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# E v o l D i r

August 1, 2004

M o n t h i n R e v i e w

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## Forward

This listing is intended to aid researchers in population genetics and evolution. To add your name to the directory listing, to change anything regarding this listing or to complain please send me mail at [Golding@McMaster.CA](mailto:Golding@McMaster.CA).

Listing in this directory is neither limited nor censored and is solely to help scientists reach other members in the same field and to serve as a means of communication. Please do not add to the junk e-mail unless necessary. The nature of the messages should be “bulletin board” in nature, if there is a “discussion” style topic that you would like to post please send it to the USENET discussion groups.

Instructions for the EvolDir are listed at the end of this message.



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## Conferences

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### BertinoroItaly ComparativeGenomics Oct16-19

#### Call For Papers

#### Second RECOMB Satellite Workshop on Comparative Genomics

Location: BICI Bertinoro International Center for Informatics, Bertinoro, Italy, see

<http://www.cs.unibo.it/bici/> IMPORTANT DATES: Submission Deadline: August 30, 2004. Notifications to Authors: September 16, 2004. Workshop: October 16-19, 2004 Information on participation, registration, accommodations, and travel can be found at:

<http://www.nada.kth.se/~jensl/recombcg2004.html>

Organizers: Jens Lagergren, Stockholm Bioinformatics Center & KTH; Aoife McLysaght, Trinity College; Nancy Moran, University of Arizona Bernard Moret, University of New Mexico; David Sankoff, University of Ottawa.

Scope: The increasing availability of complete genomes from diverse organisms offers unprecedented research opportunities. Intergenomic comparison of various kinds of maps is revelatory of many types of genomic events central to biological, medical and bioinformatics research in the post-genomic era. Computational biology has a key role to play in many aspects of this work: understanding patterns and processes of genomic evolution, mapping genome-level mutational events, and

the effective use of these maps by bioinformatics tools. Genomic data offer an alternative approach to phylogenetic reconstruction, based on genome-level events rather than nucleotide or amino-acid substitutions.

The core of comparative genome analysis is the establishment of the correspondence between genes (orthology analysis) or other genomic features in different organisms. It is these intergenomic maps that make it possible to trace the evolutionary processes responsible for the divergence of two genomes. A multitude of evolutionary events acting at various organizational levels shape genome evolution. At the lowest level, point mutations affect individual nucleotides. At a higher level, large chromosomal segments undergo duplication, lateral transfer, inversion, transposition, deletion and insertion. Ultimately, whole genomes are involved in processes of hybridization, polyploidization and endosymbiosis, often leading to rapid speciation. The complexity of genome evolution poses many exciting challenges to developers of mathematical models and algorithms, who have recourse to a spectra of algorithmic, statistical and mathematical techniques, ranging from exact, heuristic, fixed parameter and approximation algorithms for problems based on parsimony models to Monte Carlo Markov Chain algorithms for Bayesian analysis of problems based on probabilistic models.

The RECOMB Satellite Workshop on Comparative Genomics is a forum on all aspects and components of this field, ranging from new quantitative discoveries about genome structure and process to theorems on the complexity of computational problems inspired by genome comparison.

David Sankoff <sankoff@uottawa.ca>

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## Gordon Jul31-Aug5

The Gordon Conference on evolutionary and ecological functional genomics (EEFG) is focused on the genes that affect ecological success and evolutionary fitness in natural environments and populations. This interdisciplinary research area seeks to understand the functional significance of genomic variation for wild organisms (microbial, plant, and animal) in natural biological communities. The EEFG Gordon Research Conference will showcase the successes and achievements of the field to date; examine novel models of collaboration, interdisciplinary training, and information management; and map out future directions and priorities.

When: Jul 31 - Aug 5, 2005

Where: Queen's College, Oxford, UK

Organizers: Chair - Thomas Mitchell-Olds Vice-Chair - Greg Wray

We are soliciting suggestions and advice for outstanding potential speakers in this area. Self-nominations are welcome. Beginning about 25 July 2004 we plan to organize the list of invited speakers for this conference. Please send suggestions to <mailto:tmo@ice.mpg.de>tmo@ice.mpg.de. Thanks for your help.

Thomas Mitchell-Olds <tmo@ice.mpg.de>

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## Hinxton TranscriptDiversity Nov22-23

Title: Symposium on Alternate Transcript Diversity - Data, Biology, and Therapeutics Date : Nov 22-23, 2004 Venue: European Bioinformatics Institute, Hinxton, Cambridgeshire, UK URL : <http://www.ebi.ac.uk/information/events/atd-sympo/> Alternative splicing is a major versatile mechanism that generates diversity in the human transcriptome. Its regulation is complex and is an important means of physiological control. Its disruption is associated with many diseases, including cancer, multiple sclerosis, heart failure and neurodegenerative disorders. The realization

that alternative splicing is an important way of controlling gene expression has spawned several large-scale efforts to create bioinformatics resources on alternate transcripts and protein isoforms. These include: computational methods and tools to delineate and characterize alternate transcript structures; databases of alternate transcripts and protein isoforms; and annotations that describe the physiology, pathology and evolution of alternate transcript generation. These efforts require community-based collaborations involving computational biologists, bioinformaticians and experimental biologists. This symposium aims to bring together this community to discuss these resources.

=== Programme Committee ===

Ewan Birney (EMBL-EBI, UK) Ian Dix (AstraZeneca, UK) Daniel Gautheret (INSERM, France) Stefan Stamm (University of Erlangen, Germany) Alphonse Thanaraj Thangavel (EMBL-EBI, UK) - Chair

=== Local Organizing Committee (all at EMBL-EBI, UK) ===

Cath Brooksbank Liz Ford Paul Matthews Lisa Mullan - Chair Jean-Jack Riethoven Alphonse Thanaraj Thangavel Eleanor Whitfield

=== Speakers ===

\* Ewan Birney (EMBL-EBI, UK) \* Laurent Bracco (ExonHit Therapeutics, France) \* Steven Brenner (Univ. California Berkeley, USA) \* John Castle (Rosetta Inpharmatics, USA) \* Ian Dix (AstraZeneca, UK) \* Daniel Gautheret (INSERM, France) \* Winston Hide (SANBI, South Africa) \* Tim Hubbard (Sanger Institute, UK) \* Tadashi Imanishi (NIAIST, Japan) \* Adrian Krainer (CSHL, USA) \* Christopher Lee (Univ. California Los Angeles, USA) \* Christopher Smith (Univ. Cambridge, UK) \* Rotem Sorek (Compugen, Israel) \* Stefan Stamm (Univ. Erlangen, Germany) \* Alphonse Thanaraj (EMBL-EBI, UK) \* Eleanor Whitfield (EMBL-EBI, UK) This list will be updated as further speakers are confirmed.

In addition to the talks by invited speakers, oral presentations of selected poster submissions will be arranged.

=== Programme ===

The full programme will be posted in due course on the symposium web pages <http://www.ebi.ac.uk/information/events/atd-sympo/>. The programme will include a combination of invited talks, poster sessions and talks selected from poster abstracts. Topics include, but are not limited to:

\* High-throughput identification and computational documentation of alternate transcripts and protein isoforms \* Regulation of alternative splicing and computa-

tional tools to identify regulatory motifs \* Elucidating the causes and effects of variant formation \* Disease-relevant variants and therapeutic applications

Abstracts of the invited talks and poster presentations will be made available in the symposium proceedings.

=== Registration ===

DEADLINE: 30 September, 2004.

Please register online using the form at [www.ebi.ac.uk/information/events/atd-sympo/registration](http://www.ebi.ac.uk/information/events/atd-sympo/registration). When you register you will be sent an automatically generated e-mail message that includes your registration number. Please keep a record of this as you will need it to submit your poster abstract.

The registration fee is £GBP 150. This covers the cost of lunches and refreshments, an abstract book and the conference dinner. Registration payments should be made in GBP (pounds sterling) by bank transfer or personal cheque.

Payment by cheque: Please make personal cheques payable to 'Industry Workshops' and send with your name and registration number (this will be sent to you when you register online) to the following address:

Liz Ford EMBL-EBI Wellcome Trust Genome Campus Hinxton Cambridge, CB10 1SD UK

Payment by bank transfer: If you wish to pay your registration fee by bank transfer, please contact Liz Ford, [ford@ebi.ac.uk](mailto:ford@ebi.ac.uk) for more details Bottom of Form

=== Poster-abstract submission instructions ===

ABSTRACT-SUBMISSION DEADLINE: 30 September 2004

Abstracts will be considered for presentation in poster sessions. Selected posters will be included for oral presentation. \* Authors whose abstracts are selected for poster and/or oral presentation will be notified by October 20, 2004. \* Please submit your abstract using the online submission form at

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

**KansasCity Genes Ecology Oct2-3**

Please help us inform members of your EvolDir Directory about our upcoming Ecological Genomics Symposium. Detailed information can be found at our website, [www.ksu.edu/ecogen](http://www.ksu.edu/ecogen). You are invited to attend the 2nd Annual "Genes in Ecology, Ecology in Genes" Symposium on October 2 & 3, 2004, at the DoubleTree Hotel in Overland Park, Kansas (Kansas City metro area). Ecological Genomics is an emerging field at the interface of ecology, evolution and genomics that seeks to place the functional significance of genes and genomics into an ecological and evolutionary context. Symposium participants will learn about this new interdisciplinary field from leaders at the forefront of ecological and evolutionary functional genomics. (See the featured speaker list below.) The Kansas ecological genomics initiative comprises over 30 faculty from three universities. Learn about their research, too.

Participants are invited to share their own research at a poster session on Saturday. Poster topics are not limited to Ecological Genomics.

If you have any questions, please contact us at (785) 532-3482 or [ecogen@ksu.edu](mailto:ecogen@ksu.edu). The attached brochure and links for registration and hotel reservations are now posted to our website, [www.ksu.edu/ecogen](http://www.ksu.edu/ecogen). Please share this announcement with colleagues and students who are interested in learning more about the emerging field of Ecological Genomics.

Act now to finalize your Symposium registration and hotel reservation before 5 p.m. on Tuesday, August 31st.

"Ecology in Genes, Genes in Ecology" Featured Speakers: Joy Bergelson, University of Chicago, "The evolution of disease resistance in Arabidopsis" Hopi Hoekstra, University of California, San Diego, "Genetic architecture of adaptive coloration in beach mice" Robert B. Jackson, Duke University, "Ecological genomics and ecosystems" Michael Lynch, Indiana University, "The origins of genome complexity" Alison E. Murray, Desert Research Institute, "Microbial genomics goes to the environment - where some like it hot, and others like it cold" Michael Purugganan, North Carolina State University, "Ecological genomics of Arabidopsis flowering" W. Kelley Thomas, Hubbard Center for Genome Studies, University of New Hampshire, "Daphnia: An emerging model system for ecological and evolutionary genomics" Thomas G. Whitham, Merriam-Powell Center for Environmental Research, Northern Arizona University, "Community and ecosystem genetics: A consequence of the extended phenotype"

Funding for this symposium is provided by Kansas NSF EPSCoR and The Kansas Technology Enterprise Corporation.

Thank you!

Doris R. Merrill Administrative Assistant Ecological Genomics of Kansas KSU Division of Biology 231 Ackert Hall Manhattan, KS 66506-4901 Voice: 785-532-3482 Fax: 785-532-6653 E-mail: dmerrill@ksu.edu <http://www.ksu.edu/ecogen/>

Doris Merrill <dmerrill@ksu.edu>

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## Krakow European Society Evol Biol 2005

REMINDER: CALL FOR SYMPOSIA for the 10th Congress of the European Society for Evolutionary Biology, Krakow, Poland, 2005

We would like to kindly inform that the deadline of symposia submission is July 31, 2004: All submissions should be made by website <http://www.eko.uj.edu.pl/eseb/>. Any enquiries should be send to [eseb2005@eko.uj.edu.pl](mailto:eseb2005@eko.uj.edu.pl) with "symposium" written as a subject.

INTERNET RESOURCES: Congress website: <http://www.eko.uj.edu.pl/eseb/> Full text of symposia call available at: <http://www.eko.uj.edu.pl/eseb/call.html> PDF version of symposia call: [http://www.eko.uj.edu.pl/eseb/Call\\_for\\_symposia.pdf](http://www.eko.uj.edu.pl/eseb/Call_for_symposia.pdf)

10th Congress of the European Society for Evolutionary Biology Krakow, Poland, 2005  
www: <http://www.eko.uj.edu.pl/eseb/> email: [eseb2005@eko.uj.edu.pl](mailto:eseb2005@eko.uj.edu.pl)

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## Leiden Endosymbionts Sep6

This is a first announcement for the one-day symposium:

Acquired Genomes: Evolutionary consequences of endosymbionts 6 september 2004 Leiden, The Netherlands

The role of symbiosis in the creation of biodiversity has been amply demonstrated by Lynn Margulis in her recent book *Acquired Genomes* and in her previous work in which she has compiled convincing evidence that mitochondria of the eukaryotic cell and chloroplasts in

plant cells have evolved into essential organelles from a free living micro-organisms. These acquired genomes represent major innovative steps in evolution.

Exploring how the acquisition and domestication of initially free-living organisms proceeds is an exciting field of study. Intracellular symbionts and their eukaryotic hosts have initially conflicting interests, and the evolutionary arms races between them do not necessarily result in mutualistic relations between previous enemies, as the Eukaryotes might lose the race and end up being hijacked by the symbiont.

This symposium aims at bringing together researchers in the field of endosymbionts.

Confirmed invited speakers (titles and abstracts will follow, check the website <http://www.bio.leidenuniv.nl/~eew/G1/index.html> for details):

Lynn Margulis (University of Massachusetts/Amherst, U.S.A.) Fabrice Vavre (Université de Claude Bernard-Lyon 1, France) Richard Stouthamer (University of California Riverside, USA) Rob Butcher (University of Bath, UK) Hans Breeuwer (University of Amsterdam, The Netherlands) Bart Pannebakker (Leiden University, The Netherlands)

Contributed presentations in the form of poster presentations are welcome. Posterboards will be available during the breaks.

Please register by sending an e-mail with your contact details and whether you wish to present a poster to: Gerdi Dijkstra: [oeecologie@rulsfb.leidenuniv.nl](mailto:oeecologie@rulsfb.leidenuniv.nl)

We aim at keeping the symposium free of charge.

Kind regards,

Bart Pannebakker

Bart A. Pannebakker Institute of Biology - Leiden University Van der Klaauw Laboratory - Section of Animal Ecology / Section of Evolutionary Biology P.O. Box 9516, 2300 RA Leiden, The Netherlands Tel. (+31) 71 527 4990 ; Fax (+31) 71 527 4900 Email: [pannebakker@rulsfb.leidenuniv.nl](mailto:pannebakker@rulsfb.leidenuniv.nl) <http://www.bio.leidenuniv.nl/~pannebakker/index.html>

Bart Pannebakker <[pannebakker@rulsfb.leidenuniv.nl](mailto:pannebakker@rulsfb.leidenuniv.nl)>

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## MEEGID VII

Dear All:

**FINAL SCIENTIFIC PROGRAMME OF MEEGID VII** A total of 455 Abstracts have been accepted for MEEGID VII, including papers for both MEEGID Sessions and MEEGID-EMOP shared sessions. The Organising Committee apologies for the delay in making this programme available, only due to several keynote speakers sending their summaries very late (up to even the beginning of July). The very large number of delegates makes it impossible to send an email to each participant individually notifying details about their communications. Therefore, we kindly request you to look for the details in the entry “Definitive Scientific Programme of MEEGID VII” of the NEWS of the MEEGID VII web-site:

<http://www.uv.es.emop9/MEEGID> **HOW TO KNOW DATE, TIME, SESSION AND ROOM FOR YOUR PRESENTATION(S)** To find a paper and know date, time, session and room for presentation, proceed as follows: 1.- Enter in <http://www.uv.es.emop9/MEEGID> 2.- Click “Definitive Scientific Programme of MEEGID VII” in the NEWS. 3.- Click MEEGID VII PROGRAMME to directly obtain the whole MEEGID VII Programme on your computer desktop (Acrobat Reader file). 4.- In this Programme, MEEGID sessions include Abstract Nos. 1-43 and can be easily followed by looking at Plenary Sessions, Express Debates and MEEGID Symposia directly at the beginning of the Programme, as abstracts are numbered consecutively. 5.- MEEGID-EMOP shared Symposia, Workshops and Monographic Sessions include Abstracts Nos. 44-455. MEEGID-EMOP shared communications show the MEEGID VII number at left and the EMOP IX number at the end of the title in parentheses. To know date, time, session and room for presentation in MEEGID-EMOP shared communications, whether download the MEEGID VII PROGRAMME pdf file to your computer and simply use search for name in your Acrobat Reader program or go to the entry “Definitive Scientific Programme of EMOP IX” in the NEWS of the EMOP web-site << [>>](http://www.uv.es/emop9) and follow the instructions noted by using the Author Index.

**PRESENTATION GUIDELINES** Details about communications for (i) Keynote presentations, (ii) Express debates, (iii) Oral papers and (iv) Poster presentations available in the entry “Presentation Guidelines” in the NEWS.

**HONORARY COMMITTEE** Already available in the corresponding entry “Honorary Committee” in the NEWS.

**NEW INFORMATION** Details on Doc Reception and Last Registration, a modification related to the Get Together Party of Sunday July 18, the Time Table

and Transport for Social Events, and the Shuttle Service available in the entry “Modif.& New Info” in the NEWS.

According to the very large number of papers received from very numerous delegates from countries from all continents, we are pleased to say that this meeting has been very successful. We hope you will enjoy the very rich scientific programme and wish you a pleasant stay in Valencia.

MEEGID VII Organising Committee

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## Marseilles EvolBiol

Dear all,

The 8th evolutionary biology meeting’s preliminary program is already available for consultation on our web site [www.up.univ-mrs.fr/evol/congres](http://www.up.univ-mrs.fr/evol/congres) and we invite you to come and see it!

Considering the great number of participants to this new appointment, we had this year to look for a new place to meet and found a very convenient localisation near the main train station of the town. Thus, the meeting will take place at Saint Charles University, place you will also be able to discover on our web site.

To conclude, we draw your attention to the fact that you still have the possibility to present one poster, therefore, we invite you not to hesitate if you wish to do so.

Hoping hearing from you very soon,

Gaëlle, for the organizers of the 8th evolutionary biology meeting. [congres\\_evolution@hotmail.com](mailto:congres_evolution@hotmail.com)

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## Marseilles EvolBiol Sep22-24 2

Association pour l’étude de l’évolution biologique. Université Aix-Marseille I centre Saint Charles Laboratoire EGEE (Evolution, Génome, Environnement) 3 place Victor Hugo 13331 Marseille cedex 03 FRANCE

Dear colleagues, I inform you that the definitive scientific program of the 8th evolutionary biology meeting at Marseilles as well as the social events are now available

on <http://www.up.univ-mrs.fr/evol/congres/> . Moreover, we exceptionally still accept a few inscription for posters. If you were interested, please send us an abstract and register directly on the meeting web site. Best regards,

Pierre Pontarotti. [congres\\_evolution@hotmail.com](mailto:congres_evolution@hotmail.com)

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## NorthCarolina SEEPAGE Sept10-12

SEEPAGE 2004

September 10-12, Swannanoa, North Carolina

Please note the corrected URL for the SEEPAGE 2004 website:

<http://salamander.uky.edu/SEEPAGE/> David Weisrock, Ph.D. University of Kentucky T. H. Morgan School of Biological Sciences  
<http://salamander.uky.edu> David Weisrock  
[<weisrock@uky.edu>](mailto:weisrock@uky.edu)

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## QuebecCity PlantGenomics Aug29-Sep1

Final Announcement The 2nd Canadian Plant Genomics Workshop is being held in Québec City, August 29 - September 1st 2004, at the Loews Le Concorde Hotel.

