E v o l D i r

May 1, 2006

Month in Review

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.

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.

____/ ____

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Conferences

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Bangkok MEEGID VIII Nov30-Dec4

MEEGID VIII Bangkok, Thailand. 30th November-4th December 2006. Call for conferences/symposia proposals and papers

The 8th International Meeting "Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases" (MEEGID VIII) will be held in Bangkok, Thailand, 30th November-4th December 2006. As for the 7 first MEEGID meetings, it will be co-organized by the Centers for Disease Control and Prevention (CDC; http://www.cdc.gov/) in Atlanta and the Institut de Recherche pour le Développement (IRD; http://www.ird.fr/) in France. Mahidol University (http://www.mahidol.ac.th/) will be an offficial co-organizer of the meeting, which will be supported also by the French Embassy (http://www.ambafrance-th.org/).

The MEEGID meetings are organized in synergy with the new journal Infection, Genetics and Evolution (Elsevier; http://www.elsevier.com/locate/meegid), which scientific topic is identical to that of the MEEGID. Launched only 4 years ago, Infection, Genetics and Evolution is now published with 6 issues per year, and is covered by Medline and Index Medicus, starting from the 1st issue. It has been quoted 3.5/5.0 ("very good") by the US National Library of Medicine.

It is now covered by ISI and an official impact index will be available soon.

Communications on genetics, genomics, proteomics, population biology, mathematical modelling, bioinformatics are welcome. They can deal with the host, the pathogen, or the vector in case of vector-borne diseases. Papers considering host + pathogen or pathogen + vector (co-evolution) are particularly encouraged. All pathogens are within the scope of MEEGID: viruses, parasitic protozoa, helminths, fungal organisms, prion. All infectious models can be considered, including those of veterinary or agronomical relevance.

The papers communicated for MEEGID VIII will be published in a special issue of Infection, Genetics and Evolution, as already done for MEEGID VI (Paris, July 2002). MEEGID VIII will include 10-15 plenary lectures, about 20 specialized symposia, 12-15 "express-debates" (20 mn presentation by only one speaker followed by 40 mn free discussion) and several poster sessions.

Special emphasis through plenary lectures and symposia will be given to health problems of particular interest to Thailand and South-East Asia: avian flu, SARS, malaria, dengue, tuberculosis. Pleanary lectures and symposia will also deal with trasnversal topics such as population genetics or species concepts. The congress is still open to proposals of conferences and symposia.

Awards will be attributed to the best communication,

the best communication by a student and the best communication by a scientist from the Southern World on a problem specifically relevant to these areas.

For the first time, a satellite meeting will be organized in the framework of MEEGID VIII by the think tank "Biology, Medicine and Society". Societal problems linked to genetics, evolution and transmissible diseases will be discussed in several roundtables.

Abstract submission deadline: 30th September.

Registration Fee: 200.00 euros or equivalent in other currencies; Students pay only meals and coffee breaks

Place: The Royal River Hotel http://-Preliminary registration www.royalrivergroup.com and abstract submission are possible by email (below). Please provide last name, first name, title, gender, nationality, scientific speciality, professional address, phone, fax, email and website if available. Abstract should follow the format recommended for Infection, Genetics and Evolution for list of references, reference citations, etc. and should not exceed 300 words. Please express your request, either orgal communication or poster.

More information available soon at http://-www.th.ird.fr . Contact:

Michel Tibayrenc, MD, PhD Editor -in-chief Infection, Genetics and Evolution (Elsevier) http://www.elsevier.com/locate/meegid IRD representative in Thailand IRD Representative Office French Embassy 29, Thanon Sathorn Tai, Bangkok 10120, Thailand Tel: + (66 2) 627 2190 Fax: + (66 2) 627 2194 Cel: + (66 1) 82 64 056 E-mail: (direct): Michel.Tibayrenc@ird.fr (secretary) ird_th@ksc.th.com Website: http://www.th.ird.fr Michel.Tibayrenc@ird.fr

BejaiaAlgeria EvolEcol Nov7-9

Dear all, Please find below an annoucement for an Ecology meeting in the nice city of Bejaïa, Algeria.

The University A.MIRA of Bejaïa (Algeria), the Faculty of Nature and Life Sciences and the Laboratory of Ecology & Environment organize the first:

Mediterranean Meetings on Ecology in Bejaïa, 7- 9 november 2006

Objectives This seminar aims to assess the state of knowledge and the impact of human activities on the

various ecological aspects (systematics, chorology, biogeography...) of plant and animal species, natural populations and their habitats within the diverse ecosystems (wetlands, forests, maquis, agro-ecosystems, steppes and deserts) throughout the Mediterranean geographical area. These meetings will be also an opportunity to exchange ideas and views concerning methodologies of analyses, inventories, cartographies and development of disciplines such as biogeography, conservation biology and natural spaces management. Alongside the communication sessions, workshops will be organized about the following topics: 1/ Rehabilitation of ecology, 2/ Projects of inventories, atlases and cartographies, guides, floras and faunas, 3/ Necessity of a scientific journal.

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Retained topics: - Ecology of species, - Taxonomy and Phylogeny, - Population Biology and Genetics, - Modelization and management in ecology, - Conservation methods and Ecosystem planning.

Calendar 05 june 2006: Reception of communication abstracts. 20 june 2006: Notification to authors. 15 sept. 2006: Reception of communication final versions (texts to be published in the Proceedings).

Presentation Abstracts of communications should be presented in at most one page using Word format and Times New Roman, characters. Abstracts should include: - Title of communication (14 bold), -Names and surnames of the authors underlining the communicating author (10 regular), - Six key words at most, - Text written in english or french (12 regular, 1.5-spaced). The final complete versions of accepted communications should not exceed 8 pages presented following the above mentioned guidelines and forwarded as diskettes or attached e-mail files.

Correspondance:

Pr. MOALI Aïssa Faculté des Sciences de la Nature et de la Vie. Université A. Mira de Béjaïa. Targa Ouzemmour. 06000 Béjaïa - Algérie. Tel : 213 34 21 47 62 213 71 72 23 08 Email : remedeco@yahoo.fr rencontreecologie06@yahoo.fr

errol.vela@free.fr

BrockU OntarioEcology May5-7

FINAL REMINDER AND CALL FOR REGISTRANTS

The Brock University Department of Biological Sciences is proud to be hosting the 2006 Ontario Ecology and Ethology Colloquium.

This is a conference organized by graduate students to provide graduate and advanced undergraduate students, at any stage in their thesis research, the opportunity to present in a supportive atmosphere dominated by student peers and friendly faculty. The conference location rotates around Ontario. In May 2005 it was hosted by Carlton University; in May 2004 it was hosted by University of Toronto at Mississauga. This conference encompasses all aspects of ecology, behaviour, and evolution. This is also one of the largest regional graduate student run conferences in North America on these topics.

This year we are honoured to have 4 plenary speakers: Barbara Rosemary Grant, Princeton University; Ellie Prepas, Lakehead University; Linda Corkum, University of Windsor; and Marie-Josée Fortin, University of Toronto.

This years conference will be held May 5 to May 7 2006.

Early registration and abstract submission deadline is April 14, 2006. All information is available on the website www.oeec.ca . Thanks very much,

2006 OEEC Organizing Committee oeec@brocku.ca oeec@brocku.ca

HalleGermany POPBIO2006 May24-27

Herewith we would like to remind you on the *deadline for submission of talks/posters and the deadline for reduced fee registration (31.3.2006)* for the

*19th Annual Meeting of the Plant Population Biology Meeting of the Ecological Society of **Germany**, **Switzerland** and **Austria** (GfOe),*

taking place in Halle, Germany, from 24 May to 27 May 2006 organized jointly by the UFZ-Centre for Environmental Research and the Geobotanical Institute of the University of Halle.

The annual meeting is being held in English and usually attended by more than one hundred people from all over Europe. Priority is given to young researchers to present results from their PhD theses. The focus of the meeting in 2006 is on interactions of plants with

other species, recognizing that plants have to cope with a large number of competitors, herbivores, pathogens and symbionts. Therefore, to understand the population biology of plants, botanist would have to broaden their scope and incorporate these interactors in their studies. Presentations from the whole field of plant population biology are welcome.

Keynote speakers include: - *Claire de Mazancourt*, Imperial College at Silwood Park - *Jacqui Shykoff*, CNRS-Paris - *Jürgen Kroymann*, Max Planck Institute for Chemical Ecology, Jena - *Amots Dafni*, University of Haifa

Please distribute this invitation freely among your colleagues! Please visit the PopBio2006-webpage at http://www.ufz.de/popbio2006 for further information and registration.

Looking forward seeing you,

Alexandra Erfmeier & Isabell Hensen – University of Halle

Daniel Prati, Harald Auge & Walter Durka – UFZ email to: PopBio2006@ufz.de

Hanoi Rodents Aug28-Sep1

CALL FOR ABSTRACTS:

RE: 3RD INTERNATIONAL CONFERENCE ON RODENT BIOLOGY AND MANAGEMENT

Dear Colleagues, We envision bringing together a symposium at the 3rd International Conference on Rodent Biology and Management, to be held 28th August to 1st September 2006, Hanoi, Vietnam.

Our symposium would be one of many that deal with aspects of the biology and management of rodents worldwide.

The symposium 'Adaptation and Diversification in Rodents', which we envision, shall bring together presentations on findings derived from the molecular analysis of adaptation in rodents. In other words, we are keen on bringing together studies on adaptive molecular evolution in rodents. Examples of such studies range from the selection for resistance to rodenticides, coat color variation, phylogeography, and other examples of molecular evolution in rodent species. Because of their potential to identify genes underlying adaptation, we are particularly intrigued by studies that have the iden-

tification of functional genetic differences between rodent populations and species to their focus. Note that a symposium on the Evolutionary Biology and Systematics, chaired by Ken Aplin (Ken.Aplin@csiro.au), also will be held in conjunction with this symposium, and you will be able to attend both symposia.

We strongly feel that there are numerous possibilities for presentations that would fit within our symposium. Potentially, the mechanisms and evolution of rodenticide resistance, the mapping and identification of its genetic underpinnings, and the patterns of selection on the locus, might merit their own symposium. This will depend on the number of scientists who express interest in a separate session.

We cordially invite you to join us in our effort to make this a great symposium by contributing a paper. We encourage you, or any of your students or postdocs, to contact us at your earliest convenience with informal inquiries or abstracts on work in this or related research areas. Opportunities for funding for student travel are in place.

See http://icrbm2006.ioz.ac.cn/index.html for information on this conference, and please note these critical dates: 1 June 2006 (Deadline submission of abstracts for oral or poster presentation), 22 June (Deadline for early registration). 1 May (Deadline for submission of applications for developing country & student travel support).

We are looking forward to hear from you.

Thank you very much for your consideration.

Yours sincerely,

Michael H. Kohn Rice University Ecology & Evolutionary Biology & the Institute of Biosciences and Bioengineering MS170, P.O. Box 1892 Houston, Texas, 77251-1892 Phone: 713-348-3779 Fax: 713-348-5232 hmkohn@rice.edu

Hans-Joachim Pelz Federal Biological Research Center for Agriculture and Forestry Institute for Nematology and Vertebrate Research Toppheideweg 88 D-48161 Münster, GERMANY Email: j.pelz@bba.de Phone: +49 251 871 0640

Michael Kohn hmkohn@rice.edu

HongKong Bioinformatics Jan15-17

The Fifth Asia-Pacific Bioinformatics Conference, APBC2007, will be held in Hong Kong during 15 - 17 January 2007. See http://www.cs.hku.hk/apbc2007. The Asia-Pacific Bioinformatics Conference series is an annual forum for exploring research, development, and novel bioinformatics applications. The aim of this conference is to bring together researchers, professionals, and industrial practitioners for interaction and exchange of knowledge and ideas. We invite submissions that address conceptual and practical issues of bioinformatics.

Typical, but not exclusive, topics of interest include:

Sequence analysis Motif Finding Recognition of Genes RNA Analysis Population genetics/SNP/Haplotyping Physical and Genetic Mapping Comparative Genomics, Genome rearrangements Evolution and Phylogeny Protein structure analysis Microarray design Proteomics Transcriptome, Gene Expression Pathways, Networks and Systems Databases and Data Integration Ontologies Text Mining Applications

IMPORTANT DATES Submission of papers: Jul 15, 2006 Notification of paper acceptance: Sep 15, 2006 Submission of posters: Sep 30, 2006 Camera-ready copy & Author registration: Oct 10, 2006 Notification of poster acceptance: Oct 20, 2006 Conference: Jan 15 - 17, 2007

CONFERENCE CHAIR Francis YL Chin, The University of Hong Kong, Hong Kong PROGRAM CHAIRS David Sankoff, The University of Ottawa Lusheng Wang, The City University of Hong Kong

PROGRAM COMMITTEE Tatsuya Akutsu, Miguel Andrade, Stephane Aris-Brosou, Joel Bader, Serafim Batzoglou, David Bryan, Jeremy Buhler, Peter Donnelly, Dannie Durand, Nadia El-Mabrouk, Robert Giegerich, Carole Goble, Concettina Guerra, Dan Gusfield, Michael Hallett, Sridhar Hannenhalli, Daniel Huson, Gavin Huttley, Jenn-Kang Hwang, Tao Jiang, Uri Keich, Anand Kumar, Tak Wah Lam, Doheon Lee, Jinyan Lim, Wentian Li, Guohui Lin, Michal Linial, Zhejie Liu, Bin Ma, Satoru Miyano, Laxmi Parida, Mark Ragan, Marie-France Sagot, Akinori Sarai, Vincent Schachter, Steven Skiena, Yun Song, Robert Stevens, Edward Susko, Alfonso Valencia, Michael Waterman, Ken Wolfe, Stacia Wyman, Hong Yan, Qiang Yang, Kaizhong Zhang, Liqing Zhang, Louxin Zhang

SUBMISSION GUIDELINES APBC2007 invites high-quality original papers on any topic related to Bioinformatics. Papers should be no more than 10 pages in length, all- inclusive - title, addresses, abstract, text, figures, tables, and references, conforming to the formatting instructions for the series Advances in Bioinfor-

matics and Computational Biology (instructions available at the APBC2007 website). Papers will be judged on originality, significance, correctness, and clarity. Authors should submit a PDF file according to the instructions on the APBC2007 Paper Submission Website. The full paper must be submitted by 15 July 2006. The proceedings will be published as a volume in the series Advances in Bioinformatics and Computational Biology by Imperial College Press. Expanded version of selected papers will be invited for publication in the Journal of Bioinformatics and Computational Biology. Inclusion of a paper in the proceedings is contingent on one of the authors registering and presenting at the conference.

David Sankoff <sankoff@uottawa.ca>

InstZooLondon IslandEvol Apr26 2

An update on this symposium advertised a couple of weeks ago.

The Centre for Ecology and Evolution in London and the Centre for Population Biology, Imperial College, are running a one day symposium, Evolution and Ecology on Islands, at the Meeting rooms, The Institute of Zoology, London, on Wednesday 26th April.

Speakers include: George Turner (Hull), Brent Emerson (UEA), Lindell Bromham (Sussex), Michael Monaghan (NHM), Sam Berry (UCL), Fred Rumsey (NHM), Ally Phillimore (Imperial), Victoria Herridge (UCL), Shai Meiri (Imperial) & Paul Pearce Kelly (Insitute of Zoology). A current programme can be found at http://www.ucl.ac.uk/~ucbtcee/cee/events.html The symposium begins at 9:45 am and we will run through to a drinks reception at 5:30.

Registration is not mandatory, but it would be helpful if you could register with Mark Carine on <mailto:m.carine@nhm.ac.uk>m.carine@nhm.ac.uk, so that we can cater appropriately for tea and coffee. Entry will be 3 pounds, to cover the costs of tea/coffee, and payable on the day.

The meeting rooms of the Institute of Zoology are roughly opposite the main entrance to the zoo. Access to the Meeting Rooms is from the Outer Circle, Regent's Park. Nearest bus - No. 274; Underground station - Camden Town.

(Dr) Greg Hurst Reader in Evolution and Ecology Dept Biology, University College London 4 Stephenson Way London NW1 2HE UK +44 20 76795072 (t) +44 20 76795052 (f) http://www.ucl.ac.uk/%7Eucbtghu/

g.hurst@ucl.ac.uk g.hurst@ucl.ac.uk

Leiden EvolTradeOffs Apr27

A one-day symposium on

Traits Traded Off: on recurring structures in evolutionary ecology.

(to go with the PhD defense of Claus Rüffler)

27 April 2006

"grote collegezaal" Van de Klaauw laboratory, Kaiserstraat 63 2311GP Leiden, the Netherlands

9.45 Opening (Hans Metz, Leiden)

10.00-10.40 Evolution of resource consumption strategies in spatially distributed populations: a kin selection perspective (Prof. Troy Day, Kingston)

10.40-11.20 Evolution of specialization and speciation, with particular reference to either nitrogen-fixing bacteria Sinorhizobium sp. associated with Medicago or plant-mites interactions (or both !). (Prof. Isabelle Olivieri, Montpellier)

11.20-11.35 Coffee break

11.35-12.15 Specialists and generalists in variable environments (Prof. Peter Abrams, Toronto)

12.15-12.55 Traits Traded Off (Claus Rüffler, Toronto)

12.55-14.15 Lunch Break

14.15 Official defense in the Academy-Building

15.00 Reception in the Academy-Building

16.15-16.55 The long-term evolution of multi-locus traits under frequency-dependent disruptive selection (Dr. Sander van Doorn, Groningen)

16.55-17.35 The emergence of polymorphism in pleiotropic traits with trait-specific dominance (Dr. Tom Van Dooren, Leiden)

Participation in the symposium is open to anyone interested. Please register by email to vdooren@rulsfb.leidenuniv.nl.

vdooren@rulsfb.leidenuniv.nl

Madrid ForestPopGenet Oct1-6

Dear friends,

This is the first call of the IUFRO Conference: "Population Genetics and Genomics of Forest Trees: from Gene Function to Evolutionary Dynamics and Conservation", which is scheduled to take place in Alcalá de Henares, Madrid (Spain) October 1-6 2006. This event will be held jointly with the final meeting of the COST Action E-28 "Genosilva: European Forest Genomics Network".

Registration, abstract submission, hotels and general information about the meeting will be available by April 1st at the website www.genfor2006.fgua.es . For further information please contact the Congress Secretariat (M Luisa Rodriguez Frade, mluisa@fgua.es).

We would like to invite you to attend the meeting, and we would be very grateful if you distribute this information.

Looking forward to seeing you in Alcalá de Henares, Madrid

Sincerely,

M Luisa Rodríguez Frade Fundación General Universidad de Alcalá C/ Imagen 1-3 28801 Alcalá de Henares - Madrid Tfno. (34) 91 879 74 30 Fax: (34) 91 879 74 55 e-mail: mluisa@fgua.es

santiago@inia.es

$Marseilles\ 10 Evol Biol\ Sep 20-22$

10th Evolutionary Biology Meeting at Marseilles-France-20/22 September, 2006

First accepted abstracts are available on: http://www.evolutionary-biology.org We remember you that registrations and abstract submissions for the 10th Evolutionary Biology Meeting at Marseilles are on line and until June 30th, 2006.

The general scheme of the conference will be similar to the one proposed the former years. The following topics will be discussed: Systematic, Biodiversity, Comparative genomic and post-genomic (at all taxonomic levels), Functional phylogeny, Environment and evolution. This year, we would also like to touch on: - Evolutionary biology concepts for biological annotation. - Probalistic models and statistic tools for concepts in evolution.

For more information, please see the web site http://www.evolutionary-biology.org Or, contact us at egee@up.univ-mrs.fr

– Nadege BARDIOT Logistical Organisation Committee

EA 3781 Evolution Biologique Université d'Aix Marseille I - case 19 Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 http://www.up.univ-mrs.fr/evol We are organizing the 10th Evolutionary Biology Meeting at Marseilles http://www.evolutionary-biology.org http://www.up.univ-mrs.fr/evol-cgr/ egee@up.univ-mrs.fr

McMasterU GenomicsOriginHumanity Aug3-5

You are invited to a summer workshop on The Genomic Revolution and the Origin of Humanity that will be held at McMaster University, Hamilton, Ontario, Canada from August 3-5, 2006.

Attendees at this Origin Institute summer workshop will explore links between genomics and the origin of humans and human culture. A group including 6 world class scientists and leaders in the fields of genomics, evolution, and health has been invited to initiate activity that is connected with key international research efforts in population and reproductive biology, molecular medicine, gene and stem cell therapies, and environmental health. Invited speakers include: Andrew Clark, Marc Feldman, Kenneth Morgan, David Serre, Mark Stoneking, Sarah Tishkoff.

Space is limited. For information and registration please visit the website: http://origins.mcmaster.ca/-genomics/registration.html Dr. Rama S. Singh, Professor Department of Biology Life Science Building 540 McMaster University Hamilton, Ontario CANADA L8S 4K1 Tel: (905) 525-9140 ext. 24378 Fax: (905) 522-6066

singh@mcmaster.ca

Chairs

Rob Tempelman <tempelma@msu.edu>

MichiganStateU AnimalFuncGenomics May16-19 2

Re: 2nd ISAFG to be held on May 16-19, 2006 at Michigan State University

This notice serves as the final call for registration/abstract submission for the 2nd International Symposium on Animal Functional Genomics (2nd ISAFG) to be held on May 16-19, 2006 at Michigan State University. The objective of the 2nd ISAFG is to bring together international researchers, industry representatives, and administrators who seek updated information on the design, analysis, interpretation, integration, and application of high throughput gene expression profiling for the study of cells and organ systems that underlie economically relevant phenotypes in agricultural animals. Featured areas of the 11 invited speakers and international delegates include Statistical Genomics, Bioinformatics and Data Mining, Animal Health, Reproduction, and Growth and Metabolism (program details available at the 2nd ISAFG web site: http://www.isafg.msu.edu http://www.isafg.msu.edu). Delegates presenting completed research in these and relates areas have an opportunity to participate in an invited cluster submission of technical papers to Physiological Genomics, which will serve as the Symposium Proceedings and is scheduled for an August/September 2006 issue release. Please contact Jeanne Burton (burtonj@msu.edu) for details about this publishing opportunity.

In light of this publishing opportunity, several registrants have requested an extension for abstract submission. Accordingly, the registration/abstract submission deadline has been extended to April 15, 2006. Please note that you must register on line at the Symposium web site before you can submit an abstract. Once registered, you will receive an email message from us containing a userid and password that you will require for abstract submission. Our web site was designed to accept one abstract per registrant.

If you wish to submit more than one abstract per registrant, please send additional abstracts via email by April 15, 2006 to Dr. Rob Halgren at halgren@msu.edu.

We look forward to greeting you at Michigan State University in May! Jeanne Burton (burtonj@msu.edu) and Guilherme Rosa (rosag@msu.edu) 2nd ISAFG Co-

Seattle StatGenetics June 24

The 2006 Seattle Showcase Symposium in Statistical Genetics will be held at the University of Washington on Saturday June 24, 2006.

Confirmed speakers include Charles Brenner, Bill Hill, Gil McVean, Ross Prentice, Eric Schadt, and John Storey.

Registration details listed with those of the Summer Institute in Statistical Genetics at http://www.biostat.washington.edu – Bruce S. Weir Professor and Chair, Department of Biostatistics University of Washington Seattle, WA 98195-7232 Phone (206) 221-7947. Fax (206) 543-3286.

Bruce Weir

bsweir@u.washington.edu>

Sydney SocConservBiol July10-13

Mark your calendars: the Australasian section of the Society for Conservation Biology invites you to its inaugural regional meeting of conservation scientists

When: July 10-13, 2007

Where: University of New South Wales, Sydney, Australia

Topic: The Biodiversity Extinction Crisis, a Pacific and Australasian response

The world faces its sixth great extinction event, driven mainly by humans. Our region faces special challenges including: island ecology, rising sea levels, changing rainfall, and land and water degradation. These issues are overlaid by the general problems of habitat loss and fragmentation, invasive species, pollution and overharvesting.

This conference identifies the major problems for biodiversity conservation in our region, existing and potential solutions and links to the global biodiversity initiatives. Real opportunities can be found in the nexus between conservation science and policy-makers, man-

agers and the community. There will be five major themes: (1) Regional challenges (particular issues for our part of the world); (2) Managing threatening process of universal importance; (3) Case studies of conservation in action, including biodiversity monitoring and assessment; (4) Conservation science and policy and; (5) Conservation science and the community (nongovernment organisations, indigenous people).

Information on the meeting, as well as registration and abstract submission will be forthcoming.

We look forward to seeing you in Sydney in 2007

Richard.kingsford@unsw.edu.au

On behalf of the SCB-Australasia 2007 Conference Organizing Committee

Dr Karen Firestone Conservation Biologist Adjunct Lecturer Australasian Conservation Genetics Centre Rm 565 School of BEES Zoological Parks Board of NSW University of NSW PO Box 20 Sydney, NSW 2052 Australia Mosman, NSW 2088 Australia P: +61 (02) 9385 3446 (office) P: +61 (02) 9978 4608 P: +61 (02) 9385 8236 (lab) F: +61 (02) 9978 4613 F: +61 (02) 9385 1558

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kfirestone@unsw.edu.au kfirestone@unsw.edu.au

UAlaskaAnchorage Sticklebacks Jul30-Aug4 2

CONFERENCE: The Fifth International Conference on Stickleback Behavior & Evolution University of Alaska Anchorage July 30th - August 4th, 2006 http:/-/fish.uoregon.edu/sb/stickleback2006 A reminder that the Fifth International Conference on Stickleback Behavior & Evolution will be held on the campus of the University of Alaska Anchorage from Sunday July 30 (evening reception) through Friday August 4 (breakfast). We have worked to keep costs at a minimum while providing for an engaging conference. Regular early registration (due by May 1) costs US \$300, while the student rate (undergraduate or graduate) is \$200. The optional banquet is \$40 and the optional field trip is \$40 regular/ \$20 student. Various housing options are available and detailed on the website. If you are

coming from a developing country and need a reduced rate below the regular registration fee, please contact one of the organizers. Keep in mind that rates go up after May 1.

Information on the meeting, as well as registration and abstract submission, can be found at:

http://fish.uoregon.edu/sb/stickleback2006 The website also includes links to help plan a vacation around the conference. Alaska is a wonderful place to visit, and we anticipate that many attendees will be able to have an exciting adventure to go along with a stimulating meeting. Any questions about the conference can be directed to one of the meeting organizers:

Frank A. von Hippel, affvh@uaa.alaska.edu Michael A. Bell, mabell@life.bio.sunysb.edu William A. Cresko, wcresko@uoregon.edu Susan A. Foster, sfoster@clarku.edu

We look forward to seeing you in beautiful Alaska at the end of July.

Sincerely,

The 2006 Stickleback Conference Organizers wcresko@uoregon.edu

UBuffalo EGLME May6 2

Final call for registrants for the Eastern Great Lakes Molecular Evolution Meeting to be held at the University at Buffalo on May 6. Registration is free.

The deadline for submission of talks and poster abstracts has been extended to April 15. There are three invited speakers already booked on the program and the speakers selected from submitted abstracts will be informed very shortly after April 15. Those attendees that have already registered via e-mail are asked to please re-enter their information into the newly-created web-site (http://www.waterflea.org/register/index.html) in order to facilitate the creation of a final booklet containing information on participants and talk and poster abstracts.

We would encourage everyone planning on attending the meeting to also register on the web site (http://www.waterflea.org/register/index.html) to help us estimate the necessary amount of food and drink to keep people happy throughout the day.

