOMOLOGICAL SOCIETY OF QUEENSLAND INC

NEWS BULLETIN

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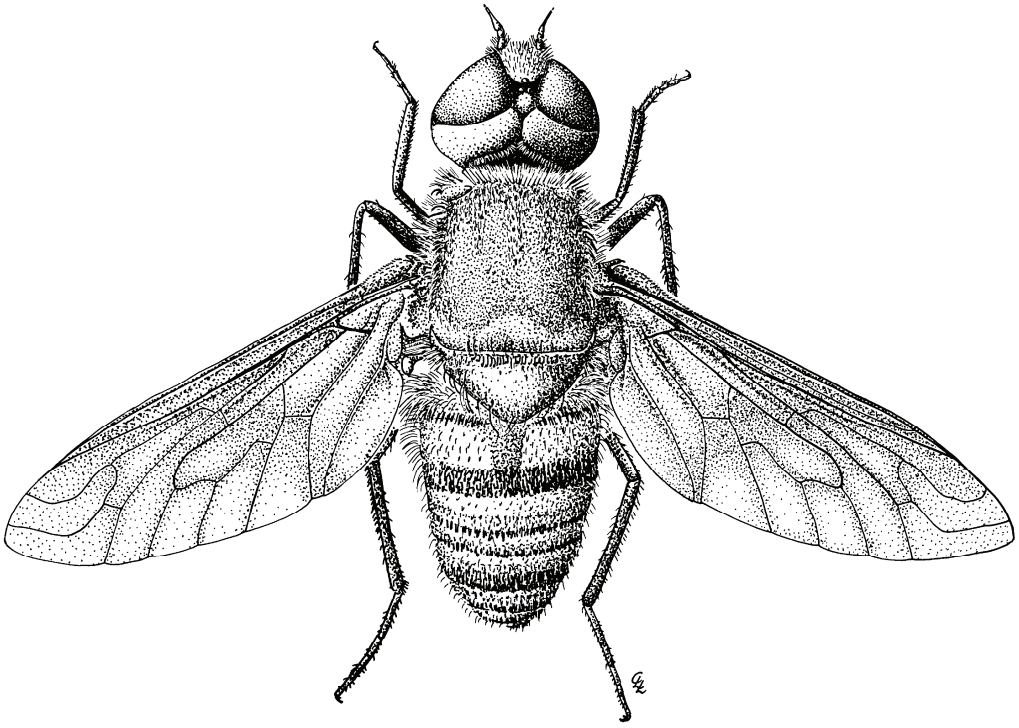

Volume 37, Issue 2, April 2009

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The **ENTOMOLOGICAL SOCIETY OF QUEENSLAND INC.**, since its inception in 1923, has striven to promote the development of pure and applied entomological research in Australia, particularly in Queensland. Membership is open to anyone interested in Entomology. The Society promotes liaison among entomologists through regular meetings and the distribution of a *News Bulletin* to members. Meetings are announced in the *News Bulletin*, and are normally held on the second Monday of each month (March to June, August to December), or on Tuesday if Monday is a public holiday. Visitors and members are welcome. Membership information can be obtained from the Honorary Secretary, or other office bearers of the Society.

Contributions to the *News Bulletin* such as items of news, trip reports, announcements, etc are welcome and should be sent to the News Bulletin Editor.

The Society publishes **THE AUSTRALIAN ENTOMOLOGIST**. This is a refereed, illustrated journal devoted to Entomology in the Australian region, including New Zealand, Papua New Guinea and the islands of the South Western Pacific. The journal is published in four parts annually.

EMBLEM: The Society's emblem, chosen in 1973 on the 50th anniversary of the Society, is the king stag beetle, *Phalacrognathus muelleri* (Macleay), family Lucanidae. Its magnificent purple and green colouration makes it one of the most attractive of all Australia Coleoptera. It is restricted to the rainforests of northern Queensland.

COVER: Habitus of ***Atrichochira commoni*** Lambkin & Yeates 2003 by Chris Lambkin. Invertebrate Systematics 17:p854.

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The Entomological Society of Queensland
Minutes of General Meeting April 14, 2009

Held in the Large Conference Room, CSIRO Entomology, Long Pocket Labs, 120 Meiers Road, Indooroopilly, on Tuesday April 14th, 2009, 12.00 midday.

The meeting was chaired by President, Chris Lambkin.