Keynote Speakers: Marc Vidal, Harvard Medical School, Boston MA Interactome Networks John Quackenbush, The Institute for Genomic Research, Rockville, MD Expression profiling for the analysis of biological systems Joseph Ecker, The Salk Institute, La Jolla, CA Genome-wide discovery of transcription units and functional elements in Arabidopsis James Zhang, Mendel Biotechnologies, Hayward, CA Functional genomics of plant transcription factors - from Arabidopsis in the lab to tomatoes in the field Fathey Sarhan, Université du Québec à Montréal, Montréal, QC Functional genomics and discovery of novel genes associated with abiotic stresses in cereals Gerald Tuskan, Oak Ridge National Laboratory, Oak Ridge, TN The International Populus Genome Consortium Intended to promote and enhance networking, this workshop will bring together renowned

international and Canadian genomics researchers, all within the context of one of the most historic cities in North America. Functional genomics will be the major theme, with prominent speakers addressing a diverse range of subjects, spanning from the C. elegans interactome to the International Populus Genome Consortium. Morning symposia will be followed by concurrent workshops in the afternoon that will address a number of technical and biological topics. These will include proteomics, metabolomics, transgenomics, expression profiling and bioinformatics.

Deadline for the reduced rate for the Loews Le Concorde hotel (800-463-5256) has been extended to Thursday, 29July04 and the early registration extended to 30July04.

The complete program, registration instructions, list of partners and organizing committee members are available at [www.cpgw-acgp.ca](http://www.cpgw-acgp.ca) . <<Final Announcement-En.pdf>>

“Rutledge, Bob” <[BRutledge@exchange.cfl.forestry.ca](mailto:BRutledge@exchange.cfl.forestry.ca)>

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## ReadingUK PopGenetics Dec14-17

This is a preliminary announcement that the the 38th Population Genetics Group Meeting (Pop Group) will be held in Reading, UK, from the evening of Tuesday 14 December to lunchtime Friday 17 December, 2004. Invited speakers are

Rasmus Nielsen (Cornell/Copenhagen) Steve Oliver (Manchester) Sara Via (Maryland)

The cost of board and lodging plus conference fee will be around 190 GBP. Registration details will be announced at the beginning of August.

Mark Beaumont

– Mark A. Beaumont, School of Animal and Microbial Sciences, University of Reading, Whiteknights, P.O. Box 228, Reading RG6 6AJ, UK

Tel 0118 987 5123 X 7707 Fax 0118 931 0180  
 Email: [m.a.beaumont@reading.ac.uk](mailto:m.a.beaumont@reading.ac.uk) WWW: <http://-www.rubic.rdg.ac.uk/~mab/>

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**SandbjergDenmark EvolStress**  
**Aug22-26 2**

Second announcement:

Symposium

Progress in Environmental Stress, Adaptation and Evolution

August 22-26, 2004 at Sandbjerg, Denmark

Sponsors:

European Society of Evolutionary Biology (ESEB)

Center for Environmental Stress Research and Faculty of Sciences, University of Aarhus (DK)

Aim:

Most organisms and populations have to cope with hostile environments, threatening their existence. Their ability to respond phenotypically and genetically to these challenges and to evolve adaptive mechanisms is, therefore, crucial. The aim of the symposium is to understand, from an evolutionary perspective, the impact of stress on biological systems. We have invited speakers that at different organizational levels, from genes to individuals and populations, explore how organisms adapt to (extreme) environments genetically and physiologically, how stress changes genetic structure and affects life histories and how environmental and genetic stress shape selection pressure and causes extinction of populations.

These issues have already been dealt with in a symposium on stress and evolution during the 5th International Congress of Evolutionary Biology and Systematics in Budapest (1966), and in the end resulted in a book edited by us Environmental Stress, Adaptation and Evolution (1997) published in the Birkhäuser EXS series (EXS 83). It is now nearly ten years later and knowledge and (genomic) techniques in this research field have progressed rapidly. Therefore, we are thinking a follow-up to be timely and are organising this small, 3 day symposium on the same issues

Structure:

The number of participants will be limited to around 50, of which 15 are reserved for invited speakers (for list see below). There will be room for maximal 40 presentations of which 25 are open for contributed talks (25 min.). In conjunction with the symposium a special

thematic issue of the Journal of Evolutionary Biology will be published on the topic that will contain high quality papers by the invited speakers. In addition, it will be possible for contributed papers to be included in this special issue of JEB. This will ensure that the papers get lots of exposure in this thematic setting. Papers for the special issue will be selected by the organisers of the symposium and the chief editor of JEB, Juha Merila. Mind that all manuscripts, including those of the invited speakers, will not be treated favourably for this special issue. They are subject to normal, rigorous peer-review and scope limits of the journal: they have to address important evolutionary, and not purely functional, problems.

Participation:

Those that are interested in the symposium topic and want to participate and/or present a paper are kindly invited to contact the organisers from now on. Please do send your application to Corneel Vermeulen (<mailto:c.j.vermeulen@biol.rug.nl> c.j.vermeulen@biol.rug.nl) who will collect and structure applications (but for safety do send also a cc to both Volker Loeschcke (<mailto:volker.loeschcke@biology.au.dk> volker.loeschcke@biology.au.dk) and Kuke Bijlsma (<mailto:r.bijlsma@biol.rug.nl> r.bijlsma@biol.rug.nl)), not later than the 7th of June. As we, in addition to the invited speakers, can only accommodate around 35 participants, the symposium might easily become full. If this is the case the organisers will select participants and contributions that seem to fit that symposium and the special volume of JEB the best. Therefore it is important that tentative participants provide a few lines about their research interests, and if they want to present a contribution, please provide also a title and a substantial abstract (up to 200 words). Membership of ESEB is not prerequisite, but gives a discount of the conference fee and might give some priority.

Practical information:

Title: Progress in Environmental Stress, Adaptation and Evolution

Date: August 22-26, 2004

Deadline: June 7, 2004 (you will hear about acceptance not later than June 15, 2004).

Organisers: Volker Loeschcke, Dept. of Ecology and Genetics, University of Aarhus (DK)

Kuke Bijlsma, Evolutionary Genetics, University of Groningen (NL)

Place: Sandbjerg Manor House, in the south of Jutland,



Denmark. This is a conference centre of the University of Aarhus in a very nice and rural setting, easily reached by train and plane. For info see: <<http://www.sandbjerg.dk/en/>> www.sandbjerg.dk/en/ .

Participants: maximal number approximately 50 (except for some invited speakers allotted to ESEB members).

Costs: The conference fee is Euro 450 for ESEB members Euro 550 for non-members. (Thus ESEB members get a discount of Euro 100, which is more than twice the yearly membership fee including the printed version of

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## SandbjergDenmark EvolStress Aug22-26 3

Due to late withdrawl we have still 3 to 4 places vacant for the ESEB sponsored workshop on environmental stress, adaptation and evolution, Aug. 22-26, Sandbjerg, Denmark; for further information on the symposium see below; if you are interested to attend, send asap an email to Corneel with cc to Kuke and me (for email addresses see below); if you want to give an oral presentation, also send an abstract; we will accept on first come first served basis to fill the last spots. kind regards Kuke and Volker

Symposium:

Progress in Environmental Stress, Adaptation and Evolution

August 22-26, 2004 at Sandbjerg, Denmark

Sponsors:

European Society of Evolutionary Biology (ESEB)

Faculty of Sciences and Center for Environmental Stress Research, University of Aarhus (DK)

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The number of participants will be limited to around 50, of which 15 are reserved for invited speakers (for list see below). There will be room for maximal 40 presentations of which 25 are open for contributed talks (25 min.). In conjunction with the symposium a special thematic issue of the Journal of Evolutionary Biology will be published on the topic that will contain high quality papers by the invited speakers. In addition, it will be possible for contributed papers to be included in this special issue of JEB. This will ensure that the papers get lots of exposure in this thematic setting. Papers for the special issue will be selected by the organisers of the symposium and the chief editor of JEB, Juha Merila. Mind that all manuscripts, including those of the invited speakers, will not be treated favourably for this special issue. They are subject to normal, rigorous peer-review and scope limits of the journal: they have to address important evolutionary, and not purely functional, problems.

Participation:

Those that are interested in the symposium topic and want to participate and/or present a paper are kindly invited to contact the organisers from now on. Please do send your application asap to Corneel Vermeulen (<<mailto:c.j.vermeulen@biol.rug.nl>> c.j.vermeulen@biol.rug.nl) who will collect and structure applications (but for safety do send also a cc to both Volker Loeschcke (<<mailto:volker.loeschcke@biology.au.dk>> volker.loeschcke@biology.au.dk) and Kuke

Bijlsma (<mailto:r.bijlsma@biol.rug.nl>  
r.bijlsma@biol.rug.nl)). As we, in addition to the  
invited speakers, can only accommodate around 35  
participants, the symposium might easily become over-  
booked. If this is the case the organisers will select  
participants and contributions that seem to fit that  
symposium and the special volume of JEB the best.  
Therefore it is important that tentative participants  
provide a few lines about their research interests, and  
if they want to present a contribution, please provide  
also a title and a substantial abstract (up to 200  
words). Membership of ESEB is not prerequisite, but  
gives a discount of the conference fee and might give  
some priority.

Practical information:

Title: Progress in Environmental Stress, Adaptation  
and Evolution

Date: August 22-26, 2004

Organisers: Volker Loeschke, Dept. of Ecology and  
Genetics, University of Aarhus (DK)

Kuke Bijlsma, Evolutionary Genetics, University of  
Groningen (NL)

Place: Sandbjerg Manor House, in the south of Jutland,  
Denmark. This is a conference centre of the University  
of Aarhus in a very nice and rural setting, easily reached  
by train and plane. For info see:

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To read the entire message look it up at <http://life.biology-mcmaster.ca/~brian/evoldir.html>

## Shropshire EvolBiol Aug29-Sept3

Final announcement for participants

10th Meeting of PhD Students in Evolutionary Biol-  
ogy 29th August-3rd September 2004 Preston Montford  
Field Centre, Shropshire, UK

There are around 15 places still available on this con-  
ference. It aims to bring together PhD students from  
all over Europe to discuss current topics in evolution-  
ary biology; topics range from molecular evolution to  
conservation biology.

Please see <http://students.bath.ac.uk/bspght> for fur-  
ther details. As the conference is quite soon please  
note that, once registration has been confirmed, pay-  
ment should be set up within 5 days.

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## GradStudentPositions

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**France INRA**  
**AnimalGenomeExpression**

Dear colleagues,

We are pleased to inform you that the INRA Jouy-en-  
Josas research centre site ([www.jouy.inra.fr](http://www.jouy.inra.fr)) has been  
accepted as a Marie Curie Early Stage Training site

in the field of the Regulation and Variability of Animal Genome Expression (named the RIVAGE project). We will soon welcome several students for Ph.Ds and shorter training stages. You will find more informations at the following internet address: <http://mc-opportunities.cordis.lu/results.cfm> fellowships number: 63 to 75

Information on the RIVAGE project will be posted at the following address: <http://www.jouy.inra.fr/europe/rivage/index.shtml> Eligibility conditions are explained at <http://europa.eu.int/comm/research/fp6/mariecurie-actions/action/level.en.html#> we are a non-international organisation and a mono partner EST.

At present, 5 Ph-D fellowships are open to european students :

Genetic variability and immunity in hens, contact [pinard@dga2.jouy.inra.fr](mailto:pinard@dga2.jouy.inra.fr)

Replication or propagation of TSE infectious agent: role of specific cell types contact [vilotte@jouy.inra.fr](mailto:vilotte@jouy.inra.fr)

Mechanisms involved in melanoma regression, contact [VINCENTN@dsvidf.cea.fr](mailto:VINCENTN@dsvidf.cea.fr)

Genome expression and cell differentiation, contact [vignon@jouy.inra.fr](mailto:vignon@jouy.inra.fr)

Role of fatty acids in embryonic development, contact [Gilles.Charpigny@jouy.inra.fr](mailto:Gilles.Charpigny@jouy.inra.fr)

If you are aware of students that could be interested, could you please pass on the information to them. Please do not hesitate to contact us at [rivage@jouy.inra.fr](mailto:rivage@jouy.inra.fr)

Thanking you very much in advance for your help,  
Yours sincerely,

On behalf of the RIVAGE committee, Etienne Verrier  
-

Prof. Etienne VERRIER [verrier@inapg.fr](mailto:verrier@inapg.fr) UMR Genetique et Diversite Animales INA Paris-Grignon / Depnt. Sciences Animales / GER Genetique Elevage et Reproduction INRA / Depnt. Genetique Animale 16 rue Claude Bernard, 75235 PARIS cedex 05, France [verrier@inapg.fr](mailto:verrier@inapg.fr)

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## Leuven FishGenomics

cellence funded by the European Commission

PhD studentship in bioinformatics and fish genomics

A 3 year PhD studentship funded by the FP6 NoE "Marine Genomics Europe" (<http://www.sb-roscoff.fr/marine-genomics-europe/MGE-PhD-announcement-KULeuven.pdf>) is available at the Laboratory of Aquatic Ecology of the Katholieke Universiteit Leuven starting 1 October 2004. Topic: analysis of EST data from seabass and seabream. Initial training in bioinformatics and programming will be provided at Bielefeld University (Prof. Folker Meyer) and advanced training in genomic analysis at NERC-British Antarctic Survey (dr. Melody Clark). You will have access to the "Marine Genomics Europe" fish EST data and in doing so will work closely with CCMAR, Univ. do Algarve, Faro (Prof. Adelino Canario). You will learn how to automatically analyse, annotate and submit EST data and prepare a database to combine the fish ESTs. Examples of analysis include: overall statistics, gene discovery/diversity ratios, gene content by tissue, gene functional content, comparative analysis of both the seabass and seabream ESTs, cluster analysis, polymorphism screening, plus comparison to publicly available data in Fugu, Zebrafish and Medaka. There will be time to follow a related project of his/her own choosing such as population SNP frequencies.

The K.U.Leuven was founded in 1325 and has a student enrollment of 28,000. Leuven (<http://www.leuven.be/>) is an historical university town with a very high and pleasant standard of living.

Candidates with a M.Sc. or equivalent in either life or engineering sciences and some training in bioinformatics, a very strong academic record, an interest in marine sciences and perfect knowledge of English (TOEFL score of at least 580), should send a letter of motivation, their CV (including course transcripts) and three letters of recommendation before 15 August 2004 to: Prof. Filip Volckaert Katholieke Universiteit Leuven Laboratory of Aquatic Ecology, Research Group on Fish Genetics Ch. de Bériotstraat 32 B-3000 Leuven, BELGIUM Phone: +32 16 32 39 72 (office) or +32 16 32 39 66 (secretariat) Fax: +32 16 32 45 75 <<mailto:filip.volckaert@bio.kuleuven.ac.be>> [Mailto:filip.volckaert@bio.kuleuven.ac.be](mailto:filip.volckaert@bio.kuleuven.ac.be)

URL: <<http://www.kuleuven.ac.be/bio/eco>> <http://www.kuleuven.ac.be/bio/eco>>

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## Paris EvoDevo NerveCells

Paris, EvoDevo Nerve cell

Ph-D position in Universite Pierre et Marie Curie, Paris

A three years Ph-D fellowship is available in our team "Evolution and Development" (Department Systematics, Evolution, Adaptation), University Pierre et Marie Curie, Paris, to work on the origin and early evolution of nerve cells. The work will aim at isolating and characterizing molecules involved in the process of neuronal differentiation in selected species of phyla Ctenophora and Cnidaria. Currently we work with *Pleurobrachia pileus* (a ctenophoran), *Clytia hemisphaerica* and *Podocoryne carnea* (hydrozoan cnidarians). Experimental strategies will involve the search for homologues of key molecules, known from bilaterian models to act in neuronal differentiation, by PCR search and through the analysis of EST sequences (4000 EST sequences from *P. pileus* and 4000 from *C. hemisphaerica* will be available next fall at the beginning of the Ph-D). Candidate molecules will be further characterized through expression pattern studies and functional experiments (mRNA injection, RNAi / morpholino). Together with embryos and adults of the model species, gene function will be tested in the context of in vitro transdifferentiation of jellyfish muscle cells into neurons. Results will be interpreted in a phylogenetic framework in order to formulate hypotheses on the origin and early evolution of nerve cells. Our collaborations include Evelyn Houliston (Villefranche, France), Volker Schmidt (Bale, Switzerland) and Mark Martindale (Hawaii, USA). The Ph-D will start at the beginning of next October. The salary will be 1 040 € monthly. Candidates should be under 25 years old at the end of 2004, and be citizens of the European Union, or at least they should have obtained their Master degree in a country belonging to the European Union or one of the following European countries: Andorra, Bulgaria, Croatia, Russia, Iceland, Norway, Rumania, Switzerland, Turkey, Vatican. Candidates should be highly motivated and have a good background in developmental biology and genetics, and an experience with molecular biology techniques. Competences in zoology, phylogeny and genomics will be appreciated. To apply send a CV, motivation letter and a letter of recommendation to Michael.Manuel@snv.jussieu.fr (or by post mail to the address below) before August 25. There will be an interview of pre-selected candidates on

Monday 6th September in Paris.

Dr. Michael MANUEL Maitre de Conferences (Assistant Professor) Universite Pierre et Marie Curie (Paris 6) Equipe Evolution et Developpement, UMR 7138 "Systematique, Adaptation, Evolution" Bat. B, 7eme etage, piece 705 9 quai St Bernard 75 005 Paris, FRANCE

tel. 33 (0) 1 44 27 34 69 33 (0) 6 14 65 48 05 fax 33 (0) 1 44 27 32 58 e-mail Michael.Manuel@snv.jussieu.fr

" ( Michael Manuel 25/04/2001 ) "  
<mmanuel@snv.jussieu.fr>

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## UBern AdaptiveRadiation

Two PhD positions in Ecology and Genetics of Adaptive Radiation

Two 3-years PhD projects are available in the research group of Ole Seehausen in both the Aquatic Ecology section of the Institute of Zoology, University of Bern, Switzerland and the Limnological Research Station of the EAWAG, Kastanienbaum, Switzerland, to investigate the interaction between ecological processes and geographical events in the speciation and adaptive diversification of whitefish (*Coregonidae*) in alpine lakes.

One PhD project would involve building a molecular phylogeny for many populations and ecotypes of alpine coregonids using AFLPs and mitochondrial DNA sequence variation and collection of morphological and ecological data for the same populations. The data will be used to reconstruct colonization and hybridization scenarios and test hypotheses for morphological and ecological adaptation. Another project will revolve around quantification of ecological resource profiles available for whitefish populations in different lakes and experimental quantification of diet preference profiles to generate adaptive landscapes. These will be used to predict ecological whitefish diversity. Morphological and ecological diversity and gene flow (molecular markers) will be quantified between ecotypes within lakes, and will be compared with predictions derived from the environment.

We are looking for enthusiastic, dedicated students with a master's degree or equivalent (e.g. Diplom) in Biology and background in evolutionary and ecological theory and/or population genetics. The phylogeny project will involve a large amount of work in the laboratory, extracting DNA, PCR, fragment separation

and sequencing on automated sequencers, genetic data analysis and phylogenetic methods. The project will also involve morphometric data collection and analysis and some fieldwork for collection of samples. Some experience in the molecular lab and/or with genetic data analysis will be advantageous. The population project will involve work in the molecular lab too, but will also have a large component of field work in Swiss lakes, morphometrics, and a component of experimental work with life fish in aquaria. Experience with quantitative aquatic field work, and/or morphometric or population genetic data analysis will be advantageous, as will be experience with handling and maintaining life fish. A clean driving licence will be required, and a diving licence might be helpful. Both students must be able to work independently, as well as in small teams. They will interact with the large community of population biologists, ecologists and geneticists at the Institute of Zoology (<<http://www.zoology.unibe.ch/index.php>><http://www.zoology.unibe.ch/index.php>) and the population and system ecologists at the Limnological Research Station (<[http://www.eawag.ch/research\\_e/kastanienbaum/e\\_index.html](http://www.eawag.ch/research_e/kastanienbaum/e_index.html)>[http://www.eawag.ch/research\\_e/kastanienbaum/e\\_index.html](http://www.eawag.ch/research_e/kastanienbaum/e_index.html)). Besides research, PhD students are expected to contribute to undergraduate teaching and supervision (teaching load not exceeding 10 percent of working time). Salaries will be according to Swiss National Science Foundation (SNF) salary schemes.

