

Annual Report for Period:07/2004 - 07/2005**Submitted on:** 06/24/2005**Principal Investigator:** Wiegmann, Brian M.**Award ID:** 0334948**Organization:** North Carolina State U**Title:**

AToL: Building the Dipteran Tree: Cooperative Research in Phylogenetics and Bioinformatics of True Flies (Insecta: Diptera)

Project Participants

Senior Personnel

Name: Wiegmann, Brian**Worked for more than 160 Hours:** Yes**Contribution to Project:**

Lead PI, organization and development of project objectives, oversight of project management, budget and data collection. Molecular phylogenetic data collection, analysis, graduate and undergraduate student training in molecular systematics.

Name: Courtney, Gregory**Worked for more than 160 Hours:** Yes**Contribution to Project:**

Co-PI, organization and development of project objectives - especially pertaining to the lower Diptera, oversight of project management, morphological data collection, supertree construction, interactive keys, taxon sampling. Phylogenetic data collection, analysis, graduate and undergraduate student training in morphological systematics, collecting and curation, natural history data informatics.

Name: Friedrich, Markus**Worked for more than 160 Hours:** Yes**Contribution to Project:**

Co-PI, organization and development of project objectives - especially pertaining to mitochondrial genome sequencing and oversight of project management. Phylogenetic data collection, analysis, graduate and undergraduate student training in molecular genetic techniques and systematics.

Name: Meier, Rudolf**Worked for more than 160 Hours:** Yes**Contribution to Project:**

Co-PI, organization and development of project objectives - especially pertaining to the Cyclorrhapha, oversight of project management, morphological data collection, supertree construction, taxon sampling. Phylogenetic data collection, analysis, graduate and undergraduate student training in molecular and morphological systematics, collecting and curation, natural history data informatics, combined data analysis.

Name: Yeates, David**Worked for more than 160 Hours:** Yes**Contribution to Project:**

Co-PI, organization and development of project objectives - especially pertaining to the lower Brachycera, oversight of project management, morphological data collection, supertree construction, interactive keys, taxon sampling. Phylogenetic data collection, analysis, graduate and undergraduate student training in morphological systematics, collecting and curation, natural history data informatics.

Name: Thompson, F.

Worked for more than 160 Hours: Yes

Contribution to Project:

Data management coordinator, organization and development of project objectives - especially pertaining to the natural history informatics, website development, nomenclature, databases, interactive keys.

Name: Kampmeier, Gail

Worked for more than 160 Hours: Yes

Contribution to Project:

Website development and implementation, database development, web tools development.

Name: Irwin, Michael

Worked for more than 160 Hours: Yes

Contribution to Project:

Collecting, data management, database development, taxon sampling, biodiversity inventories and comparative analysis of lower brachyceran flies.

Name: Beckenbach, Andrew

Worked for more than 160 Hours: Yes

Contribution to Project:

Beckenbach serves as a consultant contributor to the mitochondrial genomic sequencing components of the project.

Post-doc

Name: Blagoderov, Vladimir

Worked for more than 160 Hours: Yes

Contribution to Project:

Dr. Blagoderov is collecting morphological and paleontological data on basal dipteran lineages in the Courtney lab at Iowa State University. He is responsible for morphological scorings, image capture and databasing, collecting and rearing lower Diptera and data analysis.

Name: Lambkin, Christine

Worked for more than 160 Hours: Yes

Contribution to Project:

Dr. Lambkin is coordinating morphological dataset compilation and analysis, scoring lower brachyceran Diptera, and conducting supertree analysis. She is organizing datasets for the first tier analysis of Diptera.

Name: Barr, Norman

Worked for more than 160 Hours: Yes

Contribution to Project:

Dr. Barr is sequencing multiple nuclear genes in the Wiegmann lab (NCSU) for the first tier Diptera analysis. Barr is responsible for nuclear gene primer design and for multigene phylogenetic analysis to determine phylogenetic utility of genes.

Name: Kim, Jung-wook

Worked for more than 160 Hours: Yes

Contribution to Project:

Dr. Kim is sequencing multiple nuclear genes in the Wiegmann lab (NCSU). He is responsible for development of primers and characterization of the GART locus in Diptera and 5 additional loci.

Graduate Student

Name: Trautwein, Michelle

Worked for more than 160 Hours: Yes

Contribution to Project:

Project PhD student collecting data for thesis research on fly phylogeny; Graduate stipend and tuition are supported.

Name: Bertone, Matthew

Worked for more than 160 Hours: Yes

Contribution to Project:

Project PhD student collecting data for thesis research on fly phylogeny; Graduate stipend and tuition are supported.

Name: Kutty, Sujatha

Worked for more than 160 Hours: Yes

Contribution to Project:

Fulltime sequencing of Coelopidae, Sepsidae, and Calyprates. Graduate stipend funded through National University of Singapore

Name: Balasubramanian, Suchitra

Worked for more than 160 Hours: Yes

Contribution to Project:

Wayne State University Biotechnology Master's Program student. Dipteran mitochondrial genome sequencing, stipend partially supported by project funds.

Name: Walker, Mitchell

Worked for more than 160 Hours: Yes

Contribution to Project:

Wayne State University Biotechnology Master's Program student. Dipteran mitochondrial genome sequencing, stipend partially supported by project funds.