Attendance: Justin Bartlett, Felix Bianchi, Bradley Brown, Lyn Cook, Gio Fichera, Regis Goebel, Lynita Howie, Chris Lambkin, Anna Marcora, Gunter Maywald, Penny Mills, Lindsay Popple, Matt Purcell, Don Sands, Nancy Schellhorn, Noel Starick, Desley Tree

Visitors: Karen Bell, Nate Hardy, Greg Harper, Juan A. Villanueva-Jimeanez

Apologies: Richard Bull, Mike Furlong, Ross Kendall, Geoff Monteith, Geoff Thompson, Belinda Walters, Richard Zietek

Minutes: The minutes of the last General Meeting of December 2008, were circulated in the News Bulletin Vol. 36, Issue 9, 2008.
Any business arising from those minutes?

Moved the minutes be approved: Desley Tree
Seconded: Justin Bartlett

Membership Nominations and Elections:
No nominations were received.

General Business

Chris Lambkin informed members that the member Lindsay Barton-Brown had died at the end of March, and briefly described his entomological history.

Chris Lambkin reminded members that the closing date for applications for the Student Award was Friday April 19, and encouraged any member who knew of a student completing Honours, Postgraduate Diploma,

or Fourth Year project in Entomology in a Queensland institution to suggest they apply. Details in the Bulletin.

Chris Lambkin asked members who had topics to discuss at the June Notes and Exhibits to contact Council members.

Main Business

The Chairperson welcomed Nate Hardy who completed his PhD with Penny Gullan at the University of California, Davis in 2008, and was the recipient of several prizes for his thesis work, and invited him to address the meeting on: "Mealybug Classification and Endosymbiosis"

Mealybug Phylogeny and Endosymbiosis

Nate Hardy
Queensland Primary Industries and Fisheries Entomology Collection, 80 Meiers Road, Indooroopilly, Qld 4068

Entomologists who appreciate insects as aesthetic entities may find mealybugs hard to love, but in terms of their relationships with other organisms, mealybugs are fascinatingly complex. Mealybugs are phloem-feeding plant parasites. Because they are sessile, the relationship between mealybug and host can be described as intimate. Because phloem is protein poor, mealybugs need the help of endosymbiotic microorganisms to synthesize amino acids. Because mealybug excreta are sweet, mealybugs often enter into mutualistic exchanges with other arthropod species, especially social Hymenoptera. Most care about mealybugs for another reason: many species are devastating agricultural pests.

Mealybugs get their name from powdery secretions that cover the bodies of the immature stages and adult (paedomorphic) female. Mealybugs are found world-wide, and feed on a great diversity of plant hosts. Some of the cosmopolitan pest species are extremely polyphagous; for example, the long-tailed mealybug *Pseudococcus longispinus* (Targioni Tozzetti) has been recorded from more than 85 families of vascular plants (Ben-Dov, 2007).

Nearly 2000 species of mealybugs have been described and placed in 279 genera. Five subfamily names have been proposed for mealybugs: Pseudococcinae, Phenacoccinae Šulc, Rhizoecinae Williams, Trabutininae Silvestri, and Sphaerococcinae Cockerell. Authors have applied various combinations of these names to various ranks, and none are very popular, in part owing to the inadequate definition of groups, in terms of either their generic composition or their diagnostic morphology.

Downie & Gullan (2004) inferred the mealybug phylogeny using DNA sequence data from three nuclear genes from 64 species. They recognized only three subfamilies, Rhizoecinae, Phenacoccinae, and Pseudococcinae, and within the Pseudococcinae recognized the tribes Pseudococcini, Planococcini and Trabutinini. Excepting the Trabutinini, none of these groupings were well supported, i.e. none had ≥95% Bayesian posterior probability or ≥70% parsimony bootstrap support in analyses of the combined data. Furthermore, the Rhizoecinae and the Phenacoccinae were under-sampled, and the type genera of the Trabutinini (*Trabutina* Marchal), and Sphaerococcinae (*Sphaerococcus* Maskell) were not included.

To improve our estimate of the mealybug phylogeny, PJ Gullan, CJ Hodgson and I did the following: (i) added DNA sequence data from an additional 33 species to the analysis, including *Trabutina mannipara* (Hemprich & Ehrenberg), the type species of *Sphaerococcus*, *S. casuarinae* (Maskell), and a number of putative members of the Rhizoecinae and Phenacoccinae, one of which [*P. aceris* (Signoret)] is the type species of *Phenacoccus*; (ii) added a morphological dataset with characters from adult females, adult males and first-instar nymphs; and (iii) performed partitioned model-based inference procedures. We also created the first useful subfamily-level classification by: (i) identifying morphological features, especially of the adult female, that can be used to diagnose the subfamilies; and (ii) providing a list of all genera included in each subfamily.