Conceptual background: The theory of speciation has often been polarized between the views that speciation is driven by external (geographical) events that isolate populations, or by environmental pressures and ecological processes within populations. The geographical hypothesis came to the forefront during the modern synthesis and dominated speciation theory for several decades. The ecological hypothesis, which originated in the early days of evolutionary theory, has seen a revival in the last decade. The mechanisms associated with these alternative ideas have often been studied in isolation, except in the framework of reinforcement. A different and possibly more general form of interaction between ecological processes and external events is now in discussion: that the merging of lineages after periods of independent evolution (hybridization) generates populations with genetic properties that allow adaptive sympatric diversification in response to ecological pressures, and that are unlikely to arise in continuously panmictic populations. Although speciation would be sympatric, driven by ecology, transient geographical isolation would generate the genetic variation that makes adaptive evolutionary responses possible.

Our research group been investigating the adaptive radiations of African cichlid fish, e.g. the roles of ecology, historical contingency and hybridization in speciation. Alpine radiations of salmoniform fish are

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## UEastAnglia MHC

Gastrointestinal parasites, MHC genes and fitness in a wild avian population

Within vertebrates, the major histocompatibility complex (MHC) genes within an individual determine how well it copes with the array of parasites it encounters in its environment. An individual's fitness (survival and reproductive success) will therefore, at least in part, depend upon the MHC genes it contains. Gastrointestinal parasites (GI) occur worldwide and can be extremely detrimental to the fitness of individuals. Few studies have assessed the impact of GI parasites from an evolutionary perspective, and even fewer have taken into account the affect of the MHC. None have done so using birds. This project will investigate the affect of GI parasites and their interaction with the MHC in the simple and isolated system provided by the Cousin Island population of Seychelles warbler (*Acrocephalus sechellensis*). PCR-based molecular protocols will be used to screen MHC, while microscopic investigation of eggs within faecal samples will provide a non-invasive method for determining the intensity of GI parasites within individuals. Fieldwork to continue the population monitoring and the collection of samples and fitness data will be done in conjunction with the Seychelles warbler research project team. The results will contribute towards determining the importance of MHC variation and parasite-mediated selection in wild animal populations.

Dr David S. Richardson and Prof. Jan Komdeur: Jointly funded by UEA and JK (University of Groningen, Holland) for three years starting January 2005.

Further details

We are looking for an enthusiastic, dedicated and resilient student with an interest in evolutionary and molecular ecology. The student will spend a large part

of their time in the laboratory, isolating parasite eggs from faeces, extracting DNA and using basic molecular techniques such as PCR and DGGE. Therefore, although not essential, molecular lab experience will be an advantage, as will good organisational skills. Fieldwork will be for 2-3 months per year and, as the field site is small and isolated, the student must be able to work well independently, or within a small group. The studentship will be based at UEA with D. S. Richardson, but will visit Groningen each year.

This PhD is being re-advertised as the start date has now been delayed until January 2005. Previous applicants do not need to re-apply. This position is open to all EU citizens. Although there is no official deadline please apply ASAP. We expect to interview candidates in early September

Please send the completed UEA application form, two references (completed reference forms) ASAP. Both forms and application details are available at <http://www.uea.ac.uk/bio/studentships/welcome.html> When complete, please sign, date and return the form with all the necessary documentation to:

Graduate Studies Office +44 (0)1603 593002

Science Group Fax +44 (0)1603 593045

University of East Anglia Email [scipg@uea.ac.uk](mailto:scipg@uea.ac.uk)

Norwich NR4 7TJ UK Web site 0000,0000,FF00<http://www.uea.ac.uk> For informal enquiries contact

Dr. David S. Richardson

Telephone 01603 591496

email [david.richardson@uea.ac.uk](mailto:david.richardson@uea.ac.uk)

FAX 01603 592250

Dr. David S. Richardson School of Biological Sciences, University of East Anglia, Norwich NR4 7TJ England

Telephone 01603 591496 email [david.richardson@uea.ac.uk](mailto:david.richardson@uea.ac.uk) FAX 01603 592250

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## UEdinburgh GenomeAnalysis

Dear Everyone

The MSc Quantitative Genetics and Genome Analysis course ([www.QGen.co.uk](http://www.QGen.co.uk)) at the University of Edinburgh has been awarded 3 BBSRC and 6 NERC studentships from September to students from the UK. This year there has been a high number of non-UK stu-

dents applying to attend the MSc course and for some reason a low number of UK applicants.

As a result, there are three NERC studentships currently unallocated and I would appreciate if you could direct any students, whose interests lay in the relevant subject area, towards the MSc course.

Many thanks Neil Cameron

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Neil Cameron Institute of Cell, Animal and Population Biology University of Edinburgh King's Buildings, West Mains Road, Edinburgh EH9 3JT Direct line +44 131 650 5490 FAX +44 131 650 6564 E-mail [n.cameron@ed.ac.uk](mailto:n.cameron@ed.ac.uk) Web [www.QGen.co.uk](http://www.QGen.co.uk)

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## UNewSouthWales ConservationBiology

2 x Ph. D. positions (ARC Australian Postgraduate Awards-Industry)

Conserving our Carnivores: the application of molecular genetics to the conservation management of quolls

The University of New South Wales, in conjunction with its research partners (NSW Department of Environment and Conservation, Vic Department of Sustainability and Environment, WA Department of Conservation and Land Management, NT Department of Infrastructure, Planning and Environment, Environment ACT, TAS Department of Primary Industries, Water and Environment, and the Zoological Parks Board of New South Wales) is seeking two PhD students in molecular ecology, population genetics and forensic identification of quolls.

Quolls, the largest native marsupial predators on mainland Australia, occupy a pivotal ecological niche. All species are declining and are threatened by a variety of interacting environmental processes. This program brings together seven wildlife agencies in a nationwide partnership for understanding and protecting quolls. We will provide new genetic data to test current population and conservation theories using four species of quolls as model taxa to inform us about past histories of populations and to measure parameters of importance to on-ground managers. Results of these projects will help guide management practices for both short- and long-term conservation of these species.

Both scholarships offer an annual tax-free stipend of \$23,294, relocation and thesis production expenses, and ample field work in spectacular but remote and rugged regions. These positions are available from July 2004. Applicants must be permanent residents in Australia or Australian/NZ citizens and should hold a first class honours degree, or equivalent qualification in a discipline such as molecular ecology, conservation genetics, ecology or a related field. Interested applicants should submit a cover letter with a detailed CV (including two referees) to Dr Karen Firestone, Zoological Parks Board of New South Wales, PO Box 20, Mosman, NSW 2088. Applications will be accepted until the positions are filled. Further details and enquiries should be directed to [kfirestone@zoo.nsw.gov.au](mailto:kfirestone@zoo.nsw.gov.au) or phone (02) 9978 4608.

Dr. Karen Firestone

Conservation Biologist Adjunct Lecturer Zoological Parks Board of NSW Biological Earth & Environmental Sciences PO Box 20 University of NSW Mosman, NSW 2088 Sydney, NSW 2052 Australia Australia

ph: +61 2 9978 4608 ph: +61 2 9385 2198 fax: +61 2 9978 4613 fax: +61 2 9385 1558 email: [kfirestone@zoo.nsw.gov.au](mailto:kfirestone@zoo.nsw.gov.au) email: [kfirestone@unsw.edu.au](mailto:kfirestone@unsw.edu.au)

“Firestone, Karen” <[KFirestone@zoo.nsw.gov.au](mailto:KFirestone@zoo.nsw.gov.au)>

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## UPotsdam EvolBiol

PhD grant for 30 months (prolongation possible)

A PhD grant for 30 months (prolongation possible) is immediately available in the newly established graduate school “Earth Surface Processes”:

“Recent and fossil DNA as indicators of past environmental change”

In this project, the distribution of limnic organisms will be assessed in lake sediments of different age (recent to several 10,000 years old), making use of modern molecular genetic techniques. The project objective is to reveal the impact of climatic change on limnic organisms. This is a joint project of the Institute of Biochemistry and Biology and the Institute of Geosciences at the University of Potsdam.

Applicants must hold a university degree (Diplom oder Master of Science, preferably in biology or biochemistry). They should appreciate interdisciplinary research. Familiarity with modern molecular genetic

techniques (PCR etc.) is desired.

The University of Potsdam is an equal opportunity employer. If equally qualified, disabled applicants will be preferably considered. The University of Potsdam aims at increasing the number of female researchers and encourages qualified females to apply.

Please send your application before 31st of July 2004 to: Prof. Dr. Ralph Tiedemann, University of Potsdam, Institute of Biochemistry and Biology, Evolutionary Biology/Systematic Zoology, Karl-Liebknecht-Str. 24-25, Haus 26, D-14476 Potsdam, Germany, Email: [tiedeman@rz.uni-potsdam.de](mailto:tiedeman@rz.uni-potsdam.de)

Prof. Dr. Ralph Tiedemann Universität Potsdam Institut fuer Biochemie und Biologie Evolutionsbiologie/Spezielle Zoologie Karl-Liebknecht-Str. 24-25, Haus 25 D-14476 Potsdam Germany Tel: +49-331-977-5249, -5253 (Sekretariat) Fax: +49-331-977-5070 Email [tiedeman@rz.uni-potsdam.de](mailto:tiedeman@rz.uni-potsdam.de) <http://www.bio.uni-potsdam.de/spezzoo/index.htm>

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## USussex NeuralGeneEvol

The University of Sussex has a BBSRC funded PhD position open for this coming year on the “Evolution of Neural Genes”. The content of the project is flexible but topics which might be considered are adaptive evolution of neural genes, and the evolution of neural gene specific anti-sense RNA genes. The PhD will be supervised by Adam Eyre-Walker (<http://www.lifesci.sussex.ac.uk/CSE/members/-aeyrewalker/aeyrewalker.htm>) and Michael O’Shea (<http://www.sussex.ac.uk/biology/profile2007.html>). It is funded by the BBSRC so UK citizens receive fees and a stipend (EU citizens only get their fees paid). Please send a CV to Adam Eyre-Walker ([a.c.eyre-walker@sussex.ac.uk](mailto:a.c.eyre-walker@sussex.ac.uk)) with a list of three referees. Applications must be received by the end of end of July.

Adam Eyre-Walker Centre for the Study of Evolution & School of Biological Sciences University of Sussex Brighton BN1 9QG

tel : 01273 678480

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## UWalesBangor ConservationGenetics

UWales Bangor: Conservation genetics/forensics studentship

Title: The development and application of genetic markers for wildlife forensics.

University of Wales Bangor, School of Biological Sciences. PhD Studentship available to eligible EU persons with an intended start date of 4 Oct 2004.

The supervisor Prof. R.S. Thorpe and the small business sponsor is Wildlife DNA Services Limited.

Project outline: This project aims to explore the application of population genetic markers to the problem of individual identification in wildlife crime. The work will focus on investigating the ability of species-specific markers to discriminate between closely related individuals, and determining the minimum size of reference population necessary to present DNA profiles as forensic evidence. Some work will be carried out on birds of prey but the remit is broader.

For application forms contact Studentship.enquiries@sbs.bangor.ac.uk it is intended to lodge further information on <http://-biology.bangor.ac.uk/research/opportunities/>

– Professor R S Thorpe School of Biological Sciences University of Wales Bangor Gwynedd LL57 2UW

Tel 01248 382312 Fax 01248 371644 email r.s.thorpe@bangor.ac.uk

“Prof. R S Thorpe” <r.s.thorpe@bangor.ac.uk>

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## Jobs

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## ETHZurich HostParasite

ASSISTANT POSITION Evolutionary ecology of host-parasite interactions

ETH Zurich

We seek to fill the position of an Assistant (senior re-

searcher) in the group of Ecology & Evolution (Experimental Ecology, P. Schmid-Hempel). The ideal candidate works in the field of evolutionary ecology of host-parasite interactions, which can also include the study of immune defences. Interest in using insects as a model system and experience in molecular techniques is advantageous. We expect willingness to collaborate with other people in the group and to contribute to its teaching commitments. Salary according to qualification and local scale; starting date negotiable. Positions



are typically held for 2 - 6 years. More information on [www.eco.ethz.ch](http://www.eco.ethz.ch) and by email (psh@env.ethz.ch - after 15 Aug). Review of applications with CV, publication list and addresses of referees starts 25 Sept 2004.

Prof. Paul Schmid-Hempel ETH Zurich, Ecology & Evolution ETH-Zentrum NW CH-8092 Zurich Ph: +41 1 633 6033 or 6048 Fax: +41 1 632 1271 psh@env.ethz.ch [www.eco.ethz.ch](http://www.eco.ethz.ch) Paul Schmid-Hempel <psh@env.ethz.ch>

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### LeidenU Phycologist

SYSTEMATIC PHYCOLOGIST (tenure track) Vacancy number: 4-169

The candidate should have a PhD degree and subsequent experience in the taxonomy and molecular systematics of algae, an excellent publication record, and knowledge of herbarium curation. The candidate should also have experience in integrating molecular data into traditional systematics. The establishment of an active research program and pursuit of external funding is part of the job requirements. A strong commitment to the teaching of undergraduate and graduate students is mandatory. Supervision of the molecular research of PhD and MSc students working on higher plants and macrofungi will also belong to the tasks of the successful candidate. The ability to speak Dutch or the willingness to learn Dutch is required.

Salary in the first two years ranging from EURO 2179,- / 3344,- per month depending on experience. The tenure track formula implies that following a probationary period of two years, a further three year contract with adapted salary scale will lead to tenure if all task elements of the job descriptions are successfully fulfilled.

Please send your application, stating research interests and specific research goals/targets (the research goals should fit into the general mission statement and research programme of the NHN and PCNE (see our website at [www.nationaalherbarium.nl](http://www.nationaalherbarium.nl)), a CV and the names of 3 references to: Prof. dr. P. Baas, Einsteinweg 2, room A216, 2333 CC Leiden The Netherlands or <mailto:BAAS@NHN.leidenuniv.nl>

publicatiedatum WEB: 26-7-2004 closing date: 1 September 2004

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Joe Zuccarello <[zuccarello@nhn.leidenuniv.nl](mailto:zuccarello@nhn.leidenuniv.nl)>

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### LincolnU Entomology

Lecturer in Entomology Bio-Protection and Ecology Division Lincoln University, New Zealand Vacancy 04/59

Due to a recent retirement, we are seeking a Lecturer in Entomology. The successful candidate will have entomological skills and experience in one or more of the following areas: biodiversity, evolutionary biology, biosystematics, biosecurity, molecular biology. The appointee will teach first year biology and advanced entomology classes, make a contribution to Masters level subjects, as well as supervise the research of postgraduate students.

Research activity is an important part of academic performance, and the appointee will be encouraged to publish widely and actively seek external research funding. To support this outcome, the appointee will be closely associated with the Entomological Research Museum and the National Centre for Advanced Bio-Protection Technologies.

For an Information Pack please visit our website [www.lincoln.ac.nz/jobs](http://www.lincoln.ac.nz/jobs), or contact the Human Resources Section, phone +64 3 325-3613, fax +64 3 325-3870, email [trottc@lincoln.ac.nz](mailto:trottc@lincoln.ac.nz) Please quote the correct vacancy number on your application.

Adrian Paterson

[Patersoa@lincoln.ac.nz](mailto:Patersoa@lincoln.ac.nz)

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### MelbourneU GeneticsLecturer

LECTURER POSITION - The Department of Genetics at the University of Melbourne seeks a Lecturer who will conduct research in the area of Genetics and will be expected to teach in the areas of evolutionary and population genetics, genomics and bioinformatics. The position will be expected to conduct research which leads to publication in quality international journals and will contribute to teaching and course design at undergraduate and postgraduate levels including supervision of B.Sc(Hons) and postgraduate students. For more in-

formation contact Assoc. Prof. James Camakaris or Assoc. Prof Chris Cobbett, tel: + 61 3 8344 6246, email genetics-info@unimelb.edu.au or for a position description and details on how to apply please go to: <http://www.hr.unimelb.edu.au/jobs/> Many thanks

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Veronique Bergeron Manager Department of Genetics The University of Melbourne Ph: +61 (0)3 8344 6250 Fax: +61 (0)3 8344 5139 Email: [bergeron@unimelb.edu.au](mailto:bergeron@unimelb.edu.au)

Veronique Bergeron <[bergeron@unimelb.edu.au](mailto:bergeron@unimelb.edu.au)>

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## NSF Director

Directorate for Biological Sciences Office of the Assistant Director

June 28, 2004

Dear Colleague:

The Directorate for Biological Sciences (BIO) announces a nationwide search to fill the position of Deputy Director, Division of Environmental Biology (DEB).

The Deputy Division Director works closely with the Division Director in overseeing and carrying out the day-to-day operations and management of the Division. They work together as a team providing strong advocacy for program activities within the context of BIO long range plans and NSF's strategic plan and managing resources effectively to nurture new and emerging science opportunities as well as ongoing efforts. In the absence of the Division Director, the Deputy must be prepared to assume this role.

The Division of Environmental Biology (DEB) is responsible for programs with a total annual budget of approximately \$108 million. These programs are currently identified by four clusters- ecosystem science which supports investigations of whole-system ecological processes and relationships in ecosystems across a diversity of spatial and temporal scales; ecological biology which supports studies of community ecology and population interactions that reveal causal mechanisms and patterns for a wide range of habitats and taxa; population and evolutionary processes which supports studies of population properties that lead to variation within and among populations; and systematic biology and biodiversity inventories which supports general sci-

ence of systematics, including the inventory of global species diversity and studies of predictive classification systems that reflect the history of life.

Deputy Division Directors in the BIO Directorate come to their positions with an established record of scientific research and demonstrated leadership experience. Deputy Division Directors must work well with people, be effective communicators and act as mentors to continuously develop the diversity of talents and skills of their colleagues, especially those representing underrepresented minority groups and persons with disabilities.

This position is a career appointment in the Federal Senior Executive Service. You may access the position announcement that includes information on application procedures at

<http://www.nsf.gov/pubs/2004/s20040091/-s20040091ac.pdf> General inquires should be directed to:

Dr. Michael R. Willig Division of Environmental Biology Tel: (703) 292-8480 Fax: (703) 292-9064 E-Mail: [mwillig@nsf.gov](mailto:mwillig@nsf.gov)

Applications may be transmitted electronically to [execsrch@nsf.gov](mailto:execsrch@nsf.gov) or mailed to :

National Science Foundation Executive Personnel and Development Branch Division of Human Resource Management 4201 Wilson Boulevard, Room 315 Arlington, VA 22230

The Executive Personnel and Development Branch may be reached by telephone at (703) 292-8755.

I look forward to any help you may be able to offer in this search for outstanding candidates and encourage you to consider your interest in this position. The deadline for receipt of applications is July 23, 2004.

Sincerely,

Mary E. Clutter Assistant Director [mcourtne@nsf.gov](mailto:mcourtne@nsf.gov)

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## PurdueU LabManager

A Lab Manager is needed to help run a large genetics lab at Purdue University. This is a multi-investigator lab-not a core facility-that serves four Principal Investigators (PIs) and their associated staff. The incumbent will: maintain supplies and equipment; train students and staff in laboratory procedures and equipment operation; develop and improve laboratory protocols;

maintain laboratory equipment and ensure compliance with radiation and other safety requirements; submit compliance paperwork as required; and provide regular briefings to PIs.

The position requires a degree in Biology, Botany, Zoology, Genetics or a closed related field. One year experience in molecular biology and the previous supervision of technical personnel is required, as is fluency in spoken and written English. Experience with microarrays and automated DNA sequencers desired. Interested parties should contact J. Andrew DeWoody (dewoody@purdue.edu), Dept. of Forestry & Natural Resources, 1159 Forestry Building, Purdue University, West Lafayette IN 47907-1159. Women and minorities are encouraged to apply. Purdue University is an equal opportunity employer.