Name: Petersen, Matt

Worked for more than 160 Hours: Yes

Contribution to Project:

Iowa State University PhD student. Phylogeny and systematics of Tipuloidea; project supports some research funds, stipend support from BS&I project of co-PI Courtney.

Name: Curler, Greg

Worked for more than 160 Hours: No

Contribution to Project:

Iowa State University MS student. Phylogeny and systematics of Psychodidae; project supports some research funds, stipend support from BS&I project of co-PI Courtney.

Name: Caravas, Jason

Worked for more than 160 Hours: Yes

Contribution to Project:

Wayne State University Ph.D. graduate student (also NSF IGERT program fellow); Mitochondrial genomics of Diptera, project funds provide partial support of research costs.

Name: Petersen, Frederik

Worked for more than 160 Hours: Yes

Contribution to Project:

Petersen is a Graduate Student of the University of Copenhagen, Zoological Museum. He is conducting molecular and morphological studies of the fly superfamily Hippoboscoidea. He is supported by a ZMUC fellowship; NSF project funds supported some research costs for an 8-month molecular systematics internship in the Wiegmann lab (NCSU) 10/03- 5/04.

Name: Su, Kathy

Worked for more than 160 Hours: Yes

Contribution to Project:

Ms. Su is working on phylogenetics of the Sepsidae in the laboratory of Rudolf Meier, NUS.

Undergraduate Student

Name: Singh, Dang

Worked for more than 160 Hours: Yes

Contribution to Project:

Sequencing of fly family Coelopidae, project supports materials and supplies.

Name: Hanrahan, Bob

Worked for more than 160 Hours: No

Contribution to Project:

Mr. Hanrahan is contributing to mitochondrial genome data collection and analysis in the Friedrich lab (Wayne State Univ.)

Name: Shiyang, Kwong

Worked for more than 160 Hours: No

Contribution to Project:

Undergraduate research in Meier lab (NUS) on Sepsidae phylogenetics.

Name: Lim, Gwynne

Worked for more than 160 Hours: No

Contribution to Project:

Undergraduate research in Meier lab (NUS) on Dolichopodidae phylogenetics.

Name: Hwang, Wei Song

Worked for more than 160 Hours: No

Contribution to Project:

Undergraduate research in Meier lab (NUS) on Dolichopodidae phylogenetics.

Technician, Programmer

Name: Cassel, Brian

Worked for more than 160 Hours: Yes

Contribution to Project:

Amplification and sequencing of nuclear genes for phylogenetic objectives in the Wiegmann lab. Project funds support a portion of salary.

Other Participant**Research Experience for Undergraduates****Organizational Partners****Illinois Natural History Survey**

INHS servers host FLYTREE project website; support research of senior personnel Kampmeier

Iowa State University

Subcontract award supports contributions of co-PI Courtney and students.

University of Illinois at Urbana-Champaign

Subcontract supports contributions of senior personnel, Irwin and Kampmeier

Wayne State University

Subcontract agreement supports contributions of co-PI Friedrich and students.

National University of Singapore

co-PI Meier is supported by facilities and salary resources provided by NUS.

CSIRO Division of Entomology

CSIRO supports project co-PI Yeates and postdoctoral associate Lambkin

Simon Fraser University

Simon Fraser supports the participation of molecular systematist Andrew Beckenbach

University of Copenhagen

Other Collaborators or Contacts

Art Borkent (Royal British Columbia Museum, Victoria)

Jeff Skevington (CNC, Ottawa)

Jeff Cumming (CNC, Ottawa)

Brad Sinclair (Museum Koenig, Bonn)

Shaun Winterton, (California Department of Agriculture, Sacramento)

Thomas Pape (Zoological Museum, Copenhagen)

Bernhard Merz (Museum d'Histoire Naturelle, Geneva)

Sonja Scheffer (USDA, ARS, SEL, Beltsville).

Steve Marshall (University of Guelph, Guelph)

Stephen Gaimari (California Department of Agriculture, Sacramento)

Wayne Mathis (Smithsonian Institution, Washington DC)

Neal Evenhuis (Bishop Museum, Honolulu)

Urs Schmidt Ott (University of Chicago, Chicago)

Jerry Wilkinson (University of Maryland, College Park)

Marco V. Bernasconi, Zoological Museum, University of Zurich-Irchel

Patrick Grootaert, Royal Belgian Institute of Natural Sciences David

Barroclough (Natal Museum, Pietermaritzburg)

J. Kevin Moulton (University of Tennessee, Knoxville)

Marion Kotrba (Zoologische Staatssammlung, Munich)

Dalton de Souza Amorim (Unversidade de Sao Paulo)

Adrian Pont (Oxford University)

Activities and Findings

Research and Education Activities:

Diptera ATOL (FLYTREE)

Taxa for first and second tier phylogenetic projects have been gathered from multiple sources. The 42-taxon first tier taxon set is assembled and is being distributed among collaborators. Specimens of immature life stages are being accumulated by collaborators and distributed.

Postdoctoral associates Barr and Kim in the Wiegmann lab are generating data from 10 nuclear genes for first tier taxa. Sequencing is being completed for 42 taxa for the nuclear genes

CAD, GART, 28SrDNA, 18SrDNA, SIA, SNF, PER, TANGO, ARS, and EF1-a.