We reconstructed phylogenies using maximum parsimony (MP), Bayesian, and maximum likelihood (ML) inference methods. For the model-based inferences, the data were partitioned by data type (DNA and morphology), by gene, and by codon position for Ef-1α. The mk1 model, with gamma-distributed rates and coding set to variable, was applied to the morphological dataset. A general time reversible nucleotide substitution model (GTR) with gamma distributed among-site rate variation (+ γ) was applied to each DNA partition. Support for the optimal topology was estimated with non-

paramentric bootstrapping, for MP and ML analyses, and by calculating the posterior probabilities (PP) for each node, for Bayesian analyses. The Majority rule consensus tree with support values is shown in Figure 1.

We recovered two primary clades within the Pseudococcidae: moderate support (94% PP) for the Downie & Gullan (2004) concept of Pseudococcinae, and strong support (100% PP) for a clade comprising the hypogaeic mealybug genera *Geococcus* Green, *Neochavesia* Williams & Granara de Willink, and *Rhizoecus* Künckel d'Herculais plus a number of additional genera including *Phenacoccus* Cockerell and *Rastrococcus* Ferris. Feeling good about the support for our tree, we advanced a new concept of the subfamily name Phenacoccinae by including the hypogaeic mealybugs as a subclade. The monophyly of the hypogaeic mealybugs was strongly supported (100% PP), and we applied the tribal name Rhizoecini to this group.

Surprisingly, mealybug subfamilies can be most reliably distinguished on the basis of a pair of rather unremarkable tarsal characters. Phenacoccine mealybugs have a denticle on each claw, and tarsal digititules with fine apices. Pseudococcine mealybugs have claws without denticles, and tarsal digitules with expanded apices. Phenacoccines also tend to have quinquelocular pores and nine-segmented antennae, but these features are also found in some pseudococcine species. We used our diagnostic features to predict the subfamily placement of each mealybug genus not represented in our analysis. The morphology of the type species of each genus was assessed either by examination of type material, or, as was most often the case, with published descriptions. We placed 69 genera in the Phenacoccinae, and 201 genera in Pseudococcinae, leaving 9 genera as *incertae sedis*.

We sought phylogenetic trends in mealybug biogeography and host use. We found next to none. What we did notice was that the two mealybug subfamilies had very different microbial ecologies.