Thanks,

Antonia Monteiro William Piel Derek Taylor Antónia Monteiro <monteiro@buffalo.edu>

UMichigan Biodiversity May6

UNIVERSITY OF MICHIGAN YOUNG SCIENTISTS SYMPOSIUM: MICROEVOLUTIONARY PROCESSES UNDERLYING BIODIVERSITY

On Saturday May 6, 2006, The Ecology and Evolutionary Biology Department at the University of Michigan will sponsor the University of Michigan Young Scientists Symposium. This one-day symposium is focused on the topic of microevolutionary processes underlying biodiversity. Eight outstanding young scientists will present current research on the genetics and evolutionary processes underlying phenotypic diversity, reproductive isolation and speciation across a wide range of plants and animals:

Hopi Hoekstra (Assistant Profesor, UCSD) "Molecular basis of complex color pattern in beach mice: from QTL to QTN"

Kirsten Bomblies (Posdoctoral Fellow, Max Planck Institute) "Postzygotic reproductive isolation in Arabidopsis thaliana."

Scott Rifkin (Postoctoral Fellow, Harvard) "The impact of mutation, migration, and selection on intraspecific differences in gene expression."

Matt Hahn (Assistant Professor, U. of Indiana) "Creation, extinction, and evolution of gene families in primates"

Daniel Bolnick (Assistant Professor, U of Texas - Austin) "Testing factors that promote and constrain phenotypic diversity in sticklebacks"

Briana Gross (Graduate Student, U. of Indiana) "The origin of Helianthus deserticola: hybridization and speciation"

Patrik Nosil (Graduate Student, Simon Fraser University) "Microevolutionary processes and the formation of new species"

Daven Presgraves (Assistant Professor, U. of Rochester) "Genetics and molecular evolution of hybrid incompatibilities in Drosophila"

The symposium will end with a plenary talk ("Allele frequency and the size of allelic effects") by Dr. Andrew Clark of Cornell University, a leader in the field

of evolutionary genetics.

Registration is FREE and INCLUDES DINNER on Saturday night, but space is limited. To register, see http://sitemaker.umich.edu/yss2006. Graduate students are invited to join speakers for lunch on Saturday and can express preferences on the registration form.

For more information, please see the Symposium website: http://sitemaker.umich.edu/yss2006.

Organizing committee: Jianzhi George Zhang jianzhi@umich.edu_ Priscilla Tucker ptuck@umich.edu Patricia Wittkopp wittkopp@umich.edu Ondrej Podlaha opodlaha@umich.edu

wittkopp@umich.edu

Uppsala EuropeanSocEvolBiol Aug20-25

XI CONGRESS OF THE EUROPEAN SOCIETY FOR EVOLUTIONARY BIOLOGY UPPSALA 2007

CALL FOR SYMPOSIA

The 11th Congress of The European Society for Evolutionary Biology will be held in Uppsala, Sweden, August 20-25, 2007.

The structure of the congress is similar to previous meetings, each day starting with a plenary keynote speaker, followed by parallel symposia. About 25 symposia will be accepted. A symposium will typically consist of three invited talks and 8-10 contributed talks.

The congress will cover the field of evolutionary biology in a wide sense, but with emphasis on processes and mechanisms of evolutionary phenomena.

We invite everyone to propose subjects for symposia during the XI Congress of ESEB. Proposals should include the following:

- 1. Title
- A short description of the subject area and motivation why the symposium is of interest to Evolutionary Biology.
- 3. A tentative list of possible invited speakers.
- 4. Names and addresses of the organisers (two persons) including their affiliation and e-mail address.

Symposia proposals should be sent to the following e-mail address no later than June 15, 2006:

eseb@ebc.uu.se

Information about the Congress and Uppsala can be found at:

http://www-conference.slu.se/eseb2007/index.html

2007 is the 300 year anniversary of the birth of Carolus Linnaeus. Uppsala University will celebrate its most famous professor of all times during the entire year.

Jon Agren Dept. of Plant Ecology Evolutionary Biology Centre Uppsala University Villavagen 14, SE-752 36 Uppsala, Sweden Phone: +46-18-471 2860 Fax: +46-18-55 34 19

ductive options in social Hymenoptera without morphological caste

best wishes, Jay E

Dr. Jay Evans USDA-ARS Bee Research Lab BARC-East Bldg. 476 Beltsville, MD 20705 USA 301-504-5143 FAX 301-504-8736 evansj@ba.ars.usda.gov http://www.ba.ars.usda.gov/beelab/index.html

WoodsHole Behavior May27

WashingtonIUSSI SocialInsectCongress Jul30Aug4

Please attend the XV IUSSI Congress in Washington, D.C. July 30-Aug. 4, at which evolution will be used to make sense of the following Symposium topics, along with contributed talks and posters. Early registration/abstracts by April 15, online and onsite registration thereafter.

http://www.iussi.org/IUSSI2006.html

Current Symposia

Ant community ecology Ant phylogenetics: New molecular trees to address old problems in ant biology Body size and natural history Building behavior and the control of climate in social insects Caste Interactions and Social Reproduction Coevolution between social insects and their macroparasites Collective and Individual Intelligence Conflict and cooperation in symbioses between social insects and micro-organisms Conflict Resolution in Insect Societies Current topics in reproductive physiology Evolution and development in caste differentiation of termites Evolution of termite life histories Genes, genomics and social biology Genetic and reproductive structure of termite colonies Invasive Ants Molecular and hormonal signaling pathways in caste development and reproduction Neuroethology of Social Insects Pheromonal mediation of honey bee social behavior Phylogeny and Evolution of Bees: a tribute to Charles Michener Social complexity from solitary circuits: A new paradigm for insect sociality Social insect semiochemicals Social recognition Structure, function and dynamics of social networks The consequences of polyandry for colony organization The immune system of social insects: challenges of a colonial life The myth of the sterile worker: A reconsideration of worker repro-

Reminder

Fourth Annual Woods Hole Behavior Symposium

Saturday, May, 27, 2006 10 AM 6 PM

Lillie Auditorium Marine Biological Laboratory Woods Hole, MA Sponsored by the Marine Biological Laboratory and the Boston University Marine Program

Call for papers

We welcome presentation on any aspect of animal behavior. Please submit an abstract for a talk (12 min plus 3 min for questions) or for a standard-sized poster by April 30, 2006 as an attached word file to <mailto:ggerlach@mbl.edu, (subject: Woods Hole Behavior symposium abstract).

Please indicate your name, affiliation, preference (talk or poster), title of the presentation and any special needs.

A powerpoint projector and PC laptop will be provided.

Prizes will be awarded for the best undergraduate and graduate student presentations.

Registration (at the entry): PIs: \$15 Postdocs \$10 students \$5 This will defray some costs for coffee breaks and student prizes.

For more information contact

Gabi Gerlach, MBL (<mailto:ggerlach@mbl.edu>ggerlach@mbl.edu)

Co-organizer: Hans Hofmann, Harvard

Visit http://www.mbl.edu/research/labs/gerlach/index.html for an updated program and directions

Gabriele Gerlach, PhD Assoc. Scientist Marine Biological Laboratory 7MBL Street Woods Hole, MA 02543-1015 USA

Telephone office 508 289 7120 Telephone lab 508 289 7391 FAX 508 289 7900 Email gger-lach@mbl.edu http://www.mbl.edu/research/

labs/gerlach/index.html> http://www.mbl.edu/-research/labs/gerlach/index.html Gabi Gerlach <ggerlach@mbl.edu>

GradStudentPositions

CNRSFrance InvasiveInsects	TexasStateU BehavEcol SailfinMollies	۲۶
ETHZurich host-parasiteinteractions	UBern PopGenetics	16
ETH Zurich 2 PlantEvol	UBerne TheoEvolEcol	33
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Frankfurt DaphniaGenetics	ULeeds EvolAging	21
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LeidenU EvolBirdsong	UPlymouth TermitePopulations	23
LiverpoolU Coevolution	USussex AdaptiveEvol	24
NZ Bioinformatics	UVienna MathematicsEvol	24
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Stockholm Astrobiology		
StockholmU Phenotypic polymorphism		

CNRSFrance InvasiveInsects

A PhD position is available in France, on the population genetics of an invasive insect pest in central and South America.

Hosting laboratory: Evolution et Ecologie des insectes tropicaux IRD-CNRS, CNRS, laboratoire Evolution, Génomes et Spéciation, Bat. 13, BP1, 91198 Gif-sur-Yvette.

/Subject summary /: Several invasive species experience ecological sucess despite important reduction in genetic diversity in their invasion area. Tecia solanivora is a potato tubermoth that recently invaded south american Andes. The PhD student will 1) develop nuclear markers to describe the genetic structure of T. solanivora in its invaded and origin areas, 2) determine the exact origin of the pest, 3) search for selected loci, 4) confront molecular data to data on genetic diversity and heritability of traits related to fitness differences

between invaded and introduced area.

/Profile/: Master II in evolutionary genetics, population genetics and/or quantitative genetics. Interest in developing models or analysing data in population genetics and/or quantitative genetics. Interest for lab molecular work. Availability for field periods in South America.

/Fellowship/: 1188.31 EUR / month

/Detailed description of the subject/ : http://eddv.snv.jussieu.fr /Contacts :/ silvain@pge.cnrs-gif.fr dupas@pge.cnrs-gif.fr

– Stephane Dupas I RD c/o CNRS Laboratoire Populations Genetique et Evolution 1 av de la Terrasse 91198 Gif sur Yvette + 33 1 69 82 37 04 fax : + 69 82 37 36 http://www.cnrs-gif.fr/pge/index.html http://www.cnrs-gif.fr/pge/index.php?lang=en

Stephane.Dupas@pge.cnrs-gif.fr

ETHZurich host-parasiteinteractions

Centre of Excellence in Evolutionary Research (University of Jyväskylä, Finland) announces a

PhD-STUDENT POSITION IN EVOLUTION OF HOST-PARASITE INTERACTIONS

in the group of Prof. Jukka Jokela (ETH-Zürich, Institute of Integrative Biology / Department of Aquatic Ecology, EAWAG)

Our group is focused on evolutionary ecology of host parasite interactions. We study ecological genetics of immunesystem function, maintenance of sexual reproduction by coevolution between host and the parasite, and genetic architecture of infectivity in parasites with multiple host life-cycles. We are looking for a student who is interested in genetics, immunology, ecology and evolutionary biology of host-parasite interactions. We provide a stimulating research environment, demanding but supportive supervision and well-worked out model systems for research. Position is available for 3 years, starting when a suitable candidate is found.

The position is based at the department of Biological and Environmental Science in University of Jyväskylä as a part of the Centre of Excellence, and the student will be enrolled in the graduate programme of University of Jyväskylä. The group has strong connections to ETH-Zürich (Prof. Jokela) and University of Helsinki (Dr. Maarit Haataja) allowing a versatile co-operation network, excellent infrastructure, as well as possibilities to address broad-scale research questions. Ideal candidate is willing to spend some time in Switzerland (Zürich) each year. Overall, this training will provide excellent preparation for a successful career in science, which is one of the goals of the Centre of Excellence.

Salary for a PhD-student in Finland is about 2000 / month (all benefits included), which after taxes provides a comfortable standard of living allowing 100% commitment to science.

Send your application with CV and contact details of two references to Dr. Anssi Karvonen (anskarv@bytl.jyu.fi) by 30th of April.

More information and present project outlines are available at our webpage http://www.jyu.fi/evolresearch jukka.jokela@eawag.ch

 $2~\mathrm{PhD}$ positions in plant reproductive ecology at ETH Zürich

ETH Zurich 2 PlantEvol

Two PhD positions funded by the SNF are available at the plant ecological genetics group at the ETH Zürich (Switzerland) to study the molecular basis and evolutionary ecology of plant-pollinator interactions in Silene. One PhD project will focus on the idenfication of odor genes, by transcript profiling and functional study of candidate genes. For this project I am looking for one candidate with a background in molecular biology (ecology) or biochemistry, organism biology with good knowledge of molecular techniques.

The second project will investigate mechanisms and consequences of specific pollinator attraction in a Silene species-pair, involving investigations on floral signals (scent), behavioural experiments with pollinators and plot experiments in the field. For this PhD, a background in (chemical) ecology, evolution, or plant/insect biology etc. is desirable. The two PhD candidates are expected to closely collaborate with each other.

The two projects are embedded in a larger framework of evolutionary studies in Silene. (www.geobot.ethz.ch). We are currently a group of 3 academic staff one PostDoc, and 5 PhD students that use Silene as a model system to investigate topics such as pollinator mediated selection, reproductive isolation, hybridisation, and habitat adaptation. The institute houses modern molecular and chemical ecology labs, including a wind tunnel for behavioural experiments with pollinators. Greenhouses and climate chambers for plant cultivation are also available. Zürich has a large and very active research community at the ETH (www.ethz.ch < http://www.ethz.ch/>) and University of Zürich (www.unizh.ch http://www.unizh.ch/->) dealing with various aspects of organismal and molecular biology (www.lifescience-zurich.ch http:/- /www.lifescience-zurich.ch/>). The city also offers excellent quality of life through active cultural programs and infrastructure, as well as an attractive surrounding including the alps in proximity.

If you are interested in one of the jobs, please send a letter describing your motivation for the application, C.V., copy of degrees, publications (manuscripts) if any, and e-mail addresses of two academic referees. If you have further question, don't hesitate to contact me.

PD Dr. Florian Schiestl Plant Ecological Genetics / Institute of Integrative Biology ETH Universitätsstrasse 16 CH-8092 Zürich florian.schiestl@env.ethz.ch

florian.schiestl@env.ethz.ch

ETH Zurich InsectBehaviour

We are seeking a motivated and creative PhD Student in Entomology with a Diploma degree in Biology or related University degree.

The PhD project will focus on insect mobility of an invasive herbivore pest species of fruit trees. Mobility will be quantified in the laboratory with a computer-linked actograph, and strains of diverging mobility will be bred by selection. Such strains will be used to address challenging questions on trade-offs between dispersal and reproductive performance. Further, insects will be sampled in the field from core and peripheral regions. They will be categorized according to their mobility, and their genetic differentiation assessed using molecular markers. Results are expected to contribute to a better understanding of the behavioural ecology of insect dispersal and to improve sustainable pest management.

Languages spoken in the group are mainly German and English.

Education: Diploma degree (or MSc) in Biology or related University Degree. Start: Position open until filled, immediate start possible.

Send curriculum vitae, certificates and addresses with phone numbers of three references to:

Prof. Dr. Silvia Dorn Reference Code PhD-Mobility Institute of Plant Sciences/ Applied Entomology ETH Zurich Schmelzbergstr. 9 / LFO CH - 8092 Zurich

silvia.dorn@ipw.agrl.ethz.ch

For further information contact Dr. Dominique Mazzi (dominique.mazzi@ipw.agrl.ethz.ch, phone +41 44 632 3936)

Our homepage: www.em.ipw.agrl.ethz.ch dominique.mazzi@ipw.agrl.ethz.ch dominique.mazzi@ipw.agrl.ethz.ch

Frankfurt DaphniaGenetics

Ph.D. STUDENT POSITION IN ECOLOGICAL GENETICS OF DAPHNIA

A Ph.D. STUDENT POSITION is available in the framework of an international project funded by the European Science Foundation (ESF). The main focus of the research program is the study of connectivity, dispersal and priority effects as drivers of biodiversity and ecosystem function in pond and pool communities (BIOPOOL). The main hypotheses are to (1) characterize the relative importance of dispersal (determined by regional factors), historical effects (i.e. priority effects, mediated by propagule-banks build up) and assemblage processes (driven by local factors) on biodiversity, and (2) to quantify the effect of diversity and genetic variation on ecosystem functioning.

Microcrustaceans, such as Daphnia, are ideal model organisms since they are well suited for laboratory and field (quantitative genetic) experiments and many genetic markers and techniques have been developed. Specifically, we would like to a) monitor species and clonal establishment in newly created habitats during two or three consecutive years, and b) to monitor artificial communities (inoculated with different genotypes) through time using molecular markers.

The successful candidate should have the equivalent of a master's degree or diploma in Biology, a firm background in evolutionary biology, experience with molecular techniques and a strong commitment to basic research. The position is open starting May/June 2006 and available initially for two years, with likely extension for maximum one further year. Pay and conditions are according to the German BAT-IIa/2 scale for civil servants (ca. ??? 18K p.a. net income, depending on family status).

Interested applicants should send the following information to k.schwenk@zoology.uni-frankfurt.de: curriculum vitae, a brief statement of research interests, a description of the MSc or Diplom research, names and contact information for three references. Closing date for applications is April 26st 2006. Please feel free to contact K. Schwenk (Department of Ecology & Evolution, J.W. GOETHE-UNIVERSITY FRANK-FURT AM MAIN, Siesmayerstraße 70, 60054 Frankfurt am Main, Germany) or visit http://www.unifrankfurt.de/"kschwenk/ for clarification or additional

information.

Klaus Schwenk <k.schwenk@zoology.uni-frankfurt.de>

http://www.ijm.jussieu.fr/developpement_des_nematodes.php STRAINS: http://www2.ijm.jussieu.fr/worms Marie-Anne Felix
<felix@ijm.jussieu.fr>

JacquesMonodInst CaenorhabditisEvol

PhD FELLOWSHIP IN CAENORHABDITIS EVO-LUTION Jacques Monod Institute, Paris Dr. Marie-

Anne Felix (felix@ijm.jussieu.fr)

A PhD fellowship is available in the laboratory of Marie-Anne Felix at the Jacques Monod Institute in Paris, France, from 1st October 2006.

The funded research project concerns the evolution of the molecular network underlying vulval development in the nematode genus Caenorhabditis. In C. elegans, an intercellular signaling network including Ras, Notch and Wnt pathways determines cell fates of the vulval precursors. From preliminary work, it is clear that this intercellular signaling system varies among species of the Caenorhabditis genus, including large variations in C. briggsae and C. remanei (whose genomes are sequenced) compared to C. elegans. These variations in developmental mechanism can be described as quantitative changes in the relative activities and crosstalks between signaling pathways. In this evolutionary systems biology perspective, the student will determine the relative roles and activities of these molecular pathways in the different Caenorhabditis species, and use the known Caenorhabditis phylogeny to polarize evolutionary changes in the network.

More information lab interests the can be found at: http://www.ijm.jussieu.fr/developpement_des_nematodes.php#anglais fellowship is provided by the French CNRS for up to 3 years (1439 Euros/month before taxes). candidate should be less than 27 years old, and have a European Master or equivalent (by October 1). Information on these fellowships (in French) is available at: http://www.sg.cnrs.fr/drh/emploi-nonperm/bdi.htm To apply, please send a CV, a letter indicating your motivation for this project, and the names of referees to felix@ijm.jussieu.fr. Knowledge of French is not required.

Marie-Anne Felix Institut Jacques Monod, Tour 43, 2 pl. Jussieu, 75251 Paris Cedex 05, France Tel: +33-1-44-27-40-88; Fax: +33-1-44-27-52-65

KansasStateU SkunkEvol

GRADUATE POSITION IN MOLECULAR ECOL-OGY OF SKUNKS AT KANSAS STATE UNIVER-SITY. One graduate assistantship is available at Kansas State University to investigate the effects of urbanization on the striped skunk. Field research will involve trapping and tissue collection of striped skunks in the Flint Hills region of eastern Kansas. The emphasis of this project will be population genetics and epidemiological modeling based on microsatellite marker data. Responsibilities will include: locating suitable study sites and coordination of field and lab research. Applications will be accepted at a PhD level; qualified applicants should have a minimum of a Masters of Science in Biology and competitive GPA and GRE scores. Previous experience with mesocarnivores, molecular lab work, GIS software, and organization of field projects is desirable. The annual stipend for graduate positions will be \$21,000 per year including tuition. Information on graduate programs at K-State and current projects is available at www.ksu.edu/wiselylab. The start date will be August 15th, 2006. Interested individuals should send a cover letter outlining experience and research interests, a detailed curriculum vitae, unofficial copies of university transcripts and GRE scores, and contact information for three references to DR. SAMANTHA WISELY, Division of Biology, 232 Ackert Hall, Kansas State University, Manhattan, KS 66506-4901 (PH: 785-532-0978, FX: 785-532-6653, EM: wisely@ksu.edu;). Applications by e-mail are welcome, and will be accepted until the position is filled.

Dr. Samantha M. Wisely Assistant Professor, Wildlife Biology Division of Biology Ackert Hall Kansas State University Manhattan, KS 66506-4901 Office:785.532.0978, Lab:785.532.6413 Fax:785.532.6653, email: wisely@ksu.edu http://www.ksu.edu/wiselylab wisely@ksu.edu

LeidenU EvolBirdsong

Two PhD positions available

Closing date: 30 April 2006.

Behavioural Biology, Institute of Biology, Leiden University

BIRDSONG, SPEECH AND LANGUAGE Human speech and birdsong share several striking similarities which are such that learned birdsong is considered to be the closest animal analogue to language and both linguists and biologists have suggested that results from one field could yield hypotheses, or even answers to questions, for the other. The following two projects, for which we seek candidates, also aim to contribute to this rapidly growing field of comparative research.

1 - Bird song structure and language syntax: a comparative interdisciplinary approach.

One key feature distinguishing human language from other animal vocal communication systems concerns the presence of a rule based syntax underlying linguistic utterances. But are humans really unique in their abilities to detect and use syntactical rules, or do they share some of these properties with other species? This project will address this issue by analyzing the syntactical abilities of a songbird, the zebra finch. It will focus on two questions: 1) Are zebra finches capable of detecting and distinguishing between different types of (experimentally constructed) grammars? 2) What are the species specific grammar rules which guide zebra finch song production and development? The project will involve a bioacoustic analysis of song structure in zebra finches, different types of experiments to analyze syntactical capabilities (e.g. habituation/dishabituation tasks, operant tasks involving discrimination learning, etc.) and developmental studies on the role of experience in structuring song syntax.

2 - Bird Speech? On the production and perception of formants in bird vocalisations.

Human speech conveys language, and much research effort concerns the production and perception of acoustic features that encode linguistic meaning in speech. An important feature are formants, which are timevarying frequency bands that are emphasized in the broad-band spectrum of speech. Formant patterns result from acoustic resonances of the vocal tract, the

characteristics of which are rapidly modulated using articulators such as the tongue, lips, and soft palate. Studies of birdsong have hardly addressed the role of formants, although several findings indicate their presence. The proposed project aims to provide a comprehensive analysis of formant mechanisms in birds. It will address the following questions: 1) To what extent do vocal tract resonances cause formant patterns in natural bird vocalizations, and how do vocal tract articulators modulate such patterns? 2) What are the perceptual sensitivities of birds to formant patterns in natural bird vocalizations? 3) Are formant patterns in natural bird vocalizations affected by vocal production learning? The project will involve morphological, physiological and bioacoustical analyses and experimental studies on the vocalization systems of zebra finches and budgerigars, together with experiments on the perception of formant variants.

The projects are based in the research group Behavioural Biology. This is an active, internationally oriented research group with a strong focus on (vocal) communication in animals. The group currently consists of three tenured staff, several postdocs, PhD students and MSc-students. More information: http://biology.leidenuniv.nl/ibl/S8/index.html Requirements: Candidates are expected to have an MSc (drs) degree in Biology, Linguistics (phonetics/phonology) or other relevant discipline; to have a strong interest in experimental and interdisciplinary studies, and to be interested in international collaboration (part of project 2 will be carried out in collaboration with research groups in Germany (Dr Beckers, Seewiesen) and the US).

Appointment: The appointment is for a period of 4 years and is expected to lead to completion of a dissertation. The gross monthly salary is 1.877 in the first year and increases progressively each year to 2.407 in the fourth year. Salary and fringe benefits conform to the Collective Employment Agreement for Dutch Universities. We hope to fill the vacancies as soon as possible.

Applications: Written applications (mentioning BehavBiol-PhD-1 and/or -2), including a CV with marks obtained and the names, telephone numbers and email addresses of at least two referees (who have agreed to be contacted) should be submitted to: Leiden University, Faculty of Mathematics and Natural Sciences, attn. Mr S. Brandsma, Human Resource Department, P.O. Box 9502, 2300 RA Leiden, the Netherlands, or by email: s.brandsma@science.leidenuniv.nl. Closing date: 30 April 2006.

Further information: prof dr Carel ten Cate, ten-

ten-

cate@rulsfb.leidenuniv.nl, tel. +31-71-5275040. tencate@rulsfb.leidenuniv.nl cate@rulsfb.leidenuniv.nl

actions. American Naturalist 161, 827-836. 3 Sasaki A (2000) Host-parasite coevolution in a multilocus genefor-gene system. Proc R Soc Lond B Biol Sci 267, 2183-8.

Please apply by email, including a summary of your research interests and a CV. Review of applications is ongoing.

Mike Brockhurst <michael.brockhurst@liverpool.ac.uk>

LiverpoolU Coevolution

Experimental coevolution with multiple parasites

Dr. M.A. Brockhurst (michael.brockhurst@liverpool.ac.uk), Dr. A. Fenton (a.fenton@liverpool.ac.uk)

Antagonistic coevolution between hosts and parasites, the reciprocal evolution of host defence and parasite counter-defence, is ubiquitous and there is a considerable body of work exploring this issue in simple onehost-one-parasite systems (e.g., Sasaki 2000; Restif & Koella 2003). However, coevolution with multiple parasite species is likely to be a major selection pressure for host organisms in nature? there may be various positive and negative interactions, each modifying the optimal strategies of the component species, affecting the evolutionary dynamics of the community. While exposure to multiple parasites is likely to have far reaching ecological, evolutionary and health implications no experimental studies (and few theoretical ones) have looked at coevolution between a host species and multiple parasite species.

An experimental evolution approach using populations of bacteria and their viral parasites (bacteriophage) is ideal for studying host-parasite coevolution, due to the rapid generation time of hosts and parasites, and the ease of experimental manipulation. We have previously demonstrated rapid coevolution between Pseudomonas fluorescens and phage phi2 (Brockhurst et al. 2003). This project will extend previous findings using a mixture of experimentation and theory to investigate the effect of exposure to multiple parasite species on: i) coevolutionary dynamics; ii) resistance evolution including costs and epistasis; iii) host and parasite local adaptation. As such, this project brings together ideas concerning host-parasite coevolution, the evolution of life history strategies and community ecology and will appeal to anyone interested in testing evolutionary theory.

References 1 Brockhurst MA, Morgan AD, Rainey PB and Buckling A (2003) Population mixing accelerates coevolution. Ecology Letters 6, 975-979. 2 Restif O and Koella JC (2003) Shared control of epidemiological traits in a coevolutionary model of host-parasite inter-

NZ Bioinformatics

Scholarships

Biomatters Enterprise Scholarships for Top-achievers (BEST scholarships) are available to top students to undertake honors, masters or PhD level research in bioinformatics. Successful candidates will work in Auckland's Bioinformatics Institute. BEST scholars are advertised internationally and successful candidates are expected to have excellent skills in molecular biology as well as a very high level of programming proficiency. Areas include but are not limited to statistical alignment algorithms, HMM, sequence alignment, Bayesian learning, MCMC analysis. Biomatters are building Geneious, a ubiquitous JAVA-based platform for bioinformatics research.