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### Seattle FishGenetics

The Genetics and Evolution Program at the Northwest Fisheries Science Center, Seattle, is looking for a highly motivated recent graduate (undergraduate or masters) for an internship in fishery genetics. The successful applicant will work in our genetics laboratory on a project using genetic techniques to estimate fish abundance. The one year position is funded through the Oak Ridge Institute for Science and Education (ORISE – <http://www.ora.gov/orise.htm>), and pays approximately \$40,000. We are looking for someone with molecular genetics experience who is interested in applying molecular methods to problems in natural resource management. If interested, please send a CV and brief (1/2 page or less) letter of interest to Michael Ford (mike.ford@noaa.gov). Position is limited to US citizens. We are looking for some to start as soon as possible, and the position will remain open until filled. See <http://www.nwfsc.noaa.gov/> for more information about the Northwest Fisheries Science Center.

mike.ford@noaa.gov mike.ford@noaa.gov

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### UAlaska Fairbanks MammalianEcol

The Department of Biology and Wildlife and the Institute of Arctic Biology at the University of Alaska

Fairbanks seeks applications for a tenure-track position in Wildlife Ecology at any level. Applicants must have earned a Ph.D. in Wildlife Ecology or a closely related discipline. Postdoctoral and teaching experience, a strong record of extramural funding, the ability to supervise graduate students, to collaborate with fellow faculty, and to interact with state and federal resource management agencies are preferred.

We seek a broadly trained mammalian ecologist to conduct quantitative research that addresses basic and applied questions relevant to sustainability, harvested species, or predator-prey systems that have applicability at the state, national, and international levels. This position is 50% research and requires a teaching load of two courses per year, to include an undergraduate wildlife course and development and collaboration on graduate offerings. Numerous field stations and laboratory facilities are available at IAB to conduct research on captive and wild animals, including the R.G. White Large Animal Research Station, Animal Quarters, Toolik Field Station, Bonanza Creek LTER site, Spatial Ecology Laboratory, Alaska Center for Environmental Statistics, Alaska Geobotany Center, and the DNA Sequencing Core Facility. Extensive collections are available for study at the Univ. of Alaska Museum. The successful candidate will have the opportunity to interact and collaborate with 30 faculty studying a diverse array of topics. The Biology and Wildlife department has approximately 300 undergraduate and 110 graduate students, including 40 Ph.D. students. Applicants are encouraged to consult the Institute/departmental website, and faculty profiles at <http://mercury.bio.uaf.edu> before applying.

Applications will be reviewed starting 17 September 2004. Please provide an applicant form ([http://www.alaska.edu/hr/forms/PDF\\_ent/-applicant\\_form\\_ent.pdf](http://www.alaska.edu/hr/forms/PDF_ent/-applicant_form_ent.pdf)), cover letter, curriculum vitae, statement of research interests, statement of teaching interests, letters from 3 references and submit to: Eric Rexstad, C/O UAF Human Resources, P.O. Box 757860, Fairbanks, Alaska 99775-7860, Phone (907) 474-7700, Fax (907) 474-5859. Please reference: PCN#20245, REQ# FF20424501. If you have specific questions about this announcement, please contact Eric Rexstad, (907) 474-7159, e.rexstad@uaf.edu.

The University of Alaska Fairbanks is an Equal Opportunity/Affirmative Action Employer and Educational Institution. Women, protected, and minority applicants are encouraged to apply.

Link Olson <Link.Olson@uaf.edu>

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## UAngers EvolBiology

Position in Evolutionary biology at University of Angers (France)

Un poste de maître de conférence en biologie animale évolutive est susceptible d'être ouvert à l'université d'Angers (section 68 CNU). La date de prise en fonction serait le 01/02/05 ou le 01/09/05. Il concerne des candidats ayant réalisé un stage post-doctoral, justifiant d'une expérience en écologie et maîtrisant les techniques de génétique des populations. Le candidat devra également être inscrit sur les listes d'aptitude au poste de maître de conférence. ([http://www.education.gouv.fr/personnel/-enseignant\\_superieur/enseignant\\_chercheur/-antares.htm](http://www.education.gouv.fr/personnel/-enseignant_superieur/enseignant_chercheur/-antares.htm))

Enseignement: l'enseignant-chercheur devra participer à la formation des étudiants en biologie animale et écologie et plus particulièrement dans les domaines de l'écologie des zones humides, de la systématique et de la biologie des populations. Une bonne connaissance du fonctionnement des zones humides et l'utilisation des outils de génétique écologique serait appréciée

Recherche : le travail de recherche concerne les problématiques de dispersion et de distribution des vertébrés développées dans l'UMR Paysages et Biodiversité. Ce poste est inscrit dans une perspective de spatialisation des données génétiques dans les structures de paysage. Le chercheur devra travailler notamment à l'étude de la diversité génétique et des flux de gènes à différentes échelles (des individus aux espèces). Des applications à l'écologie évolutive, la biologie de la conservation ou l'écologie comportementale sont possibles. Une expérience de la modélisation constituerait un plus apprécié. Pour des informations complémentaires, veuillez contacter (voir ci-dessous)

A permanent position in evolutionary biology is expected to start at the university of Angers (France) on February 1st 2005 or September 1st 2005. This position (maître de conférences) includes 192 h teaching per year. The candidate should be recorded on the list of aptitude to the position of maître de conférences section CNU 68. Teaching is to be done in French. ([http://www.education.gouv.fr/personnel/-enseignant\\_superieur/enseignant\\_chercheur/-antares.htm](http://www.education.gouv.fr/personnel/-enseignant_superieur/enseignant_chercheur/-antares.htm))

Teaching: the applicant will teach animal biology and ecology, with a special focus on wetland ecology, systematics, and population biology. Good knowledge on wetland ecology and population genetics would be much appreciated.

Research: the applicant should have a post-doctoral experience in ecology and justify skills in population genetics. Research will focus on vertebrate dispersion and distribution and is to be integrated in the themes of the research unit Landscapes and Biodiversity. The researcher will focus on the study of genetic diversity and gene flow at different scales (from individuals to species) with the main objective to analyze genetic data in relation with landscape structure (landscape genetics). Applications to evolutionary ecology, conservation biology or behavioral ecology are possible. Experience in modelisation would be welcome. For further information, please contact:

Professeur Thierry Lodé Laboratoire d'écologie UMR Paysages et Biodiversité Université d'Angers

thierry.lode@univ-angers.fr Phone: 33.2.41.73.53.53. Fax: 33.2.41.73.53.52. <http://sciences.univ-angers.fr/-ecologie> Laboratory of Animal Ecology UMR Landscape and Biodiversity University of Angers Faculté des Sciences Campus de Belle-Beille 2 bvd Lavoisier F-49045 Angers France +33/ 2 41 73 50 30

<http://sciences.univ-angers.fr/ecologie/> Jean Secondi <jean.secondi@univ-angers.fr>

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## UBritishColumbia MicrobialGenomics

Below I've pasted a job ad from the Department of Microbiology and Immunology at the University of British Columbia.

I'm not sure exactly what prokaryotic enviromics is, but I'm sure it overlaps with evolution. Several of us in the Dept. of Zoology are working on microbial evolution and ecology (myself, Sally Otto, and Michael Doebeli), and we'd love to have another colleague nearby.

Don't let the priority given to Canadians put you off - UBC hires on scientific merit. And you couldn't ask for a better place to live than Vancouver.

Rosie Redfield

THE UNIVERSITY OF BRITISH COLUMBIA

The Department of Microbiology and Immunology, University of British Columbia, has two tenure track positions available for investigators whose research interests lie within one of the following two broad areas: 1) prokaryotic gene regulation, enviromgenomics of environmentally relevant organisms or communities, ecology, 2) cellular microbiology, innate immunity. At least one of the selected candidates would be eligible for a Canadian Research Chair, a prestigious funding program that was created to attract and retain outstanding young scientists. Although we anticipate hiring at the Assistant Professor level, appointment at a more senior level is possible for suitably qualified applicants. The Department of Microbiology and Immunology has a strong research record and a thriving graduate program. The nominated candidates will benefit from shared departmental equipment and modern laboratory facilities within a newly erected Life Sciences Building that will be home to more than 100 multidisciplinary research teams. The University of British Columbia hires on the basis of merit and is committed to employment equity. All qualified applicants are encouraged to apply; however, Canadian citizens and permanent residents will be given priority (applicants should identify citizenship and/or immigration status). Interested individuals should send their CV, summary of proposed research activity over the next five years, and the names of three referees to Nancy Kan, Secretary to the Head, Department of Microbiology and Immunology, 300 - 6174 University Boulevard, Vancouver, BC, V6T 1Z3, Canada. Electronic (PDF) submissions can also be sent to [nancyk@interchange.ubc.ca](mailto:nancyk@interchange.ubc.ca). The deadline for applications is August 15, 2004.

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### UFribourg EcoEvol

The Faculty of Science of the University of Fribourg (Switzerland) invites applications for a position of

FULL PROFESSOR IN ECOLOGY AND EVOLUTION

in the Unit of Ecology and Evolution of the Department of Biology, starting as soon as possible.

The successful candidate will conduct his/her own research, attract external funding, contribute to the teaching programme for students in Biology and Environmental Sciences and take turns in directing the Department. Teaching is in French or German, and

the candidates should be willing to acquire a working knowledge of the other language.

Candidates are requested to send before September 30, 2004 a curriculum vitae (including a list of publications and a record of both funding and teaching experience) and a one page description of his/her research projects to Prof. Marco Celio, Dean, Faculty of Sciences, University of Fribourg, Musée 6a, CH-1700 Fribourg.

Further information under [www.unifr.ch/biol](http://www.unifr.ch/biol) or by [Jean-Pierre.Metraux@unifr.ch](mailto:Jean-Pierre.Metraux@unifr.ch), head of the Department. [Jean-Pierre.Metraux@unifr.ch](mailto:Jean-Pierre.Metraux@unifr.ch), head of the Department.

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### UHawaii Tech

[http://workatuh.hawaii.edu/zoom\\_job.php?2996](http://workatuh.hawaii.edu/zoom_job.php?2996) Research Support PBB, Coral Molecular Biology Research Technician, position number 0077572T, UHM Hawaii Institute of Marine Biology, (Coconut Island, Kaneohe Bay), temporary, NTE Jun-30-2005, renewal subject to funding availability, satisfactory performance and program needs Duties: Coordinate and facilitate research activities in Dr. Gates's laboratory; set up microcosms for experimental manipulations, collect samples, isolate tissues by dissection; perform and troubleshoot molecular biology tasks including the extraction and quantification of nucleic acids, PCR, 3 and 5' RACE, cDNA library construction, cloning and sequencing; develop, hybridize and scan microarrays; analyze DNA sequence and microarray data using a variety of software packages; perform routine microscopy; implement appropriate university, state, and federal fiscal and safety policies; perform other duties as assigned. Minimum qualifications: Completion of a pertinent baccalaureate educational degree and relevant professional experience; competency in technical knowledge, critical thinking skills, communication skills and interpersonal skills; demonstrated hands-on experience in a biological laboratory setting; working knowledge of the principles, practices and techniques of cell and molecular biology; demonstrated ability to operate and maintain personal computers, and working knowledge of the software necessary to complete analyses of the data generated in the laboratory; demonstrated ability to supervise subordinates, manage work priorities and projects, and manage employee relations; alternatively, any equivalent combination of education and/or professional work experience that provides the required education, knowledge, skills and abilities as indicated. Desirable quali-

fications: Practical experience with cell and molecular techniques including nucleic acid extraction, plasmid purification and restriction digests, protein and nucleic acid analysis, molecular cloning, and sequencing; experienced diver and boat operator; knowledge of form and style of research analyses and writing. Pay range: minimum \$3056/month To apply: Submit cover letter indicating how you satisfy the minimum and desirable qualifications, official transcripts, 3 letters of recommendation, UH Form 64 Application address: P.O. Box 1346, Kaneohe, HI 96744 Inquiries: Dr. Ruth D. Gates 808-236-7420 rgates@hawaii.edu Date posted: Jul-14-2004 Closing date: Jul-29-2004

The University of Hawai'i is an equal opportunity/affirmative action institution. All qualified applicants will be considered, regardless of race, sex, age, religion, color, national origin, ancestry, disability, marital status, sexual orientation, or status as disabled veteran or veteran of Vietnam era.

Employment is contingent on satisfying employment eligibility verification requirements of the Immigration Reform and Control Act of 1986. Appointments to positions are subject to campus recruitment guidelines and the collective bargaining agreement.

APT applicants with re-employment rights or priority status are responsible for informing the recruiting unit, which will verify eligibility with the employing unit as provided by the BU 08 contract.

Rob Toonen <toonens@hawaii.edu>

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### UHawaiiHilo TempAssistProf

Assistant Professor of Biology: Position No. 86432T, University of Hawaii at Hilo, College of Arts & Sciences, temporary, nine-month appointment to begin approximately August 2004 and NTE July 31, 2005; pending position clearance and funding, with possibility of reappointments.

Duties: Teach undergraduate courses in cell and molecular biology, evolution and general ecology and introductory biology.

Minimum Qualifications: Ph.D. from an accredited college or university in a biological science discipline appropriate to the position, demonstrated expertise in conservation biology/genetics.

Desirable Qualifications: Teaching experience at the

college or university level, familiarity with Hawaiian ecosystems and conservation issues. Salary: Competitive. To Apply: Submit curriculum vitae, letter of application, and the names and e-mail addresses of three recent references to: Dr. Donald Price, Biology Department, University of Hawai'i at Hilo, 200 W. Kawili St., Hilo, Hawai'i.

Inquires: Dr. Donald Price, ph. 808-974-7365, fax 808-974-7393, email donaldp@hawaii.edu.

Dr. Donald K. Price co-Project Director - Hawaii NSF EPSCoR Program Director - TCBES Masters Program - UH Hilo Associate Professor of Biology - UH Hilo Ecology, Evolution and Conservation Biology - UH Manoa 200 W. Kawili Street University of Hawaii Hilo, HI 96720 808-974-7365 fax 808-974-7693 email: donaldp@hawaii.edu

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### UHouston EvolBiol

#### FACULTY POSITION IN EVOLUTIONARY BIOLOGY

The Department of Biology and Biochemistry at the University of Houston invites applications for a tenure-track Assistant, Associate or Full Professor position in Evolutionary Biology to complement existing strengths within the Division of Ecology and Evolution. Candidates are welcomed from all areas of evolutionary biology, including those using theoretical, molecular, ecological, or experimental approaches. The position requires an earned doctorate and postdoctoral experience. The successful candidate is expected to maintain a nationally competitive externally funded research program and participate in graduate and undergraduate teaching. The Department has spacious laboratories and offers competitive startup packages. Please submit curriculum vitae, list of publications, statement of research interests, and arrange for three letters of recommendation to be sent directly to: Dr. Dan Graur, Chair, Evolutionary Biology Search Committee, Department of Biology and Biochemistry, University of Houston, Houston, TX 77204-5513 (E-mail: dgraure@uh.edu). All materials must be received by October 1, 2004.

UH is an Equal Opportunity/Affirmative Action Employer. Minorities, women, veterans and persons with disabilities are encouraged to apply.

- Dan Graur, Ph.D. John and Rebecca Moores Profes-

Department of Biology & Biochemistry University of Houston Houston, TX 77204 USA

email: dgraur@uh.edu Tel: 713-743-7236 Fax: 713-743-2636 Homepage: nsm.uh.edu/~dgraur

Dan Graur <dgraur@uh.edu>

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## ULausanne ResTech

A research technician position is available at the University of Lausanne, Switzerland from October 1st or later, as part of a project on the evolution of reproductive traits in the plant *Silene latifolia*, Caryophyllaceae (<http://www.unil.ch/dee/page7005.en.html>). Applicants would ideally have laboratory experience and familiarity with experimental work. The tasks include laboratory work (microsatellite DNA; assays of pollen viability, pollen tube growth rates, enzyme activity), and collaboration with greenhouse experiments. The position is for initially 2 years, and may prolonged.

If interested, please contact:

Dr. G. Bernasconi Swiss NSF Professorial Fellow Current address: Institute of environmental Sciences University of Zurich Winterthurerstr. 190 CH 8057 Zurich Switzerland Email: bernasco@uwinst.unizh.ch

Application deadline: 15th August 2004 For application send: CV, name and address of two referees.

The Department of Ecology and Evolution of the University of Lausanne, Switzerland, provides a very lively intellectual and social environment (<http://www.unil.ch/dee/page5090.en.html>).

Lausanne, located in Switzerland at the shore of Lake Geneva, offers very high quality of life and outstandingly beautiful surroundings (Alps, Jura mountains, Lake; see <http://www.lausanne-tourisme.ch/>).

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## UMontreal programmer

Company/Institution: Robert-Cedergren Centre for Bioinformatics & Genomics, Universite de Montreal

Job Title: Development Programmer

Job Description: The position entails primary respon-

sibility for the maintenance and development of web interfaces for the two bioinformatics databases GOBASE (<http://megasun.bch.umontreal.ca/gobase/>) and PEPdb (<http://amoebidia.bcm.umontreal.ca/public/-pepdb/agrm.php>), written principally in PHP but also involving Java. The candidate will further be responsible for the maintenance of existing bioinformatics-related software and development of new code, including Perl scripts and C programs. The development will occur in a primarily Linux-based environment. The successful candidate will be a member of a closely integrated development team comprised of other programmers and database curators.

Requirements:

At least 3 years' programming experience Proficiency in Perl/PHP and SQL Familiarity with C and Java Strong Linux background Good communication skills A working familiarity with the concepts of molecular biology would be highly useful

Availability: The position is available immediately.

Contact:

Emmet A. O'Brien, Database Group Leader Departement de Biochimie Universite de Montreal Pavillon Roger Gaudry (P. principal) H-307-13 2900 Edouard-Montpetit Montreal QC, H3T 1J4 eobrien@bch.umontreal.ca

Emmet O'Brien <eobrien@BCH.UMontreal.CA>

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## UMuenster PlantEvolEcol 2

The University of Muenster (Germany) seeks to appoint a

Full Professor of Botany (C4/W3 salary scale)

in succession of Prof. von Willert.

Candidates should have an excellent track record of research in EVOLUTIONARY ECOLOGY and should have worked on genotypic and phenotypic adaptation in natural populations using experimental techniques.

The candidate is expected to contribute in part to compulsory teaching units, including basic botany (plant evolution; plant functional morphology and adaptation; field trips). Applicants must hold a doctorate and have a postdoctoral track record of independent academic research and teaching (German Habilitation or equivalent experience). Foreign candidates are expected to

acquire sufficient language skills for teaching in German within 2 years after taking up the position.

The position is substantially equipped, comprising an annual budget and core funding for scientific and technical posts.

The professorship will play a central role in a new institute in evolutionary biology and biodiversity studies which will be formed by the merger of the existing institutes of "Plant Ecology and "Animal Evolution and Ecology. In 2005 another professorship in the area of Botany will be advertised in this unit.

The WWU seeks to increase the proportion of female staff members in the faculty and therefore urges interested female candidates to apply. In case of equal qualifications, preference will be given to disabled applicants.

Applicants should send their CV, copies of transcripts and degree certificates, a list of publications and grant income to date, and a research plan not later than 6 August 2004 to the Dean of the School of Biological Sciences, University Münster, Hindenburgplatz 55, 48143 Münster, Germany. Electronic submissions in pdf-format and informal inquiries should be sent to: dekanat.bio@uni-muenster.de.