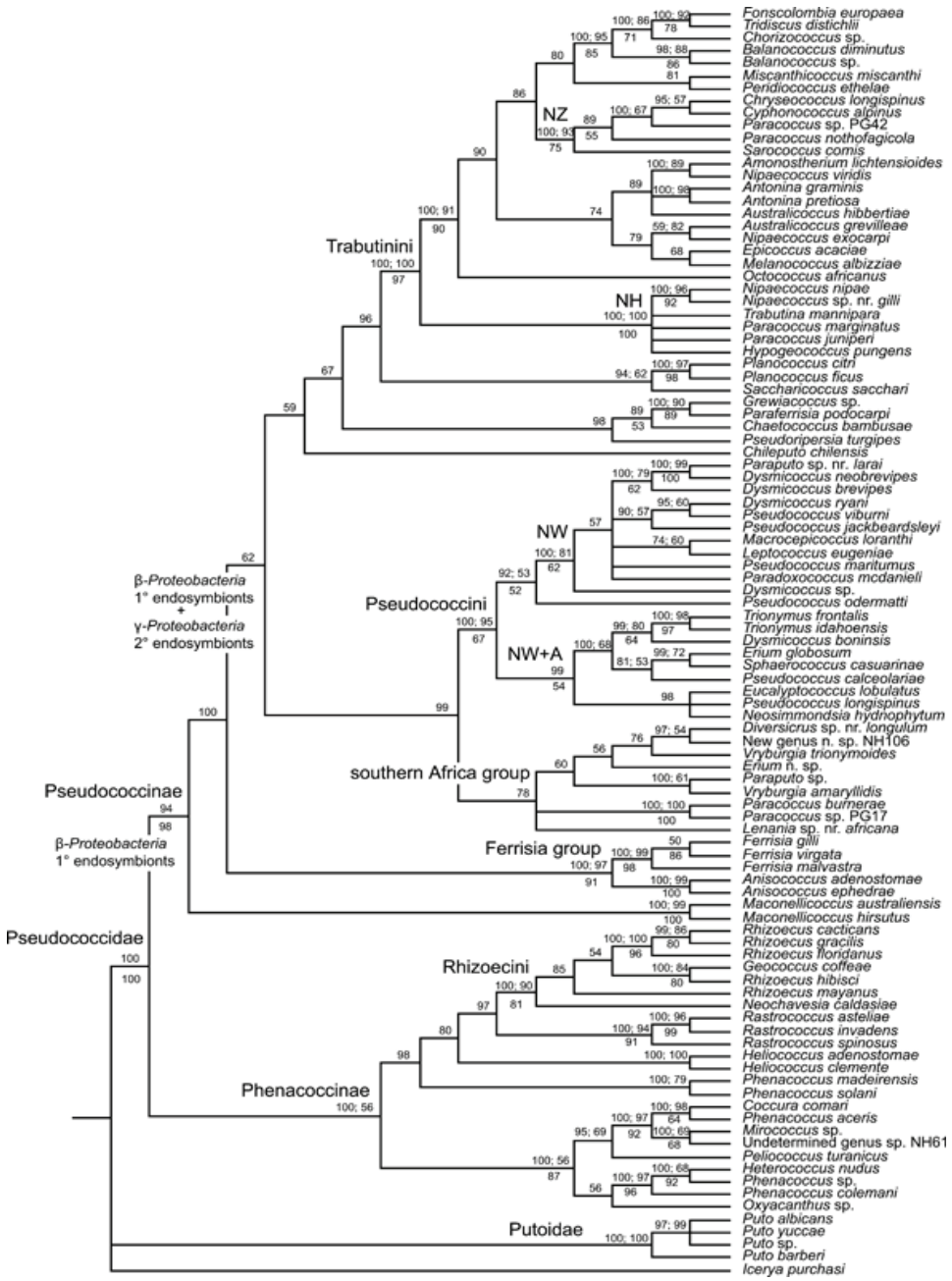
Many mealybugs are unusual in having γ-Proteobacteria secondary endosymbionts residing within primary β-Proteobacteria endosymbionts (most insect endosymbionts are γ-subdivision). Using 16S–23S ribosomal DNA sequence data to infer the phylogenies of the primary and secondary endosymbionts of 22 mealybug species, Thao et al. (2002) found that: (i) the primary endosymbionts formed a monophyletic group; (ii) the primary endosymbionts had been infected multiple times by different precursors of the secondary endosymbionts; and (iii) the primary endosymbiont phylogeny seems to reflect the

mealybug phylogeny. The strength of this last conclusion was limited by a mealybug phylogeny with only four taxa. Downie & Gullan (2005) compared the primary endosymbiont phylogeny with a mealybug phylogeny inferred from a multi-gene dataset of 21 of the 22 mealybug hosts of the primary endosymbionts examined by Thao et al. (2002), and found strong phylogenetic congruence. All mealybug species included in the aforementioned endosymbiont studies are members of the subfamily Pseudococcinae.

In his monumental histological work, Buchner (1965) examined the endosymbionts of numerous scale insects, including ca 20 mealybug species. Buchner observed that the mycetome of all species in genera that we place in the Pseudococcinae contains mucous spherules [now known to correspond to the primary β-Proteobacteria endosymbionts characterized by von Dohlen et al. (2001)], and that the mycetome of all species in genera we have placed in the Phenacoccinae, including Rhizoecini, lack mucous spherules. Thao et al. (2002) were unable to find secondary symbionts in Ferrisia and Maconellicoccus, although their primary endosymbionts are related to those found in other pseudococcines in their analysis. Thus within the Pseudococcinae, there is a clear sequence of (i) infection by β-Proteobacteria primary endosymbionts, followed by (ii) infection (or multiple infections) of the primary endosymbionts by γ-Proteobacteria secondary endosymbionts (Fig. 1). Matt Gruwell's unpublished DNA sequence data from phenacoccine endosymbionts support this scheme.

In conclusion, from our phylogenetic studies of meaybugs we can infer that endosymbiosis has played a fundamental role in mealybug diversification – perhaps even more significant than host interactions or biogeography. Our classification reflects these important differences in biology. The results of this study were published in Hardy et al. (2008).

Figure 1 (right): a) Majority rule consensus tree resulting from Bayesian analysis of combined DNA sequence and morphological data. Nodal support indicated by posterior probabilities (above left); ML bootstrap proportions (above right); and parsimony Figure 1: a) Majority rule consensus tree resulting from Bayesian analysis of combined DNA sequence and morphological data. Nodal support indicated by posterior probabilities (above left); ML bootstrap proportions (above right); and parsimony the posterior probability. Names of clades discussed in the body of the text appear above nodes. Abbreviations: NH, Northern Hemisphere; NW, New World; NW + A, New World plus Australia; NZ, New Zealand. Below two nodes we have shown the type of endosymbionts believed to be associated with each clade.