To register interest in a BEST scholarship, email contact@biomatters.com

daniel@biomatters.com

RoyalHolloway ModellingDisease

Call for applications to a PhD studentship on:

Modelling the dynamics of disease propagation on social networks"

This project aims to model the spread of diseases on social networks. This is an area in which there is currently much interest, both from a theoretical and applied point of view. Within this project we will study the spread of infectious agents on networks. As a biological inspiration we will use the spread of diseases like measles in the human population, and how this spread is affected by control measures that humans can exert

in order to influence their chances of becoming infected. By introducing this extra complexity in the spread of the disease we will need to introduce elements of game theory in the modeling. We aim to gain insight in the general principles underlying the epidemiology of disease and the importance of network structure therein by modelling such systems by means of simple mathematical models or simulation models.

This project is part of an interdisciplinary study in which the dynamic behaviour of large interacting systems on random networks is studied and is funded by the EPSRC under their Novel Computation initiative at Royal Holloway and the Universities of Sheffield, Leeds and Southampton (see http://amorph.group.shef.ac.uk/ for further details about this programme). Close interaction with a postdoctoral research assistant at Royal Holloway, and similar groups in Leeds, Sheffield and Southampton is expected. The project is suitable for those with a degree (UK equivalent 2.1 or higher) in a quantitative science such as Mathematics, Physics or Computer Science and who have an affinity to biology and epidemiology, or for Biology graduates with a proven ability to work with mathematical models or computer models. The studentship is fully funded, EPSRC eligibility criteria apply, i.e. the studentship is open to those with a relevant connection with the United Kingdom (UK), usually through residence. For further information about the studentship contact vincent.jansen@rhul.ac.uk, telephone + 44 1753 862526.

To apply, use the application form at http://www.rhul.ac.uk/Graduate-School/-App%20form%20RESEARCH.pdf and send this together with a cover letter and CV to Prof. Vincent Jansen School of Biological Sciences Royal Holloway, University of London Egham, Surrey TW20 0EX UK

Or by Email: vincent.jansen@rhul.ac.uk.

Closing date: 5/5/06 —

Jansen Vincent < Vincent.Jansen@rhul.ac.uk >

Stockholm Astrobiology

Eight PhD positions at the Astrobiology graduate school at Stockholm University Astrobiology is a new and rapidly expanding field of science that aims to understand the origin, evolution and diversity of life on Earth, and investigate possible emergence of life elsewhere in the Universe. The newly established Graduate School of Astrobiology brings together the following departments:

Astronomy

Geology & Geochemistry

Molecular biology & Functional Genomics

Physics

Students excited by the prospect of working in a dynamic multidisciplinary environment are invited to apply. Successful applicants will enter PhD programmes (4 years full-time) that include courses spanning the diversity of astrobiology research.

The deadline for application is May 15th 2006. Further information about the individual research programmes for the eight positions and instructions on how to apply can be found at

http://www.astrobiology.physto.se anthony.poole@molbio.su.se anthony.poole@molbio.su.se

StockholmU Phenotypic polymorphism

PhD Position in Theoretical Evolutionary Biology Stockholm University

The evolution of phenotypic polymorphism

A PhD position in theoretical evolutionary biology is available at the Department of Zoology, Stockholm University, Sweden. Research topics for the position include the evolution of phenotypic polymorphism and the evolution of individual variability, viewed from the perspective of modern developmental biology.

Phenotypic polymorphism is a widespread phenomenon, with examples like males and females in sexual species, alternative male mating types and winged and wingless individuals in certain insects. Variation in so-called personality between individuals of social species could also be regarded as phenotypic polymorphism. The basic issue concerns the evolution and development of alternative phenotypes, in particular, the evolution of developmental systems of phenotype determination. Such systems can implement genetically controlled polymorphisms and phenotypic plasticity, as well as stochastic (randomizing or bet-hedging) polymorphisms.

The position can be either full-time over four years or 80% over five years (with a possibility of 20% teaching assistantship), with a starting full-time yearly salary of 232800 SEK (around 24800 EUR). The starting date is flexible, but should be in the second half of 2006. Applicants should have a MSc (or equivalent background) in a field like evolution, ecology or population genetics, or possibly physics and applied mathematics. Candidates with a strong interest in evolutionary theory and good conceptual, analytical and computer programming skills are preferred. The position is open until filled, but primary consideration will be given to applications received by 15 May 2006. To apply, send a signed letter of application, containing a statement of research interests and skills, addressed to the Head of the Department of Zoology, Stockholm University, SE-106 91 Stockholm, Sweden. Attach your CV, copies of degree certificates, copies of your masters thesis (or equivalent thesis), any published or in-press papers, and contact information for two references. Informal inquiries (by email to olof.leimar@zoologi.su.se) about the position are welcome.

Olof Leimar, Professor Department of Zoology Stockholm University SE-106 91 Stockholm Sweden

olof.leimar@zoologi.su.se http://www.zoologi.su.se/-research/leimar/ olof.leimar@zoologi.su.se olof.leimar@zoologi.su.se

TexasStateU BehavEcol SailfinMollies

BEHAVIORAL ECOLOGY OF SAILFIN AND AMAZON MOLLIES

Graduate Research/Teaching Assistantship for M. S.

Applications are being sought for one student interested in pursuing an academic career studying behavioral ecology (mate choice and fitness consequences) of sailfin and Amazon mollies starting fall 2006. Amazon mollies, Poecilia formosa, are a unisexual (all female) fish species that are essentially sexual parasites on the closely related bisexual sailfin molly, P. latipinna. Conflict exists between male sailfin mollies benefiting more from mating with their own species, and the unisexual females sexually parasitizing these males. Dr. Andrea Aspbury and I have some funding (1 year) and departmental teaching assistantship for the second year for a master's level research assistant to work on this system. Some skills in molecular genetic techniques are

preferred. See http://www.bio.txstate.edu/~gabor/gabor.htm for details about our research interests.

The Department of Biology offers a strong environment in evolutionary ecology as the basis for training in behavioral ecology and degrees can be obtained in the Biology or Population and Conservation Biology Program.

San Marcos, Texas is located 30 miles South of Austin, the Live Music Capitol. Both San Marcos and Austin are rich cultural and recreational environments in which to live and study. The Texas State campus overlooks the city of San Marcos and the headwaters of the crystal clear San Marcos River (http://www.aquarena.txstate.edu/). San Marcos and Austin are NOT the Texas you see or think of from TV!

For information on applications see http://www.bio.txstate.edu/grad/GradGuide.html (Disregard application deadlines). Please also see the Department of Biology for admission information (http://www.bio.txstate.edu/) and Texas State University (http://www.txstate.edu/) web sites for more information.

To apply for this position, please send a letter of interest to Dr. Gabor (gabor@txstate.edu) & Dr. Aspbury (aspbury@txstate.edu) stating why you are interested in doing this work. Also send a CV/resume of related research, coursework, grades, GRE scores and any other relevant experience via email (preferably) or snail mail. We will respond as soon as we get this information and will consider candidates until a suitable one is found. —

Caitlin R. Gabor, Ph. D. Associate Professor Texas State University (Formerly SWT) Department of Biology, Supple Building Room 384 San Marcos, TX 78666-4615 Work: (512) 245-3387; Fax: (512) 245-8713 Email: gabor@txstate.edu

http://www.bio.txstate.edu/ ~ gabor/gabor.htm Caitlin Gabor <gabor@txstate.edu>

UBern PopGenetics

PhD position in population genetics, University of Bern, CMPG

The Computational and Molecular Population Genetics lab (CMPG) is looking to fill the position of a PhD candidate to work on the effects of selection and local adaptation on molecular diversity. Among other things,

the project aims to determine the relative importance of directional and balancing selection in natural populations using genome scans (AFLPs and potentially other molecular markers). The project will focus on a system of Microtus vole populations with morphological and molecular evidence for local adaptation, and known evolutionary and demographic history. The position will be lab-based, potentially with limited field work.

We are looking for a highly motivated candidate with experience in the establishment, application and analysis of molecular markers, combined with a vivid interest in population genetics, evolutionary biology and ecology. This is a three year position funded by the Swiss National Science Foundation, and the student will be supervised by Gerald Heckel and Laurent Excoffier. The anticipated starting date is June 1st 2006 or very soon thereafter.

Please send applications (letter of motivation, CV, names and email addresses of at least two referees) by email to gerald.heckel@zoo.unibe.ch (by April 21, 2006 or until filled). Further information on the CMPG, the University of Bern, or life in Bern can be obtained from http://www.cmpg.unibe.ch/ and by email (gerald.heckel@zoo.unibe.ch).

Dr. Gerald Heckel Computational and Molecular Population Genetics (CMPG) Zoologisches Institut Universitaet Bern Baltzerstr. 6 CH-3012 Bern Switzerland Tel.: +41 (0)31 631 30 29 Fax: +41 (0)31 631 31 88 Email: gerald.heckel@zoo.unibe.ch http://www.cmpg.unibe.ch/ gerald.heckel@zoo.unibe.ch

UBerne TheoEvolEcol

PhD-POSITIONS IN THEORETICAL AND BE-HAVIOURAL ECOLOGY

Dept. Behavioural Ecology, Institute of Zoology, University of Berne, Switzerland.

1) PhD THEORETICAL ECOLOGY: We investigate how environmental conditions experienced early in life may cause ontogenetic changes on life histories through phenotypic plasticity. The successful applicant will develop and study general evolutionary models, as well as models parameterized with experimental lab and field data of African mouthbrooding cichlids. Eligible candidates will have a master's degree (or Diplom) in Biology, Mathematics, or Theoretical Physics and dispose

of a sound background in theoretical and evolutionary biology. Research experience in evolutionary modeling is highly welcome. The successful candidate will work part-time at the International Institute for Applied Systems Analyses (IIASA) in Laxenburg (Austria), where the thesis project will be co-supervised by PD Dr. Ulf Dieckmann. The collaboration between IIASA and the University of Bern will provide extensive guidance in Mathematical Biology and Behavioural Ecology. Duration three years; supervisor: Barbara Taborsky.

2) PhD BEHAVIOURAL ECOLOGY: This PhD-study will investigate (i) proximate and ultimate causes of maternal effects on offspring size and (ii) physiological responses to the environment during early ontogeny, in African mouthbrooding cichlids. The study will involve experimental manipulation of ecological conditions and behavioural observations in the lab, ecological surveys and collection of samples in the field for genetic analysis. Eligible candidates will have a masters degree (or Diplom) in Biology and research experience in animal behaviour, a genuine understanding of evolutionary theory and a strong commitment to basic science. Practical skills in the work with fish, both in the lab and field and/or the measurement of physiological parameters will be very helpful. Duration three years; supervisor: Barbara Taborsky.

The successful candidates will join an active research group consisting currently of 5 advanced research staff, 6 PhD-students and a varying number of guest scientists and masters students. Besides the Behavioural Ecology group, the ecologically oriented Zoological Institute of the University of Bern consists of research groups on Aquatic Ecology (Ole Seehausen), Conservation Biology (Raphael Arlettaz), Evolutionary Ecology (Heinz Richner), Population Genetics (Laurent Excoffier) and Synecology (Wolfgang Nentwig). Salaries will follow the schemes of the national funding organizations of Switzerland and Austria. Besides research, PhD students assist in undergraduate teaching and supervision.

Closing date: Open until filled, but all application materials, including CV, a summary of research experience, copies of any published or in-press papers, and two letters of recommendation should be received by April 15, 2006 to ensure full consideration. The positions will start at the earliest possible date. Candidates should indicate in a cover letter for which of the two positions they apply and when they could take up the position. Please send all application material to the secretarys office, c/o Marlis Gerteis, Dept. Behavioural Ecology, University of Bern, Wohlenstrasse 50A, CH-3032 Bern, Switzerland; or as e-mail attachments to marlis.gerteis@esh.unibe.ch. For inquiries please con-

tact barbara.taborsky@esh.unibe.ch.

Please see also http://www.zoology.unibe.ch/behav/index_e.php for further information on our department.

Dr. Barbara Taborsky Zoological Institute Behavioural Ecology University of Bern Wohlenstrasse 50A CH-3032 Hinterkappelen Switzerland

e-mail: barbara.taborsky@esh.unibe.ch tel: +41/31/6319 157 fax: +41/31/6319 141

barbara.taborsky@esh.unibe.ch

ULausanne WhitefishAdaptation

PhD studentship available (3 years) in the Laboratory for Conservation Biology, Department of Ecology and Evolution, University of Lausanne, Switzerland.

We are looking for a Ph.D. candidate who would be involved in a project aiming at a better understanding of local adaptation processes and response to anthropogenic pressures in Alpine whitefish (Coregonus sp), a salmonid. This research program is based on the study of neutral and adaptive genetic variation in a population for which temporal demographic data are also available. The project will involve mainly genetic analyses (microsatellites, SNPs and AFLPs) as well as some field work and experiments. This project will be carried out in close collaboration with the group of Prof. C. Wedekind. We are seeking a highly motivated candidate interested in conservation genetics and evolutionary biology, and possibly having laboratory expertise.

Start: September 2006 or earlier. Salary: according to the guidelines of the Swiss National Science Foundation. The Department of Ecology and Evolution in Lausanne provides a lively and stimulating environment for research. It harbours research programs in conservation biology, ecology, behaviour end evolution, and has excellent facilities for molecular genetics and genomics (www.unil.ch/dee).

To apply, please send a cover letter describing your research interests, a complete CV and names of two references by e-mail only to Luca.Fumagalli@unil.ch. The position will stay opened until 15th May 2006 or until filled.

Dr Luca Fumagalli Laboratory for Conservation Biology Department of Ecology and Evolution, Biophore University of Lausanne 1015 Lausanne (Switzerland)

Luca.Fumagalli@unil.ch

ULeeds EvolAging

THE ECOLOGY AND EVOLUTION OF AGING

A PhD studentship, concerning the ecology and evolution of aging, is available from October 2006 for an applicant from the UK or EU, under the supervision of Dr. Steven Sait and Dr. Ian Hope at The University of Leeds and Dr. Mike Boots at the University of Sheffield.

BACKGROUND The evolution of ageing remains one of the most challenging of research topics today. Theory predicts that populations experiencing high mortality due to external factors (e.g. from disease or competition) evolve earlier maturity and invest more in reproduction. Theory also assumes that individuals are equally vulnerable to external mortality. However, several papers have recently demonstrated that the pattern of ageing evolution is sensitive to complexities associated with age-dependent vulnerability to mortality. The project will investigate the feedback between the individual and the population in variable environments and explore the impact of contrasting selection pressures on the evolution of ageing.

This project will use the nematode worm Caenorhabditis elegans as a model species, for which the conservation of ageing mechanisms is astonishingly conserved from worm to man. The project will investigate the ecology and evolution of ageing of C. elegans over multiple generations and for a range of environmental conditions, combining population ecology of model systems with genome analysis of C. elegans.

The project takes place within the context of vibrant and diverse research on ecology, evolution, genetics and genomics. In addition to the postgraduate training programme, the student would receive training in molecular and genomics approaches, including their application in ecology and evolution, as well as opportunities to develop models and theory with collaborators at Sheffield. The student would become familiar with experimental design and complex statistical analyses, as well the presentation of results to a variety of audiences and in a variety of formats. This broad research experience will benefit further by extensive interactions with two other related PhD projects and partners at Sheffield and York within a White Rose-funded network.

Informal enquiries can be made to Dr. Steven Sait (s.m.sait@leeds.ac.uk) and Prof. Tim Benton (t.g.benton@leeds.ac.uk).

Further project and network details are available at: http://www.leeds.ac.uk/rds/schol/wrs-info.htm. Application forms are available from http://www.leeds.ac.uk/rds/schol/wrs-app06.htm or from Mrs Shirley Yeadon, Scholarships Office, The University of Leeds, Leeds LS2 9JT (scholarships@leeds.ac.uk).

Note - Please return applications and a CV to Mrs. Catherine Bennett, Faculty of Biological Sciences Graduate School, Garstang Building, University of Leeds, Leeds, LS2 9JT, UK.

Dr. Steven M. Sait, Ecology and Evolution Research Group, Institute of Integrative and Comparative Biology, L.C. Miall Building,

University of Leeds, Leeds, LS2 9JT. Tel.: 44(0)113 3437039 Fax: 44(0)113 3432835

Steve Sait <S.M.Sait@leeds.ac.uk>

ULille EvolFloweringTime

Henk van Dijk Laboratoire de Genetique et Evolution des Populations Vegetales UMR CNRS 8016 Batiment SN2 Tel: +33 3 20 43 69 99 Universite de LILLE 1 Fax: +33 3 20 43 69 79 59655 Villeneuve d'Ascq Cedex FRANCE mailto:Henk.Van-Dijk@univ-lille1.fr http://www.univ-lille1.fr/gepv A PhD studentship is available at the University of Lille, France, for an applicant from a foreign European country to work on "The evolution of flowering time in perennials: Beta vulgaris vs. Arabidopsis thaliana" in the group of Prof. Henk van Dijk, Laboratoire de Genetique et Evolution des Populations Vegetales, UMR CNRS 8016, Villeneuve d'Ascq, France.

For plants living in a seasonal environment information about the progress of the season is crucial in order to flower at the right moment. In the course of evolution sophisticated mechanisms have been developed, especially with respect to temperature and day length. The most important genes involved in the sensitivity to these environmental cues are now known, in particular in the annual plant model species Arabidopsis thaliana.

The sea beet, Beta vulgaris subsp. maritima, the ancestor of cultivated beet, is an iteroparous perennial.

The data on B. vulgaris available in our group suggest that perennials and annuals differ in certain aspects of the mechanism of flowering initiation. The plausible argument behind this difference is that perennials should also to invest in survival in order to get offspring later in life and therefore should be more restrictive in the conditions for starting flowering. An interesting point is the memory of winter (vernalization) which is based on an epigenetic mechanism. In A. thaliana the epigenetic state is reset every generation during meiosis in order to regain the non-vernalized state for the new seedling. A perennial plant, on the contrary, would be better off by regaining the vegetative stage each summer, thus being able to become prepared for the coming winter. The epigenetic mechanism could therefore be regulated in an essentially different way.

The main aspects of this thesis are the analysis of crosses, both on the phenotypic and the molecular level; the search for homology with A. thaliana and the interpretation of the results in an ecological and evolutionary perspective.

The successful applicant should have some practical experience in standard molecular biology techniques, but also be interested in how natural selection happens in the field.

Send your application with statement of research interest and CV to Prof. Henk van Dijk, henk.van-dijk@univ-lille1.fr, together with the contact details of two references ASAP but before 2 May 2006.

Henk.Van-Dijk@univ-lille1.fr Henk.Van-Dijk@univ-lille1.fr

UMontreal SymbioticFungiEvol

Graduate positions on genomics, molecular genetics and evolution of symbiotic fungi.

Two PhD and one MSc student positions are available at the Plant Biology Research Institute at the Department of Biological Sciences http://www.bio.umontreal.ca/ of the University of Montreal. A major focus of our research is the genomics, molecular genetic and evolution of symbiotic fungi, combining information on gene polymorphism at intraspecific level and gene function with studies of cellular and molecular imaging. Arbuscular mycorrhizal fungi (AMF) are known to form symbiotic associations with more 80% of plant species, increasing the ability of roots

to explore a soil volume for immobile phosphorus. The objective of our research is to analyze AMF genetics and genomics to better understand how this important group of fungi has co-evolved with plants. The application of live cellular and molecular imaging technologies will be necessary in order to elucidate their mode of reproduction in the absence of sex.

We are looking for candidates with strong laboratory expertise in molecular genetics and genomics, a solid theoretical background in evolutionary biology, as well as expertise in bioinformatics. The start date is flexible.

To apply, please send a cover letter describing your research interests, a CV and names of two references by e-mail. <mailto:Mohamed.Hijri@umontreal.ca>

For more detail of these projects please contact me

Plant Biology Research Institute http://www.irbv.umontreal.ca/index_e.htm is located within the Montreal Botanical Garden http://www2.ville.montreal.qc.ca/jardin/jardin.htm, which is one of the largest and most prominent botanical gardens in the world.

Mohamed HIJRI Plant Biology Research Institute University of Montreal 4101 Rue Sherbrooke Est Montreal, Quebec, Canada H1X 2B2 Tel.: +1 (514) 868-5136 Fax: +1 (514) 872-9406 Email: Mohamed.Hijri@umontreal.ca

Mohamed Hijri <mohamed.hijri@umontreal.ca>

UPlymouth TermitePopulations

PhD position, University of Plymouth & The Natural History Museum, London

Stipend: £13,750 per annum for 36 months

We are seeking an independent and motivated graduate to fill a NERC CASE studentship investigating rain forest termite community structure. Candidates should have a demonstrable enthusiasm for insect ecology, taxonomy, and/or community ecology, and a minimum of an upper second class degree in Biology, Ecology or a related subject. Usually only UK students are eligible to apply due. The project is a joint venture between Dr Mairi Knight, Dr Sarah Donovan and Prof. Rod Blackshaw at the University of Plymouth, and Dr Paul Eggleton at the Natural History Museum, London.

Project background Termites are highly abundant in

lowland tropical rainforests. In their role as ecosystem engineers they have a major influence on soil structure, plant decomposition, carbon mineralisation, nutrient availability and the stimulation of microbial activity. As key soil invertebrates, termite diversity patterns are well characterised at regional and global spatial scales. However, two major questions remain unanswered: (1) How big are colonies? (2) How are those colonies distributed in the soil? Our lack of knowledge of these parameters has been identified as a major obstacle to our understanding of fundamental ecological processes, and of the factors driving population distributions. This studentship will tackle these two questions directly, using a combination of field surveys, taxonomic tools, molecular techniques (microsatellite markers) and spatial analyses. Over the three year period the successful candidate will spend roughly one third of their time working at the Natural History Museum, London, one third in the School of Biology at the University of Plymouth, and the other third conducting field work (in Cameroon and Malaysian Borneo).

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Experience required Full training will be given in all techniques, as well as initial assistance in the field, so no previous experience in insect identification, spatial analyses or molecular ecology is essential. Experience in any of these areas would, however, be an advantage. The candidate will be expected to spend considerable periods of time working in potentially basic and/or challenging tropical field conditions.

Application procedure Interviews will be held on the 3 May 2006 in Plymouth with an anticipated start date of October 2006. Applicants should send a curriculum vitae with the names and addresses (including email) of three referees along with a covering letter to Dr Mairi Knight, School of Biological Sciences, University of Plymouth, Drake Circus, Plymouth, PL4 8AA. Applications should be submitted before the end of April (2006). All informal enquiries should be directed to Dr Sarah Donovan via email (sarah.donovan@plymouth.ac.uk) or telephone (01626 325 880).

Dr Mairi Knight School of Biological Sciences University of Plymouth Drake Circus Plymouth PL4 8AA

tel: +44 (0)1752 238 633 fax: +44 (0)1752 232 970 email: mairi.knight@plymouth.ac.uk

mairi.knight@plymouth.ac.uk

USussex AdaptiveEvol

A 4-year PhD studentship is available to study adaptive evolution and the rates and fitness effects of new mutations in the lab of Adam Eyre-Walker at the University of Sussex in Brighton, UK. Unfortunately this studentship is only available to UK citizens or UK residents. Further information about the lab can be found at http://www.lifesci.sussex.ac.uk/CSE/members/aeyrewalker/aeyrewalker.htm. Applications (CV + names and email addresses of 3 referees) or enquiries should be addressed to Adam Eyre-Walker at a.c.eyre- walker@sussex.ac.uk. Applications will be considered as they are received.

a.c.eyre-walker@sussex.ac.uk

UVienna MathematicsEvol

Vienna, April 7, 2006 Research Positions in Statistical Genetics

Applications from highly qualified candidates are invited for a research position at the Ph.D. level at the University of Vienna. A two-year contract is offered. The successful candidate will participate in the research project

Mathematics and Evolution: Mathematical and Statistical Analysis of Ecological and Genetic Diversity, aiming at a close interaction between mathematics, statistics, and evolutionary genetics and ecology. (Associated researches are: Reinhard Bürger, Ulf Dieckmann, Andreas Futschik, Christian Schlötterer.) Upon appointment, the applicant is expected to participate in the development and evaluation of statistical methods for genomic approaches aiming at the identification of selected genomic regions (hitchhiking mapping).

Qualifications: A master degree either in statistics, mathematics, or evolutionary genetics; high motivation for interdisciplinary research on the development and evaluation of statistical methodology for population genetic problems. Strong background in computer programming. The starting date of the contract is negotiable. The salary follows the university scheme for

researchers at the respective levels of qualification.

This is about 23.000 Euros per year (before taxes and social insurance). Applicants should send a statement of research interest including possible starting dates, a curriculum vitae including publications, and two reference letters either by mail or by e-mail to:

Dr. Andreas Futschik Dept. of Statistics University of Vienna Universitaetsstr. 5/9, A-1010 Vienna Austria e-mail: andreas.futschik@univie.ac.at The search will continue until the position is filled.

Andreas Futschik Dept. of Statistics Tel. xx-43-1-4277-38634 University of Vienna Fax. xx-43-1-4277-38639 Universitätsstr. 5/9 A-1010 Vienna AUSTRIA

Andreas Futschik <andreas.futschik@univie.ac.at>

UWisconsin FishGenetics

GRADUATE POSITION IN FISHERIES GENETICS/MOLECULAR ECOLOGY AT THE UNIVERSITY OF WISCONSIN-STEVENS POINT. Position to begin June, 2006. Two or more graduate assistantships are available within the Cooperative Fisheries Research Unit to investigate the genetic effects of streamsiderearing facilities for Lake Michigan Lake Sturgeon rehabilitation and the relation between genetic integrity, population dynamics, habitat, and lake type on the quality of walleye populations. Other projects are available beginning August 2006 and January 2007.

Research work is primarily laboratory-based but responsibilities will include significant field responsibilities during spawning seasons.

Applications will only be accepted at the M.S. level; qualified applicants should have a minimum 3.0 GPA and cumulative GRE scores of 1000 (verbal and quantitative). Previous experience with molecular lab work, statistical software, and field projects is desirable. The annual stipend for graduate positions will be \$16,000 per year with tuition remission.

Interested individuals should send a cover letter outlining experience and research interests, a detailed curriculum vitae, unofficial copies of university transcripts and GRE scores, and contact information for three references to Dr. Brian Sloss, Wisconsin Cooperative Fisheries Research Unit, College of Natural Resources, 800 Reserve Street, University of Wisconsin-Stevens Point,

Stevens Point, WI 54481; FAX: 715-346-3624; Applications by e-mail are welcome and should be sent to andrea.musch@uwsp.edu, and will be accepted until the position is filled. Information on the College of Natural Resources and the University of Wisconsin-Stevens Point can be found at www.uwsp.edu. Brian L. Sloss,

Ph.D. Assistant Unit Leader Wisconsin Cooperative Fisheries Research Unit U.S. Geological Survey College of Natural Resources University of Wisconsin-Stevens Point 800 Reserve St. Stevens Point, WI 54481

Unit Office: 715-346-2178 Fax: 715-346-3624 Brian.Sloss@uwsp.edu Brian.Sloss@uwsp.edu

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DukeU LabManager EvolGenetics

ASSOCIATE IN RESEARCH (LAB MANAGER), EVOLUTIONARY GENETICS

An Associate in Research (lab tech) position is available in the Duke University laboratory of Biology Department Associate Professor Mohamed Noor beginning summer, 2006. Responsibilities: 35% Isolation and molecular analysis of DNA using PCR and other techniques; 30% Maintenance of fruit fly cultures and collection of unmated flies; 15% Supervision of undergraduates; 10% Data entry and analysis of results from molecular and phenotypic assessments; 10% Ordering and laboratory maintenance. Required qualifications:

B.S. or B.A. degree in biology or related field, some experience with basic laboratory techniques. Additional qualifications desired: experience with molecular biology protocols, experience with handling of Drosophila fruit flies, experience with supervising others. Applications will be reviewed as they are received until candidate is selected. Please ONLY send an e-mail of intent (no attachments!) that indicates your experience and interest to: Dr. Mohamed Noor, NOOR@DUKE.EDU . Duke University is an Equal Opportunity/ Affirmative Action Employer.