Primers have been designed and synthesized to amplify these genes.

Graduate student Michelle Trautwein

is sequencing CAD and 28S rDNA for relationships of Bombyliidae

and lower Brachycera. Graduate student Matthew Bertone has sequenced full-length 28S rDNA for 40 species of lower Diptera (Nematocera). Phylogenetic analysis have been conducted for lower Diptera and lower Brachycera for meeting presentations and to assess phylogenetic utility of sampled genes. Bayesian phylogenetic analysis of protein encoding genes, SIA, SNF, PER and TANGO were conducted to assess phylogenetic signal.

Collaborating scientists, Jeff Skevington (CNC, Ottawa) and Sonja Scheffer (USDA, ARS, SEL) are generating molecular data sets based on multiple gene regions for basal Aschiza and Cyclorrhapha (Skevington) and Agromyzidae/Opomyzoidea (Scheffer).

Co-PI Meier and students at NUS are compiling the following project data sets:

Calyptrates:

A data set with 42 taxa from 12 of the 13 families was generated and analyzed using DNA sequences from 12S, COI, CytB, 28S, 18S.

Scathophagidae:

A data set with 67 of the approximately 200 species from 22 genera was generated and analyzed using DNA sequences from 12S, COI, CytB, 28S, 16S, Ef1a, and RNA Polymerase subunit II.

Sepsidae:

Data set extended from 44 species to 71 species. Increase in gene coverage from 5 genes (COI, COII, 12S, 16S, Ef1a, 28S) to 7 (additional genes: CytB, Histone 3)

Coelopidae:

Data set with 32 species extended to also include CytB and Histone 3 in addition to 12S, 16S, COI, 28S, and Ef1a.

Hippoboscoidea:

Extension of Petersen & Wiegmann data set with 42 taxa (CAD, 28S) to also include COI and 16S.

Dolichopodidae:

Start of combined sequencing and morphological project for the SE Asian radiations of Teuchophorus and Thinophilus.

Morphological Research:

Research on the first-tier taxa is ongoing in preparation for the Morphology workshop in mid-July in Copenhagen. Training in confocal microscopy for the imaging of insect specimens at the American Museum of Natural History. Successful transfer of the technique to the confocal microscope at the National University of Singapore.

Research is beginning on the Calyptratae; a specimen collection with 76 species was assembled and the DNA extractions and sequencing has started.

All gene sequences for 6 genes from Genbank and two morphological data sets for Calyptrates have been compiled into a supermatrix

The FLYTREE website <http://www.inhs.uiuc.edu/cee/FLYTREE/> debuted 23 April 2004. The website features information about the Diptera Tree of Life project, its participants and collaborators; information about flies and links to more information for many interests and interest levels about flies; fly

morphology and phylogeny, including a current conception of supertree of the Diptera; links to the BioSystematic Database of World Diptera and the Tree of Life; publications and products related to the project; and pictures or links to pictures of flies. Species pages for the targeted species in the 1st tier study are under development.

Co-PI Friedrich and students at Wayne State Univ. Species have completed sequencing the full coding region of the mitochondrial genomes of the following species:

Haematopota pluvialis, *Musca domestica*, *Glossina morsitans*

Lonchoptera uniseta.

Species for which mt genome sequencing is currently in progress:

Sepsis cynipsea, *Delia radicum*, *Sarcophaga bullata*

Sequence assembly and evaluation are now fully computationally executed using Phred and Phrap software on a designated PC work station.

Suchitra Balasubramanian defended her M.S. thesis: Sequencing the mitochondrial genome of the horse fly, *Haematopota pluvialis*

Beckenbach and students are generating full mitochondrial genome sequences for 8 dipteran taxa: *Bradysia amoena* (25% complete), *Mayetiola destructor* (25% complete), *Nymphomyia dolichocheza* (10% complete), *Edwardsina gigantea* (50% complete); *Chironomus tepperi* (30% complete), *Exeretonevra angustifrons* (20% complete)

Hermetia illucens (35% complete), *Bombylius major* (50% complete).

Co-PI Yeates, CSIRO has continued the development of the interactive key to fly families, and the interactive glossary of fly anatomy. In addition Yeates, Lambkin, Wiegmann, and Meier continued analyses of supertrees covering the entire order Diptera.

Lambkin is completing a paper on her supertree analyses which summarize 24 phylogenetic studies using modern techniques to produce the first overall phylogeny for the family Therevidae.

Lambkin has amalgamated a morphological character list developed for the lower Diptera (Courtney), lower Brachycera (Yeates and Sinclair), and Schizophora (Pape, Meier, Thompson) including immature, pupal, and adult characters. This list describing 405 characters and states has been disseminated, in both word and NEXUS formats, to all groups for preliminary scoring and refinement.

Co-PI Courtney, postdoctoral associate Blagoderov, and students compiled morphological matrix for lower

Diptera, especially 1st tier and other taxa. Special emphasis was given to image capture and scoring larval morphology of lower dipteran taxa, including Axymyiidae, Nymphomyiidae, Tanyderidae, Thaumaleidae, Trichoceridae, Lygistorrhinidae, and Keroplatidae.