Fonscolombia europaea
Tridiscus distichlii
Chorizococcus sp.
Balanococcus diminutus
Balanococcus sp.
Miscanthicoccus miscanthi
Peridiococcus ethelae
Chryseococcus longispinus
Cyphonococcus alpinus
Paracoccus sp. PG42
Paracoccus nothofagicola
Sarococcus comis
Amonostherium lichtensioides
Nipaecoccus viridis
Antonina graminis
Antonina pretiosa
Australicoccus hibbertiae
Australicoccus grevilleae
Nipaecoccus exocarpi
Epicoccus acaciae
Melanococcus albizziae
Octococcus africanus
Nipaecoccus nipae
Nipaecoccus sp. nr. gilli
Trabutina mannipara
Paracoccus marginatus
Paracoccus juniperi
Hypogeococcus pungens
Planococcus citri
Planococcus ficus
Saccharicoccus sacchari
Grewiacoccus sp.
Paraferrisia podocarpi
Chaetococcus bambusae
Pseudoripersia turgipes
Chileputo chilensis
Paraputo sp. nr. larai
Dysmicoccus neobrevipes
Dysmicoccus brevipes
Dysmicoccus ryani
Pseudococcus viburni
Pseudococcus jackbeardsleyi
Macrocepicoccus loranthi
Leptococcus eugeniae
Pseudococcus maritumus
Paradoxococcus mcdanieli
Dysmicoccus sp.
Pseudococcus odermatti
Trionymus frontalis
Trionymus idahoensis
Dysmicoccus boninsis
Erium globosum
Sphaerococcus casuarinae
Pseudococcus calceolariae
Eucalyptococcus lobulatus
Pseudococcus longispinus
Neosimmondsia hydniophytum
Diversicrus sp. nr. longulum
New genus n. sp. NH106
Vryburgia trionymoides
Erium n. sp.
Paraputo sp.
Vryburgia amarylidis
Paracoccus burnerae
Paracoccus sp. PG17
Lenania sp. nr. africana
Ferrisia gilli
Ferrisia virgata
Ferrisia malvastra
Anisococcus adenostomae
Anisococcus ephedrae
Maconellicoccus australiensis
Maconellicoccus hirsutus
Rhizoecus cacticans
Rhizoecus gracilis
Rhizoecus floridanus
Geococcus coffeae
Rhizoecus hibisci
Rhizoecus mayanus
Neochavesia caldasiae
Rastrococcus asteliae
Rastrococcus invadens
Rastrococcus spinosus
Heliococcus adenostomae
Heliococcus clemente
Phenacoccus madeirensis
Phenacoccus solani
Coccura comari
Phenacoccus aceris
Mirococcus sp.
Undetermined genus sp. NH61
Peliococcus turanicus
Heterococcus nudus
Phenacoccus sp.
Phenacoccus colemani
Oxyacanthus sp.
Puto albicans
Puto yuccae
Puto sp.
Puto barberi
Icerya purchasi
Trabutinini
NZ
NH
NW
NW+A
Pseudococcini
southern Africa group
Ferrisia group
Rhizoecini
Phenacoccinae
Putoidae
Pseudococcinae
Pseudococcidae
β-Proteobacteria
1° endosymbionts
+
γ-Proteobacteria
2° endosymbionts
β-Proteobacteria
1° endosymbionts

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Downie, D.A. & Gullan, P.J. (2004) Phylogenetic analysis of mealybugs (Hemiptera: Coccoidea: Pseudococcidae) based on DNA sequences from three nuclear genes, and a review of the higher classification. Systematic Entomology, 29, 238–260.

Downie, D.A. & Gullan, P.J. (2005) Phylogenetic congruence of mealybugs and their primary endosymbionts. Journal of Evolutionary Biology, 18, 315–324.

Hardy, N.B., Gullan, P.J. & Hodgson, C.J. (2008) A subfamily-level classification of mealybugs (Hemiptera: Pseudococcidae) based on integrated molecular and morphological data. Systematic Entomology, 33, 51–71.

Thao, M.L., Gullan, P.J. & Baumann, P. (2002) Secondary (γ-Proteobacteria) endosymbionts infect the primary (β-Proteobacteria) endosymbionts of mealybugs multiple times and coevolve with their hosts. Applied and Environmental Microbiology, 68, 3190–3197.