Mohamed A. F. Noor noor@duke.edu Associate Professor Tel: 919-613-8156 DCMB Group/ Biology Lab: 919-613-8193 Box 91000 FAX: 919-613-8177 Duke University Durham, NC 27708 USA http://www.biology.duke.edu/noorlab/ noor@duke.edu noor@duke.edu

EAWAG Switzerland EvolBiol

Eawag (Swiss Federal Institute for Aquatic Science and Technology) is a Swiss-based and internationally linked aquatic research institute committed to an ecological, economical and socially responsible management of water.

Our Aquatic Ecology Department is offering a senior position for a

AQUATIC ECOLOGIST / PHYTOPLANKTON RESEARCHER (PHD)

Suitable candidates, full of enthusiasm and team spirit, should meet the following criteria - excellent research record in Aquatic Ecology / Evolutionary biology (persons already conducting research on phytoplankton are especially encouraged to apply) - Experience in leading an externally funded research group and potential to attract external funding from competitive sources

and are furthermore expected to: - establish a research group to complement the diverse ecological and evolutionary research activities in the department - supervise PhD students - participate in department activities (teaching, administration)

Eawag's Department of Aquatic Ecology supports 10 research groups in diverse areas of aquatic research and collaborates in several research projects with groups of other departments of Eawag, ETH-Zurich and internationally. Our researchers may therefore also teach at ETH-Zurich (Prof. Jukka Jokela - Aquatic Ecology, Institute of Integrative Biology, Department of Environmental Sciences). The teaching profile can be tailormade.

Aquatic Ecology is present at two locations (Duebendorf and Kastanienbaum on the shore of Lake Lucerne). Both locations offer excellent facilities, including technical staff to assist in research. The working place is negotiable.

As a top research institute in Aquatic Sciences Eawag gives excellent support for high quality research and provides a stimulating research environment. The Aquatic Ecology department has access to breeding facilities for aquatic invertebrates and there is potential for developing experimental phytoplankton research. To state a few recent investments in Aquatic Ecology and mention other equipment installed:

- a molecular genetics facility in Duebendorf (16 capillary ABI, 2 real time PCR machines, option for preand post PCR robots, a cluster of PCR machines) - several flow cytometers, several HPLC machines and a fully equipped water chemistry laboratory - complete package for research in aquatic ecology, including research vessels and technical staff

The position will be available from the beginning of 2007. Working language in the group is English and the position is open to all nationalities.

Your CV and application letter (including your research interests as well as names and addresses of 3 references) should be sent to: Personnel Department, Eawag, Ueberlandstrasse 133, 8600, Duebendorf, Switzerland.

Application deadline: June 1st, 2006.

For further information about the position email to Prof. Jukka Jokela (jukka.jokela "at" eawag.ch)

jukka.jokela@eawag.ch jukka.jokela@eawag.ch

EAWAG Switzerland LabTech

Eawag (Swiss Federal Institute for Aquatic Sciences and Technology) is a Swiss based and internationally linked aquatic research institute.

Our Aquatic Ecology Department is looking for a:

RESEARCH TECHNICIAN / LAB MANAGER (in evolutionary ecology)

Suitable candidates should have basic laboratory skills (e.g. evolutionary genetics, molecular biology and immunology) and the willingness to participate in laboratory and field work, involving freshwater invertebrates.

The position is open for persons at different levels of expertise. It is suitable for a person having completed a PhD, who wants to participate in ecological research but is not interested in pursuing an independent research career. That applicant could be considered as a Lab Manager. Alternatively, a person with laboratory skills but no research experience could be considered as a research technician.

The tasks include: - assistance in animal breeding (freshwater invertebrates) - field work (New Zealand, Switzerland, Finland) - allozyme electrophoresis (one of the main tasks) - work at the molecular genetics laboratory (PCR, microsatellites, AFLP's, etc.) - basic protein electrophoresis (SDS-page, 2D electrophoresis)

- training and supervision of laboratory work conducted by PhD- and Masters students - supervision and organization of the laboratory work in the group of Prof. Jukka Jokela

Training for the above tasks is provided by the group. Initially the position will be available as a part time job (60%, e.g. 3 days/week), but it's likely to change to a full time employment later in 2006.

Eawag's Aquatic Ecology department houses 10 research groups in diverse fields of Aquatic Ecology. Our 15 - 20 PhD students work on projects varying from ecosystem processes to molecular genetics, and our 7 - 9 technicians participate in challenging tasks of field and laboratory research. The research group of Prof. Jokela is focused on the role of coevolution for maintenance of sexual morphs in the New Zealand snail Potamopyrgus antipodarum. This is a long term research project with a unique mix of genetic and ecological questions and data. The project provides challenging field work in New Zealand (6 weeks / year) and intensive laboratory work on genotyping the field samples. Willingness to function as a coauthor in the resulting publications is a bonus. This project will continue for 3 - 5 years and the person is expected to be available for at least 3 years.

The position will be available for the beginning of May 2006. Working language in the group is English and the position is open to all nationalities.

Your CV and application letter (including a description of your specific skills as well as names and addresses of 2 references) should be sent to: christiane.rapin"at"eawag.ch

Your applications should reach us no later than April 30, but the search will continue until a suitable candidate has been found.

For further questions about the position, ask Prof. Jukka Jokela (jukka.jokela "at" eawag.ch).

jukka.jokela@eawag.ch jukka.jokela@eawag.ch

HarvardMedSchool Bioinformatics

Bioinformatician position in Department of Genetics, Harvard Medical School

We are searching for a bioinformatician to support multiple research projects at a laboratory that carries out a wide variety of projects in medical genetic and evolutionary biology. Typical projects include the alignment of many millions of bases of DNA in multiple species to study ancient speciation, or building and maintaining a database to study patterns of variation and find disease genes in diverse human populations. This will be a challenging position where the successful applicant will have the opportunity to substantially extend their skill-set.

Required Skills:

- . B.A in Computer science or related field
- . Fluency in C, Perl, Oracle databases
- . At least 3 years experience in bioinformatics, especially comparisons of DNA or protein sequences. Some familiarity with standard tools such as BLAST and Phred and knowledge of statistics.

Laboratory experience is not an advantage for this position.

Please apply via the Harvard Employment site:

http://employment.harvard.edu, requisition # 25991

David Reich <reich@genetics.med.harvard.edu>

HarvardMedSchool LabManager

Research specialist / lab manager position in Dept. of Genetics, Harvard Medical School

We are looking for an individual who will work independently on large-scale genotyping and sequencing experiments, involving collection of millions of datapoints and robotic analysis of the data, for study of questions in medical genetics and human evolution in the Reich laboratory (Harvard Medical School Department of Genetics).

The successful applicant will be responsible for quality control/assurance of large data sets. The applicant will also be responsible for manipulation, processing and analysis of large data sets in PERL, EXCEL, or both. Will handle all storage and retrieval and tracking of >10,000 DNA samples and laboratory management, including staff management and purchasing. This position is grant-funded through April 30, 2009.

Requirements

Bachelors degree required, MA degree in molecular genetics or a related field strongly preferred, and at least 3+ years' experience including high-volume sample processing. Must have experience in genetics and genomics

lab work, including high-throughput sequencing and genotyping, and PCR. The successful candidate will also have experience storing, extracting, and shipping DNA and PCR primers. The successful candidate will demonstrate experience in quality control and assurance of large data sets.

Please apply via the Harvard Employment site:

http://employment.harvard.edu, requisition # 26030

David Reich <reich@genetics.med.harvard.edu>

IndianaU GenomicsBioinformatics

Employment Opportunities at the Center for Genomics and Bioinformatics

Three Project Scientists for research in genomics of arthropods:

The Center for Genomics and Bioinformatics (Indiana University, Bloomington - http://cgb.indiana.edu) carries out research that focuses on using genomic tools for ecological and evolutionary investigations. The Center has strengths in functional genomics using microarrays, genome-wide studies of DNA polymorphisms, and is exploring new technologies to gain knowledge on how genomes are shaped by evolution. We currently have three openings in our Genomics Laboratory for Project Scientists. Our research projects are mostly on arthropods (Daphnia, Drosophila, Hyalella, Amblyomma, and Nasonia). The positions are associated with a subset of these projects, namely the Drosophila Genomics Resource Center, the Daphnia Genome Project, and the Hyalella Microarray Project.

The successful candidate(s) will participate within units that specialize on fundamental approaches to genomic research: creating cDNA libraries, producing and testing microarrays, gene expression profiling by microarray and quantitative PCR, microsatellite and SNP genotyping. The Project Scientist will gain experience in using specialized equipment (e.g., Biomek Liquid Handling Robot, microarray printers and scanners, thermal cyclers) and various molecular biology techniques (e.g., RNA isolation, labeling and hybridization).

We seek individuals with a Bachelor's or a Master's degree in Biology or Biochemistry and some laboratory experience in molecular biology or genomics, although specialized on-the-job training will be provided. However, we will consider candidates with minimal previous experience and/or degrees in other scientific fields.

Please send only inquiries to the email address below; do not send your materials via email.

The position is open now and applications will be accepted until it is filled. Those received by May 31, 2006, will be assured full consideration. Interested candidates may contact (jobs@cgb.indiana.edu) for further information.

Please submit a CV and a description of your background and interests, and have three (3) letters of recommendation sent directly to the address below. Be sure to refer to Project Scientist - 007 in your cover letter.

Position #CGB-007 Attn: Project Scientist Center for Genomics and Bioinformatics Indiana University 1001 E. 3rd St. Bloomington IN 47405-3700

Indiana University is an affirmative action equal opportunity employer.

jcolbour@cgb.indiana.edu

IndianaU ResAssoc BirdEvol

POSITION AVAILABLE in the lab of Dr. Ellen D. Ketterson: Full-time Research Associate to administer laboratory and participate in laboratory and field research on birds. Three-year commitment and Master's degree or comparable experience required. Duties will include lab administration (permits, billing, keeping accounts, ordering supplies, data management and analysis, hiring of assistants), laboratory work (e.g. hormone assays, genotyping, immune assays), and managing an animal facility. Depending on the season, there is likely to be field work and some may be away from Bloomington. Depending on experience, there may be opportunities to mentor undergraduate research students. Actual duties will reflect candidate's experience and interests; opportunities for research available. Seeking cheerful, cooperative, quick, independent, and experienced person with lab and field skills. Position has served as a post-doctoral one in the past but candidates should understand that duties of Research Associate are part of the job. Start date 15 June, 2006, with room for negotiation. For further inquiries, please contact Ellen D. Ketterson at ketterso@indiana.edu. All applications including CV and names of references with contact information should be sent via email to mal-

ockha@indiana.edu, enter Ketterson - RA position, in the subject line. Indiana University is an equal opportunity affirmative action employer.

– Ellen D. Ketterson 812 855-6837 (office) Professor of Biology 812 855-6705 (fax) Department of Biology ketterso@indiana.edu Indiana University 1001 E. Third Street Bloomington, IN 47405-7005

http://www.bio.indiana.edu/facultyresearch/faculty/-Ketterson.html http://www.indiana.edu/~kettlab/-index.html http://www.indiana.edu/~reprodiv/-index.htm http://www.indiana.edu/~animal/ Ellen Ketterson < ketterso@indiana.edu>

KewGardens ResAssist Barcoding

Graduate or postgraduate research assistant to analyse plant DNA barcoding data.

Closing date: 14th April

We are seeking a data analyst for an international collaborative project devising new markers for plant DNA barcodes. You would compile sequence data generated by the project, implement phylogenetic and statistical analyses to judge the accuracy with which species can be identified, and prepare results for publication. The post would be ideal for a graduate interested in gaining research experience, someone with good bioinformatics skills or a postgraduate interested in strengthening their computing skills. You will have an undergraduate degree in biology, computing or related area and be familiar with phylogenetics, bioinformatics, or programming. You will also have excellent communication skills, problem solving ability, and team working experience.

The post will be based at the Royal Botanic Gardens, Kew or at the Silwood Park Campus of Imperial College London, with some flexibility on main location. It will last for 9 months from June 2006.

Application details are on http://www.rbgkew.org.uk/aboutus/jobs/ref1255.htm For more information on the project, see http://www.rbgkew.org.uk/barcoding/index.html or contact Tim Barraclough at t.barraclough@imperial.ac.uk.

Timothy Barraclough < t.barraclough@imperial.ac.uk >

MBL WoodsHole ResAssist EvolGenomics

POSITION: Research Assistant I Josephine Bay Paul Center Marine Biological Laboratory Woods Hole, MA 02536

Full-Time

Position Description: A full-time Research Assistant I position is available in the Josephine Bay Paul Center for Comparative Molecular Biology and Evolution at the Marine Biological Laboratory. This position is part of an evolutionary genomics research program and will involve interconnections among parasitology, genomics, evolutionary biology, and phylogenetics. The successful candidate could start as soon as possible. Questions can be addressed to sbordenstein@mbl.edu and additional information about the Center or Bordenstein lab can be found at: http://jbpc.mbl.edu/bordenstein . Duties/Responsibilities: Wolbachia are a genus of obligate intracellular bacteria that span the spectrum of symbiotic associations from parasitism in arthropods, mutualism in nematodes, and pathogenesis in humans. Primary research projects will focus on, but are not limited to, the molecular evolution of Wolbachia genes and the purification of symbiont genomic DNA from insect hosts. Primary responsibilities comprise molecular biology activities such as preparation of large scale insect homogenates, purification of symbiont DNA, insect rearing, primer design, PCR, southern hybridizations, high-throughput DNA sequencing, phylogenetic analysis and genetic database searching. Skills in some of these duties are required and should be highlighted in your cover letter.

Conditions: Position is available as early as soon as possible. Continuation is contingent on performance and available funds. The position includes generous benefits and coauthorship.

Educational/Experience/Skills: B.A./B.S. degree and experience in Microbiology, Molecular Biology, Evolution, Genetics, or a related field. Training in some molecular biology techniques required, including polymerase chain reaction, gel electrophoresis, sequence alignments, phylogenetics, or genomics. Familiarity with computational skills, GenBank, Mac OS, Windows, and Linux/Unix a plus. The successful applicant is expected to have good team skills, but work with a high level of independence under broad supervision.

Candidates with interest and experience in Molecular Biology, Parasitology, Evolution, Genetics, or Comparative Genomics may find this position particularly rewarding.

Instructions: Applicants should submit a cover letter, curriculum vitae or resume, transcripts, and list of three references including telephone numbers and email address. Please see the Marine Biological Laboratory Employment Website for full instructions: http://www.mbl.edu/inside/what/human_resources/employment.html .The MBL is an Equal Opportunity/Affirmative Action Employer/Nonsmoking workplace. Contact Dr. Seth Bordenstein (sbordenstein@mbl.edu) with specific questions.

Application Deadline: Until a suitable candidate is identified.

sbordenstein@mbl.edu sbordenstein@mbl.edu

Marseilles DirectorEvolOceanology

The Center of Oceanology of Marseilles is seeking a new director to start 2006 October 1st. Weblink: http://www.marbef.org/modules.php?name=-Jobs&p=vdetails&id=86

Didier

aurelle@com.univ-mrs.fr aurelle@com.univ-mrs.fr

MichiganStateU QuantGenet

The Department of Animal Science at Michigan State University welcomes applications for a full time Research Assistant position in Quantitative Genetics and Genomics. This person is expected to provide research support for animal genetics researchers in quantitative genetic analysis, statistical genomics analysis and database management. Projects will include classical animal breeding problems based on linear mixed model analysis, estimation of quantitative trait loci effects, functional genomics, simulation studies for statistical genetics research, and genetical genomics (i.e. the interface between genetics and genomics). A good working knowledge of statistical software, such as R or SAS, solid training in linear model analyses, and pro-

ficiency with basic programming (FORTRAN, C++, or C) and/or scripting languages (Java or Perl) is absolutely essential. Graduate training in quantitative genetics, mixed model analysis and bioinformatics is highly desired. It is imperative that the candidate be willing to develop and learn new skills in these areas as the need for these skills arise. Also, the candidate should have very good communication and technical writing skills and be able to interact with a diverse body of animal genetics researchers and graduate students.

The successful candidate should have at least a Masters of Science degree in animal breeding, quantitative genetics, statistics, genetic epidemiology, bioinformatics, or related field. The successful candidate would also be able to pursue a PhD in animal genetics at MSU along the themes of any of the projects listed previously, if that opportunity is desired.

Interested individuals are encouraged to submit a letter of application, names and email addresses of two references, and an updated resume by June 1, 2006 to Rob Tempelman (tempelma@msu.edu).

Robert J. Tempelman Department of Animal Science Michigan State University East Lansing, Michigan U.S.A. 48824-1225 Phone: (517)355-8445 Fax: (517) 353-1699 Email: <mailto:tempelma@pilot.msu.edu> tempelma@msu.edu

${\bf Munich} \\ {\bf Graduate Program Coordinator} \\$

The department of Biology, LMU Munich looks for a coordinator for a new graduate program (Master and PhD) in Evolution, Ecology, and Systematics. The ideal candidate should have a degree (preferably PhD) in Biology or a related field. S/he should be highly motivated have good communication skills. Proficiency in English and German is required. Any experience with administration or curriculum coordination is an advantage.

The coordinator will organize summer schools and workshops, contribute to the development of the curricula and function as an interface between university administration, teachers, and students.

The position is available at 50% (BAT IIa/2 according to German salary scale) from October 1st 2006 for initially three years. Informal inquiries and applications including letter of motivation, CV, and two references

should be sent until end of May preferably by email to

Dr. Joachim Hermisson Department Biology II, LMU Munich Bio-Center, Grosshadener Str. 2 82152 Planegg-Martinsried

joachim.hermisson@lmu.de

NHMLondon ResAssist PolychaeteEvol

Department of Zoology The Natural History Museum, London

Research Assistant Polychaete Research Group Salary £23,000 - £24,000

Molecular genetics of deep-sea polychaetes A 12-month research position is available to join a research project on polychaetes from chemosynthetic ecosystems such as whale-falls, wood-falls and hydrothermal vents. The aim of the molecular part 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 is required with sound laboratory skills and an interest in the fields of phylogenetics, phylogeography and population genetics of deep-sea invertebrates. The candidate should have a PhD in a relevant field of molecular biology, or equivalent lab experience. Experience in deep- sea biology, invertebrate zoology and polychaete systematics is desirable, but not essential. The successful candidate will be expected to take an active role in our whale-fall field program in Sweden and the United Kingdom.

This project will be jointly supervised by Dr Adrian Glover (The Natural History Museum) and Dr Thomas Dahlgren (Tjärnö Marine Biological Laboratory, Sweden). Please send informal enquiries to <a.glover@nhm.ac.uk>. To formally apply, please see instructions below.

For further information and details of how to apply, please send an A5 SAE (1st class) to The Natural History Museum c/o Tribal Resourcing, The Atrium, Wollaton Street, Nottingham NG1 5FW or email:

NHM@tribalresourcing.com

Please quote reference: NHM/RA/KB

Closing date: 28 April 2006

To confirm receipt of your application call the Museum response line on 0870 241 9031 between 11am to 2pm Monday to Friday only. No telephone requests for details will be accepted.

At the Natural History Museum we value the diversity of our employees and the unique perspectives they bring to our business.

Dr Adrian Glover Zoology Department The Natural History Museum Cromwell Rd., London SW7 5BD, U.K

+44 (0)20 7942 5056 (office) +44 (0)77 666 484 40 (mobile)

http://homepage.mac.com/adrianglover a.glover@nhm.ac.uk

NHM London 2 Taxonomy

Tow EU-funded jobs (4.5 year contracts) are currently being advertised (see Nature 30th March).

Band 4 Researcher in delivery of web-based taxonomy

We seek an IT specialist to work on EDIT, the European Distributed Institute of Taxonomy, a Network of Excellence funded by the European Commission with the aim of better integrating the effort of taxonomists across Europe: see http://www.mnhn.fr/edit. The post will be a key member of the workpackage entitled 'Unifying revisionary taxonomy', the aim of which is to encourage expert taxonomic task groups to migrate taxonomic data to an internet platform.

Band 4 Insect Taxonomist

To work on EDIT, the European Distributed Institute of Taxonomy, a Network of Excellence funded by the European Commission with the aim of better integrating taxonomy across Europe. The preferred target taxon is Lepidoptera, although other insect taxa are not excluded at this stage. The successful applicant will be a key member of the workpackage entitled 'Unifying revisionary taxonomy', the aim of which is to encourage expert taxonomic task groups to migrate taxonomic data to an internet platform being constructed in a related workpackage.

Details can be found at http://www.jobsgopublic.com/ and search for NHM as keyword.

Cheers, Dave

Dr D.McL. Roberts, Tel: +44 (0)20 7942 5086 Dept. Zoology, Fax: +44 (0)20 7942 5054 The Natural History Museum, Cromwell Road, London SW7 5BD Great Britain Email: d.roberts@nhm.ac.uk Web page: http://www.nhm.ac.uk/zoology/extreme.html The Monster Raving Loony Party, founded in 1963, included in its manifesto the vote at 18, local radio and all day drinking.

d.roberts@nhm.ac.uk

NHM London CollectionManager

Still time left to apply for a collections management job with a lot of variety (and time for research):

Invertebrate Collections Curator, Department of Palaeontology, Natural History Museum (London), London, UK Posting Date: 3 March 2006 Closing Date: 27 April 2006 Invertebrate Collections Curator (Ref: NHM/ICC/KB) Starting Salary £25,500 - £30,000 per annum (depending on experience) The Department of Palaeontology of The Natural History Museum, London is seeking a curator to help manage its mollusc and sponge collections. We are looking for a dynamic, selfmotivated individual with a broad range of skills to join the Invertebrates & Plants Curation B-Team, which is responsible for the collections of fossil molluscs, brachiopods, sponges, and 'worms'. Together, these collections comprise more than fifty per cent of the Palaeontology Department's holdings. The successful candidate will be expected to support the Museum's collections management activities by curating the mollusc (with principal initial responsibility for cephalopods) and sponge collections. This includes strategic collections development, supporting departmental research programmes, making collections information available to a wide audience, managing loans, enquiries, and scientific visitors, developing and implementing remedial and preventative conservation procedures (in association with the Palaeontology Conservation Unit), and promoting use of the collections. In addition, you will be expected to take an active role in the support of and contribution to external income generation activities, as well as participating in the Museum's outreach programmes through the Darwin Centre and Earth Lab.

A BSc degree (or equivalent) in museum studies, earth sciences or biological sciences, with two years experience in collections management of natural history collections is essential. Familiarity with the use and role of collections databases and good written/verbal communication skills is also considered essential. An interest in invertebrate palaeontology, active involvement in a professional organizations, a history of publication, participation at international conferences, and active participation in other professional activities (e.g., teaching) are desirable. The position will be a permanent appointment after a one-year probationary interval. Additional details can be requested from Allie Bailey <a.bailey@nhm.ac.uk>

or by sending an A5 self-addressed envelope (1st class) to: The Natural History Museum c/o Tribal Resourcing The Atrium, Wollaton Street Nottingham NG1 5FW UK Please quote the appropriate reference number.

NZ Bioinformatics

Employment in Bioinformatics Development at Biomatters

We are looking for people who want to work in environment that is at the crossover point between academic and commercial. The position will involve writing software modules for sequence alignment, and other ares such as HMM and MCMC for our Geneious product. At the same time you have the opportunity to do research and publish papers for a company co-located at a University inside a world-leading bioinformatics institute. We offer benefits, an excellent team, autonomy and flexibility, plus the opportunity to benefit directly through the growth of the company and your contribution to it - in an environment where everyone is highly motivated.

Our team includes world leaders in bioinformatics, vis-

iting international experts and several national programming championship winners. We are seeking new people who will feel at home in this environment. We use Java, XML, and webservices technologies.

We are based in Auckland, New Zealand, but also have people who are working for us remotely. We work flexible hours and after an initial training period are open to a number of employment arrangements that allow considerable autonomy to the right candidate.

You can find out more about us at www.geneious.com. To apply, send your CV to careers@biomatters.com.

Daniel Batten

CEO, Biomatters P: +649-3795064 F: +649-3737688 M: +6421-747131 www.biomatters.com daniel@biomatters.com

OldDominionU MarineAssessment

RESEARCH ASSOCIATE POSITION IN MARINE CONSERVATION

The Department of Biological Sciences at Old Dominion University, a "Doctoral Research - Extensive" state university, has an opening for a Research Associate position in marineconservation. The appointment is for one year (potentially renewable) beginning as early as June 2006. This position involves participation in a project to assess a large number of marine species for the IUCN Red List of Threatened Species through a collaborative initiative with Conservation International and the IUCN Species Survival Commission. The successfulcandidate will be expected to participate in the Red Listing process, including backgroundresearch and international workshops and meetings, supervise research assistants, and assistteaching courses in Marine Biology and Ichthyology. At the time of employment, applicantsmust have a PhD in Biology, Zoology, Oceanography or a related field with a dissertation topic marine conservation biology of marine ecology OR a Masters degree with at least five years experience in marine conservation biology or marine ecology. Geographical Information Systemexperience is highly desirable. Please submit a curriculum vitae, statement of interest, and thenames, telephone numbers, and addresses (postal and email) of three references to: MarineConservation Search Committee, Department of Biological Sciences, Old DominionUniversity, Norfolk, VA 23529-0266 USA; or to ecolsearch@odu.edu (electronic submissionof materials is preferred). Review of applications will begin on June 1, 2006 and will continueuntil a suitable candidate is found. Women and minorities are encouraged to apply. OldDominion University is an Affirmative Action/Equal Opportunity Employer and requirescompliance with the Immigration Reform and Control Act of 1986.

amahon@odu.edu

OregonStateU ResAssociate EvolGenomics

An NIH-funded faculty research associate position to study evolutionary genetics and genomics in Caenorhabditis elegans and related nematode species is available in the Department of Zoology at Oregon State University. See announcement below for details.

Application Deadline: For full consideration, application materials must be received no later than 5pm, May 2, 2006.

Starting Date: June 2006

Position: The Department of Zoology invites applications for a Faculty Research Assistant. This position will be under the direction of principal investigator Dr. Dee Denver in the Department of Zoology. The laboratory conducts research on genome evolutionary processes using the model nematode Caenorhabditis elegans and related species.

Responsibilities: The duties of this position include: 1. supervision of 1-2 undergraduate workers, who make solutions and prepare C. elegans agar plates; 2. execution and analysis of a large-scale, high-throughput PCR and DNA sequencing screen for mutations and polymorphic nucleotide sites in experimental C. elegans populations - work will involve extensive setup of PCR reactions, DNA sequencing reactions, running of agarose gels, and communication with the OSU Center for Genome Research and Biocomputing core facility personnel; 3. maintaining long-term experimental C. elegans populations in the laboratory; 4. analyze and prepare data for presentation in scientific research articles and meetings; 5. general laboratory coordination and maintenance includes ordering and organizing equipment and supplies, and maintaining laboratory databases. About 50% of these duties requires the knowledge base provided by a BS degree to design the experiments, interpret the data, read the scientific lit-

erature and write up the data for publication.

Qualifications: Required qualifications include: BS or BA from accredited institution, and experience in molecular biology, microbiology, and/ or laboratory coordination.