Prof. Dr. Nico K. Michiels Institute of Animal Evolution and Ecology Westphalian Wilhelms-University Muenster Huefferstrasse 1, D-48149 Muenster, Germany

Tel. +49 (0)251 83 24661 Mobile +49 (0)170 4758003  
Fax. +49 (0)251 83 24668

michiels@uni-muenster.de <http://www.uni-muenster.de/Biologie.EvoEco/Evolbio/> Nico Michiels  
<michiels@uni-muenster.de>

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## UNebraska Fisheries

### FISHERIES ECOLOGIST

The School of Natural Resources (SNR), University of Nebraska-Lincoln, invites applications for a tenure-track, 12-month assistant professor faculty position in fisheries ecology (50% research/50% teaching). Research focus on fish ecology with a quantitative, interdisciplinary approach to addressing critical issues such as species-habitat interactions, predator-prey dynamics, and community bioenergetics preferred. Position complements and interacts with faculty in fisheries

and wildlife, the new Cooperative Fish and Wildlife Research Unit, SNR hydrological sciences, and the Nebraska Game and Parks Commission. Research responsibilities include development of a successful research program; publications in refereed journals; strong record of extramural grant funding; and supervision of graduate students and post doctoral research associates. A key faculty for the Fisheries and Wildlife major, this person must be strongly committed to undergraduate and graduate teaching. Teaching responsibilities include Ichthyology; Fisheries Science; a new graduate-level course in area of specialization (e.g., Reservoir Fisheries Ecology and Management, River Fisheries Ecology and Management, Ecological Statistics); and participation in undergraduate and graduate seminars. Requires a Ph.D. in fisheries ecology, ecology, or related field, with expertise in quantitative approaches to population, community, and/or ecosystem research, and experience with interdisciplinary and collaborative research. More information at SNR website: <http://snr.unl.edu>. Interested candidates should send a signed letter of application, curriculum vitae, statements of teaching and research interests, and three letters of reference to:

Chair, Fisheries Ecologist Search Committee School of Natural Resources University of Nebraska-Lincoln 307 Biochemistry Hall Lincoln, NE 68583-0758 E-mail: pfreeman1@unl.edu

Review of applications begins on September 15, 2004 and continues until the position is filled or the search is closed.

The University of Nebraska is committed to a pluralistic campus community through affirmative action and equal opportunity and is responsive to the needs of dual career couples. We assure reasonable accommodation under the Americans with Disabilities Act. Contact Sharon Kelly at (402) 472-9873 for assistance.

gortil@unl.edu

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## URochester ResearchTech

Description: A research technician IV position is available at the University of Rochester, in Rochester New York conducting studies of intracellular bacteria in insects. The position is part of a 5-year NSF funded project to investigate molecular genetics, ecology and evolution of Wolbachia, a widespread and important group of intracellular bacteria found in invertebrates.



Duties/Qualifications: The ideal applicant will be familiar with standard molecular genetic techniques such as DNA and RNA preparations, diagnostic and quantitative PCR, cloning, and sequencing. Some experience with programs for sequence reactions and alignments is desirable. Other duties will include maintenance of insect cultures, ordering supplies, reagent preparation, and other tasks as assigned. Must be able to work independently and maintain good records of work completed. B.S. or M.S. in Biology or related discipline.

Conditions: This position is available now and will be funded through the life of the grant (2003-2008) and possibly beyond.

Instructions: Send resume and cover letter to Cathy Westbrook via email at cwestbro@mail.rochester.edu or mail at the University of Rochester, Dept. of Biology, 226 Hutchison hall, River campus, Rochester, N.Y. 14627-0211. Phone: 585-275-3889. fax 585-275-2070

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## Other

|                                       |    |                                      |    |
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### AFLP sea anemones

Dear all,

I am about to start AFLP analysis on a population of the anemone *Condylactis gigantea*. There is little mention of AFLP analysis on Cnidarians in the literature as far as I can see.

I would be really interested to hear from anyone who may have attempted AFLP with any type of Cnidarian. I am currently struggling with the joys of getting a good yield of reasonably intact genomic DNA, but getting there I think.

Hope someone can offer some advice.

Best regards

Alex

Alexander Venn Ph.D. Candidate Department of Biology (area 2) University of York PO Box 373 York YO10 5YW UK E: Alexandervenn@yahoo.com T: +44 1904 438611

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### BSA and PCR

Hi all, Does anybody know if too much BSA (used to counter inhibition in PCR) can actually inhibit PCR itself? If yes, does anybody have a feel for the concen-

tration at which it becomes detrimental? Thanks for your help Tom Gilbert

Dr Tom Gilbert Ecology and Evolutionary Biology University of Arizona Tucson AZ 85721-0088

Tel: 520-621-1960 Fax: 520-621-9190  
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### BSA inhibition PCR answers

Dear All, Last week I wrote and asked 'Can too much BSA inhibit PCR'. I got back a lot of very useful information, and most people who wrote to me asked if I could summarize the findings. So, here goes....

The simple answer seems to be definitely yes, if its acetylated and people should be warned that a lot of the BSA that comes with restriction enzymes is acetylated, so for PCR buy specific non-acetylated BSA! New England Biolabs supplies a popular ready made solution. I personally have been using Sigma's powdered form (#B6917) that I dilute to 10mg/ml and freeze (and use 1ul in a 25ul RXN).

As for whether non-acetylated BSA inhibits, the answer seems to be yes, but the concentration at which inhibition starts all depends on the particular extract (which naturally contains a whole host of variables), and the enzyme being used for the PCR.

It seems that usual' levels of BSA used for PCR to counter inhibition are about 0.1-0.4mg/ml final concentration, but some people have observed success at up to 10mg/ml (readers should note that such cases were accidental' application, not done for any benefit!). The highest level that anybody specifically seemed to use was 3mg/ml, on unpurified alkali lysed plant extracts. In contrast however, at least one person who replied has specifically tested the issue, and in his case found BSA inhibited at any level above 0.1mlg/ml.

On a further note, various people mentioned observing the PCR becoming gelatinous during cooling above certain concentrations (eg 5mg/ml), and becoming so gelatinous above 10mg/ml that the PCR couldn't be run on a gel. From my own personal experience I will add that the concentration that this seems to become a problem appears to depend on the enzyme (or at least its buffer). For example, I have seen PCRs using ABI's Taq Gold' and Invitrogen's Platinum Taq' fill with what we like to call snot' during the PCR process, at BSA levels where Invitrogen's Platinum Taq Hifi' is fine. One

observation that may explain the difference it is that Gold and Platinum use MgCl2 as a buffer, whereas Hifi uses MgSO4 (I've no idea why, but it correlates nicely)

As for the actual inhibition, most people reported a peak' of efficiency at particular concentrations, either side of which the amplification success drops off (although fairly slowly it would seem). So overall it seems that if anyone really cares, they will need to optimize for particular sample/extraction method/enzyme combinations.

Thanks to all those who replied with very useful information: Anne Chenuil, Rob Cruickshank, Will Goodall-Copestake, Alistair Jump, Jeff Lozier, Connie Mulligan, Olivier Raspé, Dominik Refardt, Scott Santos, Henri Thomassen, Rajenda Whitlock, Sam Wisely, Craig Wilding

Hope this summary is of use to some people out there

Tom Gilbert Tom Gilbert

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### Bulked Samples

Hello Everyone,

I am a phd student working with microsatellite markers in oat. I work with bulked samples and am experiencing problems with entering these data in ordinary programs for analysis, since these only accept two possible alleles for codominant data. I get on occasion three and could in theory get even more - since the data derive from thirty individuals bulked into one test-sample. Does anyone have experience with entering this kind of data into e.g. ntsys or phylip?

thank you Louise Nersting

Cand. Scient. Louise Grau Nersting Risoe National Laboratory DK-4000 Roskilde phone +45 46 77 41 89

louise.grau.nersting@risoe.dk

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### Cephus samples

A student in our lab is working on a wide scale DNA based -phylogeographic study of the wheat stem sawfly (Cephus cinctus), a destructive insect pest of wheat in

the Northern Great Plains. We are also interested in the relationship between *Cephus* species using mt and nuclear gene sequences. However, we do not have any sample from *C. hyalinatus* which is known from eastern Asia including Japan. Is there someone who have well conserved specimen of this species (or closely related species) and is ready to send specimens to us to complement our analysis? 95%-96% ethanol is suitable for storing and shipping the material. However, we will also accept samples that have been fixed in formalin or dried.

Please contact me on the address given below.

Many thanks and best wishes,

Marie-Claude BON, PhD European Biological Control Laboratory USDA, ARS Campus International of Bailarguet 34980 Montferrier sur Lez France Tel: (33) 4 99 62 30 41 Fax: (33) 4 99 62 30 49 mcbon@ars-ebcl.org

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## Collecting plants

Dear All.

A few weeks ago I posted a summary of the responses I received following my queries about high throughput methods of preparing dried leaves for PCR. Based on these responses (from people largely working on deciduous trees and some Mediterranean shrubs) and my own experience, I suggested collecting the youngest leaves available.

I've since been contacted by Mike Fay (head of genetics at the Jodrell lab at RBG Kew) who reports difficulty in obtaining amplifiable DNA from young leaves in some groups of species. This highlights the importance of checking the methods to be used with unfamiliar species before embarking on large-scale collections of material. Mike's advice follows:

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In our experience, in some groups of plants, at least, young leaves give unamplifiable DNA due to the presence of inhibitory chemistry not present in more mature tissues. This is definitely the case in some legumes among others. It is probably due to the plant producing compounds to prevent insect predation before the leaves have hardened off.

Our standard advice is to collect fully expanded leaves that have not begun to senesce. This works well for the vast majority of plants (our DNA bank contains nearly

20K samples extracted following this recommendation).

Flowers can be used as an alternative - they produce far less by way of secondary chemistry, cuticle etc. than leaves in most cases, and in really problematic cases (e.g. some tropical orchids) for which we get next to no amp. from leaves, floral DNA performs well. It is also a way round problems with plants with succulent leaves or other tissues - e.g. cacti, many terrestrial orchids etc. We routinely extract from flowers of *Dactylorhiza*, *Orchis* etc. when these are available in preference to leaves.

\*\*\*\*\*

— Dr. A.S. Jump

Affiliation: Centre de Recerca Ecològica i Aplicacions Forestals (CREAF)

Current address:

Departamento de Genética Molecular IBMB-CSIC C/Jordi Girona 18 08034 Barcelona Spain Tel: 0034 934006100 ext 256 Fax: 0034 932045904 Fax: 0034 932045904

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## DNA Barcoding

Dear Evoldir / Taxacom / PEET members,

ANNOUNCEMENT AND REQUEST FOR HELP

Special Debate: DNA Barcoding, Thursday, 23rd September, Univ. of Illinois, Champaign-Urbana, Illinois As part of the forthcoming PEET meetings this September (<http://www.conferences.uiuc.edu/peet/>) I will be chairing a debate on DNA barcoding at the University of Illinois. Speaking in defense of barcoding will be Paul Hebert (University of Guelph), arguably the founder of the barcoding movement. Speaking against will be Kip Will (University of California), a voice of caution who has recently published on the pitfalls of molecular taxonomy. I am keen to engage the wider taxonomic community beyond PEET grant holders in this debate and this is where you can help...

I am looking for a diverse selection of questions that can be put to Paul and Kip by a student panel as part of the debate. These questions should cover the full spectrum of issues associated with the application of DNA barcoding, from its use in taxon identification and discovery, through to its practical and political ramifications if barcoding is to become more widely applied within taxonomy. If you would like to submit a

question, reply to me personally (OFF LIST PLEASE) at "vsmith@inhs.uiuc.edu", preferably with the subject line "DNA Barcoding Debate".

The proceedings of this meeting will be published (subject to peer review) in question and answer format in a forthcoming issue of Systematic Biology. All questions selected will be credited with their author unless they would prefer to remain anonymous. This is an excellent opportunity to ask questions to two of the leading authorities on genetic barcoding and get a direct answer - don't miss it!

All questions will be considered, and just to make things more interesting they will not be disclosed to Paul Hebert or Kip Will until they are asked on the day of the debate!

Thanks and apologies for cross posting,

Vince Smith

-NOTE MY NEW ADDRESS AS OF JULY 04-

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## Dried leaves extraction answers

Dear all.

Several weeks ago I posted a query regarding techniques and potential pitfalls of high-throughput systems of DNA extraction from silica-gel dried leaves. I received almost as many questions as answers in reply; the questions regarded just about every aspect of working with dried leaves from collection through to genotyping. Below is a summary of information from my experience and that of all who replied to my original query.

Regards.

Alistair Jump

1) Sample collection: Collect the youngest tissue you can. In newly unfolding leaves there are more cells per area and therefore you get a higher yield of DNA from the same mass of leaf. Even more important, the tissue is likely to contain far fewer secondary metabolites and therefore it is much easier to obtain clean DNA from young tissue. For some species it may be near impossi-

ble to use simple methods to purify DNA from mature leaves.

2) Preservation: Dry rapidly using an excess of silica gel (for example a 10:1 ratio gel:leaf by mass) a mixture of 20-200 mesh size silica gel with 6-16 mesh indicating gel is ideal. The faster the leaf samples dry - the better the DNA quality, so dry small pieces of leaf (around 2 cm<sup>2</sup>) and cut out fleshy midribs if necessary. If you have to collect very succulent tissue using desiccants then separate and discard the water storage layer and dry the photosynthetic layer of the leaf/stem. Calcium sulphate ('Drierite') can also be used to dry samples (but requires higher temperatures to reactivate it if reused). Store dried leaves with some active desiccant at room temperature or in a cold room if you have access to one. Protect them from light. When reusing desiccants, they can be baked to sterilise them. If you bake either type at too high a temperature it destroys the indicator and can impair their ability to absorb water - so check the instructions first! Chase and Hill (1991) Taxon 40:215-220 give more information on using silica gel for drying leaves for DNA extraction.

3) Sample disruption: Several people sounded almost tearful in their description of how much the tissue lyser/mixer mill had reduced the labour involved in processing hundreds of samples! The consensus is that it works well as long as you get the sample into the bottom of the tube and the steel (or preferably tungsten) bead on top (a flat piece of leaf adhering to the side of the tube will not be ground). Cooling the rack of tubes in liquid nitrogen before grinding in the machine will improve the grinding of tougher dried samples. A common problem when working with dried leaves is the build up of static electricity. This may be solved by grinding the leaves after cooling the racks in liquid N. Where this remains a problem, be very careful when opening the caps to avoid losing sample and consequent risk of cross contamination. Grinding dried leaves in extraction buffer may produce degraded DNA, whereas grinding them after freezing with liquid nitrogen will yield excellent quality DNA if they have been dried rapidly.

4) Extraction/purification method: Do not presume that the method you use for extracting DNA from fresh leaves will work as well if the same leaves are dried. In some cases, changes in the leaf chemistry during drying can cause problems. If you are going to carry out a large scale sample collection, the cautious approach is to check you can get useable DNA from dried leaves before you collect them!

In general: the Quiagen DNeasy plant 96 kit was considered well worth the money and has been used with a variety of often difficult species.

Other multiple extraction and purification protocols suggested were Mogg and Bond (2003) Molecular Ecology Notes 3: 666-668 and one from the Somers lab at U Minnesota - to be found at: [http://bioplasticscollaborative.coafes.umn.edu/-uniplate\\_DNA\\_extraction.htm#](http://bioplasticscollaborative.coafes.umn.edu/-uniplate_DNA_extraction.htm#)

Another approach is to PCR from crude plant extracts without purifying the DNA (simple alkaline lysis) - in combination with a modified PCR buffer. This has more limited applicability, but it can save a huge amount of time and money when useable. In all cases when working with crude extracts you should check the reliability of such methods against 'clean DNA' controls before commencing a large scale genotyping operation. Inhibition of PCR by components of the extract may be locus specific, so it is unwise to use them with multi-locus markers such as ISSR or for markers requiring digestion/ligation steps such as AFLP. However, they may be used with single locus markers such as microsatellites if tested properly. See Jump et al. (2003) New Phytologist 160: 359-370 and Xin et al. (2003) Biotechniques 34: 820-826 for methods.

— Dr. A.S. Jump

Affiliation: Centre de Recerca Ecològica i Aplicacions Forestals (CREAF)

Current address:

Departamento de Genética Molecular

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

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## Flow cytometry

Dear EvolDir members,

Has anyone of you had any experience with performing flow cytometry (DAPI staining) on leaf material that has been dried with silica gel? Any hints on how to optimize the procedure as well as other experiences are highly appreciated.

We use a PA from Partec with their standard mutual extraction/staining buffer, normally on fresh leaf material, with great satisfaction. However, with dried material we do not get consistent results so far. The high

resolution kit does not seem to provide any better results than the regular kit.

Thanks in advance, cheers, Marc Stift.

Institute for Biodiversity en Ecosystem Dynamics Experimental Plant Systematics Universiteit van Amsterdam [stift@science.uva.nl](mailto:stift@science.uva.nl)

[stift@science.uva.nl](mailto:stift@science.uva.nl)

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## Fluorescent Labelling

I am after advice...

I have a collection of tail feathers obtained from Long-tailed wagtails. If possible I would like to look at extra-pair paternity using these samples.

I have been unable to find microsatellite markers for this species or the genus and in any case do not have the funds to purchase microsatellite primers. But for future reference, I would like to know if there are any developed for this or closely related species or if any microsatellites have been used in this species.

As an alternative to radioactivity I have been looking at fluorescent labelling of minisatellites and wonder if anyone can tell me if fluorescent labelling might be more sensitive than radiolabelling?

If anyone has experience in using feathers in minisatellite analysis?

My reason for asking is I am wondering if the use of fluorescent labelling might provide a way to analyse these samples using minisatellite analysis.

[201302042@ukzn.ac.za](mailto:201302042@ukzn.ac.za)

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## Gel extraction

Dear all,

we currently have a problem with purification of PCR products from gels: bands cut from gels are no longer suitable for downstream applications such as restriction digests or sequencing although the purified DNA looks okay on the gel afterwards (which makes the gel extraction kits quite useless). What we already tried to solve the problem: - use different batches of kits (Qiagen,

Macherey Nagel). The kits shouldn't be the problem: using exactly the same procedure and buffers for the direct purification of PCR products, the DNA works perfectly afterwards. - use of the diluted restriction enzyme buffer for elution of DNA from columns instead of the provided elution buffer did not change the results (after the last washing step, the columns were left open and incubated at 50 degrees centigrade for a few minutes in order to completely evaporate residual ethanol from the last wash buffer - directly purified PCR products work perfectly after this treatment) - using different agaroses, different buffers (plus checking buffer components in turn), different sources of ultra-pure water for electrophoresis, different loading dyes etc. did not solve the problem. - using three different UV tables (all 312 nm), putting intensity to 70%, minimizing exposure time of bands to UV during cutting etc. also did not solve the problem. - trying it in a different lab (with our/their buffers, our/their kits, their agarose and UV table also did not improve the digest. Digests work perfectly when samples are not electrophoresed and cut from gel, but directly purified from the PCR product. But of course, if you do have extra bands in some PCRs which you can't get rid of by optimizations, you would like to use the option to excise the proper product. There is some digestion, and there is also some result from sequencing, but incomplete and of very bad quality. (In my former lab this worked as it should, for restriction digests as well as for sequencing.)

We and also the technical support from Qiagen (Czech Republic and Germany) don't have any idea left what could be wrong. The odd thing is that quality and yield of purified gel-extracted DNA when visualized on gel seem completely ordinary. So what is inhibiting the enzymes then? We suspect some damage done to the DNA somewhere in the procedure, but which and at what step does it occur?

Is anybody out there who has an additional idea or who has had the same problem and has solved it?

Best wishes,

Judith

Dr. Judith Fehrer Institute of Botany CZ-25243 Pruhonice

phone +420 2 71015215 fax +420 2 67750031 email: fehrer@ibot.cas.cz

Judith Fehrer <fehrer@ibot.cas.cz>

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## Hawaiian Gobies

Microsatellite Folks -

I'm an undergraduate at Clemson University doing my honors thesis project under Dr. Margaret Ptacek and Dr. Richard Blob looking at the genetic diversity of three different species of Hawaiian gobies (*Sicyopterus stimpsoni*, *Awaous guamensis*, and *Lentipes concolor*). I am looking for previously developed microsatellite primers that could be used for these or any closely related species (such as *Stenogobius hawaiiensis*). If you have any information that would assist me in my search, please contact me at LSDURHA@clemson.edu. Thank you.