Questions

Don Sands asked whether there was a symbiotic relationship between the mealybugs and the ants in the antplants found in Fiji. Nate said that mealybugs are often found in ant plants but this was one of the only two recorded mealybugs found within a Rubiaceous antplant (with *Pheidole* ants). Social hymenoptera such as ants usually gain honeydew from mealybugs, which is an advantage to the mealybugs as otherwise they must find some method of disposing of that waste before fungal attack becomes an issue, thus this could be considered an obligate symbiotic relationship.

Nancy Shellhorn asked for more information on the biology of mealybugs. Nate described the females as wingless, and even sometimes legless. The males are winged, but go through two non-feeding pupal stages, and are very weak and restricted in their movement. Essentially only exist to mate.

Nate was asked whether Wolbachia may be present in mealybugs, and he passed the question to Lyn who stated that Wolbachia was known from scale insects, but not from mealybugs.

Vote of thanks

Lyn Cook thanked Nate Hardy for demonstrating that Mealybugs are really worthy of interest.

Chairman's closing statement

The next meeting will be held at this venue on May 11th at 12.00 noon and will be a talk by Mary Whitehouse from CSIRO Entomology, Narrabri, on her research.

Correction to ESQ Bulletin Volume 36, Issue 10 (pg 275)

Re: Cricket Misidentification

The Malanda crickets mentioned in the Jan/Feb issue of the ESQ News Bulletin weren't *Gryllotaurus bicornis*. On our second trip to the tableland in March my wife and I had a closer look and thanks to Geoff Monteith the new, less tentative, ID is *Penalva flavocalceata* the White Kneed Cricket.

For interesting close-up images (not mine!) see the following web pages:

http://www.wettropics.gov.au/st/rainforest_explorer/Resources/Images/animals/invertebrates/WhiteKneedCricket.jpg

http://www.aussiepythons.com/forum/other-animals/white-kneed-king-cricket-and-mantis-duw-90209

Dr Bob Mesibov

Notice of Next Meeting

Entomological Society of Queensland

Monday 11th May, 2009 12pm

'*From Lynx Spiders to Cotton: Four Trophic Levels of Behaviourally Mediated Predator Effects*'

Mary Whitehouse

(CSIRO Narrabri)

CSIRO Long Pocket Laboratories
Large Conference Room
120 Meiers Rd, Indooroopilly

ALL WELCOME

Entomological Society of New Zealand 58th Annual Conference "Islands and Hotspots" 5-8 April 2009

The conference kicked off appropriately with a field trip to Rangitoto Island on Sunday. Peggy Herbert showed us round a restored bach, and Chris Green told us about the ambitious plan to rid the island of vertebrate pests over the coming winter months. Then we walked to the summit for lunch and amazing views over the water to Auckland City and beyond.

Rosemary Gillespie from University of California, Berkeley gave the keynote presentation of the symposium 'Hotspots and Coldspots' in which she discussed how the biota of Pacific islands reveal insights into the processes shaping species and communities over evolutionary time. Nod Kay, Scion, Rotorua, presented the novel view that island communities are well defended against exotic invasion, and suggested that the Island Resource Allocation hypothesis offers a testable alternative explanation of plant defence and ecosystem invasibility to the Equilibrium Theory of Island Biogeography.

The Island Biosecurity symposium was introduced by Dennis O'Dowd's sobering description of the devastating effects of yellow crazy ant and honeydew-secreting scale insects on communities on Christmas Island through extirpation of native red crabs. Such mutualistic behaviour between invaders leading to invasional meltdown provides urgent impetus for effective biosecurity. The broad range of papers on biosecurity topics in this symposium, with emphasis on ants, supported the seriousness of the issue.

One of the highlights of the Insect–Plant interactions symposium was Dave Kelly's fascinating story of a 22-year study of the interactions between *Chio-*

nochloa pallens and three insect herbivores. Ecki Brockerhoff's Presidential address was saved until last. He gave a thorough and insightful contemporary view of forest pests in New Zealand and overseas.

There were sixty-six participants, including 3 from the USA and 2 from Australia, and 45 paper presented (Hotspots and Coldspots, 16 papers; Island Biosecurity, 15 papers; Plant-Insect Interactions, 10 papers; Contributed Session, 4 papers) plus the Presidential Address.