Database Activities

After the Tangalooma meetings (post-International Congress of Entomology, August 2004), Gail Kampmeier began building a registration database in FileMaker 7 that was to be accessible via the web to collaborators for tracking work being done or proposed on various tiers of taxa for the FLYTREE project. This database has been available since January 2005 to registered users.

Mandala 6.5, will be the last version of the Mandala database to utilize FileMaker Pro 5.x/6. The database structure is undergoing a massive overhaul in anticipation of its migration to FileMaker 7, which is significantly

different from previous versions of this database engine. Vestigial appendages in this 10 year old Mandala database structure are being pruned, all field names, relationships among files/tables, scripts, layouts, & value lists are being renamed with core conventions that should make it easier for users and future developers to find the information they need to manage their data. New features include management of bioinventories and tools for conducting a biodiversity blitz (outreach event), and the registration database will become a part of the suite once Mandala is in version 7 (with FileMaker 7). Proposed Darwin Core 2 fields <http://darwincore.calacademy.org/Documentation/DarwinCore2Draft_v1-30_HTML> are included and named as appropriate.

Expeditions:

COWEETA HYDROLOGIC LAB LTER, NC. 11/04. Courtney, Wiegmann, Blagoderov, Peterson, and Bertone collected lower dipteran larvae and adults. Several target taxa were collected including Thaumaleidae, Nymphomyiidae, Tanyderidae, Axymyidae, and Trichoceridae.

SAN BERNADINO MTNS, CALIFORNIA. 5/05. Wiegmann, Yeates, Irwin, Trautwein, Winterton, and Gaimari collected Diptera in the Angeles Crest and San Bernadino Mtns near Wrightwood and in the Owens Valley nr Lone Pine. Malaise traps, hand netting and yellow pan traps were used to obtain a large sample of important fly specimens for the ATOL project. The rare species, *Apystomyia elinguis* (Hilarimorphidae) was collected in large numbers for the first time since the 1940's.

AUSTRALIA: VICTORIA & NSW. Lambkin began a long-term trapping program for flies through the Gippsland area and the coastal regions of south-eastern Victoria, in the isolated, inaccessible Tinderry Nature Reserve and the state forests and National Parks of south-eastern New South Wales. 8 large Hocks and 20 smaller Sharkey Malaise traps were erected, and checked monthly for 5 months from early December 2004 to late April 2005, over summer and autumn. Light trapping was carried out in Tinderry Nature Reserve in December. Hand collecting occurred at each sample collection visit. Several target groups were collected including Therevids, Acrocerids, and Xylophagids.

Findings:

Sequences have been obtained for newly characterized nuclear genes for dipteran systematics. PER (period locus focus): 20 taxa, TANGO (10 taxa); CAD (35 taxa); GART (segment A and B): segment A, about 15 taxa (5 with only one direction sequences); segment B, 1 taxon
Snf: 29 taxa; Sia: 24 taxa; Pgd: 4 taxa

Postdoctoral associate Kim developed new primers for the protein encoding gene GART for a broad range of flies. The target region of GART is about 2.2K, which was divided into two segments for amplification (segment A and B). Each PCR amplification should yield 1.1K size of products. Primer modification proves necessary for amplification across broad taxonomic ranges. Both GART segments amplified well with a modified touch-down PCR program. The aligned sequences showed levels of divergence that should help resolve higher-level of dipteran relationships.

SNF and SIA:

Seven in absentia (sia or sina) is easily amplified using *Drosophila*-based

primers. Sans fille (snf) also can be easily amplified for sequencing. Modified primers for both genes were developed for easier amplification of diverse dipteran taxa.

New candidate genes:

Syntaxin, phosphogluconate dehydrogenase (pgd), and glycogen synthase are good candidates based on successful PCR amplification. After analyzing the available primers for these genes, we developed new primers based on *D. melanogaster* and *A. gambiae* sequences for taxon specific exon amplifications.

Phylogenetic analysis of full-length 28S rDNA in basal Diptera using Bayesian and parsimony methods yield well-supported clades among basal Diptera. In particular, molecular data support the monophyly of the order, a basal position for the Tipuloidea, monophyly for the Culicomorpha, Psychodomorpha, and Bibionomorpha. This data supports a the Brachycera as sister-group to the Bibionomorpha.

Phylogenetic analysis of 28S and CAD in the Bombyliidae shows only weak support for expected groupings based on comparative morphology. Notable findings include, monophyly for the family including a basal position for the Mythicomyiidae and support for several subfamilies. Increased sampling of genes and taxa is underway.

Assessment of clade support in Calyptratae based on the analysis of the supermatrix of concatenated GENBANK sequences shows little resolution among major lineages. GENBANK coverage is still too sparse to provide phylogenetic support for most dipteran lineages.

Finding immature larval and pupal stages for scoring of morphological characters is proving difficult. In many cases immature stages have never been recorded for the taxa specified, not even at the generic or tribal level. Even specialized collecting events may not provide specimens as taxonomic identification is difficult, if not impossible, unless the immature develops into an adult.

Supertree analysis for the Order Diptera based on 13 published works shows strong support for major lineages, with some areas of controversy surrounding complex morphological interpretations (basal Eremoneura) or ancient radiations (lower Diptera).

Training and Development:

Michelle Trautwein, Frederik Petersen, Jason Caravas, Sujatha Kutty, Brian Cassel, and Matthew Bertone gained valuable laboratory and analytical training in molecular genomics techniques applied to the successful amplification, sequencing and analysis of nuclear protein encoding genes for insect systematics.