Preferred qualifications include: experience in using Microsoft Office applications, managing databases, basic programming skills. Individuals with a record of promoting harmony in the laboratory setting are also desired. Preferred qualifications include a demonstrable commitment to promoting and enhancing diversity.

University & Community: OSU is one of only two American universities to hold the Land-, Sea-, Sun- and Space-Grant designations and is the only Oregon institution recognized for its "very high research activity" (RU/VH) by the Carnegie Foundation for the Advancement of Teaching. OSU is comprised of 11 academic colleges with strengths in natural resources, earth dynamics and sustainability, life sciences, and the arts and sciences. OSU has facilities and/or programs in every county in the state, including 12 regional experiment stations, 41 county extension offices, a branch campus in Bend, a major marine science center in Newport, and a range of programs and facilities in Portland. OSU is Oregon's largest public research university, conducting more than 60 percent of the research funded throughout the state's university system.

OSU is located in Corvallis, a community of 53,000 people situated in the Willamette Valley between Portland and Eugene. Ocean beaches, lakes, rivers, forests, high desert, the rugged Cascade and Coast Ranges, and the urban amenities of the Portland metropolitan area are all within a 100 mile drive of Corvallis. Approximately 15,700 undergraduate and 3,400 graduate students are enrolled at OSU, including 2,600 U.S. students of color and 950 international students.

The university has an institution-wide commitment to diversity, multiculturalism, and community. We actively engage in recruiting and retaining a diverse workforce and student body that includes members of historically underrepresented groups. We strive to build and sustain a welcoming and supportive campus environment. OSU provides outstanding leadership opportunities for people interested in promoting and enhancing diversity, nurturing creativity, and building community.

Salary and Appointment Period: \$25,000-\$35,000/12 months at full time (1.0 FTE), fixed term. Reappointment is at the discretion of hiring supervisor.

Application: Send a Letter of Application, Curriculum Vitae or Resumé, and names, addresses, phone numbers and email addresses of three references to (preferably

by email):

Dee Denver Search Committee Chair Department of Zoology Oregon State University Corvallis, OR 97331-2914 Telephone 541-737-3698 Email: denver@cgrb.oregonstate.edu

Oregon State University is an Affirmative Action/Equal Employment Opportunity employer and has a policy being responsive to the needs of dual-career couples.

denvedee@cgrb.oregonstate.edu

Roscoff MarineEvol

Station Biologique de Roscoff CNRS, UMR 7144, Groupe Plancton Oceanique Equipe ATIP: « Evolution du Plancton et Paleoceans » http://www.sbroscoff.fr/Phyto/ CONCERNS: Two positions (PhD 3 Years \$ PostDoc 2 Years) available at the Roscoff Marine Station; Team: Plankton Evolution and Paleoceans. Roscoff, April 4th 2006,

The group Plancton Oceanique at the SBR in Brittany, France, is a one of the world leader in the fields of molecular ecology, evolution, and physiology of marine unicellular plankton (http://www.sb-roscoff.fr/Phyto/-). The new team Plankton Evolution and Paleoceans (PI: Colomban de Vargas; Research Engineer: Ian Probert; PhD students: Miguel Frada and Hui Liu) explores key aspects of the biological, functional, and ecological diversities within the two main groups of pelagic micro-calcifiers: the coccolithophores and foraminifers. Having built kilometers-thick, exceptionally well preserved carbonate deposits at the ocean floor, these protists have played a fundamental role in the ecology and geology of Earth System for the last ~200 My. The biological (genomic, physiological, ecological, biogeographical), chemical (trace elements and isotopes within the micro-skeletons), and morphological (optical and electron microscopy) information we extract from living species are used to assess their mode and rate of evolution, and to re-interpret their fossil record and impact on biogeochemical cycles.

PhD project: Role of Red-Queen selection, life cycle, and sex in the evolution of marine pelagic viruses and their hosts (coccolithophores).

This project will be co-supervised by Colomban de Vargas (SBR) and Willie Wilson (Plymouth Marine Laboratory, http://www.pml.ac.uk/pml/). It is part of ESTeam, a new European PhD program of excellence in

marine genomics and molecular ecology, hosted at the SBR (http://www.sbroscoff .fr/ESTeam/).

Project Abstract: Modern optical and genomic techniques have revealed extremely abundant and diverse marine planktonic viruses. Although the influence of viruses on marine geochemical cycles (via the regulation of host populations), and prokaryote evolution (via lateral gene transfer), is well recognized, the processes creating and maintaining such huge oceanic viral diversity, including its rate of evolution, are largely unknown. Mechanisms of co-evolution between hosts and their viruses, where both are fighting to respectively decrease and increase virulence, are certainly playing critical roles. We propose to test two main hypotheses, using the coccolithophore Emiliania huxleyi as model: (A) virulence in pelagic host-virus interactions is highly specific, constrained by the boundaries between species, sub-species, or strains; (B) virulence is not species specific, but life-stages specific, and thus constrained by the sexual alternation between haploid and diploid populations. Experiments will test if Red-Queen processes are driving ecological/evolutionary diversification in coccolithoviruses and their hosts, and will address whether host evolution is driven by rapid genomic mutations, or rather by genomic restructuring through haploidization and/or genetic recombination associated with sex. Results will enhance our understanding of the nature and tempo of evolution of planktonic host-virus interactions.

The complete project can be downloaded @: http://www.sb-roscoff.fr/ESTeam//Theses/-

ESTeam_DeVargas.pdf Application dealine: May 26th 2006; Interviews: June 15-16th 2006; Starting date: Fall 2006. Salary: 1532,94 Euros net/month; in addition: travel allowance, 750 /year; mobility: 523,50 /month; career exploration: 2000 /fellow. Further detail about the ESTeam program can be found @ http://www.sb-roscoff.fr/ESTeam/ .Application form can be found @ http://www.sb-roscoff.fr/ESTeam/ and will be sent, together with a CV, a letter of motivation, and 2 recommendation letters, to houbin@sb-roscoff.fr, i.e. Mrs Celine Houbin, ESTeam operational manager, SBR/CNRS-UPMC, BP74, F-29682 cedex, FRANCE. A copy of the documents should be emailed to the Dr. Colomban de Vargas, vargas@sb-roscoff.fr; Any questions? Do not hesitate to call: 00 33 2 98 29 25 28.

CONCERNS: 2-Years PostDoc positions available at the Roscoff Marine Station; Team: Plankton Evolution and Paleoceans.

Postdoctoral Associate: Species & Skeleton Diversification in Coccolithophores

The invention of intracellular biomineralization (or

coccolithogenesis) in haptophyte microalgae ~200 Ma transferred the biological control of carbonate chemistry from coastal waters to the open oceans. This new

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

UArkansas DrosophilaDiversity

A field research position is available at the University of Arkansas for summer 2006 to survey drosophilid biodiversity in the Ozark and Ouachita mountains. The main goal of this project is to collect Drosophila and return them to Fayetteville for genetic analysis. All training (collecting techniques, species identification, fly culturing methods, etc) will be provided. Salary is included, summer housing in Fayetteville can be arranged, and transportation will be provided (field vehicle, gas, food). This position starts May 15, and should last 2-3 months. Please contact William J. Etges for details.

Applicants should submit a CV, statement of interests, and 2-3 letters of recommendation.

William J. Etges Department of Biological Sciences SCEN 632 University of Arkansas Fayetteville, AR 72701 USA wetges@uark.edu http://comp.uark.edu/~wetges/wetges.html voice: (479) 575-6358 lab: (479) 575-7437 FAX (479) 575-4010

"Those who would sacrifice liberty for security deserve neither." Ben Franklin.

wetges@uark.edu

UHertfordshire EvolComputation

Dear Colleagues,

The following posts may of interest to candidates in Evolutionary Computation, BioComputation and Systems Biology.

Best Regards,

C. L. Nehaniv

- Research Lectureships (2 posts) Computer Science

Principal Lecturers Salary: c 38,700 - 41,100 GBP per annum

These are new-blood appointments focused towards the long-term development of the existing computer science research base at the University. In the 2001 RAE this unit of assessment became the largest 4-rated unit in the sector and you will complement and strengthen these ongoing research activities. We are seeking outstanding individuals with the potential for developing international excellence in research. Preference will be given if you are active in one (or more) of the following areas:

* Automatic Differentiation of Algorithms * Biocomputation * Computer Architecture * Human-Computer Interaction * Distributed Systems and Security * Neural Computation * Information Theory and Communications * Machine Learning * Formal Methods and Requirements Engineering * Compilers * Complex Adaptive Systems (Quantitative Methods)

For an initial period of 3 years you will be given considerable support to build up, with around 70% of your workload devoted to research activities and with a funded PhD studentship available in your research area. It is anticipated within this period you will have reached the level where your research will be self-funding and your profile will make you eligible for a Readership.

Quote reference: B1642

Closing date: Monday 8 May 2006. Interview date: 12 June 2006

The University offers a range of benefits including a final salary pension scheme, professional development, family friendly policies, discounted memberships at the Hertfordshire Sports Village and generous annual leave.

Application packs are available from Personnel on +44-1707 284802 (24hr voicemail), or from our website at http://recruitment.herts.ac.uk/recruit quoting the appropriate reference number.

The University is committed to Promoting Equal Opportunities

c.l.nehaniv@herts.ac.uk

UK FieldAssist Bees

Field assistant sought for project on bees in Britain and Ireland

A field assistant is needed for the period 15 June-30 July 2006 to work on the behaviour and ecology of eusocial sweat bees (Halictus) at field sites in Britain and Ireland. The work will involve helping a postdoctoral researcher to census/observe/excavate bee nests as part of a study of the basis of sociality. During periods of weather unsuitable for fieldwork, you will carry out lab duties at UCL in London. Work will include weekends and anti-social hours where necessary. Note that sweat bees are small and do not sting, with average colony sizes of <5 individuals!

The successful applicant will be prepared to work hard, have an interest in behavioural ecology and insects, and enthusiasm for fieldwork. A driving licence would be useful but is not essential. Travel/accomodation expenses necessary for the fieldwork away from London will be provided, plus a salary of £100 per week. During labwork periods, the successful applicant will need their own accomodation within reach of UCL in London. Applicants must be able to attend an interview in London, and should send a hard copy covering letter plus CV, including e-mail addresses of the applicant and 2-3 referees, to Dr Jeremy Field, 25 Wyndham Road, London W13 9TE, UK, or e-mail to jeremy.field@ucl.ac.uk. Review of applications will begin on 15 April 2006 and will continue until the position is filled.

Dr Jeremy Field

Department of Biology, University College London, Wolfson House, 4 Stephenson Way, London NW1 2HE, UK

http://www.ucl.ac.uk/biology/academic-staff/field/field.htm - Dr Jeremy Field Dept Biology University College London Wolfson House 4 Stephenson Way London NW1 2HE, UK (currently on sabbatical)

jeremy.field@ucl.ac.uk jeremy.field@ucl.ac.uk

ULausanne Coordinator

Coordinator of the Inter-University Doctoral School in Ecology & Evolution for the Universities Lausanne, Berne, Fribourg, Geneva, Neuchâtel (job reference 545)

The newly formed doctoral school in Ecology and Evolution for the 5 Swiss-French universities seeks a coordinator. The ideal candidate should be highly motivated and with a high degree of initiative. He/ she

should have a university degree, preferably in biology and some previous experience in administration. Knowledge of ecology and evolution would be an advantage. The candidate should be able to coordinate the activities of the doctoral school including organization of workshops, seminars and courses, accreditation of doctoral students, coordination with the doctoral schools that exist in each of the 5 universities, maintenance of a doctoral school website, assure the transfer of information between doctoral students and teachers/supervisors, ability to manage the finances of the doctoral school.

The ideal candidate should be proficient in spoken and written English, should be well organised and have very good communication skills.

The candidate will coordinate the doctoral school from the doctoral school office at the University of Lausanne (Dorigny Campus).

The position is available at 60%, although an additional 20% may be available at the most busy times.

Availability: The position is available as soon as possible, after the closing date for applications.

Applications: Applications including letter of motivation, detailed CV, reference letters should be sent to Madame Delphine Martins, Service des Ressources Humaines, Château de Dorigny, 1015 Lausanne, Switzerland. You should quote the job reference number 545 in your application. Closing date for applications is 4th May 2006.

Informal enquiries: Contact Prof. Ian Sanders, Dept. of Ecology and Evolution, University of Lausanne, Switzerland by email at ian.sanders@unil.ch or by phone +41 21 692 4261.

Ian R. Sanders Professor of Evolutionary Biology Dept. of Ecology & Evolution University of Lausanne Biophore Building 1015 Lausanne Switzerland

Tel (direct): +41 21 692 4261 Tel (Secretary): +41 21 692 4260 Fax: +41 21 692 4265 Email: ian.sanders@unil.ch

http://www.unil.ch/dee/page7238_en.html Ian.Sanders@unil.ch Ian.Sanders@unil.ch

UMiami ResAssociate Aphids

Research Associate Biology Department, University of Miami, FL Position #032242

A full-time research associate position is available in the Biology Department at the University of Miami, FL in the laboratory of Dr Alex Wilson (http://www.bio.miami.edu/acwilson/home.htm).

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Primary research projects will focus on but are not limited to: the ecology, genetics and molecular evolution of aphids. Primary responsibilities comprise but are not limited to standard molecular biology activities, microarray analyses, sequence analyses, microsatellite DNA fragment analysis, extraction of nucleic acids from insects, primer design, PCR, gel electrophoresis, cloning of PCR amplicons, preparation of DNA sequencing reactions, molecular database searching, insect rearing and greenhouse tasks. Skills in some of these duties are required. The appointed person will also be required to oversee the day-to-day management of the laboratory including the purchase and maintenance of supplies and equipment, and the supervision of undergraduate research assistants.

This position is available July 1, 2006 for one year, with continuation contingent on performance and available funds. This position includes co-authorship in publications. Salary will be commensurate with experience and will include benefits.

Education: B.A. or B.S. degree and experience in molecular biology, evolution, genetics or a related field. Previous laboratory experience with molecular biology and/or genomics is preferred. Familiarity with computational skills; Mac OS, Windows and Linux/Unix is a plus. Experience with rearing insects and growing plants is preferred and familiarity with genetics is required. The successful candidate is expected to be highly motivated, to have excellent team and organizational skills but capable of working with a high level of independence.

A cover letter, curriculum vitae and the names and contact information, including email addresses and phone numbers, of at least three people who agreed to be referees are required to be considered for this position. Send to Dr. Alex Wilson, Department of Biology, University of Miami, P.O. Box 249118, Coral Gables, FL 33124. acwilson@bio.miami.edu Review of applications will begin May 1st 2006 and will continue until a suitable applicant is found.

The University of Miami is an equal opportunity/affirmative action educator and employer.

Dr Alex Wilson PERT Postdoctoral Fellow Center for Insect Science Department of Ecology and Evolutionary Biology The University of Arizona acwilson@email.arizona.edu http://cis.arl.arizona.edu/PERT/people/Wilson/index.htm

http://www.bio.miami.edu/acwilson/home.htm phone - (520) 626 8344 fax - (520) 621 2590 Mailing address: Department of Ecology and Evolutionary Biology, P.O. Box 210088, University of Arizona, Tucson, AZ 85721-0088, USA Courier address: Department of Ecology & Evolutionary Biology, Biosciences West, Room 310, 1041 E. Lowell St., The University of Arizona, Tucson, Arizona 85721-0088 U.S.A.

Alex Wilson <acwilson@email.arizona.edu>

UMuenster PlantEvolBiol

The newly founded 'Institute for Evolution and Biodiversity' (IEB) forms the core of the priority area "Evolutionary Biology" of the Biological School, University of Muenster, Germany. Within IEB, the Plant Evolutionary Ecology department is inviting applications for a

Research fellow position in PLANT EVOLUTIONARY BIOLOGY

The position starts on 1 September 2006, is non-permanent and may be extended to a maximum of five years. The salary is according to the German civil servant scale A13, thus approximately 45 000 Euro gross per year. The position is comparable to the level of an assistant professor in non-German academic systems.

We are seeking a highly motivated and enthusiastic candidate who is expected to develop his/her own research line including the acquisition of funding. Subjects that would fit particularly well into our group include

- the evolution of plant mating systems - plant metapopulation structure and dispersal - ecological and conservation genetics - evolution of host-parasite or plant-animal interactions - ecological and environmental genomics

The successful candidate must have a PhD or doctorate in Biology and a strong publication record in relation to his/her biographic phase. The position includes teaching in elementary and biodiversity aspects of botany, teaching experience would thus be advantageous. S/he will be encouraged to guide graduate students from our MSc and PhD programs and to participate in collaborative funding initiatives that are currently set up at the Biological Faculty and with the IEB as a key player.

The Plant Evolutionary Ecology Group has just started to establish this novel department. Our young group is one of four existing groups in the newly founded Institute of Evolution and Biodiversity at the University of Muenster (see www.uni-muenster.de/evolution/). When fully grown, the institute is planned to encompass 5 full groups and two junior groups working on diverse aspects of the evolution of biodiversity. The institute will be equipped with a central molecular genetic laboratory, physiological and microscopy laboratories, greenhouses and climate chambers. We intend to create a lively and stimulating work environment promoting the study of all aspects of modern evolutionary biology.

Working language in the group is English and the position is open to all nationalities. The university is an equal opportunity employer. Female candidates are particularly encouraged to apply.

Please address further inquiries to Thorsten Reusch (see address below). Applications should include information on teaching experience, three selected publications, names and addresses of 3 referees, and a research perspective. Please submit applications until 25 April 2006 to

Prof. Thorsten Reusch, Institute for Evolution and Biodiversity. Huefferstr. 1, 48149 Muenster, Germany email: treusch@uni-muenster.de <mailto:treusch@uni-muenster.de>, phone +49-251-83-21095

Thorsten Reusch kreusch@uni-muenster.de

URochester ResTech DrosophilaWolbachia

Research Technician - University of Rochester

I am seeking a full-time research technician to join our lab. Much of our current research focuses the ecology and evolution of associations between Drosophila and Wolbachia (http://www.rochester.edu/College/BIO/faculty/Jaenike.html). General responsibilities of the position include oversight of routine lab operations, maintenance Drosophila, assisting with experiments, and supervising undergraduate assistants. The specific responsibilities in the near future include field work in Arizona (optional), DNA isolation, PCR, sequencing, real-time quantitative PCR, and phylogenetic analysis of DNA sequence data.

Applicants with experience in basic molecular techniques (DNA isolation, PCR and sequencing) and a serious interest in evolutionary biology are especially encouraged. A bachelor's degree in biological science

and previous laboratory experience are preferred.

The position may begin as soon as June 1, 2006. Starting pay will be in the range of \$23,000 to \$29,000, depending on hours and prior experience. Send resume (including the names of three references) and cover letter summarizing research interests and experience to John Jaenike at joja@mail.rochester.edu (or Department of Biology, University of Rochester, Rochester, NY 14627). The University of Rochester is an affirmative action/equal opportunity employer.

Thanks very much.

John -

John Jaenike Department of Biology University of Rochester Rochester, NY 14627

Email: joja@mail.rochester.edu

Phone: 585 - 275-0009 (office) 585 - 275-5013 (lab) Fax:

585 - 275-2070

John Jaenike <joja@mail.rochester.edu>

USouthernCalifornia ConservationGenet

Laboratory Research Technician Marine Population and Conservation Genetics University of Southern California, Los Angeles

I am seeking a full-time research technician to join our lab group as early as June 15. The technician will assist with projects involving the genetics of inbreeding and outbreeding depression using a marine copepod as a model. Specific duties will include maintenance of copepod cultures, morphometric assays, various molecular assays and routine lab management. The ideal candidate would have a bachelor's or possibly master's degree in biology, a strong interest in population genetics/evolution and research experience including molecular techniques such as PCR, DNA sequencing, microsatellites and AFLPs. Specific training will of course be provided. The position is initially for one year but may be extended. Starting salary is \$28-32K.

To apply send a letter of interest, a resume, and contact information for three references to the address below via either email (preferred) or regular mail. Review of applications will begin May 15 and continue until the position is filled.

Suzanne Edmands Department of Biological Sciences,

AHF 107 University of Southern California Los Angeles, CA 90089-0371, USA sedmands@usc.edu (213)740-5548 http://www.usc.edu/schools/college/faculty/faculty1003223.html sedmands@usc.edu sedmands@usc.edu

UStirling 2 EcolEvol

We currently have four open faculty positions within the School of Biological and Environmental Sciences at The University of Stirling. Two of these posts will be Lectureships in Ecology & Evolution. They will be advertised shortly (probably within a fortnight) in Nature and on jobs.ac.uk

The School has three research clusters: Evolutionary Ecology & Conservation; Environmental Processes; Geoarchaeology & Environmental History. Following recent appointments at Chair and Readership level within the Evolutionary Ecology & Conservation research cluster the School now wishes to appoint two Lecturers who are also to join the Evolutionary Ecology & Conservation research cluster. Applicants in all areas of ecology and evolution are welcome, but preference may be given to those whose research interests ally with existing areas of expertise (http://www.sbes.stir.ac.uk/research/ecology/index.html). The salaries will be on either Lecturer A or B scale depending on experience.

Currently, the School has 10 post-doctoral scientists, approximately 35 research postgraduate students and 12 centrally funded technicians. The annual research expenditure from external grants and contracts is approximately £1M. The School teaches and administers a suite of BSc teaching programmes in the biological and environmental sciences, including Biology, Animal Biology, Marine Biology, Ecology, Environmental Science and Environmental Geography. MSc programmes are offered in Environmental Management, River Basin Management and, with the Institute of Aquaculture, Sustainable Development.

PERSON SPECIFICATION

The successful applicant will:

Have an established reputation in an appropriate area of ecology/evolution as demonstrated by publication and/or research potential and the ability to develop a vigorous research programme.

Be able to contribute to the teaching of organismal bi-

ology academic programmes.

Have the potential to develop co-operative relationships with biological and environmental scientists within the School

Be willing to play an influential role in the future development of the school.

APPLICATION PROCEDURE

Informal enquiries may be directed to Professor D. Goulson, tel: +44 (0) 1786 467759. E-mail daye.goulson@stir.ac.uk

Formal applications must include a completed application form available from Human Resources Services, details of research plans and aspirations, a complete CV and the details of three academic/scientific referees. The complete application, quoting reference (see advert on jobs.ac.uk for reference) must be sent to HR Services, University of Stirling, Stirling FK9 4LA, Scotland UK; hr-services@stri.ac.uk by May 19th.

Dr Andre Gilburn Programme Director (Animal Biology) School of Biological and Environmental Sciences University of Stirling Scotland FK9 4LA Tel: 01786 467807 Email: andre.gilburn@stir.ac.uk

Andre Gilburn <andre.gilburn@stir.ac.uk>

UWyoming Bioinformatics

2 Positions at University of WyomingService Scientist in BioinformaticsPostdoctoral Researcher in Comparative Functional

Genomics

Two positions are currently available at University of Wyoming. The first position is for a service scientist in the new bioinformatics core that is being created (details will be available through www.wyomingbioinformatics.org). The Ph.D. level service scientist will be expected to have a broad understanding of both sequence analysis and microarray statistics and be expected to collaborate with biological researchers on campus on problems in those areas. Recent Ph.D. graduates in bioinformatics or computational biology, especially those with significant biological training are welcome to apply. The starting salary is \$40,000 per year plus benefits. Applicants should send a CV and contact information for three references together with a cover letter describing their qualifications for this position by email to rex@uwvo.edu and liberles@uwyo.edu.

The second position is for a postdoctoral researcher in comparative functional genomics in the Liberles Research Group. The position has guaranteed funding for one year and the salary is \$30,000-\$35,000 plus benefits, depending upon previous experience. Applicants with either computational or experimental backgrounds are welcome and those with experience in both are particularly encouraged to apply. For more details on research in the Liberles Research Group, please see www.wyomingbioinformatics.org/LiberlesGroup. To apply, please send a CV, contact information for three references, and 2 .pdf copies of your favorite (significant) papers you have published together with a cover letter to liberles@uwyo.edu.

The application deadline for both positions is April 28, 2006.

David Liberles liberles@uwyo.edu

Other

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ABI3100 Fluorescent Dyes

ABI3130 costs

dear all, I want to use the full potential of the ABI3100 sequencer for AFLP-fragment analysis with the four dyes 6FAM (blue), VIC (green), NED (yellow), PET(red), plus LIZ-size standard. Is there any experience with respect to which dye is preferable for which selective primer? At the ECO-RI side we routinely use three selective bases with "A" as first base (AAC, AAG, ACA, ACC, ACG, ACT, AGC, AGG). What about other selective motifes (e.g. CAG)?

thanks for any suggestions Walter Durka

- **** Register for "Plant Population Biology" http://www.ufz.de/index.php?ene83 *** A conference from 24.05.-27.05.2006 in Halle, Germany *

Dr. Walter Durka Dr. Walter Durka UFZ - Centre for Environmental Research Leipzig-Halle UFZ - Umweltforschungszentrum Leipzig-Halle Dept. Community Ecology Department Biozönoseforschung Theodor-Lieser-Strasse 4 Theodor-Lieser-Str. 4 06120 Halle 06120 Halle Germany Deutschland Tel.: (+49)345/558-5314 Tel.: 0345/558-5314 Fax: (+49)345/558-5329 Fax: 0345/558-5329

INVASIONS: http://www.ufz.de/index.php?en=2773 http://www.ufz.de/index.php?en'73 Home: http://www.ufz.de/index.php?en=798 http://www.ufz.de/index.php?eny8

Our department has recently purchased an ABI 3130xl for DNA sequencing and fragment analysis. We expect that our usage of the instrument will vary, and there may be some weeks where it is only needed for a few runs. Given that, we would like to minimize our costs for consumable reagents, particularly polymer. ABI suggests changing any polymer bottle that has been on the instrument more than a week. Has anyone tried running the instrument with older polymer? If so, how old? Any adverse effects on the data or the instrument? Also, any other tips for saving on reagents during periods of inconsistent use would be greatly appreciated.

Thank you,

Dan Sloan Graduate Student Biology Department University of Virginia

dbs4a@virginia.edu

ABI3130 costs answers

Hi all,

Thank you for the many helpful suggestions for maximizing the efficiency of our ABI 3130 polymer (POP7) use. Below you can see my original question along with

all the replies I received.

Our department has recently purchased an ABI 3130xl for DNA sequencing and fragment analysis. We expect that our usage of the instrument will vary, and there may be some weeks where it is only needed for a few runs. Given that, we would like to minimize our costs for consumable reagents, particularly polymer. ABI suggests changing any polymer bottle that has been on the instrument more than a week. Has anyone tried running the instrument with older polymer? If so, how old? Any adverse effects on the data or the instrument? Also, any other tips for saving on reagents during periods of inconsistent use would be greatly appreciated.

Thank you,

Dan Sloan Graduate Student Biology Department University of Virginia

dbs4a@virginia.edu

We also are running a 3130xl and I've found that the polymer works fine for 10 days. After that, the peaks get wide and more difficult to read. We only fill the polymer bottle up to how much we think we're going to use in 10 days (but that's difficult to determine due to unpredictable use).