News from Queensland Primary Industries & Fisheries Entomology

Shaun Winterton recently was invited to attend the annual CERF Taxonomy Research Infrastructure Network [http://www.taxonomy.org.au/] meeting in the resort town of Murramurang, NSW. This group has broad goals such as:

- Reinvigorate taxonomy in Australia
- Evaluate and road test new methodologies for research and delivery of taxonomic information for a wide range of end users
- Create and maintain a modern collaborative national electronic framework for taxonomic knowledge delivery

Shaun presented is recent research on using cybertaxonomy tools to speed the process of taxonomic description for rapid biodiversity discovery. He is using tools like Life Science Identifiers (LSIDs) to value add to taxonomic papers with web resources (e.g. Zoobank name registration and active links to image and specimen databases) in the electronic version of monographs. An important aspect of this, demonstrated at the meeting, is the promotion of the old, but now repackaged, idea of Natural Language Descriptions parsed from character matrices. Shaun showed how this can be easily done using programs like Lucid Builder, to produce sophisticated taxonomic descriptions for monographs and interactive keys (e.g. fact sheets in xml and html) at the click of a button. Moreover, this technology is more powerful the more species that are needed to be described, as the per unit time taken to produce a description is significantly shorter the more taxa that are included (good news for those working on large monographs!); on average about 1/3 of the time taken to produce a monogragh normally. Descriptions are highly standardised and the NLD output is more sophisticated than previous programs (i.e. reads better), and with flexible templates for differing journal formats. For more information on using Lucid Builder to increase your speed of taxonomic description, contact Shaun or the guys from CBIT.

News from USDA ARS Australian Biological Control Laboritory

Staff in the **USDA Weeds Group** have recently been travelling extensively conducting exploratory surveys for several projects.

Tony Wright visited Thailand in April, conducting exploration for biocontrol agents of Downey Rose Myrtle, *Rhodomyrtus tomentosa*, climbing fern, *Lygodium microphyllum* and skunk vine, *Paederia foetida*. He then met with **Jeff Makinson** in Singapore to undertake similar exploration. Jeff then travelled to Hong Kong to collect stem-boring moths on climbing fern.

In April, **Ryan Zonneveld** and **Bradley Brown** conducted surveys for biocontrol agents of climbing fern, *Casuarina* and the aquatic weed *Hydrilla verticillata*. They travelled to sites around Darwin and near Kununurra in Western Australia.

Matthew Purcell visited the US during March/April. He travelled to Portland Oregon to attend a USDA ARS Overseas Biological Control Laboratories workshop and presented a lab overview at another meeting; "Biological Control in the Western USA - W2185 Biological Control in Pest Management Systems of Plants". Matthew then travelled to Arizona to visit a weevil taxonomist, Dr. Charlie O'Brien. In Florida he met with collaborating USDA ARS scientists, inspected Australian insects under evaluation in quarantine, and visited field release sites for agents released as biocontrol agents against the paperbark tree, *Melaleuca quinquenervia*, and the climbing fern. Matthew will return to the US in early May to meet with several funding bodies in Mississippi and Florida.

The **USDA Weeds group** is looking at new potential targets, Downy Rose Myrtle and the Australian tree fern, *Cyathea cooperi*, which is becoming a serious weed in Hawaii. The long-term Melaleuca project has been highly successful with the Aussie insects providing significant control across southern Florida.

News from the Queensland Museum

Jenny Beard continues her project on the systematics of Australian flat mites (Tenuipalpidae) and in the past month visited Bruce Halliday (ANIC) in Canberra where they went collecting. She's currently collecting in the south-west of Western Australia, with special focus on mites on *Banksia*.

News from School of Biological Sciences (BIOL), The University of Queensland

First year "Biodiversity and Our Environment" students have been assisting **Robbie Wilson** collect and identify dung beetles from across Brisbane and surrounding regions as part of an ARC-funded project investigating local biodiversity. Students have been trapping beetles in their backyards before identifying specimens to species in class. You can check out a news article at http://www.uq.edu.au/news/index.html?article=17713.

Two students have joined **Sassan Asgari**'s group: **Alex Abraham**, a MSc student, and **Guoqing Toh**, an Honours student, are working on the role of small RNAs (microRNAs) on insect host-virus interactions. Sassan is organizing a symposium on "Genomic aspects of polydnavirus studies" at the Society for Invertebrate Pathology conference held in Utah in August 2009. Polydnaviruses are symbiotic viruses associated with parasitic wasps facilitating parasitisation.

Francesca Frentiu has joined the **Scott O'Neill** and **Beth McGraw** labs where she will be working on the evolution of dengue virus in two of its hosts - mosquito and human. The O'Neill lab has just begun cage trials of *Wolbachia*-infected mosquitos in Cairns, investigating survival of the mosquitos in a more natural setting than the UQ lab. The cages are constructed to be similar to the underneath of a "Queenslander" type house, with surrounding plantings, to mimic natural urban conditions.