Sincerely, Lisa Durham LSDURHA@clemson.edu

"Margaret B. Ptacek" <mptacek@CLEMSON.EDU>

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## Hybridization Studies

I am doing a meta-analysis on hybridization in animal taxa looking at various factors that contribute to the frequency of hybridization and success of hybrids.

I am trying to gather all the papers I can on animal hybridization that have been conducted for any purpose (hybrid zones, repro isolation, etc).

My purpose for this message is to locate any past, unpublished studies that are sitting around in file cabinet drawers, or from obscure or non-English language journals. I am trying to prevent the "publication bias" that can affect meta-analyses, so would like to do a systematic search for any known research.

Please email me at ecowriter@ev1.net or (alternate) holtcamp@rice.edu

Thanks in advance! Wendee

Wendee Holtcamp ~ ~ ecowriter@ev1.net Freelance  
Writer & Photographer ~ ~ [www.greendzn.com](http://www.greendzn.com) Ph.D.  
Student, Rice University, Ecology & Evolutionary Biology

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## MOLPHY problems

I am currently experiencing difficulties with the online version of MOLPHY 2.3, Programs for molecular phylogenetics based on maximum likelihood (Adachi and Hasegawa, 1996), website: [http://bioweb.pasteur.fr/seqanal/interfaces/prot\\_nucml.html](http://bioweb.pasteur.fr/seqanal/interfaces/prot_nucml.html). Is anyone familiar with the workings of this particular interface as I am after some advice? Any feedback would be greatly appreciated.

Adam Miller

admiller@deakin.edu.au Postgraduate Research School of Ecology and Environment, Deakin University, PO Box 423 Warrnambool, 3280 Victoria, Australia – Adam Miller Postgraduate Research School of Ecology and Environment, Deakin University, PO Box 423 Warrnambool, 3280 Victoria, Australia Phone: 03 55633569 Fax: 03 55633462

admiller@deakin.edu.au

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## SNP data analysis

Dear Evoldir people, we would like to receive suggestion about the best statistic analysis for SNP data. We have genotyped 60 mammals populations for 12 SNP loci and we are wondering wich kind of analysis is the most suitable for them and which softwares can be suitable to peerform it. Any suggestion will be welcome. Cheers, Irene

– Dr. Irene Cappuccio Dipartimento di Produzioni Animali Laboratorio n 308, II piano Università della Tuscia Via S. Camillo de'Lellis 01100 Viterbo Office Tel. Number +390761357447 Mobile Tel. Number +393404646789 FAX Number +390761357434 E-mail: cappucci@unitus.it

Irene Cappuccio <cappucci@unitus.it>

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## Seed Ovule ratios

EvoDir members,

Lawrence Harder, Shane Richards, and I are collecting seed-ovule ratios and outcrossing estimates to evaluate some predictions we have generated regarding mixed mating in plants. These data are occasionally available in the literature, but I suspect that the collective experience of the EvoDir contains much more. We would greatly appreciate any unpublished data or pointers to published sources.

Specifically, we are looking for three things: 1) The number of ovules produced per flower; 2) The number of seeds matured per flower; 3) An outcrossing rate estimate for the species, preferably estimated with genetic markers.

If any of the unpublished data are the result of experimental manipulations of resources, pollen abundance, etc. please include some details of the manipulations.

Thanks in advance for any data.

Take care, Matt — Matthew Routley Post-Doctoral Fellow Department of Biological Sciences University of Calgary Calgary, AB, Canada T2N 1N4

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## Software Tree-Puzzle v5 2

Dear collage,

After a more or less 'silent' release 5.1, I am announcing the next TREE-PUZZLE release. (Please note: a bug has been fixed, which tended to produce less resolved trees. Hence, versions prior to 5.2 should not be used anymore!)

TREE-PUZZLE 5.2 —————

Heiko A. Schmidt, Juelich, Germany. Korbinian Strimmer, Munich, Germany. Arndt von Haeseler, Duessel-

dorf/Juelich, Germany.

July 2004

<http://www.tree-puzzle.de> DESCRIPTION ———

TREE-PUZZLE is a computer program to reconstruct phylogenetic trees from molecular sequence data applying maximum likelihood. It implements a fast tree search algorithm, quartet puzzling, that allows analysis of large data sets and automatically assigns estimations of support to each internal branch. TREE-PUZZLE also computes pairwise maximum likelihood distances as well as branch lengths for user specified trees. Branch lengths can be calculated with or without a molecular-clock assumption. In addition, TREE-PUZZLE offers likelihood mapping, a method to investigate the support of a hypothesized internal branch without computing an overall tree and to visualize the phylogenetic information content of a sequence alignment. For a set of user provided trees a consensus tree can be computed or the trees can be evaluated inferring ML value and ML branchlengths. TREE-PUZZLE also conducts a number of statistical tests on the data set and/or the set of trees provided by the user (chi-square test for homogeneity of base composition, likelihood ratio to test the clock hypothesis, 1- and 2-sided Kishino-Hasegawa test, Shimodaira-Hasegawa test, and Strimmer-Rambaut's expected likelihood weights - ELW). The models of substitution provided by TREE-PUZZLE are TN, HKY, F84, GTR, SH for nucleotides, Dayhoff, JTT, mtREV24, BLOSUM 62, VT, WAG for amino acids, and F81 for two-state data. Rate heterogeneity is modeled by a discrete Gamma distribution and by allowing invariable sites. The corresponding parameters (except for GTR in this release) can be inferred from the data set.

CHANGES ———

What's new in TREE-PUZZLE 5.2:

- TREE-PUZZLE has now implemented a faster recursive quartet puzzling algorithm giving the same result but significantly reducing the running time.
- The GTR model is now available for DNA data. However, its free parameters are not (yet) estimated automatically.
- The limits on the number of sequences to be  $4 \leq n \leq 257$  are removed for the estimation of parameters, pairwise distances as well as likelihood mapping. (The lower limit 4 is of course still valid for quartets, as is the upper limit for quartet puzzling, due to memory addressing problems by overflows. However, the second limit will be extended soon.)
- Besides the evaluation (ML branch length, ML value)

and testing (Shimodaira-Hasegawa, Kishino-Hasegawa, ELW) of a set of usertrees, now also a consensus tree can be computed for which branch lengths and ML value are estimated.

- The output file prefix can now be changed using a commandline switch (-prefix=) to ease, for example, batch analyses that are using the same datasets but different models/parameters.
- The random number generator has been changed to use the free SPRNG library which implements high quality random which in turn gives significantly better time performance (especially in parallel runs) compared to the old implementation.
- The parameter estimation now has been also parallelized (in close collaboration with E. Petzold; cf. Schmidt et al. 2003 for more details).
- Furthermore a number of bugfixes have been incorporated: - WAG matrix data has been corrected. - A bug that tended to make trees reconstructed less resolved has been rectified (old TREE-PUZZLE versions should, hence, not be used anymore). - The KH tests have been altered to not artificially reject a tree if the variance between it and the best tree is too small. - KH tests have been fixed in their precision, because they tend to reject tree topologies that are almost identical to the 'best tree', i.e., for which the variance is too small. - a number of further minor bugs.

...finally there will be pre-compiled executables again for Linux, Mac OS X, and Windows.

Best wishes, Heiko Schmidt

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 To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

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**Speciation Bottlenecks answers**



Dear all,

Thank you very much again for all your help with my question about bottleneck at speciation. As many of you asked me to put the answers received on the EvoDir directory, here they are. Best regards,

Begoña

1- Hola Begona,

lo que nosotros hacemos es calcular por simulacion de una poblacion en expansion tras un bottleneck, la probabilidad (likelihood) de obtener un nivel de polimorfismo como el que tenemos (te envio el PDF de un paper en el que hacemos ese analisis, "Demographic modelling of european population", table 1). Como ves, el bottleneck puede ser completamente independiente de la especiacion (ya que para nosotros no era importante), pero si tu sabes el tiempo de especiacion, puedes incluir ese parametro en tus simulaciones y ya esta.

2- Querida Begoña, Intenta DnaSP 4.0 - un programa escrito en Universidad de Barcelona

3- Dear Begona There is a computer programme called Bottleneck which I think uses microsatellite data. I'm sure someone else will provide the details I don't have them with me at the moment. If no one does then come back to me and I will try to find the details.

4- Hi Begoña, Have you tried that program BOTTLENECK on your microsatellite data yet? it is available at <http://www.montpellier.inra.fr/URLB/bottleneck/-bottleneck.html> 5- <http://lifesci.rutgers.edu/~hey/lab/HeylabSoftware.htm#WHI> don't think WH does quite what you want but perhaps there are modifications of that software. At least it estimates the size of the ancestral pop. which may indicate the potential for a bottleneck?

6- Hello Begoña, In response to your questions on the evodir server, Gordon Luikart and Jean-Marie Cornuet are the best references I have seen for testing bottlenecks (although your use of the word "speciation" I am unsure about—I have only used these programs for intra-specific datasets). L & C are incredibly articulate and I highly recommend you read anything they have written. They have provided empirical data on a software program written by Piry et al. There is also a program tested by Garza and Williamson that uses a different metric for testing for bottlenecks from that of L & C using usat data. You will probably have to write to Garza directly or find his website from his paper for his program (actually supported, I believe, by Williamson). Here are the references pasted from my Endnote file. Good luck. Cindy Taylor, PhD Scripps Institution of Oceanography UC, San Diego Cornuet, J.-M., and G.

Luikart. 1996. Description and power analysis of two tests for detecting recent population bottlenecks from allele frequency data. *Genetics* 144:2001-2014. Garza, J. C., and E. G. Williamson. 2001. Detection of reduction in population size using data from microsatellite loci. *Molecular Ecology* 10:305. Luikart, G., and J.-M. Cornuet. 1998. Empirical evaluation of a test for identifying recently bottlenecked populations from allele frequency data. *Conservation Biology* 12:228-237. Luikart, G., J.-M. Cornuet, and F. W. Allendorf. 1999. Temporal changes in allele frequencies provide estimates of population bottleneck size. *Conservation Biology* 13:523-530. Luikart, G. L., F. W. Allendorf, J.-M. Cornuet, and W. B. Sherwin. 1998. Distortion of allele frequency distributions provides a test for recent population bottlenecks. *Journal of Heredity* 3:238-247. Piry, S., G. Luikart, and J.-M. Cornuet. 1999. BOTTLENECK: a computer program for detecting recent reductions in the effective population size using allele frequency data. *J Hered* 90:502-503.

7- Dear Begona, A number of coalescent-based methods can estimate the population size through time of a population using genetic data. This would allow you to measure the population size at the time of speciation. BEAST, GENIE, Mark Beaumont's software and BATWING can all do this...

8- Begoña, Here's an old one for a specialized case, but you may find some ideas here: HILTON, H., R. M. KLIMAN, and J. HEY, 1994 Using hitchhiking genes to study adaptation and divergence during speciation within the *Drosophila melanogaster* species complex. *Evolution* 48:1900-1913 These guys used hitchhiking to time the split between sister *Drosophilas* sp., as I recall.

9- Begoña, I did not see your original email nor the replies sent to you. So this may be something you are already aware of, but Laurent Excoffier has written the simulation software that you need. It's called SIMCOAL and is available at <http://cmpg.unibe.ch/software/-simcoal/>. With SIMCOAL you can specify times of divergence and changes in population size, and then generate molecular data under these conditions. Typically what you would want to do is draw distributions (from the simulations) of common diversity

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## Speciation bottleneck

Dear colleagues,

Does someone know a software to test for a bottleneck at speciation either with microsatellite or sequence data?

Thanks!

Begoña

Begoña Martínez-Cruz Phd Student Department of Applied Biology Estación Biológica de Doñana Avda. María Luisa s/n 41013 SEVILLA Spain Telf. +34 954 232340 Fax +34 954 621125

Begoña Martínez Cruz <bemar@ebd.csic.es>

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## Speciation bottleneck 2

Dear all,

Thank you very much for your quick answers. However, what I am looking for is not to test for a recent bottleneck (as Bottleneck or M do) but for an historical bottleneck, at the time of speciation of two closely related taxa. I am thinking in a software based on the coalescent model that simulates the split and estimates whether the divergence resulted in a bottleneck for the descendant species at the time of split.

Thanks again,

Begoña

Begoña Martínez-Cruz Phd Student Department of Applied Biology Estación Biológica de Doñana Avda. María Luisa s/n 41013 SEVILLA Spain Telf. +34 954 232340 Fax +34 954 621125

Begoña Martínez Cruz <bemar@ebd.csic.es>

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## Tetraploid micros answers

Dear Evoldir,

Here are the responses I got for the questions regarding tetraploid microsatellite problem, which I posted in the forum about a month ago. I got some useful suggestions but in my opinion the problem is not yet completely solved. I am very much thankful to all of you who responded my question.

The question I posted was as following:

Dear evoldir,

I am a Ph.D. student in forest genetics and working with a forest tree species called sycamore (*Acer pseudoplatanus*) which is a tetraploid species. I am using nuclear microsatellite marker to study the genetic structure of above mentioned species. Since the species is tetraploid I am getting 1 to 4 bands per locus per sample and to score alleles depending on dosage effects is not working (difficult to differentiate alleles). I am getting difficulties to interpret such types of bands. I would be grateful if anyone can suggest me how to interpret such types of bands and what types genetic variation parameter can be estimated from such types of data using which programme.

ANSWERS:

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I already noticed your post at the EvolDir, but did not reply as I was a bit short on time and thought that others might also be able to help you. However, if you did not yet get the answers you needed, I can help you by giving my view on your problem.

It was nice of Ruzica to suggest my program to you, but I am afraid it might not entirely what you are looking for, though it might be of use, depending on your research question. My program is in principle meant for use with asexually reproducing species, and as most asexuals are polyploid, the program can handle polyploid data. Most of the program's functionality is rather useless if you are working on a sexual species. However, the program does allow you to calculate and export genetic distance matrices (also using Ruzica's method). You can use this matrix then to make a tree (eg. UPGMA) and draw some conclusions from that or to do other things that people usually do with genetic distances. You can find the program on [www.science.uva.nl/~meirmans](http://www.science.uva.nl/~meirmans). More useful however would be to forget about my program and do an Amova. In that case you might score your msats as if they were dominant markers and use these as an input file. Someone called JENCZEWSKI published something Amova's on polyploids in Molecular Ecology in 1999, if I remember correctly, but those were on RAPDs. If you do want to use your data as codominant, you would have to think of a way to calculate a

chi-square distance matrix for your data to use as an input.

Furthermore there is the excellent program called SPAGEDI, written by Olivier Hardy, that can calculate Fst using polyploid data. However the bias that arises from not knowing the dosage of your alleles is hard to asses, though I know people who have done Fst calculations on data from polyploids like that.

Just out of interest: are all *A. pseudoplatanus* polyploid or are there also diploids somewhere? And something that has been bugging me for quite sometime: is polyploidy as frequent in trees as it is in herbs? I never before heard of polyploid trees, though I never took the effort to look for it...

Hope I have helped you with this, if you have any further questions, don't hesitate to ask.

Greetings, Patrick

Patrick G. Meirmans Institute for Biodiversity and Ecosystem Dynamics Evolutionary Botany University of Amsterdam Kruislaan 318 1098 SM Amsterdam The Netherlands

Tel. +31 (0)20 525 7856 Fax. +31 (0)20 525 7832

<http://www.science.uva.nl/~meirmans>

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Hi,

The short answer is:

“There is no standard approach to population genetic stats in a polysomically inheriting polyploid in which you can't identify allele dosage. There is certainly no software to do so.”

However,

If you can score allele dosage, then use Spagedi (Hardy and vekemans)

If it has disomic inheritance, then I have an approach (and a beta of a text-interface program) that will give some statistics.

My program will work with a polyploid with polysomic inheritance (i.e. give you numbers), but inference would be harder.

I have attached the (very 'beta') doumentation for my program. Included are some helpful references.

Darren

Darren Obbard Plant Sciences, Oxford (Currently residing in Norwich, UK) [darren.obbard@plants.ox.ac.uk](mailto:darren.obbard@plants.ox.ac.uk)  
Mobile: +44 07968 838 635 Home: +44 01603 259 670

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I had exactly the same problem when I scored microsatellites in a tetraploid *Echium vulgare*. I did not trust the estimation of number of copies of the alleles, based on the signal intensity. I ended up noting only the presence or absence of amplified alleles. I wrote it in my primer note. Korbecka G, Vrieling K, Squirrell J, et al. (2003) Characterization of six microsatellite

— / —

This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evodir.html>

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## Water voles

I have a Masters student who wishes to carry out a phylogeographic project on the water vole, *Arvicola terrestris* using cytochrome-b sequences. We would be very grateful if anybody could send us tissue samples (hair follicles, dried tissue...) from areas away from North Wales, UK. Please note that in the UK at least, a Home Office license is needed to collect tissue from live mammals so please check your national legislation! If you are PIT-tagging, we can get enough DNA from the hypodermic needle but we would need to supply you with appropriate preservation material.

Thanks in advance.

Chris

—  
Dr. Chris Gliddon School of Biological Sciences University of Wales, Bangor LL57 2UW United Kingdom  
Tel: +44 (0)1248 382533 FAX: +44 (0)1248 382569 Mobile: +44 (0)7941 060423

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## PostDocs

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Aviv Bergman <abergman@aecom.yu.edu>

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### AlbertEinsteinCollegeMed EvolSystemsBiol

Post Doctoral Research Fellow in Evolutionary Systems Biology Seaver Foundation Program in Bioinformatics, Albert Einstein College of Medicine,

Postdoctoral research position is available in computational/systems biology. The program's focus is the study of complex gene networks and their evolution.

Applicants could have skills in any of several areas of evolutionary, molecular, computational, or systems biology and/or genetics, and development biology. We encourage applicants from any of these fields. We particularly encourage applicants working on model organisms who are interested in strengthening their theoretical and computational scholarship.

The position is available immediately and for the duration of 1-3 years; Salary (in the range of \$35K to \$40K, plus benefits) will be commensurate with experience.

If interested, please send your curriculum vitae and the names of at least two references to: Prof. Aviv Bergman Department of Pathology Seaver Foundation Program in Bioinformatics, Albert Einstein College of Medicine, Jack and Pearl Resnick Campus, 1300 Morris Park Avenue, Bronx, NY 10461.

E-mail: [abergman@aecom.yu.edu](mailto:abergman@aecom.yu.edu)

– Aviv Bergman Ph.D. Professor Albert Einstein College of Medicine 1300 Morris Park Ave. (Belfer 902A) Bronx, NY 10461 Phone (718) 430-2942 Fax: (718) 430-8541 e-mail: [abergman@aecom.yu.edu](mailto:abergman@aecom.yu.edu)

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### CornellU Drosophila Immunity

#### POSTDOCTORAL POSITION

An NSF funded postdoctoral position is available in Brian Lazzaro's lab at Cornell University to study the evolution of innate immune responses in *Drosophila*. The successful applicant will be expected to develop his or her own research project, but possible broad topic areas include a) coevolution between *Drosophila* and its microbial pathogens, or b) the relationship between genetic and phenotypic variation in immunity. Ideal applicants will have a background in population genetics, quantitative genetics or evolutionary biology and will have some experience in insect immunity, microbiology, or *Drosophila* genetics. The Lazzaro lab is in the Cornell department of Entomology, and is physically and intellectually close to the departments of Molecular Biology and Genetics and Ecology and Evolutionary Biology. The successful applicant will have the opportunity to take advantage of these and other linkages across campus.

Support for this position is available immediately, but start date is negotiable. Applications should include a CV, a brief statement of research interests and experience, and contact information for three references.

Applications and inquiries may be directed to: Brian Lazzaro, Ph.D. 4138 Comstock Hall Cornell University Ithaca, NY 14853

email: bl89@cornell.edu

Cornell University is committed to creating a more diverse and inclusive campus in which to work, study, teach and serve.

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## Dublin GenomeEvolution

Bioinformatics / Molecular Evolution

Postdoctoral Opportunities

Postdoctoral fellowships are available in Prof. Ken Wolfe's group at Trinity College Dublin (Ireland). The projects will involve using bioinformatics and comparative genomics methods to study genome evolution in eukaryotes. Particular interests in the lab include the evolution of polyploid species, clustering of functionally related genes, and fungal genomics.