Good luck, Caren Goldberg University of Idaho

We have had similar issues concerning the varying usage level of ABI. We have tried the following 2 approaches of which the latter we are now applying. At first we kept the full polymer bottle that was in use in a fridge and had water bottle attached inside the machine. Then replaced the water bottle with polymer bottle when starting run. This however resulted in considerably faster electrophoresis runtime and subsequently the results were bad. Bad meaning that as normal runtime for GS 500LIZ to travel through capillaries would be around 6000 datapoints the runtimes varied from 2500 to 5500 datapoints. This in turn results inconsistent in respect to fragment lengths between runs! The reason probably is that polymer became diluted as water was let to system. Now we are doing the following which seems to work fine. We have the 'full' polymer bottle in fridge and 'empty' polymer bottle attached to machine. 'Empty' polymer bottle always contains a minimum amount of polymer enough to have the tip of tube to be embedded in polymer thus preventing airbubbles to appear in system. Then depending on how many runs needs to be done and whether bubble removes etc. needs to be done we add the appropriate amount of polymer by pipetting with pipette with truncated tip. There is always some 'old' polymer in the bottle but as long as you run few runs per week this polymer should always change and should not result in elongated runtimes. If polymer gets old then you will observe elongated runtimes as but as long as GS500LIZ travels through between 5500-6500 datapoints, the results are very consistent and comparable. I hope this helps. Juha-Pekka Vähä

I'm using Abi310 almost on my own and many times have similar problem. I've checked that you can keep the polymer for a little longer, the longest time i run samples on the same polymer was 2 weeks and the results were still fine. I also keep the buffer for longer, usually about 10 days, but the guy from Applera told me, that it's better to be rather strict with changing buffer. Could you please post me the answers you will get, or post them on evoldir? Maybe there will be some other interesting tips. Ola Gondek Institute of Nature Conservation Polish Academy of Sciences

If you keep the room where the sequencer is palced airconditionned so that the temperature is below 20 degreeC, and if you just need fast short runs for sequencing small fragments (says, 300bp), the polymer remains fairly good for several weeks. But, this is offset by a shortened life of the capillaries (due to old polymer) to our experience.

Good luck.

De-Xing Zhang

POP7 lasts at least 15 days on the machine with no ill effect on band resolution or the capillary (1000+ runs). When our 3730xl and 3130xl have low usage we 1) do not put on a full bottle (recycle the old empty bottles) and 2) we do a blank water run every second or third day to keep the polymer from getting "stale" in the capillaries.

Lawrence C Shimmin University of Texas Houston Health Science Center Human Genetics Center

We have used polymer that was slightly past expiration with good results. However, every situation is different. Nonetheless, I would take ABI's "no more than a week" with a grain of salt.

Alan W. Meerow, Ph.D., Research Geneticist and Systematist USDA-ARS-SHRS, National Germplasm Repository

We're using a 3100 which is nearly the same as your machine. We have left polymer on the machine for more than a week (up to 2 weeks) with no ill effects. The other thing we do to cut costs is extend the length of the

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

Adjacent SNPs

Dear colleges

I'm a PhD student from Madrid. I'm working with SNPs. There are two SNPs in contiguous or adjacent nucleotides, have you ever seen it? I would like to know what is the frequence of SNPs in contiguous nucleotides in the human genome, where could I find this information?

Thank you Carmen

Allelic Diversity

We are trying to model loss of genetic variation due to drift and have a known starting genetic sample of approximately 70% of the population. Can anyone suggest how we estimate the number of alleles missed in our sample such that we can model an appropriate starting allele frequency distribution. I see this as a different problem to unequal sample sizes, since we are not trying to compare between samples but rather predict the true a llelic richness based on our subsample of known proportion (ie. we know h ow many animals were not sampled).

Thanks for your advice.

Deborah Randall

deborah.randall@zoology.oxford.ac.uk rah.randall@zoology.oxford.ac.uk

debo-

AmerGenetAssoc **SpecialEventAwards**

SPECIAL EVENT AWARDS FROM THE AMERI-CAN GENETIC ASSOCIATION

The Council of the American Genetic Association invites applications from members of the Association for support of special events that further the purposes of the Association. The Association expects to make one or two awards of approximately \$10,00015,000. Eligible events include specialized workshops open to Association members in areas of great current interest and short courses in organismal genetics, but any event that would advance the purpose of the Association is eligible for support. We encourage members to think creatively about the types of events they could offer with support from the Association and to propose topic areas that have not been previously covered.

An application for a Special Event Award should include the following items of information: 1. name(s) and title(s) of the individual(s) who will be responsible for organizing the event and overseeing the tion to which an award should be made, including the complete address of the relevant institutional department and the signature of an authorized institutional representative indicating the institutions willingness to administer the award if granted. 3. The title of the event for which an award is requested. 4. A rationale for the event explaining (a) why the event is timely or needed, (b) how the planned event will address the perceived need, and (c) how support from the American Genetic Association will improve the event, e.g., by making it possible or by making it more affordable for graduate students and post-doctoral research associates. The rationale need not be longer than 1 page. 5. A description of the event including: a list of primary participants (e.g., workshop leaders, course instructors, keynote speakers), dates and location of the event, a preliminary schedule for the event, and a plan for how participants will be selected (if participation is limited). The description need not be longer than 2 pages. 6. A budget for the event showing how funds provided by an award from the Society would be used to support event activities. If funds are also being sought from other sources, the budget should show both how funds from the Association will be used and how funds from other

sources will be used. (The sources of other funds need not be identified, but the application should indicate whether the funds are in hand.)

Applications for a Special Event Award should be sent electronically as Word or pdf attachments to the Association office (agajoh@ncifcrf.gov). The Council will review all applications received before May 15, 2006 and will decide on an award at its annual meeting in July 2006.

If you have questions about the award, please contact me (ashley@uic.edu).

Mary Ashley AGA Special Events Committee Chair

Mary V. Ashley Professor Faculty Coordinator, Ecology and Evolution University of Illinois at Chicago 845
 W. Taylor St., M/C 066 Chicago, IL 60607

http://www.uic.edu/depts/bios/ecoevo/ashley.htm Phone: (312) 413-9700 FAX: (312) 996-9462 E-mail: ashley@uic.edu

Australasian Evol Society

Australasian Evolution Society Call for Membership

We are pleased to announce that the Australasian Evolution Society is now in a position to accept memberships for 2006-2007. Membership costs Au\$40 (Au\$20 for students and retirees) and covers the period up to the end of 2007.

We have an exciting set of plans in place for 2006-7, the highlight of which is the 5th AES Conference at University of New South Wales, Sydney. The conference is likely to closely precede or follow the SSE/ASN/SSB meetings which are to be held in Auckland, NZ in June 2007. This is the first time the SSE/ASN/SSB meetings have been held outside north America, and we hope that many people coming to Auckland will include a trip to the AES meetings in Sydney.

I would encourage you to renew your membership or to join the society. Do do so, please fill out the form at http://www.eriophora.com.au/AES/About/join_online.html and pay via one of the three options presented on that form.

Please also consider providing a link to the society's webpage (www.evolutionau.org) from your own page or any other relavant sites that you manage.

School of Biological, Earth and Environmental Sciences

Collagenase Extractions

Dear EvolDir,

I wish to try out the method described in Eguchi & Eguchi (High yield DNA extraction from the snake cast-off skin or bird feathers using collagenase; Biotechnology Letters 22: 1097-1100, 2000). There is a pre-DNA extraction step where collagenase is used to disperse cells, followed by the typical lysis buffer and protease K digestion step.

Unfortunately the original authors did not specify a catalog number for a collagenase they used, and cannot be contacted. I wish to hear from anyone who has either used this method or has used collagenase for cell dispersion (in vitro, using preserved tissues). I have obtained some collagenase from the same company (although they have a great number of varieties, and mine is quite possibly different from that of the original study), but there are no instructions for its use. I read somewhere that calcium might be a cofactor needed for some collagenases to work, but does anyone have a rough protocol for a buffer to use with it or any suggestions? As the cell solution would then be used for DNA extraction, are there buffers or reagents to avoid? Does anyone know the best way of diluting the powdered form of collagenase (e.g. is ddH20 enough or should it be diluted in a buffer with Ca ions or some other buffer)?

Thank you for your assistance! Kind regards, Gabriela Ibarguchi

Gabriela Ibarguchi Department of Biology, Queen's University Kingston, Ontario, Canada, K7L 3N6 ibarguch@biology.queensu.ca or gibarguchi@biology.ca tel (613) 533-6000 ext. 75539, fax (613) 533-6617 http://www.ibarguchi.ca/>http://www.ibarguchi.ca/>

ibarguch@biology.queensu.ca guch@biology.queensu.ca ibar-

Commercial micros

Dear Colleagues,

We are working on the genetics of invasion of the horse chest nut leaf-mining moth Cameraria ohridella. We would like to get a commercial company to develop microsatellites for us. If anyone knows of a commercial company with a reliable Microsatellite Development Service please let me know. Thank you.

Carlos

– Dr. Carlos LOPEZ-VAAMONDE INRA-Orleans Forestry Zoology Unit Ardon- BP 20619 F- 45166 OLIVET FRANCE Tel: + 33 238417861 Fax: + 33 238417879 carlos.lopez-vaamonde@orleans.inra.fr

${\bf DNAB arcode Data Analysis Initiative}\\ {\bf Participation Call}$

Call for Participation

Data Analysis Challenges Arising from the DNA Barcode Initiative

The Challenge: The Data Analysis Working Group (DAWG) of the Consortium for the Barcode of Life (CBOL) has developed interdisciplinary research challenge problems in statistics and computer science arising from DNA barcoding, a method proposed as a tool for differentiating species. Students, postdocs, and researchers from all over the world are challenged to develop new approaches to these problems. Compelling solutions to these challenges will require collaboration among taxonomists, population geneticists, and evolutionary and systematic biologists, so DAWG encourages the formation of multidisciplinary teams.

Presenting Preliminary Ideas at a Workshop in Paris: Preliminary ideas for approaches to these problems will be discussed at a workshop at the National Museum of Natural History in Paris on 6-8 July 2006 (see http://dimacs.rutgers.edu/Workshops/DNABarcode/ (http://dimacs.rutgers.edu/-Workshops/DNABarcode/>
). Participation in this workshop will be limited to approximately 40 presenters

of preliminary results and attendees who can offer useful feedback to the presenters. Space will therefore be limited and all those wishing to participate in the workshop should register at http://dimacs.rutgers.edu/Workshops/DNABarcode/registnew.html no later than 29 June 2006. However, you are urged to register early as we will close registration when all spaces are filled.

Travel awards for a limited number of Europeans who would like to give presentions at this workshop will be available through funding from the Conservation Genetics Programme of the European Science Foundation. Travel awards for US presenters will also be available, pending funding agency approval. Travel support will focus primarily on increasing the participation of students, postdocs and junior faculty.

Presenting More Advanced Results at a Conference in Southeast Asia: The preliminary workshop will be followed by an international conference in southeast Asia in February 2007, during which the most promising approaches to these challenge problems will be presented. Travel awards will also be available (pending funding agency approval).

For the full Call for Participation, including the statement of the research challenges, see: http://dimacs.rutgers.edu/Workshops/-BarcodeResearchChallenges/.

For instructions on how to submit an abstract for the Paris workshop, see http://dimacs.rutgers.edu/-Workshops/DNABarcode/abstractsubmissionform.ht ml.

To apply for travel funds to give a presentation at the Paris workshop, see http://dimacs.rutgers.edu/-Workshops/DNABarcode/travelsupport.html

For information about the DNA Barcode Initiative, see: http://dimacs.rutgers.edu/Workshops/-DNAInitiative/.

Important dates:

Deadline for submission of abstracts: 2 June 2006

Deadline for submission of requests for travel support: 2 June 2006

Deadline for registration: 29 June 2006

Announcement of final agenda of presenters, awards of travel support: as early as possible after 2 June 2006

"Schindel, David" <schindeld@si.edu>

Dating supertrees

Hi there,

I was wondering if anyone came up with a method to put branch lengths on supertrees.

cheers,

Jason jas2339@yahoo.com jas2339@yahoo.com

Dibrachys wasp samples

Dear EvolDir users,

I am a PhD student at Hamburg University (Zoological Museum) and I am working on the biology and ecology of parasitoid wasps (Hymenoptera: Pteromalidae). For taxonomic and systematic studies I am looking for EtOH material of the species in the genus Dibrachys. Maybe there is somebody out there, who is collecting these small wasps or maybe even gets them as a sort of "waste product" in studies on the host species. I am also interested in (undetermined) material from some Diptera host species (not necessarily in EtOH) Earwig parasitoids Tachinidae: Triarthria spp. and Ocytata pallipes Bird blowflies: Calliphoridae: Protocalliphora spp.

If you can provide some material, please contact me. Thanks a lot and best regards

Ralph

Dipl.-Biol. Ralph Peters Zoologisches Museum Universität Hamburg Martin-Luther-King-Platz 3 20146 Hamburg Germany Phone 0049 40 428385631 0049 40 70291847 (private) Email: Ralph_Peters@Hotmail.com ralph_peters@hotmail.com

We have received a large number of requests from people who want DNA instead of live flies from the stock center. Finally we have DNA for most of the sequenced species. Would you please post the following announcement on the evoldir? Thanks, Teri Markow

The Tucson Drosophila Stock Center is now offering highly purified genomic DNA from the sequenced species of Drosophila. Currently DNA from the following 11 species (strains) are available, hopefully with more to follow. The cost is 20 μ g for \$50.00.

http://stockcenter.arl.arizona.edu/ Stock Number 0000-1005.01 D. ananassae – Matsuda (AABBg1) GENOME/BAC LIBRARY strain

Stock Number 0000-1004.01 D. erecta – GENOME/BAC LIBRARY strain

Stock Number 0000-1003.01 D. mojavensis – (Reed) CI 12 IB-4 g8 GENOME/BAC LIBRARY strain

Stock Number 0000-1008.01 D. persimilis – (Machado)MSH3 GENOME/BAC LIBRARY strain

Stock Number 0000-1006.01 D. pseudoobscura – line MV2-25 Baylor sequencing strain GENOME strain

Stock Number 0000-1001.01 D. sechellia – (Jones) Robertson 3C GENOME/BAC LIBRARY strain

Stock Number 0000-1000.01 D. simulans – (Begun) Dsim\w[501] GENOME/BAC LIBRARY strain

Stock Number 0000-1002.01 D. virilis – (McAllister) V46 Dvir\b[1]; tb[1] gp-L2[1]; cd[1]; pe[1] GENOME/BAC LIBRARY strain

Stock Number 0000-1007.01 D. willistoni – (Powell) Gd-H4-1 GENOME/BAC LIBRARY strain

Stock Number 0000-1009.01 D. yakuba – (Begun) Tai18E2 GENOME/BAC LIBRARY strain

Therese Ann Markow Regents' Professor Department of Ecology and Evolutionary Biology BSW 310 University of Arizona Tucson, AZ 85721

Office: 520 621 3323 Lab: 520 626 2772 FAX: 520 626 3522

tmarkow@arl.arizona.edu http://-cis.arl.arizona.edu/markow_lab/index.htm tmarkow@public.arl.arizona.edu

Dye Terminator dilutions

Sequenase Cy5 Dye Terminator

My lab is interested in using Sequenase Cy5 Dye Terminator made by GE Healthcare (formerly Amersham). I am looking for any information with regards to how much it can be diluted before it starts to loses effectiveness. Any other advice using the product is also welcome. My lab is about to start a massive sequencing project are we are looking to do it cheaper than Big Dye.

Thank you in advance for your help,

Whit Farnum Curatorial Assistant Museum of Comparative Zoology Harvard University 26 Oxford St Cambridge, MA 02138 617-495-8971

wfarnum@oeb.harvard.edu

Evol2006 Events AMNH

A day of special activities at the American Museum of Natural History in New York City has been arranged for registered participants of "Evolution 2006." These activities will be on June 22, 2006 and include free admission to the Museum, the Darwin exhibition (http://www.amnh.org/exhibitions/darwin/), and Sean Carroll's lecture, "Endless Forms So Beautiful: The New Science of Evo Devo."

While there is no charge for these activities, registration is necessary. Please go to http://life.bio.sunysb.edu/ee/sse2006/amnh_event.html for more information and the on-line registration form.

Michael A. Bell, Co-organizer Evolution 2006 mabell@life.bio.sunysb.edu

Fluorescent mini probes

Hi, can anyone recommend a kit for fluorescently tagging minisatellite probes for routine size screening (i.e. not mapping studies)? I would rather avoid having to use radioactivity. I will of course post a compilation of replies. Thanks in advance, Bill

Dr Bill Hutchinson Genome Analysis Suite Manager Molecular Ecology & Fisheries Genetics, Biological Sci-

ences, Hull University, HULL HU6 7RX United Kingdom

Tel:- 01482 465804 office 01482 465536 lab Fax:- 01482 465458 http://www.hull.ac.uk/biosci/staff/hutchinson.html http://www.hull.ac.uk/-GAS/ http://www.microchecker.hull.ac.uk/w.f.hutchinson@hull.ac.uk

Freezing ABI sequencer polymer

Dear All,

I would like to have you advice please.

We recently ordered some polymer from ABI for ABI sequencer. The polymer arrived frozen yesterday. I remembered that polymer cannot be frozen or it will affect the sequencing quality. But the ABI reps said that it won't and they usually do like this.

Has anyone got similar experience before? Or known if freezing will have a bad effect on the separation quality?

Thank you very much.

Sincerely, De-Xing Zhang Institute of Zoology Chinese Academy of Sciences

dxzhang@ioz.ac.cn

GeoDis problems

I am working on my thesis using GeoDis 2.4 looking at phylogeographic gene flow of Horned Lizards. The problem is that the program is having issues with my input files. Here is an example-

Clade 1-1 2 II III 1 0 1 1 1 1

Error message reads: the number of haplotypes for location X can not be one-you need genetic variation for this analysis. I do believe that II and III of line 3 represents 2 haplotypes! I've tried entering 2 i.e. 2 haplotypes at location 1-same thing (2 was entered for line 7) Also just entering 1 under location 1 just to see-same thing Another example

Clade 3-3 2 2-5 2-2 1 0 2 2 5 1 0 0 1

The program error is the same-it flags location 2 as be-

ing problematic and not 5. The same thing happens in another file and the clade is flanked before and after with clades that have the exact same scenario (clade 1-1 o.k 1-2 not o.k 1-3 fine). Why it chose the middle one and was happy with the rest-I don't know. If you have any insight into this, I would welcome your help.

Thanks, Austin austin_burt@juno.com austin_burt@juno.com

Heterozygosity

Hi all,

Does anyone help me to clear the difference between concepts of heterozygote excess in HWE and heterozygosity excess in BOTTLENECK tests?

I found in my results that most populations shown heterozygosity excess in BOTTLENECK test, but dificit of heterozygotes in HWE test.

I would really appreciate your help.

Sincerely yours

Kang Ming m.kang@uq.edu.au

Kang Ming <m.kang@uq.edu.au>

Heterozygosity Excess Answers

Hi EvolDir members, thank you very much for your answers. Since several colleagues have the same problem as me. Below I attached all of the reply on my question.

My original message: Hi all, Does anyone help me to clear the difference between concepts of heterozygote excess in HWE and heterozygosity excess in BOTTLE-NECK tests? I found in my results that most populations shown heterozygosity excess in BOTTLENECK test, but dificit of heterozygotes in HWE test. I would really appreciate your help. Sincerely yours

Kang Ming

Hi,

In HWE tests, heterozygosity excess/deficit refer to the excess/deficit of the observed heterozygosity (the proportion of heterozygotes in a population of a diploid organism) relative to the expected heterezygosity under HW, i.e. the "gene diversity" (He= 1-sum[allele freq^2]). In Bottelneck tests, heterozygosity excess/deficit refer to the excess/deficit of gene diversity (He) relative to a model predicting He from the number of alleles observed in a sample of a demographically stable population at drift-mutation equilibrium. The terminology "heterozygosity excess" for Bottleneck tests is indeed confusing because it is unrelated to the proportion of heterozygote individuals. The origin of the confusion stems from the widespread but unfortunate use of "heterozygosity" to denote He in population genetics litterature, which is meaningful only for diploid populations at HWE.

Best regards,

Olivier Hardy

Dear Kang,

heterozygote excess and heterozygosity excess are different and independent issues. The former is simply the excess of heterozygote individuals with respect to the Hardy-Weinberg equilibrium. The latter is a little more complicated concept: A bottlenecked population will transitorily show an excess of heterozygosity over that expected under the mutation-drift equilibrium. The test relies on the assumption of allele neutrality and mutation-drift equilibrium. It is based on the principle that near the mutation-drift equilibrium the expected heterozygosity equals the measured Hardy-Weinberg equilibrium heterozygosity in nonbottlenecked populations. Instead, if a population has been subjected to a recent bottleneck, the mutationdrift equilibrium is temporarily disrupted and the expected heterozygosity will be significantly greater than the HWE-heterozygosity calculated from the number of alleles sampled. The test allows the detection of the heterozygosity excess due to the faster loss of low frequency alleles and thus determines if a population has been recently bottlenecked. In fact, the loss of low frequency alleles does not account for an equal loss in heterozygosity. I used the test in MALTAGLIATI F. 2002. Genetic monitoring of brackish-water populations: the Mediterranean toothcarp Aphanius fasciatus (Cyprinodontidae) as a model. Marine Ecology Progress Series, 235: 257-262. You can download a pdf from my homepage.

ciao ferruccio

Ferruccio Maltagliati Ph.D.

Hi,

Very easy:

HWE tests for departure from the distribution of genotype frequencies expected under random mating, using the actual gene frequencies. Heterozygote deficits indicate some degree of inbreeding, due to selfing or, e.g., a Wahlund effect (structured population). Heterozygote excess are rarer, and usually involve different gene frequencies between males and females gametes. Of course selection at particular loci can also be involved, but then there are large heterogeneities of patterns among loci.

BOTTLENECK tests for past demographic bottleneck. When a population goes through a bottleneck, random diff is stronger so that gene frequencies are rapidly changed. Rare alleles are lost first, whereas the loss of heterozygotes (due to the loss of polymorphism) is occurring at a slower pace (but with no departure from HWE if indeed random mating is occurring). There are theoretical expectations with regards to the frequency of heterozygotes and number of alleles at mutation drift equilibrium in a population of constant size. So one way to suggest a recent bottleneck is to compare the level of polymorphism (as shown by heterozygote frequency) with the number of alleles. If there are too many heterozygotes compared to the number of alleles (heterozygote excess) this means you have too few rare alleles, and then you can suspect a recent bottleneck. If on the contrary there are few heterozygotes compared to the number of alleles (so too many rare alleles), you can suspect a recent expansion of the population.

In your case it looks like your population went through a recent bottleneck, and there is departure from random mating (selfing or mating preferentially with neighbours for instance).

I hope this helps Best, Isabelle

Dear Kang, Under Hardy-Weinberg assumption (random mating) you expect H=2pq, and the Fis is measuring the difference between this expected He (gene diversity, or Hardy Weinberg heterozygosity estimated on the basis of

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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

ID in Canada

Dear Colleagues,

I am distressed to bring to your attention an alarming decision made by the Canadian Social Sciences and Humanities Research Council (SSHRC) concerning the relative scientific merit of evolutionary biology vs. intelligent design. Dr. Brian Alters, Director of the Evolution Education Research Centre at McGill University recently submitted a grant to the council entitled Detrimental effects of popularizing anti-evolutions intelligent design theory on Canadian students, teachers, parents, administrators, and policymakers. As the title implies, this proposal aimed to investigate how the increasing popularity and expose of intelligent design in the United States is affecting acceptance of evolutionary biology in Canada. Dr. Alters is well respected and has a distinguished record in this area of study, including being an expert witness at the Kitzmiller v. Dover Area School Board court battle over I.D. Dr. Alters grant proposal ended up being rejected by the review committee. The committees comments are presented below in their entirety:

The committee found that the candidates were qualified. However, it judged the proposal did not adequately substantiate the premise that the popularization of Intelligent Design Theory had detrimental effects on Canadian students, teachers, parents and policy makers. Nor did the committee consider that there was adequate justification for the assumption in the proposal that the theory of Evolution, and not Intelligent Design theory, was correct. It was not convinced, therefore, that research based on these assumptions would yield objective results. In addition, the committee found that the research plans were insufficiently elaborated to allow for an informed evaluation of their merit. In view of its reservations the committee recommended that no award be made.

I dont believe that I am appropriately qualified to evaluate Dr. Alters proposal, but I believe we can all evaluate the comments made by the SSHRC evaluation committee. The statement, Nor did the committee consider that there was adequate justification for the assumption in the proposal that the theory of Evolution, and not Intelligent Design theory, was correct should set of serious alarm bells. SSHRC is one of three major granting agencies in Canada. There is clearly a problem when a major federal granting agency demands that scientists prove the validity of evolution as part of their proposals.

I have attached the summary statement from Dr. Alters proposal below (with permission). If you are so inspired you can contact the president of SSHRC (stan.shapson@sshrc.ca).

Dr. Alters has asked that he be ccd on emails

(b.alters@mcgill.ca) when messages are sent on his behalf to SSHRC.

Sincerely, David Guttman Associate Professor Canada Research Chair in Comparative Genomics Director, Univ Toronto Centre for the Analysis of Genome Evolution & Function Department of Botany University of Toronto

Detrimental Effects of Popularizing Anti-Evolutions "Intelligent Design Theory" on Canadian Students, Teachers, Parents, Administrators, and Policymakers

1) Summary of Proposed Research Never in recent decades has the cornerstone of modern biology education - evolution - been so challenged and misrepresented by an idea masquerading as science, and never has that pseudoscience obtained such ubiquitous coverage and resultant popularity. The new form of creationism is termed "Intelligent Design" and it seriously threatens to affect evolution education in science classrooms throughout North America. Intelligent Design has been reported and discussed as never before in every major Canadian and U.S. television, print, and radio outlet. Proponents of Intelligent Design have facilitated public events throughout Canada and U.S. including speaking engagements at educational institutions such as major universities. At the time of this writing (October, 2005) a high-profile U.S. Federal Court case is examining the constitutionality (church/state separation) of teaching Intelligent Design in public school science classrooms, which was reported in virtually every major media outlet worldwide. The President of the United States publicly supported teaching Intelligent Design in schools. Despite this far-reaching popularization of Intelligent Design, and the political and religious movements to legitimize it as a science to be taught in schools, every leading scientific organization in North America has resoundingly rejected Intelligent Design as science and strongly recommends that it not be taught as science in science classrooms. Moreover, every leading science education association has come out against teaching Intelligent Design in science courses. Unfortunately, the result of such consistent and massive media

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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

InsectDNA PropyleneGlycol

This paper recent paper on the use of 100% propylene glycol for preservation of spiders for later DNA extraction is exciting because propylene glycol is non-toxic (it's a food additive) and thus can be safely mailed and carried on planes etc. It effectively dehydrates the tissues.

The effects of preservatives and temperatures on arachnid DNA Author(s): Vink CJ, Thomas SM, Paquin P, Hayashi CY, Hedin M Source: INVERTEBRATE SYSTEMATICS 19 (2): 99-104 2005

I'd like to know if anyone has additional experience with this method of preservation. The authors used spiders so one might assume the method would work for all arthropods - has anyone used it with insects?

I wonder specifically if larger bodied insects might not preserve as well in PG as in ethanol if the ethanol penetrates the tissues to dehydrate them faster than PG.

I'd also like to know if propylene glycol is a viable longterm alternative to high-grade ethanol for specimens stored at -80C.

Finally, I'm curious if there are any issues with DNA extraction - does the PG need to be thoroughly removed from the specimen for successful extraction? and if so, how is this done?

I'll collect replies off-list and summarize them for a later posting.

Thanks!