Tom Gosden has joined **Steve Chenoweth**'s group as an ARC Linkage International Fellow (UQ and Ottawa). He will be investigating geographic variation in the mate preferences of Australian *Drosophila serrata*, having previously worked on Swedish damselflies. Two PhD candidates have also joined Steve's lab this year. **Scott Allen** will look at the genetic basis of sexual antagonism in *D. serrata*, and **Camille Latimer** will work on thermal dependence of locomotory activity in *Drosophila*.

Paul Lin (PhD student working on coccids in **Lyn Cook's** lab) has just arrived back from the US where he has been visiting the Smithsonian, and Penny Gullan and the Bohart museum in California. He has brought a swag of material back with him that should keeping him busy with the morphological and molecular systematics of Saisettini.

NEWS ITEM: Meat Ant makes meal of toads

By Rosslyn Beeby, Science and Environment Reporter

http://www.canberratimes.com.au/news/national/national/general/meat-ant-makes-a-meal-of-toads/1473966.aspx

The common and much-persecuted Australian meat ant has emerged as a surprise weapon in the war against the cane toad, according to new research.

Scientists have discovered the meat ant, *Iridomyrmex reburrus*, also called rainbow ant because of its iridescent sheen, poses little danger to native frogs but attacks cane toadlets that have emerged from the tadpole stage.

University of Sydney biologist Professor Rick Shine said, "We're talking about toadlets about 1cm long that are easy prey for the ants."

His research team noticed meat ants eating toadlets on mud around ponds and river banks in northern Australia. They observed native frogs quickly jumped out of the way to avoid ants, but cane toadlets seemed unaware of the threat they posed.

"They seemed to have no predator response. So we suspected there was a mismatch between the way the invading toads had evolved and the new territory they were invading.

"We hoped that evolutionary mismatch could lead to new opportunities for biocontrol."

Professor Shine and his research team have published their findings in the British Ecological Society's journal, suggesting it could be feasible to manipulate ant densities in places where large numbers of cane toadlets occur.

"Even slight increases in mortality rates [of cane toadlets] might cause significant reductions in cane toad populations in Australia," the paper says.

More than 200 million cane toads have spread across tropical Australia since the introduction of a small number in 1935 to control beetles infesting sugar cane crops in Queensland. The toads excrete a powerful poison which kills predators, and have caused widespread death of native wildlife across northern Australia.

Using a purpose-built runway, scientists tested the comparative sprint speed and endurance of frogs and cane toadlets. The frogs were much quicker off the mark. They were also more vigilant than cane toads, quickly jumping into the water when meat ants approached.

THE ENTOMOLOGICAL SOCIETY OF QUEENSLAND INC.

Founded 1923
Incorporated 1971

Dear Member,

Your subscription for 2009 is now due. If you haven't already paid, please mail or fax your payment to the address supplied.

Yours sincerely,

Desley Tree (Treasurer)

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Return to: Treasurer, Entomological Society of Queensland
PO Box 537, Indooroopilly QLD 4068

DIARY DATES 2009

Meetings held 2nd Monday of the month
(or Tuesday if Monday is a public holiday)

Monday March 9th	Dr Mike Furlong (UQ)	AGM & Presidential Address
Tuesday April 14th	Nate Hardy (QDPI)	Mealybug Classification
Monday May 11th	Mary Whitehouse (CSIRO Narrabri)	From Lynx Spider to Cotton
Tuesday June 9th	Student Award and Notes & Exhibits	
Monday August 10th	Perkins Memorial Lecture: Professor Gerry Cassis (UNSW) and BBQ	
Monday September 14th	Trevor Lambkin (QDPI)	
Monday October 12th	Chris Burwell (QM)	
Monday November 9th	Myron Zalucki (UQ)	
Monday December 14th	Notes & Exhibits and BBQ	

IMPORTANT NOTICE

The official address for the Entomological Society of Queensland and *Australian Entomologist* and to which all communications should be addressed is: **PO Box 537, Indooroopilly QLD 4068.**

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NOTICE OF NEXT MEETING

The next meeting of the Society will be held at **12:00 pm** on **MONDAY, 11th May 2009** in the **Large Conference Room**, **CSIRO Long Pocket Laboratories**, 120 Meiers Rd Indooroopilly. The main business will be an address by **Mary Whitehouse (CSIRO)** entitled:

'*From Lynx Spiders to Cotton: Four Trophic Levels of Behaviourally Mediated Predator Effects*"

VISITORS ARE WELCOME
(Please sign in at CSIRO reception before attending the meeting)

HONORARY LIFE MEMBERS OF THE SOCIETY

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