Project graduate students, Matthew Bertone, Michelle Trautwein, Sujatha Kutty and Frederik Petersen attended the FLYTREE workshop, Tangalooma Australia (9/2004).

In October 2004, Gail Kampmeier attended a 4-day intensive training course in FileMaker Pro 7 in Reston, VA, sponsored by The Support Group. Her goal

was to more quickly absorb the implications of the changes and new techniques that would be needed to convert Mandala from its current form to the new relational structure in FMP 7, with advantages in security, better web hosting, and efficiencies of a multiple table file structure.

Additional education/training efforts include:

Graduate student training in phylogenetic methods at CSIRO Entomology, supervised by Lambkin, provided to David Carlisle. Carlisle, is working on an Honours project at Australian National University, examining the phylogenetic signal from the male genitalia in the first comprehensive morphologically-based phylogeny of the Australian Therevidae, including 55 Australian taxa.

- Graduate student, Jason Caravas and postdoctoral student, Norman Barr attended the ATOL meeting, Arlington VA (11/04).

- training of two graduate and one undergraduate student (Singapore)

- grad student training in mitochondrial sequencing at Wayne State

- graduate student training in phylogenetic methods at Iowa State University.
-undergraduate research training experiences supported in the Friedrich and Meier laboratories.

Laboratory Exchanges:

Brian Wiegmann and Greg Courtney visited CSIRO ANIC September 2004 working with Yeates and Lambkin after the International Congress of Entomology.

Frederik Petersen (University of Copenhagen) came to the Meier lab for one month to add additional genes after starting the Hippoboscoidea data set in the Wiegmann lab (10/04)

Christine Lambkin visited Irwin's lab June 2004 and Wiegmann's lab in July 2004.

Wiegmann visited the Courtney lab to present a seminar, interact with students, and exchange data(3/05).

Outreach Activities:

Additional print and media releases: Diptera web products featured in Science, Web Watch, 11/04.

2005.03.18. Interview for Channel News Asia (TV).

2005.02.28. Interview for Tamil Murusa (newspaper)

2005.02.05. Interview for Vasantham Central (TV)

Gail Kampmeier coordinated the database efforts at the Busey Woods Biodiversity Blitz held in Urbana, IL 24-25 June 2005. She brought the functionality of the bioblitz recording features created for the Allerton BioBlitz in 2001 into the core of Mandala, where it may be used for future outreach events or where the number of taxa found and faunal list creation are of primary importance.

Journal Publications

- Yeates, D.K., Harvey, M. and Austin, A., "New estimates for terrestrial arthropod species-richness in Australia.", *Records of the South Australian Museum Monograph Series*, p. 231, vol. 7, (2004). Published
- Yeates, D. K. R. Meier, and B. M. Wiegmann., "Phylogeny of true flies (Diptera): A 250 million year old success story in terrestrial diversification.", *Entomologische Abhandlungen*, p. 119, vol. 61, (2003). Published
- Lambkin, C.L., and Yeates, D.K., "Partitioned Bremer support localises significant conflict in bee flies (Diptera: Bombyliidae: Anthracinae)", *Invertebrate Systematics*, p. 351, vol. 18, (2004). Published
- Wiegmann, B.M., B. K. Cassell, and D. K. Yeates., "Phylogenetic relationships of the dipteran suborder Brachycera (Insecta); a synthesis of multiple nuclear genes and morphology.", *Systematic Entomology*, p. , vol. , (). in Preparation
- Laamanen, T. R., R. Meier, M. A. Miller, A. Hille, and B. M. Wiegmann, "Phylogenetic analysis of *Themira* (Sepsidae: Diptera): sensitivity analysis, alignment, and indel treatment in a multigene study", *Cladistics*, p. , vol. , (2005). Accepted
- Savage, J., T. A. Wheeler, and B. M. Wiegmann, "Phylogenetic analysis of the genus *Thricops* Rondani (Diptera: Muscidae) based on molecular and morphological characters", *Systematic Entomology*, p. 395, vol. 29, (2004). Published
- Austin, A. D., Yeates. D. K., Cassis, G., "Insects down under - Diversity, endemism and evolution of the Australian insect fauna: examples from select orders", *Australian Journal of Entomology*, p. 216, vol. 50, (2004). Published
- Clarke, A.R., K.F. Armstrong, A.E. Carmichael, J.R. Milne, S. Raghu, G.K. Roderick and D.K. Yeates, "Invasive phytophagous pests arising through a recent tropical evolutionary radiation: The *Bactrocera dorsalis* complex of fruit flies", *Annual Review of Entomology*, p. 293, vol. 50, (2005). Published
- Wiegmann, B. M., Yeates, D. K., Hill, H.N., J.K. Moulton, Yang, L. L., Hauser, M., Holston, K. and M. E. Irwin, "Phylogeny of the Therevidae based on multiple nuclear genes", *Insect Systematics and Evolution*, p. , vol. , (). In Preparation
- Lambkin, C.L., Recsei, J.M. and Yeates, D.K., "Systematic revision of *Johnmannia* Irwin and Lyneborg (Diptera: Therevidae): Atypical metallic stiletto flies from Australian mesic habitats", *Zootaxa*, p. 1, vol. 866, (2005). Published
- Schnell e Schuehli, G., C. J. Barros de Carvalho, and B. M. Wiegmann., "Regarding the Taxonomic Status of *Ophyra*, 1830 Robineau-Desvoidy (Muscidae): A Molecular Approach.", *Zootaxa*, p. 1, vol. 712, (2004). Published
- Meier, R., and Farhan Ali, "Software Review. The newest kid on the parsimony block: TNT (Tree analysis using new technology)", *Systematic Entomology*, p. 179, vol. 30, (2005). Published
- Damgaard, J., N. M. Andersen, and R. Meier, "Effects of alignment and taxon sampling in combined molecular and morphological analyses of water strider phylogeny (Hemiptera-Heteroptera, Gerromorpha)", *Systematic Entomology*, p. 289, vol. 30, (2005). Published