These fellowships form part of a 5-year research programme supported by Science Foundation Ireland. For further information about the lab, see wolfe.gen.tcd.ie. Very competitive salaries will be available for outstanding applicants.

Previous experience in molecular evolution, bioinformatics, and/or computer programming experience in C / Perl / SQL is essential. Candidates should submit a cover letter and curriculum vitae, including the names of two referees, by mail or e-mail to: Prof. Kenneth H. Wolfe, Department of Genetics, Smurfit Institute, Trinity College, Dublin 2, Ireland (Tel. +353 1 6081253; e-mail khwolfe@tcd.ie). Informal enquiries are welcome. Closing date 8 August 2004.

Trinity College is an Equal Opportunities Employer.

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## ETHZurich HostParasite

POST-DOC POSITION Evolutionary ecology of host-parasite interactions ETH Zurich

In the group of Ecology & Evolution (Experimental Ecology, P. Schmid-Hempel) a post-doc position will be available by 2005. The project is on the evolutionary ecology of host-parasite interactions, either on questions of immune defence strategies, or on the problem of genetic interactions, depending on interest and qual-

ification. It most likely will use our established model system (bumble bees and their parasites). Experience in molecular techniques is advantageous. Salary according to local scale; starting date negotiable, the position is for 2 years and may be extendable. More information on [www.eco.ethz.ch](http://www.eco.ethz.ch) and by email (psh@env.ethz.ch - after 15 Aug). Review of applications with CV, publication list and addresses of referees starts 25 Sept 2004.

Prof. Paul Schmid-Hempel ETH Zurich, Ecology & Evolution ETH-Zentrum NW CH-8092 Zurich Ph: +41 1 633 6033 or 6048 Fax: +41 1 632 1271 psh@env.ethz.ch [www.eco.ethz.ch](http://www.eco.ethz.ch) Paul Schmid-Hempel <psh@env.ethz.ch>

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## Edinburgh AnimalBreeding

RESEARCHER, ANIMAL BREEDING & GENETICS  
Scottish Agricultural College, EDINBURGH, UK

SAC, in conjunction with the Roslin Institute, are seeking a postgraduate with experience in animal breeding or quantitative genetics to work on a project aimed to investigate the links between breeding for scrapie resistance and economically important production and health traits in sheep.

The successful candidate will join a multidisciplinary team researching the optimal breeding strategies for scrapie resistance in the context of an overall genetic improvement programme. The post is available for 3 years.

Candidates should hold a postgraduate qualification in animal breeding, quantitative genetics or a closely related discipline. Strong communication, computer and mathematical/statistical skills are required. Knowledge in epidemiological modelling and animal breeding industry and database management skills will be an advantage.

The salary will be in the region of £19,585 - £32,995 per annum. A final salary Pension Scheme is in operation.

Applications close 16 August 2004.

For further details and application packs see our website: <http://www.sac.ac.uk/jobvacancies>. Application packs are also available from Human Resources, Scottish Agricultural College, West Mains Road, Edinburgh EH9 3JG, UK.

Tel: (+44) 0131 535 4343 (answering machine), Fax:

(+44) 0131 535 4322, HumanResources@ed.sac.ac.uk.

Please quote reference R&D/SLS/103/04.

\*\*\*\*\*

Loeske Kruuk Institute of Cell, Animal and Population  
Biology University of Edinburgh Edinburgh EH9 3JT,  
UK Tel. (44) 131 650 5515 Fax (44) 131 650 6564

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Loeske Kruuk <Loeske.Kruuk@ed.ac.uk>

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## MidwesternU EvolPhysiology

### POST-DOCTORAL POSITION IN EVOLUTION- ARY PHYSIOLOGY

An NSF-funded postdoctoral position is immediately available for an individual interested in examining the evolution of respiratory patterns of terrestrial insects. The project is broadly comparative and will include insects from Arizona and southern Africa. This study will be conducted under the guidance of Dr. Michael Quinlan (Midwestern University) and Dr. Allen Gibbs (University of Nevada at Las Vegas). Dr. Steven Chown (University of Stellenbosch, South Africa) is a collaborator on this project and will provide access to the African species. The successful candidate will be based primarily in the Phoenix area, though he or she will be expected to travel to UNLV on occasion. Money is available for some travel to the Chown lab at the University of Stellenbosch.

Candidates having experience in one or more of the following areas will be given preference: (1) respiratory physiology, especially of terrestrial invertebrates, (2) phylogenetic comparisons of physiological traits, and (3) insect metabolism and water balance. A Ph.D. in biology or a related discipline is required. Initial appointment will be for one year and is renewable upon satisfactory performance. Applicants must submit a complete curriculum vitae and names and contact information for two references to Michael Quinlan, Department of Basic Science, Midwestern University, 19555 N. 59th Ave, Glendale, AZ 85308 (email [mquinl@midwestern.edu](mailto:mquinl@midwestern.edu)). Review of applications will begin immediately.

Persons interested in this position may also contact Allen Gibbs ([agibbs@arl.arizona.edu](mailto:agibbs@arl.arizona.edu)) for more information.

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## NatHistMuseum Polychaetes

Department of Zoology The Natural History Museum  
Post-Doctoral Research Assistant Polychaete Research  
Group Salary to £23,000

Molecular genetics of deep-sea polychaetes A 6-month research position is available to study polychaete worms collected from deep-sea chemosynthetic habitats on the California Slope. These habitats include hydrothermal vents, whale-carcasses, kelp-parcels and wood-parcels. The aim of the project is to obtain a variety of nuclear and mitochondrial DNA sequences in order to address questions regarding the degree of gene-flow between these ephemeral island' habitats, the genetic structure of their populations and the phylogenetic position of the species that occupy them. One of the main goals of the project is to examine the linkages between chemosynthetic habitats of geologic origin (such as hydrothermal vents and seeps) and those of biogenic origin (such as whale-carcasses). A skilled molecular biologist, with sound knowledge of phylogenetic, phylogeographic or population genetic analysis is required. Knowledge of deep-sea ecology and polychaete taxonomy is not required, but would be desirable. Although the specimens for the project have already been collected, there will be an opportunity to collect more on an oceanographic research cruise on the California slope.

This project will be jointly supervised by Dr Adrian Glover (The Natural History Museum), Dr Thomas Dahlgren (Tjärnö Marine Biological Laboratory, Sweden) and Prof Craig Smith (University of Hawaii).

For full details of requirements, a full job description and equal opportunities form please Email: [PDRA@hscientific.co.uk](mailto:PDRA@hscientific.co.uk), or write to: The Natural History Museum, c/o Hudson Shribman Scientific Recruitment, Vernon House, Sicilian Ave, London, WC1A 2QS. Application will be by CV & covering letter including a summary of your research interests.

Closing date: 20th August 2004. ----- Dr Adrian Glover Zoology Department The Natural History Museum Cromwell Rd, London SW7 5BD, U.K.

020 7942 5056 (office) 077 666 484 40 (mobile)  
----- <http://homepage.mac.com/adrianglover> <http://-homepage.mac.com/adrianglover>

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## PortlandStateU PlantEvol

### Post-Doctoral Position in the Evolutionary Ecology of Invasive Plants

A post-doctoral position is available for studies of life history evolution in a newly invasive grass in the Willamette Valley of Oregon. The work will focus on examining evolutionary changes associated with range expansion and the transition to an aggressive-invasive life history. The work includes a mixture of field and greenhouse studies with opportunities to participate in genetic marker analyses and to develop related projects of mutual interest. An individual with a background in plant ecology and field biology, and an interest in molecular markers would be particularly suitable for this position.

The work will be conducted at Portland State University and at nearby field sites in and around the Willamette Valley. The successful candidate will join an active group of graduate and undergraduate students in the Plant Ecological Genetics lab at PSU (<http://web.pdx.edu/~cruzan/>), and will have the opportunity to participate in genetic marker studies in collaboration with Alisa Ramakrishnan (<http://web.pdx.edu/%7Eramakris/index.htm>). Opportunities for interactions and collaborations with a broad range of faculty, post-docs, and graduate students are available in the Department of Biology (<http://www.bio.pdx.edu/>), and in related departments at PSU and local colleges in Portland.

Interested applicants should send a CV, statement of research interests, and a list of three referees to Mitch Cruzan (Cruzan@pdx.edu).

If you are interested in this position and plan to attend the Ecological Society of America meetings in Portland next month please contact me so we can arrange a time to meet.

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Mitch Cruzan, Associate Professor Department of Biology Portland State University, Box 751 Portland, OR 97207 Phone: 503-725-8391 Fax: 503-725-3888 Webpage: <<http://web.pdx.edu/~cruzan/>>

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## PurdueU MolEvol

A postdoc position in evolutionary genetics is available at Purdue University. The successful applicant will be highly motivated to develop one of several projects in molecular evolution, population genetics, or genetic parentage assessment. Demonstrated expertise in computer programming, automated DNA sequencers, and/or microarrays is required. Purdue is a large university (>38,000 students) and collaborations with colleagues are common. Salary and benefits are very competitive. Interested parties should send a current CV, relevant reprints, and a statement of research interests & experience to Andrew DeWoody (dewoody@purdue.edu), Dept. of Forestry & Natural Resources, Purdue University, West Lafayette Indiana. International applicants will be considered if they hold the correct visa(s). Women and minorities are encouraged to apply. Purdue University is an equal opportunity employer.

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## SUNYStonyBrook Genomics

Postdoc in metabolic genomics and molecular evolution

An NIH supported postdoctoral position is available to work on the molecular evolution, population genetics, physiology, and functional genomics of metabolic genes in *Drosophila*. The position is for two years and is available starting immediately, although there is flexibility in any start date.

Applicants could possess skills in any of several areas including *Drosophila* genetics, molecular evolution, population genetics, or physiological genetics.

If interested please contact Walt Eanes, Department of Ecology and Evolution, Stony Brook University, Stony Brook, NY 11794 or e-mail [walter@life.bio.sunysb.edu](mailto:walter@life.bio.sunysb.edu).

Walter F. Eanes Professor Dept. of Ecology and Evolution State University of New York Stony Brook, New York 11794

[weanes@notes.cc.sunysb.edu](mailto:weanes@notes.cc.sunysb.edu)

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## UArizona phylogenetics

Judith Becerra and I have postdoc funding for someone who can work with us on comparative ecology in a phylogenetic framework. The subject areas are plant-insect interactions and evolution of plant adaptive traits. Ideally we want someone who has familiarity and experience working with the theory and software used in phylogenetic comparative biology. A good background in statistics and computer programming would be a plus. This is a one or two year position, with possibility of renewal for a third. We have a very strong program in ecology and evolutionary biology with many grad students and postdocs, making this a good environment for postdoctoral work. Please contact us at Judith Becerra <becerra@Ag.arizona.edu> or venable@u.arizona.edu

The website with the job posting is: [www.UACareerTrack.com/](http://www.UACareerTrack.com/). Look under Postdocs, Ecology and Evolutionary Biology.

-Larry Venable and Judith Becerra Departments of Ecology & Evolutionary Biology and Entomology University of Arizona Our websites: <http://eebweb.arizona.edu/faculty/venable/> <http://eebweb.arizona.edu/Faculty/Becerra/> Larry Venable <venable@email.arizona.edu>

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## UBritishColumbia Phylogenetics

Computational phylogenetics postdoctoral position available in the laboratory of Wayne Maddison at the University of British Columbia

We seek a postdoctoral computational biologist or computer scientist to contribute to the NSF-funded CIPRes project (Cyber Infrastructure for Phylogenetic Research, <http://www.phylo.org>). The CIPRes project is developing a software framework to enable larger and more flexible phylogenetics analyses through a modular architecture and distributed computing. Candidates should be skilled in programming in Java, C++ or related languages. Ideally, the successful candidate would also be conversant in evolutionary biology.

The particular duties of this postdoc will be to par-

ticipate in the design and programming of (1) the general CIPRes framework and (2) Mesquite, <http://www.mesquiteproject.org>. Work on the framework will focus on the design of intermodule communication. Work on Mesquite will have as goals both the integration of Mesquite into the CIPRes system and improvement of Mesquite's analytical capabilities. Mesquite's modules span diverse areas of evolutionary analysis, from simulations of molecular evolution, to population genetics and coalescence, morphometrics and comparative method, and likelihood ancestral state reconstruction. Which area is the target of improvement may depend on the background and interests of the candidate.

Starting date can be as early as September 2004. Salary is US\$30,000, plus benefits. Funding is available for 3 years; whether we offer 1, 2 or 3 years to the successful candidate is a subject for negotiation. The University of British Columbia (<http://www.ubc.ca>) is located in Vancouver, Canada, a beautiful city nestled between mountains and sea (<http://www.ubc.ca/about/-vancouver.html>).

To apply, send to me (wmaddisn@interchange.ubc.ca and cc'd to Karen Needham <needham@zoology.ubc.ca>) the following: (1) your curriculum vitae, (2) statement of research interests, (3) statement of expertise relevant for this project, and (4) the names of 3 referees and their email addresses. Application review will commence as early as August 1 and continue until the position is filled.

I will be in the field for the month of July; if you have questions please send email both to me and to Karen Needham (needham@zoology.ubc.ca).

---

Wayne Maddison Professor and Canada Research Chair  
Departments of Zoology and Botany 6270 University  
Boulevard University of British Columbia Vancouver,  
BC V6T 1Z4 Canada

email: [wmaddisn@interchange.ubc.ca](mailto:wmaddisn@interchange.ubc.ca) FAX: (604) 822-2416

Mesquite: <http://mesquiteproject.org> MacClade: <http://macclade.org> Salticidae: <http://salticidae.org>  
Tree of Life: <http://tolweb.org> Home page: <http://salticidae.org/wpm/home.html>

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## UCDavis PlantEvol



### Post-Doc on the Evolutionary Genetics of the Invasive Barbed Goatgrass

A two-year post-doctoral position at UC Davis is available as part of a project funded by the USDA to study range expansion of the invasive barbed goatgrass (*Aegilops triuncialis*). The major focus of the post-doctoral research will involve using a variety of molecular approaches to quantify the genetic bottleneck involved in the introduction into California, and to examine the biogeography of invasive lineages in their native range. In addition, because barbed goatgrass is an allotetraploid with multiple origins, this system is ideal to address questions relating to polyploid speciation.

We are looking for a highly motivated individual with a Ph.D. degree and with the demonstrated ability to carry out outstanding research. The successful candidate must have substantial experience in high-throughput genotyping and a strong record in population genetic and phylogenetic analyses. We also emphasize the ability to interact and work collaboratively with others, as the post-doc will work closely with a technician and undergraduate researchers. In addition to the molecular ecology, the project as a whole involves substantial quantitative genetic and ecological genetic experiments. While no experience in this area is required, the candidate can expect to hone their expertise in field demography.

The position is available 1 October 2004, but the start is flexible to some degree. Salary and benefits are competitive, and UC Davis is an excellent academic environment for a post-doc in plant evolutionary biology and species invasions. Our lab group has excellent interactions with our colleagues in plant physiology, evolutionary genetics and molecular biology.

We will begin reviewing applications on September 1 2004. Please send a letter of interest and a C.V., and the names and contact information for three references to:

Prof. Kevin Rice, Agronomy and Range Science One Shields Ave, University of California Davis, Davis, CA 95616 [kjrice@ucdavis.edu](mailto:kjrice@ucdavis.edu)

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### UCIrvine SocialInsectGenetics

POSTDOCTORAL POSITION - Genetics and behavior of social insects.

The Department of Ecology & Evolutionary Biology

at UC Irvine is currently seeking a Postdoctoral Researcher in the laboratory of Dr. Neil Tsutsui.

We are seeking a Postdoctoral Researcher to study the genetics, behavior, and social structure of social insects. Previous work has focused on the invasive (but charismatic) Argentine ant (*Linepithema humile*). In this species, genetic changes during introduction have altered individual behavior and, in turn, the social organization of introduced populations. These changes have contributed to the Argentine ant's invasive success by promoting the formation of massive "supercolonies" in the introduced range. Future research will explore the ontogenetic and biochemical components of nest-mate recognition in both invasive and non-invasive social insects. Publications from previous research can be downloaded from <http://tsutsuilab.bio.uci.edu/> The successful applicant must have a strong background in molecular techniques, population genetics and data analysis, and previous experience in behavioral ecology is desired. Salary will be commensurate with experience. Generous benefits are included.

Review of candidates and applications will begin Aug. 8, 2004. Applicants should submit a curriculum vita, a brief statement of research interests, and the name, address and phone number of two references to:

Dr. Neil D. Tsutsui Department of Ecology and Evolutionary Biology 321 Steinhaus Hall University of California, Irvine Irvine, CA 92697-2525

Applications or queries can also be sent to: [ntsut-sui@uci.edu](mailto:ntsut-sui@uci.edu).

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### UCLA 2 EvolBiol

#### TWO POSTDOCTORAL POSITIONS AT UCLA

Two postdoctoral positions are available in the Center for Tropical Research, Institute of the Environment and the Department of Ecology and Evolutionary Biology at UCLA. We are seeking two broadly trained evolutionary biologists with strong backgrounds in the application of molecular genetic techniques to natural populations. The positions are available for one year with the possibility of renewal.

EVOLUTIONARY PROCESSES AND CONSERVATION - We are particularly interested in evolutionary biologists and ecologists with experience working at the intra-specific level and with broad knowledge of molecular genetic techniques, especially the application

AFLPs. The successful candidate will work as part of an interdisciplinary team investigating the evolutionary processes that give rise to and maintain biological diversity in the western Amazonian region of South America, especially Ecuador. The ultimate aim of the investigation is to develop a model that can integrate biological point locality and process data (e.g., genetic and morphological information and estimates of connectivity among populations) with remotely sensed environmental parameters to quantify patterns of species range and diversity in tropical regions. These data will be combined with data from other taxa to prioritize areas for conservation efforts.

**ECOLOGY OF AVIAN DISEASES** - The successful candidate will work as part of an interdisciplinary team investigating the effects of deforestation on the prevalence of blood-borne pathogens in African rainforest birds. Using existing CTR samples, as well as collecting new ones, and using PCR-based detection methods and molecular phylogenetics, the candidate will work collaboratively investigating how long-term anthropogenic changes in habitats affect the prevalence of infectious diseases in natural populations. The three main objectives of the study are to: 1) determine how pathogen prevalence changes over time within differing rainforest habitats, some of which have remained unaltered, and some of which have gone through habitat conversion, 2) determine the host- and habitat- specificities of blood-borne pathogens to assess the degree of host-switching that may occur in differing habitats, and 3) determine, using remote sensing data, the environmental variables that best correlate with pathogen prevalence and develop models that will aid in the prediction of how ecological change will affect disease prevalence and the likelihood of host switching.

The postdoctoral fellows will also have the opportunity to explore broader questions related to population diversification and microevolutionary processes. They will be expected to interact and collaborate with postdoctoral researchers and graduate students working on a broad range of ecological and evolutionary projects. Other Center for Tropical Research projects include: 1) investigations of the mechanisms of speciation, 2) population structure and conservation of migrant birds and connectivity, and 3) seed dispersal and forest regeneration. Interested candidates should mail or e-mail a CV, a brief description of research interests, and names and contact information for three references to:

Thomas B. Smith, Ph.D. Professor, Ecology and Evolutionary Biology (formerly Organismic Biology, Ecology, and Evolution) Director, Center for Tropical Research Institute of the Environment University of California, Los Angeles 1609 Hershey Hall Box 951496 Los Ange-

les, CA 90095-1496 USA

E-mail: [tbsmith@ucla.edu](mailto:tbsmith@ucla.edu) Phone: (310) 206-6234  
 Fax: (310) 825-5446 <http://www.ioe.ucla.edu/-ctr> and <http://www.obee.ucla.edu/> tbsmith  
 <[tbsmith@obee.ucla.edu](mailto:tbsmith@obee.ucla.edu)>

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### UCSantaBarbara LabManager MatingSystemsEvol

Postdoctoral Research/Lab Manager Position Department of Ecology, Evolution and Marine Biology Mazer Lab University of California, Santa Barbara

Life History, Developmental, and Mating System Evolution in the genus *Clarkia* (Onagraceae)

A 12-month lab manager/research position beginning in January 2005 is available to supervise a comprehensive greenhouse experiment while the principal investigator is on leave as Program Director at the National Science Foundation. The optimal candidate will also participate fully in the data management, statistical analysis, and anticipated publication of this work. While a postdoctoral candidate is the most desirable, other candidates with sufficient research, laboratory, statistical and leadership experience will also be considered. An individual with a background in plant evolutionary ecology, quantitative genetics, statistical analysis of multivariate data, and plant development would be particularly suitable for this position.