-Derek Sikes

Derek S. Sikes, Assistant Professor Division of Zoology Department of Biological Sciences University of Calgary 2500 University Drive NW Calgary, Alberta, Canada, T2N 1N4

dsikes@ucalgary.ca http://homepages.ucalgary.ca/~ dsikes/sikes_lab.htm phone: 403-210-9819 FAX:
403-289-9311

"Remember that Truth alone is the matter you are in Search after; and if you have been mistaken, let no Vanity reduce you to persist in your mistake." Henry Baker, London, 1785

Entomological Society of Alberta: http://www.biology.ualberta.ca/courses.hp/esa/esa.htm dsikes@ucalgary.ca dsikes@ucalgary.ca

Micro stutter answers

Thank you to everyone who replied! I was able to reduce the ambiguity in identifiying the 'true' alleles by implementing suggestions for PCR optimization. In particular, reducing the number of cycles and the time at each step, resulted in PCR products in which the stutter was reduced. Previously, each allele at a heterozygous individual, had exhibited several peaks of very similar size. After reducing the number of cycles and the time at each step, each allele had one larger peak with several smaller stutter peaks in front of it.

There were numerous requests to post the replies so here they are:

Here is a repeat of a post Brian made some years ago compiling responses to a similar question. Hope it helps. RESPONSES TO MICROSAT STUTTERS Below I have grouped the responses so far received to reduce stutters, thank you to everyone who has responded! The most common response was to reduce the number of cycles. Followed by reduce the MgCl concentration. Also a mix of PCR cycle options with a high initial annealing temperature either through a 'Touch down' process or a few said plain heating your PCR before you put the polymerase in. 'Two-step' PCR was mentioned more than just heating your reaction without tag. Also as popular was to reduce the extension time at the end. About 3-4 people said specifically to try hot start taq. After the combined PCR suggestions commonly stated was to just redesign reverse primers according to the 'Pig-tail' method (Brownstein et al. 1996, Biotechniques 20, 1004-1010). Since then I have reduced the number of cycles, then also shortened the extension time. Then with the shortened number of cycles and extension time varied MgCl from 1.5 to 2.5 because the person who uses them successfully now says not to go out of this range. I have also kept the 2.5 MgCl as original, but added BSA. I am currently looking over the results, but wanted to pass along the feedback I have been getting. Again THANK YOU very much to all who responded. PCR REACTION CHANGES. Varying Mg++ levels, maybe try a gradient from 1-4mM, lower MgCl helps to reduce stutters. . Use hot start Taq . Change concentration of your primers. We use a starting concentration of only 0.5uM of our labeled primer and then the reverse (unlabeled) is 2uM. My labmates have found that better bands sometimes come with changing the labeled primer to either 0.3uM or 0.7uM. We were told that it's good to have the reverse primer in higher concentration. . Try out t4 polymerase PCR CYCLE CHANGES. Reduce the number of cycles down as low as possible, 40 cycles is excessive and try 25 cycles o "increasing the number of cycles may increase nonspecific background and may lead to artifacts" (source: Qiagen multiplex pcr handbook, 2002, p.33). Use a very stringent annealing temp Set your final extension to 70 degrees or 65 degrees for 45 mins (see Profiler Plus manual for Profiler Plus kit used on humans). I had some loci which were tricky to score until our lab stumbled across the reaction conditions used for Profiler Plus kit. . 'Touch down' PCR program o start Tm at 65C or 67C and the annealing temp reduced 2C per cycle for the next cycles up to TmX, then the remaining cycles at a 58C annealing temperature o start at 60C and within the first 10 cvcles down the Ta to 50C, then keep 50C for the next 30 cycles o start at 60C and within the first 10 cycles down the Ta to 50C, then keep 50C for the next 30 cycles. "short PCR" o cycles of 15s at 94, 15s at annealing temperature and 45s at 72 and lower the number of cycles. I've heard people sometimes run only 5s at annealing temperature. Hotstart PCR with regular promega taq by performing a first denaturing step with DNA, primers and water and then lower the temperature for about 85C to add the master mix containing tag and all the other reagents. I've performed 12.5 ul reactions, primer concentrations ranging from as low as 0.03 to 1.2uM in multiplexes. Annealing temperatures were 58C for most primer sets and 60C. I also recommend the Quiagen multiplex PCR mix, that provides a tag appropriate for hotstart PCR. No 72C extension step in the cycle (I mean that I have the annealing step followed by the denaturing step and then annealing again, with the Taq extending during the ramp, for microsats is more then necessary), and only 2 minutes of final extension step. . Biotechniques suggested "abbreviated cycling times" for PCR steps. For instance, denature for only 2 seconds, anneal for 2 seconds, extend for 8 seconds. I've often used this "2/2/8" protocol (or some variant, e.g. 3/3/12) to clean up microsatellite stutter. Sometimes it fails miserably, but in about 50% of the cases it helps dramatically. . Try heating your PCR without tag in it for 15min @95C, then adding tag . Two-step PCR o 30sec at 94C and 80 sec at 50C. Also here is the reference that uses the suggested cycle Here is the reference:

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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

Micros Development answers

Dear Colleagues, Thank you to everyone who replied. I received 12 replies from researchers and 2 from commercial companies (East Malling and Ecogenics). In summary, 8 commercial companies were recommended by colleagues. GIS, Ecogenics, Newbiotechnique, SREL, Genterprise and Bioprofiles. Both GIS and Ecogenics were the most recommended commercial companies. There were several requests to post the replies so please see below my original request and all the answers I received in order of arrival. I have omitted the two commercial offers I received.

Best wishes, Carlos

Dear Colleagues, > >We are working on the genetics of invasion of the horse chest nut >leaf-mining moth Cameraria ohridella. >We would like to get a commercial company to develop microsatellites for >us. If anyone knows of a commercial company with a reliable >Microsatellite Development Service please let me know. Thank you. > >Carlos

Dear Carlos,

weve got very good results with www.ecogenics.ch . Cheers and good luck, Nora

Dipl. Biol. Nora Brede Dept. Ecology & Evolution Institute for Ecology, Evolution & Diversity

Hi Carlos,

Sounds like an interesting project.

We used a Swiss company called Ecogenics to develop Maculinea microsats, and we were very happy with the result (and the relative price).

http://www.ecogenics.ch/ Cheers David Nash David Nash Work: Department of Population Biology, Institute of Biology University of Copenhagen, Universitetsparken 15 DK-2100 Copenhagen Ø, Denmark

Hi Carlos,

Try Genetic Identification Services in California. I found them to be very efficient. The microsatellites they developed for us were highly polymorphic. They

are quite expensive, but worth every cent, with good support afterwards.

Check out their website: http://www.genetic-id-services.com/ Good luck, Liz ——

Dear Carlos

I suggest Ecogenics (www.ecogenics.ch) - they have a lot of experience and good service.

Cheers Alex ETH Zurich Alex Widmer Plant Ecological Genetics Institute of Integrative Biology Universitätstrasse 16 8092 Zurich, Switzerland ——

Dear Carlos. If you want try with this spanish company: Newbiotechique - NBT (Web Page: http://www.newbiotechnic.com/es/)

Good luck. Joaquin. Joaquin Munoz Garcia (PhD. Student) Laboratory of Molecular Ecology. Estacion Biologica Donana (CSIC). Pabellon del Peru. Avda. Maria Luisa, s/n. Apartado de Correos 1056. 41013-Sevilla. Spain.

These folks provided outstanding service and excellent results.

http://www.genetic-id-services.com/

Michael Sorenson Associate Professor Department of Biology Boston University 5 Cummington St. Boston, MA 02215

Hi Carlos, Our lab is just starting a project with this company: http://www.genetic-id-services.com/library.htm So far, they seem very good. they are easy to contact to get questions answered and they "guarantee" enrichment of an msat library of at least one motif... they have more about this on their website. If not, then the customer does not have to pay anything.

good luck! deb ——

Check out the msat development link on the left side of the screen. They're not as fast as other places, but they're good and the cheapest option out there.

http://www.uga.edu/srel/DNA_Lab/index.htm Julie

Dear Carlos.

I was very pleased with the services I received from Genetic Identification Systems (GIS) gisemail@genetic-id-services.com They were very efficient, provided me with both excellent locus identification and primer design, and are have great tech support, including clearly documented protocols and fast response to email queries. I definitely recommend them.

-Mark

Mark Fishbein Assistant Professor Portland State University Dept. of Biology P.O. Box 751 Portland, OR 97207

Hi Carlos.

I made good experiences with Genterprise company located in Mainz/Germany. For my research project on Chironomus midges they developed microsatellite markers fast and really cheap compared to other companys. As the homepage www.genterprise.de is in German, you may better directly contact Prof. Tom Hankeln hankeln@uni-mainz.de . Bye,

Carsten Nowak Institute of Ecology, Evolution and Diversity Division of Biosciences J.W.Goethe-University 60054 Frankfurt am Main

Hi Carlos,

We have very successfully used a company in the US. Its approx 10,000 US \$ for a species (3 motives incl sequencing of 40 msats containing

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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

Microsatellite stutter

I am looking for suggestions on how to reduce stutter at dinucleotide microsatellite loci.

Thank you, Katie

katieshul@gmail.com

k s <katieshul@gmail.com>

NatlEvolSynthesisCenter WorkingGroups

Call for Proposals? NESCent Working Groups and Catalysis Groups

National Evolutionary Synthesis Center (NESCent) is now accepting proposals for Working Groups and Catalysis Groups. The deadline is June 15, 2006. For more information, please see our website at http://www.nescent.org/proposals/. Karen Henry Assistant Director of Research Administration National Evolutionary Synthesis Center 2024 W. Main Street, Suite A200 Durham, NC 27705

email: khenry@duke.edu telephone: 919-668-4574 fax: 919-668-9192

Karen Henry khenry@duke.edu

Newick transforms

Dear Evoldir members,

Does any of you know if there is a function in R (or other software) to transform a file in Newick format to a data set that can be used the Phylogenetic Independence package of Abouheif (1999)? Any suggestions as to how this could be done would be appreciated.

Thank you, -

Carlos Daniel Cadena O. Department of Biology University of Missouri-St.Louis One University Boulevard St. Louis, MO 63121

Phone: (314) 516-6200 Fax: (314) 516-6233 cdc35b@umsl.edu http://www.umsl.edu/~cdc35b Carlos Daniel Cadena <cdc35b@studentmail.umsl.edu>

PAUP memory issue

Hello EVOLDIR members, I am running a bootstrap with PAUP on a MAC, but the machine keeps running out of memory and needs to be prompted to continue after one replicate or so. The bootstrap is very straightforward-no branch bindings, constraints or anything fancy-just 100 replicates/10 random additions with unweighted characters basically. Max trees are set to automatically increase by 100. The OSX is the issue, I just don't know how to allocate more memory to keep the thing up and running. Any ideas? Austin

austin_burt@juno.com

PAUP on MacIntosh Computers

Dear EvolDir members,

I have just purchased a new macintosh computer. One of the objectives was to run PAUP on it. Unfortunately, I realize now that it is not possible to run Paup, because the new Intel-based Mac's do not support the 'classic' environment (OS 9) necessary to run the current version of Paup. In the Paup website, they say that the next version will include a command-line version for Mac OSX, but this announcement was made in 2002 already. Since Macintosh has announced that all their computers will have these Intel-processors from the end of this year onward, very soon no new computer will be able to run Paup.

I would like to ask if there is some alternative, whether to hope that a new version will be made available that works with OS X, or some workaround maybe compiling the source code to work on OS X. Any suggestion would be helpful.

Thank you for your help!

Gonalo Espregueira Themudo PhD student 1. Naturalis - National Museum of Natural History Leiden, The Netherlands e-mail: themudo@nnm.nl

2. CIBIO - Centro de Investigaão em Biodiversidade e Recursos Genéticos Vairão, Portugal e-mail: themudo@mail.icav.up.pt web: http://cibio.up.pt/main.php?content=members&id=47&type=graduate

themudo@mail.icav.up.pt

PAUP on Macs answers

Dear All,

Thank you very much for all your replies. I had a mixed-feeling from the responses. Some were rather pessimistic about the future use of PAUP with MAC's, while others suggested some interesting workarounds.

Some good news is that David Swofford, has announced a new version of PAUP for this year as mentioned in the PAUP help group(http://lists.scs.fsu.edu/pipermail/pauphelp/2006-March/000220.html) This version is

supposed to run natively in Mac OSx. If you are too anxious to wait for the next version, there are two other options: 1. You can use the command-line version for UNIX http://paup.csit.fsu.edu/versions.html in MAC OSX even if you-re using the new Intel processors, by accessing the UNIX terminal in Mac OSX (don't ask me how to do it, though!) 2. You can use an emulator called SheepShaver (<a href="http://www.gibix.net/dokuwiki/en:projects:sheepshaver)that can run OS9 applications in OSx. This seems like a good option, but it might slow down your machine. I'll have to try this one.

If you are a windows user, there is also some good news: Of course you can run either the command-line version for either Windows or Dos. If you have the latter version, you can also use the PAUP-up GUI (http://www.agro-montpellier.fr/sppe/Recherche/JFM/PaupUp/main.htm) that will allow you to access most of the same menus as in the Mac version.

Of course, there are other programs that can replace PAUP, like Phylip, PhyML, etc.

Some people also mentioned Boot-camp (http://www.apple.com/macosx/bootcamp/). This is a program that allows you to boot your Intel- based Mac in Windows XP, but this would only allow to run Windows programs in Mac computers, which is exciting by itself, but another issue altogether.

I hope this helps other people too! I will try some of these alternatives myself in the near-future.

Regards, Gonalo Themudo

—Original Message— From: evoldir@evol.biology.mcmaster.ca [mailto:evoldir@evol.biology.mcmaster.ca] Sent: quinta-feira, 13 de Abril de 2006 7:12 To: themudo@mail.icav.up.pt Subject: Other: PAUP on MacIntosh Computers

Dear EvolDir members,

I have just purchased a new macintosh computer. One of the objectives was to run PAUP on it. Unfortunately, I realize now that it is not possible to run Paup, because the new Intel-based Mac's do not support the 'classic' environment (OS 9) necessary to run the current version of Paup. In the Paup website, they say that the next version will include a command-line version for Mac OSX, but this announcement was made in 2002 already. Since Macintosh has announced that all their computers will have these Intel-processors from the end of this year onward, very soon no new computer will be able to run Paup.

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Thank you for your help!

Gonalo Espregueira Themudo PhD student 1. Naturalis - National Museum of Natural History Leiden, The Netherlands e-mail: themudo@nnm.nl

2. CIBIO - Centro de Investigaão em Biodiversidade e Recursos Genéticos Vairão, Portugal e-mail: themudo@mail.icav.up.pt web: http://cibio.up.pt/main.php?content=members&id=47&type=graduate

the mudo@mail.icav.up.pt

gethemudo@hotmail.com

Population tree help

Dear members,

I have a data of mtDNA sequences from 9 populations of the same species, each population differs in size and the minimum population size is 20. I would like to draw a nj tree of the population data with bootstraping. I can draw individual tree using PAUP but i could not configure how to draw population tree by PAUP. I defined 9 taxa after the sequence data of all individuals in the input file, but it didnot take this into consideration.

When i use the genetic distance matrix (estimated using Arlequin) in PHYLIP, I can have the population tree but this time with no bootstrapping. When I enter the sequence data into Phylip, it again constructs the individuals tree, and there is no way to define the populations (that I know of).

I would really appreciate your help. I am looking forward to hear from you soon.

Sincerly, Cigdem Gokcek

cigdem_gokcek@yahoo.com

SNPsoftware answers

Question

I'm looking for software you can use to download specific SNPs from GENBANK together with specified flanking sequences and information about other SNPs in that flanking sequence. I know the software SN-Phunter (http://www.hsph.harvard.edu/ppg/software) does precisely this, but I am looking for a program in which you can do batch queries for specific SNPs using a file that lists SNPs according to their rs numbers. The batch queries of SNPhunter only involve genes, as far as I know, and my SNPs are not associated with genes.

55

Answer

I did not get any replies but found something that works for me on the net @ http://snpper.chip.org/ You can specify the snps that you want in a batch list, and then get the SNPs with specified lengths of flanking fragments and other snps in the flanking parts in an output file.

You have to register to use the webpage.

Apparently SNPhunter can also handle SNP batch queries with rs numbers, haven't tried it though

Hope this helps

Carina Schlebusch

Carina.Schlebusch@nhls.ac.za

SSE Evolution Poetry contest

Announcing the second annual SSE EVOLUTION POETRY CONTEST

YOUR CHANCE FOR GLORY Any and all poems concerning the theme of evolution are solicited; serious, funny, tragic, elegant, nonsensical, in any style including tanka, limericks, haiku, free verse, couplets, and epic poems

Winner(s) to be announced and poem(s) read at the Annual Meeting Awards Ceremony in Stony Brook Prizes remain to be determined, but assuredly will be glorious and highly desirable

Judging will be by a small, elite, biased and arbitrary team of crack evolutionary poetry experts RULES: SSE Members and non-members welcome to submit entries ONLY electronic submissions will be accepted NO previously published poems will be accepted ONLY ONE entry per person—your first entry is your last entry, others will be automatically identified as spam and

deleted—think before you submit Entries may be in any language, or combination of languages Poets retain copyright privileges for their work PLEASE FORWARD THIS TO POTENTIAL ENTRANTS IN ELEMENTARY THROUGH HIGH SCHOOLS AS WELL AS AMONG FRIENDS AND COLLEAGUES

Submit all entries to: Carey Madsen, Administrative Assistant careymadsen@bioscience.utah.edu Please put "Evolution poetry contest" into the subject line

Lacking suitable or sufficient entries, an interminably long, dull and pompous monologue will be read at the awards ceremony

Deadline May 15, 2006

Scott Starr <sstarr@allenpress.com>

SeparatingDNA answers

Dear evoldir members,

Thank you all for your suggestions on how to solve my problem. Most people so far have advised me to design internal primers to amplify fragments of 150 to 300 bp, and then assemble them to get the full gene. I also got some references to columns that allow one to remove smaller (< 200 bp or so) fragments from DNA extracts.

Below i post the replies i got so far (in order of arrival). I think i got them all, but if i forgot some answer please let me know. Also I have ommitted the email addresses (I think there is such a thing as email harvesters out there in the internet) so if you need to reply to someone, let me know and I will send you the emails.

For now it seems like my extracts contain some inhibiting substance, but that it is possible to remove it using the Qiaquick spin columns. I did a couple of "spiking" PCRs. This is when you add to a PCR two different DNA extracts, one from one sample that you know that works and another from a sample that is not working. In the first such PCR, the amplification did not occur, meaning that the extract that doesn't work probably contains inhibitors. After running these extracts through Qiaquick columns I did a new "spiking" PCR, and now it works, which probably means that I no longer have inhibitors in my non-working extract. I also tried a PCR on the extracts that I run through Qiaquick, but no amplification occurred. Thus it now seems that the problem is fragmentation of my DNA

and I will try to design primers to amplify shorter fragments.

Once again thank you all for your help

Best wishes to all of you,

cheers

Bruno

Hi Bruno,

You may not be able to see your fragments on a gel (I suppose you're talking about 2-3% low-melting agarose gel), if the DNA is degraded. It is easier to design primers for shorter target fragments (100-400bp each), than to try to fish out longer fragments, if any are still there - again, not very likely, if the DNA is degraded. Once you amplified the short amplicons, build a contig and you will be able to assemble your target sequence of 900bp.

Cheers, sergios

——— Sergios-Orestis Kolokotronis

Well, your problem looks rather strange. To have a good quality of extraction of your samples you must first be sure that the hole ethanol has evaporated before beginning. What I usually do is to cut the samples in little pieces, absorbe the ethanol on a paper, and after dry them in an autoclave (the time depend on your samples) and after it works fine. You also have to increase the quantity of proteinase to digest (2-3) times, and wait that the digestion is complete (shake gently in the autoclave). After you should maybe cheek if you have per inhibitors in your extract. Use the DNA and Primers of someone for how it works and add in the per the same amount of your sample. Make a positive control. After, try also to be sure that your primers works, what I suppose it's more the problem. Maybe you can try to amplify another fragment that is more conserved just to cheek if you have your mtDNA. Short fragment of dna to my knowledge don't inhibate the pcr, it's more enzymes and ions. You can also try in diluting your dna (sometimes it solve the problems of inhibitors). If you can, try to quantify the DNA you have in your extract.

500bp may still be too long—I had good luck with 200-300bp in the control region with degraded DNA. Good luck! — Rachel E. Simmons

Hi, Bruno, I guess, your target size is still too big...from

my experience, up to 300 bp usually work fine in older samples. If your could design internal primers (from fresh sample sequences), it might work.

Matthias

Hi Bruno Several things. Firstly I would be surprised if the number of small frags alone was the problem, but here are some things you can try.

- 1) Put the extract through a silica based PCR column, like Qiagen's Qiaquick. Stuff under 70bp (which as DNA degrades in a weird exponential like fashion will probably be the majority of fragments) will wash through, leaving you the larger fragments at the end.
- 2) If you wan't to try and get rid of stuff from a larger cutoff, you can try Biorad's PCR Kleen Spin columns. They work on a different technology and remove stuff <200bp.

The problem with the above is that you lost some of your large DNA too. Maybe you will get 80% back of what you put in. But it may help. However, I am not sure that inhibition from DNA frags is your problem. So, some more things.

Maybe your size of assay is too big. DNA really degrades fast. I would suggest that you start aiming for something small, like a 100bp fragment of the D-loop. If it works then you can increase the size. There is pretty good evidence that as you reduce size of fragment, you get an exponential increase in numbers of template molecules. So small is good.

___ / ___

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

Tenebrionid samples

Dear EvolDir readers,

I'm looking for live laboratory cultures or ethanolpreserved samples of the following Tenebrionidae beetles:

- Tribolium anaphe, T. destructor, T. audax, or other less cosmopolitan Tribolium from South America, Madagascar, Australia or New Zeeland - Latheticus prosopis ('long-headed flour beetle') - Erelus ssp. - Lyphia ssp. - Tenebrio ssp. (other than T. molitor) - Palorus ssp. (P. ratzeburgi is of particular interest) - Gnathocerus maxillosus

In general, if you find a tenebrionid in flour (or a similar dry stored foodstuff) it is likely to be of interest to me.

I am studying the development of the antennae in Tribolium, and the evolutionary context of antennal diversity in this genus. Live laboratory cultures are particularly useful for comparative developmental work, however samples from any of these species would be very useful for systematics.

Any help in this regard would be greatly appreciated! Best wishes, Dave Angelini

David R. Angelini, Ph.D. Department of Ecology & Evolutionary Biology University of Connecticut Torrey Life Sciences, U-3043 75 North Eagleville Rd Storrs CT 06269-3043 USA 860-486-6215 [lab] angelini@uconn.edu

PostDocs

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BanyulsSurMerFrance EvoDevo

POSTDOC POSITION in Evo-Devo in Banyuls sur Mer, France (http://www.k-projects.com/cnrs_postdocs/public/departement_details.php?IdDpt&Dep=-SDV&NumOffre1&Langue=en)

A postdoctoral position is available in September 2006 on the following subject: "Evolution of the embryonic axis in chordates: Role of the FGF signaling pathway in the embryonic development of the cephalochordate amphioxus."

The present project aims to understand the functional relationships between two signalling pathways implicated in the control of the axial patterning in chordates. These signalling pathways are the retinoic acid (RA) one and the FGF (Fibroblast growth factor) one. We will study the role of FGF genes and the possible crosstalk between the FGF and RA signalling pathways in the antero-posterior patterning developmental process. Taking advantage of the common evolutionary origin of all chordates, we have chosen a comparative approach (Evo-Devo). We will use the cephalochordate amphioxus as an animal model and we will try to understand how the vertebrate-specific genome duplications that generated 22 FGF genes in humans, instead of 8 in amphioxus, have contributed to the evolution of complexity and to the diversification and of the vertebrate phylum.

Applicants for this postdoctoral research project should be interested in research in the Evo-Devo field and should be capable to manage his own work. Applicants should have a background in developmental biology and evolution and should also know the most common techniques in molecular biology, developmental biology and some basic bioinformatics. Some experience in the use of the amphioxus animal model will be also much appreciated.

Email to hescriva@obs-banyuls.fr a brief statement of

research interests (< 500 words) and contact information for 2 or 3 references (name, affiliation, phone and email); attach pdf or Word files for CV.

*Héctor** Escrivà* *Groupe Evolution Développement Chordes* Observatoire des Océanologique de Banyuls sur Mer UMR 7628, "Modèles en Biologie Cellulaire et Evolutive". CNRS/UPMC BP 44 66651 Banvuls sur Mer, Cedex Tel: 33 (0)4 68 88 73 90 Fax: 33 (0)4 68 88 73 98 Mél : hector.escriva@obs-banyuls.fr <mailto:hector.escriva@obs-banyuls.fr>

hescriva@obs-banyuls.fr

Chile Biodiversity

The Institute of Ecology and Biodiversity (IEB) in Chile is offering a number of two year postdoctoral awards. Foreigners are eligible to apply. Detailed information may be found at www.ieb-chile.cl on the News page - Whats new? Deadline for applications: 30 May 2006.

Mary Kalin Arroyo <southern@abello.dic.uchile.cl>

DartmouthCollege Behavioralgenetics

I would like to announce a post-doctoral position at Dartmouth college working on any of a diverse range of topics focused primarily on behavior and genetics. I am looking to support a creative and motivated candidate with an opporunity to work collaboratively in a developing lab, confronting problems of sexual conflict, natural selection, population structure and/or maintainence of polymorphism in natural populations of lizards.

This post-doc will be independently funded and so is largely open in subject matter depending on the creativity and interests of the sucessful candidate. For some general ideas about the nature of the research programs to which this position could be applied, please refer to http://www.dartmouth.edu/ bio125/Calsbeek/pubs.html please send a CV and a statement of research interests to calsbeek@ucla.edu (my primary email will soon change to ryan.calsbeek@dartmouth.edu, but use the previous address unless after JULY 2006).

thanks Ryan calsbeek@ucla.edu

IndianaU BehavioralEvolution

We are looking for a postdoc with interests in behavioral mechanisms to work on a large, collaborative zebrafish project in the lab of Emilia Martins (http:/-/www.indiana.edu/~martinsl) at Indiana University, Bloomington. The project aims to uncover the genetic, hormonal and biochemical bases of evolutionary shifts in complex behavior seen in comparisons of natural populations of zebrafish and also in comparing the behavior of domesticated and recently-wild-caught strains. Individuals with interest and previous experience working with steroid hormones, pheromone biochemistry, quantitative genetics, fish behavioral ecology and/or fieldwork in India are especially encouraged to apply, but other combinations of skills and knowledge backgrounds may also be welcome. The position (including stipend and benefits package) is available as early as July 1, 2006, and can continue for up to two years.

The successful candidate will join IU's large and active behavior community (http://www.indiana.edu/-animal) and a Biology Department (http://www.bio.indiana.edu) especially strong in evolutionary research. Bloomington is located in the heavily forested hills of South-Central Indiana and is renowned for its attractive quality of life and modest cost-of-living. The cultural environment provided by the University is exceptionally rich in art, music and theater. For further inquiries, please contact Emilia Martins at emartins@indiana.edu. All applications (letter of interest, CV and contact information for 3 references) should be emailed to malockha@indiana.edu, enter Martins -Postdoc position, in the subject line. Please indicate in

your cover letter the date at which you are available to begin the position. Review of applications will begin immediately and continue until the position is filled.