Books or Other One-time Publications

- Yeates, D. K., and B. M. Wiegmann, "Phylogeny and evolution of Diptera: recent insights and new perspectives", (2005). Book, Published

Editor(s): Yeates, D. K., and B. M. Wiegmann
 Collection: The Evolutionary Biology of Flies
 Bibliography: Columbia University Press

Meier, R., "The Role of Dipterology in Phylogenetic Systematics: The Insight of Willi Hennig", (2005). Book, Published
 Editor(s): Yeates, D.K, and Wiegmann, B. M.
 Collection: The Evolutionary Biology of Flies
 Bibliography: Columbia University Press

Yeates, D.K., and Wiegmann, B. M., "The Evolutionary Biology of Flies", (2005). Book, Published
 Bibliography: Columbia University Press

Web/Internet Site

URL(s):

<http://www.inhs.uiuc.edu/cee/FLYTREE/>

Description:

This is the primary project website that will disseminate information on the Dipteran tree, explain project objectives, serve products from the project, and function as a portal for other Diptera websites.

www.diptera.org is being developed within the project to be a major dissemination tool for information on flies, their diversity, evolution, nomenclature and identification. This site is now undergoing changes to reflect its connection to the Diptera ATOL project (FLYTREE)

Other Specific Products

Product Type:

Teaching aids

Product Description:

Yeates, D., Hastings, A., Hamilton, J., Colless, D., Lambkin, C., Bickel, D., McAlpine, D., Schneider, M., Daniels, G. and Cranston, P. (2004). Anatomical Atlas of Flies. (Produced by: Anne Hastings, David Yeates, and Joanna Hamilton; CSIRO Entomology AUSTRALIA.) www.ento.csiro.au/biology/fly/fly.html.

This Interactive Glossary to Diptera Morphology was developed by co-PI Yeates and colleagues, with partial support from ABRS and the Diptera ATOL.

This innovative, web-based interactive anatomical atlas was featured in Science magazine's Netwatch segment in 19 November 2004 (<http://www.sciencemag.org/content/vol306/issue5700/netwatch.shtml>; Volume 306: 1269) and also in Biotechniques Journal Webwatch segment in June 2005 (<http://www.biotechniques.com>; Volume 38 (6): 845).

The Anatomical Atlas of Flies website was also chosen to be catalogued at Natural Selection (<http://nature.ac.uk/>) a subject-specific gateway to the natural world, jointly co-ordinated by The Natural History Museum in London and Biome, part of the Resource Discovery Network.

Sharing Information:

This glossary is served on the project website (<http://www.inhs.uiuc.edu/cee/FLYTREE/index.html>) and will be included in an interactive key to fly families (in development).

Product Type:

Interactive Key

Product Description:

Winterton, S.L., Skevington, J.H. & Lambkin, C.L. (2005) ?Stiletto flies of Australasia (Diptera: Therevidae)?. Lucid3 key. California Department of Food & Agriculture, CSIRO Entomology Australia, and Agriculture Canada, ver 1. (online publication). [An Interactive key to genera of Therevidae throughout Australasia; the first ever Lucid 3 key published online]. This website <http://www.cdfa.ca.gov/phpps/ppd/therevidopen.htm>, debuted in early 2005 and includes a Lucid3 interactive key to genera and taxon pages for all Australian genera of the Therevidae including biology, systematics, and numerous digital images of live flies. The website is featured on the CSIRO Divisional website and the ANIC website, and was written up in the CSIRO Divisional Bulletin ?Gnatter?, and was submitted for inclusion in the CSIRO Board Report

Sharing Information:

This website <http://www.cdfa.ca.gov/phpps/ppd/therevidopen.htm>, debuted in early 2005.

Contributions

Contributions within Discipline:

We have contributed primers and made recommendations to more 10 laboratories that are now using these nuclear genes in projects in Diptera, Hymenoptera, Neuroptera, Coleoptera, Lepidoptera, and Trichoptera. New gene development and analysis should provide several new markers for insect phylogenetics.

Divergence time estimation in Brachycera and the estimates for therevoid radiations are providing baseline data for similar studies of insect and dipteran evolutionary history.

Empirical studies of supertree methods and partitioned Bremer support (PBS) are contributing to analytical and theoretical development of these areas of systematic biology.

Studies of nucleotide alignment dynamics and sensitivity analysis provide instructive empirical examples for systematic biology.