The successful candidate will direct and conduct a comparative greenhouse study to measure genetic and ontogenetic components of gender allocation in two subspecies of *Clarkia xantiana* (Onagraceae): the predominantly outcrossing *C. xantiana* ssp. *xantiana*, and the predominantly selfing *C. xantiana* ssp. *parviflora* (see attachment for lovely photos!) The work is also designed to seek evidence for evolutionary constraints on life history and floral development rates by estimating the genetically based correlation between rates of individual and floral development. Experience in image analysis and in automated pollen-counting is desirable but not necessary (training will be provided).

The candidate will be expected to recruit and to supervise 6 - 10 undergraduate assistants at UCSB who will participate as research-for-credit interns, assisting in sample-collection and - processing in the greenhouse and lab. Depending on the experience of the candidate, there may be the opportunity to teach courses in

Botany and Introductory Biology (for additional compensation).

The work will be conducted at the University of California, Santa Barbara. The successful candidate will join an active group of graduate and undergraduate students in the Department of Ecology, Evolution, and Marine Biology at UCSB (<http://www.lifesci.ucsb.edu/eemb/faculty/mazer/index.html>), and will have the opportunity to develop independent or collaborative research.

Anticipated annual salary: ~\$34,400 with benefits (with no teaching responsibilities); \$38,000 - \$44,000 with benefits (with one or two one-quarter courses to teach; a PhD. and experience teaching plant biology are required).

Interested applicants should send a CV, statement of research interests, and a list of three referees (with e-mail addresses and telephone numbers ) to Susan Mazer ([mazer@lifesci.ucsb.edu](mailto:mazer@lifesci.ucsb.edu) <<mailto:mazer@lifesci.ucsb.edu>> and [smazer@nsf.gov](mailto:smazer@nsf.gov)). You may also reach me by phone at: 703-292-7121. In addition, if you plan to attend the Ecological Society of America meetings in Portland during August 1 - 6, 2004, please contact me so we can arrange a time to meet.

Dr. Susan J. Mazer Program Director Ecological Studies Cluster (BIO/DEB) Ecology Program National Science Foundation 4201 Wilson Blvd., rm 614 Arlington, VA 22230 Phone: 703-292-7121 FAX: 800-208-8980

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## UCopenhagen GeneDiversity

A post doc position is available at the Department of Evolutionary Biology, University of Copenhagen.

January 2003 the Carlsberg Foundation granted 5 years of support for the project Molecular Diversity and Evolution. The grant includes 10 post doc years, 2 PhD stipends and running costs.

The project has two major components: 1. Evolution of processes responsible for gene product diversity. Focus will initially be upon alternative splicing in evolution and 2. Evolution of regulatory networks based on non-coding RNA. The overall perspective for these studies is the molecular evolution of organism complexity. The intention of this research is to better understand the relationship between phenotypic evolutionary change and the evolution of basic molecular processes. The project

will focus upon molecular experimentation in collaboration with on-site bioinformaticians.

With this post doc position we specifically wish to focus on differential splicing and its regulation. The candidate will be responsible for the experimental work in this connection and supervision of PhD and Msc students. The project is internationally well connected and is in a strong bioinformatic and molecular environment.

The Post doc is potentially for 3 years with a yearly renewal. There is a three month probation.

The position is open until filled. Send applications to: Professor Peter Arctander, [parctander@zi.ku.dk](mailto:parctander@zi.ku.dk)

Information on Danish post doc and PhD rules and regulations, including salaries and taxation, are available at <http://www.ku.dk/english/> Further information from Professor Peter Arctander, [parctander@zi.ku.dk](mailto:parctander@zi.ku.dk) +45 2875 1310 Department of Evolutionary Biology, Universitetsparken 15, DK-2100 Copenhagen ?, Denmark

Arctander <[Parctander@bi.ku.dk](mailto:Parctander@bi.ku.dk)>

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## UGeorgia StatMathEpidemiology

Postdoctoral Research Associate Institute of Ecology, University of Georgia, USA

Applications are invited for a postdoctoral fellowship in Statistical and Mathematical Epidemiology, funded by the National Science Foundation. The successful applicant will be involved in the development of novel statistical and time-series methods to explore potential interactions between diseases in epidemiological data. Initially, the project will focus on childhood infections in Europe and the USA, but there is scope for studying other candidate infections in various locations around the globe.

A PhD in statistics, applied mathematics or a highly quantitative field is essential. Previous experience in the analysis of ecological or epidemiological systems would be desirable though not essential.

The position is for three years with a salary of \$35,000 per year, plus fringe benefits.

Informal enquiries may be addressed to Pej Rohani +1 706 542 9249, e-mail: <<mailto:rohani@uga.edu>>[rohani@uga.edu](mailto:rohani@uga.edu).

Candidates should send a detailed CV, together with a

statement of research interests and three references to Pej Rohani, Institute of Ecology, University of Georgia, Athens GA 30602. Electronic applications are encouraged.

Review of applications will start on August 30 and will continue until a suitable candidate has been identified.

Pejman Rohani <rohani@uga.edu>

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## ULausanne Reproduction

A postdoctoral position is available to work on the evolution of reproductive traits in the dioecious *Silene latifolia* ([http://www.unil.ch/dee/page7005\\_en.html](http://www.unil.ch/dee/page7005_en.html)) at the University of Lausanne. The position is for 18 months and is available from October 1st or later.

Applicants could have skills and interests in any of several areas of evolutionary ecology of plants (mating system evolution, pollination biology, population genetics).

If interested, please contact

Dr. G. Bernasconi Swiss NSF Professorial Fellow Current address: Institute of environmental Sciences University of Zurich Winterthurerstr. 190 CH 8057 Zurich Switzerland Email: [bernasco@uwinst.unizh.ch](mailto:bernasco@uwinst.unizh.ch)

Application deadline: 15th August 2004 For application please send: CV, publication list, name and address of two referees.

The Department of Ecology and Evolution of the University of Lausanne, Switzerland, provides a very lively intellectual and social environment ([http://www.unil.ch/dee/page5090\\_en.html](http://www.unil.ch/dee/page5090_en.html)).

Lausanne, located in Switzerland at the shore of Lake Geneva, offers very high quality of life and outstandingly beautiful surroundings (Alps, Jura mountains, Lake; see <http://www.lausanne-tourisme.ch/>).

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## USheffield ConservationGenetics

UNIVERSITY OF SHEFFIELD  
DEPARTMENT OF ANIMAL & PLANT SCIENCES

The following post was advertised (with others) in New Scientist on 19 June:

The UK Population Biology Network (UKPopNet) is a network of five Universities (Aberdeen, East Anglia, Leeds, Sheffield, York) and the Centre for Ecology and Hydrology. It is funded by NERC with additional support from English Nature to develop research in population biology in the UK. As part of a three-year programme of projects, network members are currently seeking to recruit staff.

This post will investigate the genetic significance, sustainability and adaptive potential of declining populations of plants and animals (primarily insects) using molecular markers. The appointee must have a PhD and experience in molecular and evolutionary genetics.

The post is full time for 1 year initially and is available from 1 October 2004. Funding is expected to be available for a further 2 years.

For further details go to: [http://www.shef.ac.uk/jobs/-job\\_details.php?file=job\\_list&ID=2411&start=16](http://www.shef.ac.uk/jobs/-job_details.php?file=job_list&ID=2411&start=16)

Post reference no. PR1056

Closing date 09 July 2004

Informal enquiries may be addressed to Terry Burke ([t.a.burke@sheffield.ac.uk](mailto:t.a.burke@sheffield.ac.uk) / +44(0)114 222 0096)

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## USussex Postdoc

The University of Sussex is seeking nominations for two 9-10 month Leverhulme Post-doc positions. These are open to non-UK citizens and can be taken up as late as Feb 2006. Unfortunately we need to nominate someone by July 26th. If you are interested in being nominated to work with David Waxman, Joel Peck, Lindell Bromham or Adam Eyre-Walker within the Evolution Group at Sussex, then please contact Adam Eyre-Walker ([a.c.eyre-walker@sussex.ac.uk](mailto:a.c.eyre-walker@sussex.ac.uk)). More details about the group can be found at <http://www.lifesci.sussex.ac.uk/CSE/> and about the fellowship at [http://www.leverhulme.org.uk/grants\\_awards/-grants/visiting\\_fellowships/](http://www.leverhulme.org.uk/grants_awards/-grants/visiting_fellowships/) Adam Eyre-Walker Centre for the Study of Evolution & School of Biological Sciences University of Sussex Brighton BN1 9QG

tel : 01273 678480 tel : 01273 678480

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**UWalesBangor**  
**LizardSpeciationGenetics**

UWales Bangor . Lizard Speciation Genetics

Postdoctoral position in speciation/population genetics of Caribbean anoles.

The BBSRC funded position in Prof R S Thorpe's laboratory is available for three years from 1/10/04, or as soon as possible thereafter, for someone with a PhD in molecular ecology/evolution and experience of developing/screening nuclear markers such as microsatellites and SNPS. The post involves substantial fieldwork in the southern Lesser Antilles, molecular laboratory work and data analysis. Application forms from Human Resources, University of Wales Bangor, Gwynedd, LL57 2DG. Closing date 19/08/04. Further information on <http://biology.bangor.ac.uk/research/opportunities/> – Professor R S Thorpe School of Biological Sciences University of Wales Bangor Gwynedd LL57 2UW

Tel 01248 382312 Fax 01248 371644 email [r.s.thorpe@bangor.ac.uk](mailto:r.s.thorpe@bangor.ac.uk)

“Prof. R S Thorpe” <[r.s.thorpe@bangor.ac.uk](mailto:r.s.thorpe@bangor.ac.uk)>

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**WashingtonU EvolBiol**

This is a second notice, but note the addition of a second position. ——— 2 POSTDOCTORAL FELLOWS WASHINGTON UNIVERSITY in ST. LOUIS TYSON RESEARCH CENTER Washington University in St. Louis, Missouri invites applications for two [2] Postdoctoral Fellowships in Ecology, Environmental Sciences, or Evolutionary Biology to be based at the Tyson Research Center, a 2,000-acre tract of land located 20 miles from campus. The fellows will be responsible for developing research programs independently or in conjunction with Washington University faculty and involving undergraduates in research conducted at the Center. In addition, the fellows will be expected to teach one course during the school year. One fellow will teach Conservation Biology, and this position can start no later than Jan. 1, 2005. The other fellow will teach a course to be determined later and can start no later than June 2005. More information on Tyson can be found at <http://www.biology.wustl.edu/tyson/>. Applicants should include a curriculum vitae and a statement of the research to be conducted at the Center, and arrange to have two letters of recommendation sent on the applicant's behalf. In addition, state which position and start time interests you most, and what sort of flexibility you have. If applying for the second position, also include a brief statement of the course you might teach. All materials should be sent electronically to Jonathan Losos, Ph.D., ([losos@biology.wustl.edu](mailto:losos@biology.wustl.edu)), and to Jon Chase, Ph.D. ([jchase@biology2.wustl.edu](mailto:jchase@biology2.wustl.edu)). Applicant review will begin July 31 and continue until the positions are filled. Washington University is an Equal Opportunity Employer.

Jonathan Chase <[jchase@biology2.wustl.edu](mailto:jchase@biology2.wustl.edu)>

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**WorkshopsCourses**

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| ColdSpringHarbor ComputationalGenomics Nov5-11 | UFribourg ExperimentalEvol Oct4-5 | 47 |
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## ColdSpringHarbor ComputationalGenomics Nov5-11

Course announcement - Application deadline, July 15, 2004

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Cold Spring Harbor COMPUTATIONAL GENOMICS  
NOVEMBER 5 - 11, 2003

INSTRUCTORS:

Pearson, William, Ph.D., University of Virginia, Charlottesville, VA  
Smith, Randall, Ph.D., SmithKline Beecham Pharmaceuticals, King of Prussia, PA

Beyond BLAST and FASTA - This course presents a comprehensive overview of the theory and practice of computational methods for gene identification and characterization from DNA sequence data. The course focuses on approaches for extracting the maximum amount of information from protein and DNA sequence similarity through sequence database searches, statistical analysis, and multiple sequence alignment. Additional topics include gene recognition (exon/intron prediction), identifying signals in unaligned sequences, and integration of genetic and sequence information in biological databases. The course combines lectures with hands-on exercises; students are encouraged to pose challenging sequence analysis problems using their own data. The course makes extensive use of local WWW pages to present problem sets and the computing tools to solve them. Students use Windows and Mac workstations attached to a UNIX server; participants should be comfortable using the Unix operating system and a Unix text editor.

The course is designed for biologists seeking advanced training in biological sequence analysis, computational biology core resource directors and staff, and for scientists in other disciplines, such as computer science, who wish to survey current research problems in biological sequence analysis.

The primary focus of the Computational Genomics Course is the theory and practice of algorithms used in computational biology, with the goal of using current methods more effectively and developing new algorithms. Students more interested in the practical aspects of software development are encouraged to apply to the Cold Spring Harbor Bioinformatics - Writing Software for Genome Research Course.

For additional information and the lecture schedule and

problem sets for the 2003 course, see:

<http://www.people.virginia.edu/~wrp/cshl03>

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To apply to the course, fill out the form at:

[http://meetings.cshl.org/course\\_app.htm](http://meetings.cshl.org/course_app.htm)

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## Denmark Hybridization Nov27-30

First Announcement of Workshop and Ph.D. course:

“Natural hybridization and introgression: from genomics to ecology” Denmark, November 27. -30. 2004

The goal of this workshop is to discuss genetics, genomics and ecology of hybridization and gene introgression. We will concentrate on newer findings on the effects of specific genes and -interactions, genotype x environment interactions, changes in genomes subsequent to hybridization, gene expression, regulation etc. The role of hybridization in evolution is more debated and empirically better supported than ever, due to new insights into genetics, genomics and ecology of hybrids. It is now widely recognized that hybridization may have a variety of evolutionary and ecological consequences, and a major goal is to understand their frequencies, conditions and mechanisms. At the same time, hybridization and introgression is becoming increasingly relevant for human management of e.g. survival of indigenous populations, invasive species, genetically modified organisms, maintenance of genetic resources, etc.

Three invited speakers will take part in the workshop: Allison Snow, Professor at Dept. of Evolution, Ecology, and Organismal Biology, Ohio State University (<http://www.biosci.ohio-state.edu/~asnowlab/allison.htm> <<http://www.biosci.ohio-state.edu/~asnowlab/allison.htm>>): “Effects of hybridization between crops and their weedy relatives: the potential for rapid evolutionary change.” Michael Arnold, Professor at Dept. of Genetics, University of Georgia ([http://www.genetics.uga.edu/faculty/bio-Arnold\\_.html](http://www.genetics.uga.edu/faculty/bio-Arnold_.html) <[http://www.genetics.uga.edu/faculty/bio-Arnold\\_.html](http://www.genetics.uga.edu/faculty/bio-Arnold_.html)>), “Natural Hybridization and evolution: from genetics to ecology and back again”. Andreas Madlung, Assistant Professor at Biology Department, University of Puget Sound (<<http://www.ups.edu/biology/faculty/madlung.htm>>): “Genomic structure and stability, epigenetic changes

and transposon activity in auto- and allopolyploid hybrids of Arabidopsis.”

In addition, there will be oral and poster presentations by participating researchers and Ph.D. students. But most importantly, there will be plenty of time for discussion and exchange of ideas.

The course will take place at a course facility ca. 50 km north of Copenhagen. Participation fee, including room and board, will be 270 EUR maximum, possibly lower. Travel at the participants own expense. A maximum of 30 persons can take part in the workshop. Students will receive a certificate stating their participation (active, if presenting research, or passive) to be used for university credits. For preliminary registration (to be confirmed later), send an e-mail to Mette Hansen, mha@kvl.dk. Please indicate whether you would like to give an oral presentation or poster, and enclose a brief abstract of its content (please note: only few presentations will be accepted). For more information, contact thure.hauser@risoe.dk <mailto:thure.hauser@risoe.dk>, fax: +45 4677 4160. Organizing committee: Thure Hauser, Senior Scientist, Risø National Lab.; Christian Damgaard, Senior Scientist, National Environmental Research Inst.; Erik Kjær, Professor, Forest Genetics, Royal Veterinary and Agricultural Univ.; Dorte Bekkevold, Scientist, and Einar Eg Nielsen, Senior Scientist, Danish Institute for Fisheries Research.

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## UFribourg ExperimentalEvol Oct4-5

Experimental Evolution Workshop 4-5 October 2004

Application deadline extended!

Fribourg Ecology & Evolution Days 2004

University of Fribourg, Departement of Biology, Fribourg, Switzerland,

<http://www.unifr.ch/biol/ecology/expevo04/-index.html> When does natural selection favor the evolution of ecological specialization as opposed to a generalist lifestyle, and why? Does conflict between

the sexes lead to an evolutionary arms-race? What factors affect the evolution of parasite virulence? Is mutation rate molded by evolution? Is evolution repeatable and reversible? Studying evolution in real time under experimental conditions is a powerful way of addressing these questions.

This workshop will bring together several invited speakers and a number of younger researchers using experimental evolution to address diverse questions. The talks will be followed by plenary discussion. The symposium will be free (no registration fee).

Confirmed invited speakers: \* James B. Anderson (University of Toronto, Canada) \* Graham Bell (McGill University, Montreal, Canada) \* Angus Buckling (University of Bath, UK) \* Santiago Elena (University of Valencia, Spain) \* William Rice (University of California, Santa Barbara, USA) \* Gregory Velicer (Max-Planck Institute of Developmental Biology, Tübingen, Germany)

We have time for about 15 contributed talks of 20 min.

The workshop is supported by the University of Fribourg, Switzerland and the TROISIÈME CYCLE de CONFÉRENCE UNIVERSITAIRE DE SUISSE OCCIDENTALE. (<http://www.cuso.ch/3e-cycle/biologie.html>)

Organizers: Tadeusz Kawecki & Dieter Ebert University of Fribourg, Departement of Biology, Fribourg, Switzerland Email: tadeusz.kawecki@unifr.ch dieter.ebert@unifr.ch

For more information on the workshop and for registration check: <http://www.unifr.ch/biol/ecology/expevo04/index.html> For more information on Ecology and Evolution in Fribourg check: <http://www.unifr.ch/biol/ecology/index.html> –

Dieter Ebert [ [Mailto:dieter.ebert@unifr.ch](mailto:dieter.ebert@unifr.ch) ] Université de Fribourg, Departement de Biologie, Ecologie et Evolution, Chemin du Musee 10 1700 Fribourg, Switzerland <http://www.unifr.ch/biol/ecology/index.html> Tel. +41-(0)26-300 88 69, Fax +41-(0)26-300 96 98

Please visit the web-page dedicated to the late W.D. (Bill) Hamilton: <http://www.unifr.ch/biol/ecology/-hamilton/hamilton.html> <http://www.unifr.ch/biol/ecology/hamilton/hamilton.html>

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains one of the keywords “Conference, Grad, Job, Other:, Postdoc, Workshop” and then the message stands a better chance of being correctly parsed.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. So please do not expect an instant response.

## Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by L<sup>A</sup>T<sub>E</sub>X do not try to embed L<sup>A</sup>T<sub>E</sub>X or T<sub>E</sub>X in your message (or other formats) since my program will strip these from the message.