Conferences & Workshops Organized

David Yeates is co-organising the following symposia at the International Congress of Entomology (August 2004)

1. With Dr Thomas Pape-Global goals and collaboration: Diptera in the 21st Century
2. With Dr Lyn Cook-Evolutionary radiations of Australian Terrestrial Arthropods: biological success stories from the driest continent

Yeates was invited to organize two workshops (one on Supertrees, and another on Interactive Keys) at the biennial Partnerships Enhancing Expertise in Taxonomy conference in Champaign, Illinois in September 2004. He is currently chair of the organizing committee of the combined conferences of the 7th Invertebrate Biodiversity and Conservation Conference, Australian Entomological Society, Society of Australian Systematic Biologists, and other groups, in Canberra in December 2005 (<http://www.invertebrates2005.com>).

A large group of FLYTREE participants and collaborators met at Tangalooma, Moreton Island, Queensland from the 22-26 August 2004 for a combined Therevid PEET and FLYTREE Conference. Wiegmann, Yeates, Courtney, Meier, Pape, Kampmeier, Thompson, Irwin, Lambkin, Winterton, Skevington, Trautwein, Bertone, Petersen, and Kutty spent three days discussing the progress so far, web-based registration system of specimens, species pages for first tier taxa, a Morphobank for Diptera, and the morphological character list prepared by Lambkin from amalgamation of Yeates, Courtney, and Pape studies. Many morphological characters for Schizophora were added by Meier, Pape, Thomson, and Skevington.

Gail Kampmeier organized the Database Mania workshop for the PEET V conference δ Spatial & Temporal Issues in Taxonomy δ held in Urbana, IL September 2004. She was also Secretary of the organizing committee for the conference.

Invited Presentations

Yeates, D.K. 2004. Supertrees, Supermatrices, and Hennig δ s Legacy: The Relationships of Diptera. Departmental Seminar, State University of Iowa, Ames, Iowa, February.

Lambkin, CL, DK Yeates, B Wiegmann and ME Irwin Evolutionary Radiation of Stiletto Flies in Australia Terrestrial Arthropod Radiations. Biodiversity & Biogeography, International Congress on Entomology 2004 (ICE 2004) in Brisbane, Australia, 15 - 21 August 2004.

Lambkin, CL, ME Irwin, GE Kampmeier, DK Yeates, and BM Wiegmann Rewards and Challenges of Global, Collaborative taxonomy: The Paradigm Shift Offered by PEET Global Goals & Collaboration: Diptera In The 21st Century. Systematics & Phylogeny, International Congress on Entomology 2004 (ICE 2004) in Brisbane, Australia, 15 - 21 August 2004.

Wiegmann, BM, and JK Moulton Comparative Genomics of Diptera: Mining Data Resources from GenBank to FlyBase. Diptera In The 21st Century. Systematics & Phylogeny, International Congress on Entomology 2004 (ICE 2004) in Brisbane, Australia, 15 - 21 August 2004.

Wiegmann, BM, R Meier, DK Yeates, GW Courtney, and FC Thompson. FLYTREE: Cooperative Research in Phylogenetics and Bioinformatics Towards a Dipteran Tree of Life. Diptera In The 21st Century. Systematics & Phylogeny, International Congress on Entomology 2004 (ICE 2004) in Brisbane, Australia, 15 - 21 August 2004.

Wiegmann, B. M. Multigene Systematics of Diptera: Pathways Toward a Fly Tree of Life Systematics and Biodiversity Seminar, CSIRO, Entomology, Canberra, Australia, September 2, 2004.

Trautwein, M. 2004. The phylogeny of bee flies. Entomological Society of American Annual Meeting, Salt Lake City Utah, November, 16, 2004.

Wiegmann, B. M. Flies in the Tree of Life: Strategies for Taxon Sampling in the FLYTREE ATOL, Symposium Speaker, Challenges of Incorporating Large BS & I Grants, TOL and Other Major NSF Programs, Entomological Collections Network, Meeting, December 13, 2004.

Wiegmann, B. M. FLYTREE: Cooperative Research in Phylogenetics and Bioinformatics Toward a Dipteran Tree of Life' National Science Foundation, Assembling the Tree of Life (ATOL) Conference, December 17, 2004.

Wiegmann, B. M. Flies in the morphological, fossil and molecular record Department of Entomology, The University of Illinois, Champaign-Urbana, 1/05.

Wiegmann, B. M. Genes, Fossils and the Evolutionary History of Flies, Seminar Speaker, Department of Entomology, Iowa State University, Ames, IA, 3/05.

Kampmeier, G., and M. E. Irwin. Tracking Specimens, Taxonomic Nomenclature, and Literature in Mandala. Bernice P. Bishop Museum, Honolulu, HI, February 2005.

Kampmeier, G., and M. E. Irwin. Tracking Specimens, Taxonomic Nomenclature, and Literature in Mandala. Canadian National Collection, Ottawa, Canada, March 2005.

Kampmeier, G.E. Databasing experiences from the therevid PEET project. Invited GBIF (Global Biodiversity Information Facility) workshop on Identifying the Impediments to Databasing Entomological Collections, Columbus, OH 23-24 February.

Lambkin C, Yeates, D. and Wiegmann, BM 2004 Supertree Analyses, NSF-PEET Conference, University of Illinois, Urbana-Champaign, September, 23, 2004.

Other presentations:

Lambkin, CL, DK Yeates ME Irwin, and BM Wiegmann 2004. Supertree Analyses with Little Taxon Overlap Joint Meeting of the Society for the Study of Evolution, Society of Systematic Biologists, and American Society of Naturalists at the Colorado State University in Fort Collins, Colorado, USA in June 2004.

Kampmeier, G.E. and Irwin, M.E. Meeting the interrelated challenges of specimen, nomenclature, and literature data tracking in Mandala. Electronic poster, International Congress of Entomology 2004, Brisbane, Australia, 15 - 21 August 2004.

Kampmeier, G., and M. E. Irwin. Tracking Specimens, Taxonomic Nomenclature, and Literature in Mandala. Electronic poster. Abstract p. 63. PEET V conference 'Spatial and Temporal Issues in Taxonomy,' Urbana, IL 20-23 Sept.

Poster Presentations

Trautwein, M.D., Wiegmann, B.M. and D.K. Yeates. Phylogeny of the Bee Flies (Diptera: Bombyliidae). International Congress of Entomology 2004, Brisbane, Australia, 15 - 21 August 2004.

Wiegmann, B. M. Meier, R., Yeates, D.K., Courtney, G.W., Friedrich, M.F., Kampmeier, G. , and F.C. Thompson. FLYTREE (ATOL Diptera) Cooperative research in phylogenetics and bioinformatics of true flies. NSF ATOL PIs Meeting, Arlington VA. November, 2004.

Bertone, M. and B. M. Wiegmann. Molecular Phylogeny of the Nematoceros Diptera: The Earliest Diversification of Flies. Entomological Society of America, Southeastern Branch Meeting, Tunica, Mississippi. March 2005.

Jason Carvas, Suchitra Balasubramanian, Mitchell Walker, Robert Hanrahan, Mithun Neral, Vipin Chaudhary and Markus Friedrich: Towards a mitochondrial genome phylogeny of schizophoran flies. Poster presentation at 2005 IGERT program meeting, Washington DC.

Professional Meetings Attended

Lambkin C.L. Joint Meeting of the Society for the Study of Evolution, Society of Systematic Biologists, and American Society of Naturalists at the Colorado State University in Fort Collins, Colorado, USA in June 2004

PEET V meeting, University of Illinois at Urbana-Champaign, 20-23 September 2004. Irwin, Yeates, Wiegmann, Kampmeier, Thompson.

Yeates, Wiegmann, Courtney, Meier, Thompson, Kampmeier, Irwin, Trautwein, Bertone, Petersen, Kutty, Winterton, Skevington, Pape. International Congress of Entomology 2004, Brisbane, Australia, 15 - 21 August 2004.

Wiegmann, B. M., Meier, R, Kampmeier, G.E., Courtney, G. W., Thompson, F.C. Trautwein, M., Annual Meeting of the Entomological Society of America, Salt Lake City, UT, November 2004.

Wiegmann, B.M., Kampmeier, G. E. Insect Collection Network, Annual meeting, Salt Lake City, UT November 2004.

Kampmeier, G.E. Invited conference of the 22 awardees of NSF Assembling the Tree of Life grants (2001-2004) on databasing and data management, Arlington, VA, November 2004.

Gail Kampmeier and Mike Irwin participated in post-congress (ICE) meetings at Tangalooma (Moreton Island, Australia) 22-26 August 2004 for the NSF FLYTREE grant.

Grants funded:

Terrestrial Arthropod Survey of Fiji. Subcontract to M.E. Irwin and G.E. Kampmeier from Bishop Museum for National Science Foundation Biodiversity Surveys and Inventories program. 8/2004-7/2007. \$68,843, funded.

Proposals Submitted:

Evolution, Structure, and Function of bHLH-PAS Proteins. Atchley, W. R.,

Estes, P., Rose, B. and Wiegmann, B. National Institutes of Health, 12/2005-11/2010 \$1.25M, pending.

Microsporidia PEET Project. L.F. Solter, J.J. Becnel, D.G. Boucias, PI/Es
National Science Foundation Partnerships for Enhancing Expertise in
Taxonomy. 5 years. pending

Contributions to Other Disciplines:

Contributions to Human Resource Development:

D.K. Yeates co-organised and taught an undergraduate course in Entomology at the Australian National University (BIOL 3115).

Lambkin is co-supervising an Honours student, David Carlisle, at the Australian National University, enrolled July 2004 to May 2005. Two papers on the spatial and temporal emergence patterns of therevid larvae and the phylogenetic signal from the male genitalia in Australian Therevidae (with the description of a new genus of Therevidae) are planned from this work.

Gail Kampmeier created step-by-step tutorials in PowerPoint for novice data entry personnel using Mandala for the Busey Woods Biodiversity Blitz. One tutorial focused on entry of specimens and observations; the other on the creation of new taxonomic names.

Contributions to Resources for Research and Education:

Contributions Beyond Science and Engineering:

Special Requirements

Special reporting requirements: None

Change in Objectives or Scope: None

Unobligated funds: less than 20 percent of current funds

Animal, Human Subjects, Biohazards: None

Categories for which nothing is reported:

Contributions: To Any Other Disciplines

Contributions: To Any Resources for Research and Education

Contributions: To Any Beyond Science and Engineering