Indiana University is an Equal Opportunity / Affirmative Action Employer. Women and minority candidates are especially encouraged to apply.

emartins@indiana.edu emartins@indiana.edu

LSU VertSystematicsPopGen

Postdoctoral Position in Vertebrate Population Genetics and Systematics

The Museum of Natural Science at Louisiana State University is seeking an enthusiastic and highly motivated Postdoctoral Researcher to join our multidisciplinary research team working on various aspects of vertebrate systematics and population genetics.

The successful candidate will conduct independent research in coordination with one of the Curators. The candidate will also be responsible for helping with the laboratory supervision of graduate and undergraduate research assistants and management of the Museum molecular genetics core facility. Ongoing projects in the lab include systematics and population genetic studies of birds, mammals, reptiles, and amphibians.

Minimum qualification requirements are: 1) Ph.D. or equivalent degree in biology or related discipline; 2) extensive experience in molecular methods, evolutionary biology, and computational biology; 3) strong publication record; 4) ability to manage an active laboratory used by a diverse population of researchers (undergraduates, graduate students, postdoctoral researchers, and Curators). Annual salary is \$30,000 plus health and retirement benefits. This is a full-time, one-year (renewable up to two years) position. Baton Rouge is a vibrant and culturally diverse city with a low cost of living.

Review of applications will begin 1 June 2006, and the position has a desired start date of late Summer or Fall 2006. Applicants should email the following information to Robb Brumfield (brumfld@lsu.edu): CV, statement of research interests, and three letters of reference. LSU is an Equal Opportunity-Affirmative Action employer.

brumfld@lsu.edu brumfld@lsu.edu

MichiganStateU EvolGenomics

Montpellier InterplantTransfers

Postdoctoral Position in Evolutionary Genomics

A postdoctoral position is available starting the Fall of 2006 in the lab of Shin-Han Shiu at Michigan State University. Research in the lab focuses on (1) comparative genomics of gene families, (2) the functional divergence of duplicate genes, (3) polyploidy and gene fate, and (4) prediction of novel genes and cis-regulatory elements using the model plant Arabidopsis thaliana. The successful candidate will use both computational and experimental approaches to address questions in one or more these focus areas.

Interested applicants should have expertise in one or more of the following areas: molecular genetics and developmental biology, comparative genomics and bioinformatics, and/or evolutionary and population genetics. Michigan State University has a strong biological research community with various programs and interactive groups in ecology/evolution, genetics, systems biology, and genomics. The PI is associated with: the Plant Biology Department, the Genetics program, the Ecology, Evolutionary Biology, and Behavior program, and the Quantitative Biology and Modeling Initiative. The training environment is highly interdisciplinary, diverse, and intellectually challenging. For move information about the Shiu lab, see the homepage: http:/-/shiulab.plantbiology.msu.edu Applicants should send the following information to shius@msu.edu: (1) CV, (2) brief statement of research interests (1 page), (3) info for 3 references (names, affiliations, e-mail addresses, and phone numbers), and (4) 2 selected publications (PDFs, send Word file if draft). Applications will be reviewed as they are received. Informal inquiries are welcome.

Dear Colleagues,

Here the description of an open post-doc position. Feel free to send it around !

Marc-André

— TWO YEAR RESEARCH POSITION IN MONT-PELLIER (FRANCE)

Centre d'Ecologie Fonctionnelle et Evolutive - CNRS

Exploring inter-plant carbon transfers mediated by mycorrhizal fungi in orchids

Fields of interest of our team: we focus on plant-toplant interactions mediated by mycorrhizal fungi in temperate ecosystems. Among other aspects, we are interested in plants that rely on the carbon provided by mycorrhizal fungi shared with other plants - the latter being the ultimate carbon source. This situation is allowed by the low specificity of mycorrhizal interactions, which entail sharing of fungal symbionts by plants of different species, i.e. the formation of a mycorrhizal network linking several plants of a given community. Fungal carbon is a partial C source for some plants (mixotrophy, where photosynthesis still contributes to the plant's carbon budget) or can be the exclusive source of C for others (achlorophyllous plants called mycoheterotrophs'). Our work so far has focused on (1) describing mycorrhizal fungal partners of various plants, to demonstrate such networks and (2) establishing indirectly (by methods based on stable isotopes of C and gas exchange) that mixotrophic or mycoheterotrophic plants exist. Our main models are orchids from a temperate forest tribe, the Neottieae, but we are now turning to other plant species. See publications at http:/www.cefe.cnrs.fr/coev/MA_Selosse.html . Working project in which the associated researcher would be involved: Little is known on (1) the impact of of mixotrophy or mycoheterotrophy on the fitness of the fungal and plant partners and (2) how these \pm heterotrophic plants recover the carbon from their mycorrhizal fungus. By using orchids or other models studied by our team, we aim at accomplish the following:

- (1) Conduct in situ labelling experiments to track carbon flows;
- (2) Establish of carbon budgets for mixotrophic species in situ;

(3) In microcosms, develop experimental designs allowing (2a) analysis of parameters related to fitness of the various partners and (2b) assessment of the biochemistry of the exchanges by way of labelling experiments on finer time-scales.

In this two-year project, we will collaborate with other teams more experienced in plant C metabolism (C. Damesin, Laboratoire d'Ecologie Systématique et Evolution, Univ. Paris-Sud, France) and/or microcosm experiments on mycoheterotrophic plants (D. J. Read, Univ. Sheffield, UK). We have 3-years of financial support from the CNRS (ATIP The functional and evolutionary ecology of mycorrhizal networks: using "cheaters" to explore inter-plant carbon transfers and stability of plant-fungus interactions' to M.-A.S) and a grant of the French Orchid Society (SFO).

Our team is part of larger a team focusing on coevolution in several models, including orchids or figs and their pollinators; domesticated plants and man; or ants and plants. We are part of the Centre d'Ecologie Fonctionnelle et Evolutive (ca 150 researchers on ecology and evolution). We are located in Montpellier, near the Mediterranean Sea, in a scientifically rich environment both for plant sciences and for evolutionary ecology.

Requested experience: applicants should not have the French nationality. They should be experienced (as demonstrated by published papers) in at least three of the following domains:

- 1 Microcosm (gnotobiotic) experiments manipulating plants and micro- organisms
- 2 Physiology of nutrient transfers between symbiotic partners
- 3 Mycorrhizal fungi of orchids and/or ectomycorrhizal plants
- 4 In situ use of isotopic labelling in plant metabolism
- 5 In situ use of methods to assess gas exchange in plants and C metabolism/budget
- 6 In vitro fungal culture
- 7 Transmission electron microscopy

Duration: 2 years, starting in October 2006. Salary ranges from 2 020 euro/month to 2 762 euro/month depending on applicant's experience and diploma.

Contact: Marc-André SELOSSE (Professeur à l'Université Montpellier II), CEFE-CNRS, UMR 5175, Equipe co-évolution, 1919 Route de Mende, 34 293 Montpellier cédex 5, France. Tel. 33(0)4 67 61 32 31; Fax 33(0) 4 67 41 21 38

In your first email/letter, please list your fields of experiences using the numbers (1-7) listed above as well as the name and e-mail address of two referees.

Marc-André SELOSSE

Professeur à l'Université Montpellier II CEFE-CNRS, UMR 5175, Equipe Interactions Biotiques 1919 Route de Mende, 34 293 Montpellier cedex 5, France Tel. 33(0)4 67 61 32 31; Fax 33(0)4 67 41 21 38 Mobile 33(0)607 1234 18



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

NCStateU QuantGenet

POSTDOCTORAL RESEARCH ASSOCIATE Molecular and Quantitative Genetics of Aggressive Behavior in Drosophila

Applications are invited for a postdoctoral research associate to participate in a collaborative project between Drs. Trudy F. C. Mackay and Robert R. H. Anholt (Department of Genetics and the W. M. Keck Center for Behavioral Biology, North Carolina State University) on the molecular basis of quantitative genetic variation for Drosophila aggressive behavior.

The major goals of this NIH-funded project are to identify networks of genes affecting Drosophila aggressive behavior; the subset of genes responsible for naturally occurring variation in aggression; and to determine how interactions between genetic networks and environmental factors shape the expression of aggressive behavior. The project will involve a forward genetic screen to identify new candidate genes affecting aggressive behavior and determine their interactions; whole genome transcriptional profiling of mutant alleles to identify coregulated genetic networks affecting aggression; mapping quantitative trait loci (QTLs) affecting naturally occurring variation in aggressive behavior with high resolution; and using linkage disequilibrium mapping to identify molecular polymorphisms that are associated with naturally occurring genetic variation in aggressive behavior.

Candidates will be required to have a PhD in Ge-

netics, Biology or related field. The ideal candidate will be creative, have excellent molecular biology and statistical skills, a background in population and/or quantitative genetics, and experience working with Drosophila. The salary is in accordance with NIH guidelines. Review of applications will begin immediately, and continue until the position is filled. Please contact trudy_mackay@ncsu.edu or anholt@ncsu.edu for further information.

To apply, please submit applications, including a CV and the names and contact information of three references at our website at http://jobs.ncsu.edu and use the position number 01-09-0603 to locate this posting.

Women and members of other underrepresented groups are especially encouraged to apply. AA/EOE. In addition, NC State University welcomes all persons without regard to sexual orientation. ADA: call 919-515-3148.

trudy_mackay@ncsu.edu

NorthCarolinaStateU InsectPopGenet

NCSUpopgenepidemiology

Job description: We are searching for an evolutionary biologist with experience in computer simulation modeling (C++ preferred) to work on an NIH-funded project. The successful candidate will build computer simulation models that link insect population dynamics and population genetics in a way that can contribute to improving strategies for releasing transgenic mosquitoes to reduce the incidence of human disease. Once the insect modeling is complete, disease epidemiology models will be built and linked to the insect models. The fellowship is for 2 years. In addition to working on model development and testing, the person in this position will collaborate in an interdisciplinary group funded by the Gates Foundation composed of mosquito ecologists, disease epidemiologists, molecular biologists, biomathematicians, ethicists, and scientists from disease-endemic countries, in efforts to develop novel transgenic strategies for disease reduction. The person in this position will work with the PI and at least one other postdoc in organizing a workshop to teach other researchers how to use the models. There will be an opportunity for some empirical research (if desired), and for interactions with other members of the lab who are working on other evolutionary and modeling research.

Qualifications: Candidates should have doctorates in ecology, evolutionary biology, genetics, biomathematics, epidemiology, entomology, or a related field. A working knowledge of computer programming is essential. Rigorous training in population dynamics, population genetics and/or biomathematics are prerequisites for the position. Candidates with knowledge of entomology, disease epidemiology, and advanced computer programming would be preferred.

Salary: Salary will be commensurate with experience ranging from \$32,000 to \$40,000.

Source of funds: NIH grant 5-23612

fred_gould@ncsu.edu

OregonStateU EvolGenomics

A two-year postdoctoral research associate position in evolutionary genomics is available in the Department of Zoology at Oregon State University. See announcement below for details.

Application Deadline: For full consideration, application materials must be received no later than 5pm, May 12, 2006.

Anticipated Starting Date: December 1, 2006.

Position: Postdoctoral Research Associate, full-time, 12-month, fixed-term position with reappointment at the discretion of the supervisor.

Responsibilities: The postdoctoral research associate will work in the laboratory of Dr. Dee Denver in the Department of Zoology at Oregon State University. A diverse range of exciting research projects in the general area of evolutionary genetics and genomics are available and include: 1. application of high-throughput DNA sequencing and genomic-scale methodologies to study mutation processes and genome evolution in experimental and natural Caenorhabditis nematode populations; 2. analysis of Caenorhabditis transcriptome evolution using microarray approaches; 3. investigation of the evolution of mutation rates through experimental evolution methodologies involving mutator C. elegans strains; and 4. phylogenomic analyses that examine the evolution of eukaryotic DNA repair proteins and pathways. In addition to leading in the execution and analysis of research projects, the postdoctoral research associate will also be expected to contribute to

the training of graduate students, faculty research associates, and undergraduates in the Denver lab, and participate in OSU scientific community activities. For additional information on the Denver lab, visit: http://www.cgrb.orst.edu/faculty/denver/index.html Qualifications: Required qualifications include: Ph.D. in Evolutionary Biology or Molecular Biology (requirements must be completed prior to start date), experience and a demonstrated record of achievement.

Preferred qualifications include: experience in high-throughput and/or genomic-scale methodologies, an interdisciplinary training background in evolutionary biology, population genetics, phylogenetics, molecular biology, and genomics, experience with statistical analysis softwares (i.e. SAS, R) and/or familiarity with microarray analysis platforms and software. Individuals with a record of promoting harmony in the laboratory setting are also desired. Preferred qualifications include a demonstrable commitment to promoting and enhancing diversity.

University & Community: OSU is one of only two American universities to hold the Land-, Sea-, Sunand Space-Grant designations and is the only Oregon institution recognized for its very high research activity (RU/VH) by the Carnegie Foundation for the Advancement of Teaching. OSU is comprised of 11 academic colleges with strengths in natural resources, earth dynamics and sustainability, life sciences, and the arts and sciences. OSU has facilities and/or programs in every county in the state, including 12 regional experiment stations, 41 county extension offices, a branch campus in Bend, a major marine science center in Newport, and a range of programs and facilities in Portland. OSU is Oregons largest public research university, conducting more than 60 percent of the research funded throughout the states university system.

OSU is located in Corvallis, a community of 53,000 people situated in the Willamette Valley between Portland and Eugene. Ocean beaches, lakes, rivers, forests, high desert, the rugged Cascade and Coast Ranges, and the urban amenities of the Portland metropolitan area are all within a 100 mile drive of Corvallis. Approximately 15,700 undergraduate and 3,400 graduate students are enrolled at OSU, including 2,600 U.S. students of color and 950 international students.

The university has an institution-wide commitment to diversity, multiculturalism, and community. We actively engage in recruiting and retaining a diverse workforce and student body that includes members of historically underrepresented groups. We strive to build and sustain a welcoming and supportive campus environment. OSU provides outstanding leadership opportu-

nities for people interested in promoting and enhancing diversity, nurturing creativity, and building community.

Salary and Appointment Period: The minimum starting annual salary is \$35,000, includes a benefits package including several options for health/dental/life insurance, and will be based upon skills and experience. Reappointment is at the discretion of hiring supervisor.

Application: Send a letter of application, C.V., 1-page statement of professional and research objectives, and names, addresses, phone numbers and email addresses of three references to (email applications preferred):

Dee Denver Search Committee Chair Department of Zoology Oregon State University

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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

UBerne TheoEvolEcol

POST-DOC POSITION IN THEORETICAL AND BEHAVIOURAL ECOLOGY

Dept. Behavioural Ecology, Institute of Zoology, University of Berne, Switzerland.

1) POST-DOC: Theoreticians are invited to apply for a postdoctoral research position to study evolutionary mechanisms of conflict and cooperation, with particular emphasis on reciprocity. Applicants must be experienced in modeling and should have a sound background in theoretical issues in evolutionary biology. The position is initially for two years and can be prolonged. Supervisor: Michael Taborsky.

The successful candidate will join an active research group consisting currently of 5 advanced research staff, 6 PhD-students and a varying number of guest scientists and masters students. Besides the Behavioural Ecology group, the ecologically oriented Zoological Institute of the University of Bern consists of research groups on Aquatic Ecology (Ole Seehausen), Conservation Biology (Raphael Arlettaz), Evolutionary Ecology (Heinz Richner), Population Genetics (Laurent Excoffier) and Synecology (Wolfgang Nentwig). Salaries will follow the schemes of the national funding organizations of Switzerland. Besides research, Post-docs assist in undergraduate teaching and supervision.

Closing date: Open until filled, but all application materials, including CV, a summary of research experience, copies of any published or in-press papers, and two letters of recommendation should be received by April 15, 2006 to ensure full consideration. The positions will start at the earliest possible date. Candidates should indicate in a cover letter when they could take up the position. Please send all application material to the secretarys office, c/o Marlis Gerteis, Dept. Behavioural Ecology, University of Bern, Wohlenstrasse 50A, CH- 3032 Bern, Switzerland; or as e-mail attachments to marlis.gerteis@esh.unibe.ch. For inquiries please contact barbara.taborsky@esh.unibe.ch.

Please see also http://www.zoology.unibe.ch/behav/-index_e.php for further information on our department

Dr. Barbara Taborsky Zoological Institute Behavioural Ecology University of Bern Wohlenstrasse 50A CH-3032 Hinterkappelen Switzerland

e-mail: barbara.taborsky@esh.unibe.ch tel: +41/31/6319 157 fax: +41/31/6319 141

barbara.taborsky@esh.unibe.ch

UCDavis SimulationModeling CADMS

POSITION AVAILABLE: Postdoctoral Researcher. Located at the Center for Animal Disease Modeling and Surveillance, University of California, Davis

SALARY/TERMS: Salary between \$40,000 and \$60,000, commensurate with experience and skills. Full benefits, including vacation, health, dental and 403b. Position renewable on an annual basis. Start date negotiable.

QUALIFICATIONS: Proficiency in spatial/evolutionary simulation modeling and programming languages are essential. A solid analytical, conceptual and/or statistical background is required. Strong personal skills.

RESPONSIBILITIES: Continue development of a spatially-explicit, individually based, stochastic simulation model to study the spread of animal diseases, and the processes of antigenic shift and antigenic drift. The major target systems are foot-and-mouth disease within and between livestock herds in the United States, and a global surveillance of avian influenza genetics. Examples of other projects include toxoplasma in sea otters

and pasteurella in bighorn sheep. Knowledge of disease dynamics or agricultural systems is not required; post-docs are encouraged to take the project in a direction that dove-tails with their previous experience and expertise. Must be willing to interact/collaborate with researchers in wildlife, veterinary medicine, agricultural, military and government fields. Extensive international travel may be required for certain projects.

APPLICATION PROCESS: Position is open until filled, application review will begin immediately. Interested applicants should submit: 1) a letter of intent outlining particular interests in the position, overall related qualifications including, but not limited to, computer programming skills and genetic or genomic analysis techniques and experience; 2) curriculum vitae including citizenship; and 3) the names and addresses of three references to:

Dr. Tim Carpenter, Co-director Center for Animal Disease Modeling and Surveillance (CADMS) Attn: Marlene Mooshian (mmooshian@ucdavis.edu) VM: CADMS Department of Medicine & Epidemiology School of Veterinary Medicine University of California Davis, CA 95616

Individuals who have responded to previous postings for postdoctoral positions at CADMS will have their applications reconsidered without further action on their part.

The University of California, Davis and the Department of Medicine and Epidemiology, School of Veterinary Medicine, are interested in candidates who are committed to the highest standards of scholarship and professional activities, and the development of a campus climate that supports equality and diversity. The University of California is an affirmative action/equal opportunity employer.

Brad Dickey bfdickey@ucdavis.edu

UCSanDiego EvolTheory

POSTDOC POSITION in evolutionary theory at UC San Diego

A postdoctoral position is available beginning Fall 2006 to develop models of community dynamics and diversification. This will involve a combination of analytical and computer investigation of processes in speciation, extinction, coevolution and/or macroevolution. Applicants should have a background in population or

quantitative genetics theory, and be proficient at computer programming. Salary will depend on experience. Email to rlande@ucsd.edu a brief statement of research interests (< 500 words) and contact information for 2 or 3 references (name, affiliation, phone and email); attach pdf or Word files for CV and two reprints or manuscripts. –

Russell Lande Division of Biology 0116 University of California, San Diego 9500 Gilman Drive La Jolla, CA 92093

rlande@biomail.ucsd.edu rlande@biomail.ucsd.edu

UCanterbury Genetics

Senior Research Associate in Genetics (A085-06J) School of Biological Sciences, College of Science University of Canterbury New Zealand

We are currently seeking a Senior Research Associate with interests in genetics, ecology and evolution to work with Associate Professor Neil Gemmell and members of the Molecular Ecology Laboratory on research projects that span analyses of mating systems through to the identification of genes of adaptive significance in species of conservation importance. The key role of the appointee will be to spearhead several new projects in our lab that seek to reduce the extinction risk to New Zealand's fauna by identifying and conserving relevant genetic diversity. In addition, the appointee will assist in the further development of our research group via submission of research grant applications and the management of projects and research students.

The ideal candidate will be motivated and organised, with several years experience in both molecular genetics and population genetics. You will be a highly competent laboratory worker, with experience of all routine molecular genetic techniques, particularly genotyping, sequencing and real time PCR analyses. You should also be computer literate with experience in database management, statistical and population genetic analyses. Most importantly, you will have a desire to forge a career in research science, as witnessed by a track record of publication commensurate with your experience.

The successful applicant will join a thriving Molecular Ecology Group, which uses advanced molecular genetic technologies to elucidate complex ecological and evolutionary problems in organisms ranging from marine invertebrates to iconic New Zealand species. The

group is well equipped with dedicated sequencing facilities, PCR, microbiology and genomic facilities etc. For more information on the Molecular Ecology Laboratory and the School of Biological Sciences see the web page www.biol.canterbury.ac.nz.

Minimum qualifications: MSc or PhD in Genetics, Molecular Biology, Molecular Ecology or equivalent with at least 3 years of laboratory experience.

Term of Contract: Fixed Term of 4 Years Closing Date: 19 May 2006

More detailed vacancy descriptions and how to apply can be assessed at: http://vacancies.canterbury.ac.nz/-positiondetail.asp?p=2982

Interested applicants are encouraged to make informal enquires to Assoc. Prof. Neil Gemmell, in the first instance.

Applications should include a curriculum vitae, names and addresses of three referees, university transcripts, a copy of your best paper, and a brief statement of research interests and goals.

For further assistance regarding applications please contact the Human Resources Administrator, College of Science, University of Canterbury, Private Bag 4800, Christchurch, New Zealand, Email: hr@science.canterbury.ac.nz

Dr Neil J. Gemmell Senior Lecturer in Genetics Molecular Ecology Laboratory School of Biological Science University of Canterbury Private Bag 4800 Christchurch, New Zealand Phone: +64 (0) 3 364 2009 Fax: +64 (0) 3 364 2590 www.biol.canterbury.ac.nz/-people/gemmell.shtml

neil.gemmell@canterbury.ac.nz neil.gemmell@canterbury.ac.nz

UCologne MouseAdaptation

A postdoc position is available within the collaborative research center SFB 680 in the group of Dr. Bettina Harr. Our group employs a combination of genomics techniques, evolutionary bioinformatics and cytogenetics to study the molecular basis of adaptation and speciation in natural populations of the house mouse. The main focus of our work is on the evolution of gene expression within and between subspecies of house mice but the successful applicant will be encouraged to develop his/her own research project within this general

framework. Researchers interested in molecular cytogenetics are particularly encouraged to apply. The position is initially for up to four years with the possibility of extension. Applicants should send an e-mail outlining research interest and motivations, including C.V. and contact details to: harrb@uni-koeln.de. More information about our work is available on the website: http://tina-10-1.genetik.uni-koeln.de/~website/.

The SFB680 is devoted to study the "Molecular Basis of Evolutionary Innovations". The research themes include studies on the evolution of developmental processes, characterization of adaptive trait genes in natural populations as well as computational analysis, modeling and theory of adaptive evolution. An overriding theme in most projects is the analysis of evolutionary changes in regulatory interactions and regulatory networks. The groups working in the SFB combine expertise in developmental biology, population genetics and statistical physics. Facilities for functional genomics and high throughput marker analysis are associated. The SFB activities include a seminar and guest researcher program, a PhD program and the organisation of bi-annual international meetings. Cologne is located in the center of Germany in close proximity to international airports and has a rich cultural life. The city as well as the Institute has a very international atmosphere and working language is English.

Bettina Harr PhD Research Group Leader Abteilung fuer Evolutionsgenetik Institut fuer Genetik Universitaet Koeln Zuelpicher Strasse 47 50674 Koeln - Germany

Tel: ++49 221 470 2324 Fax: ++49 221 470 5975 http://tina-10-1.genetik.uni-koeln.de/ ~ website/harrb@uni-koeln.de

UMinnesota PlantInsect

Announcing a postdoctoral position in

Molecular Ecology of Plant/Insect Interactions

Support from the National Science Foundation and the Packard Foundation is available for postdoctoral research in the area of molecular ecology of plant/insect interactions. Candidates are expected to contribute to an existing project and to develop a line of independent research. Interests in our group are diverse and currently include:

- Comparative phylogenetic studies of plant/insect food

webs and coevolution - Host specificity of insect herbivores feeding on tropical trees in New Guinea - Species delimitation (DNA barcoding) - Comparative methods in community ecology

Applicants should indicate an interest in one or more of these topics in a cover letter. This flexible position enables postdocs to pursue personal research interests in parallel. Starting date in Summer/Fall 2006 is negotiable. Please send a cover letter, vitae, names & addresses of three references, and examples of recent publications. Applications are accepted until the position is filled. Electronic submission is preferred.

Dr. George Weiblen Department of Plant Biology University of Minnesota 220 Biological Sciences 1445 Gortner Avenue Saint Paul, MN 55108 USA

Tel: 612-624-3461 Fax: 612-625-1738 Email: gweiblen@umn.edu Web: http://geo.cbs.umn.edu gweiblen < gweiblen@umn.edu>

URennes CanopyArthropods

Dear all

— Sorry for cross-posting —

The below position is re-posted due to recent with-drawal of a candidate. Please apply as soon as possible, *review of applications starts immediately*. Thank you.

Postdoc in Canopy Arthropod Ecology for 3 years available at University of Rennes 1, France (highly qualified MScs are invited to send a statement of interest).

Arthropods in the canopy represent one of the highly diverse, most widespread, and least studied communities in temperate regions. In the present project we will study the role of atmospheric stress (desiccation, NH3 imissions) and island biogeographic processes (colonization,, extinction) on arthropod biodiversity. We thus envision the canopy as an archipelago of tree crown islands in a sea or air. We will study diversity at species level, but also at a historical, i.e. phylogenetic level. We will also explore consequences of the diversity of arthropods for their functional role, particularly as grazers and dispersers of cryptogams. Approaches include detailed observational studies, as well as transplant and exclusion experiments with arthropod communities in cryptogams. Canopy access will be ensured flexibly by

cherry pickers and climbers. Up to date spatial statistical procedures will be applied. The external and internal collaboration may permit possible additional sideline studies on geno- or phenotypic differentiation of populations, tritrophic interactions, arthropod / cryptogam interactions, or habitat-use behavior.

The host institution is the Research Unit Ecosystems, Biodiversity, Evolution, co-funded by University of Rennes 1 and Centre National de la Recherche Scientifique, harboring 58 researchers and docents. Several further research institutions in ecology and evolutionary biology exist at Rennes. Rennes has approximately 200 000 inhabitants and is the capitol of the Bretagne region with exceptional coastal and mainland landscapes, and a french-celtic heritage (http://www.region-bretagne.fr/CRB/-Public/rubriques_thematique/visiter_la_bretagne/la_bretagne_une_reg/la_bretagne_en_image/). English is spoken everywhere in Academia, but not necessarily outside.

The project is for 35 months, pending approval of the intermediate report after 1.5 years. Salary is approximately 1450-1500 Euros / month net (1 Euro = 1.23 Dollars, many 2 bedroom apartments are available at 400 500 Euros / month, all inclusive), additional funds might become available. For an entire family this salary is at the limit, but families of foreign scientists receive full family aids by the state (around 200 Euros per month) and child care is extremely well organized and cheap in France. Moreover spouses of scientists receive a special visa and a work permit (if the scientist is member of the European Union, a non-European spouse can even work without further visa, permit etc.)

The candidate should ideally contribute (1) Taxonomic expert knowledge on a major group of mesofauna (Collembola, oribat mites, Psocoptera) or of phytophages (aphids, Heteroptera, Curculionids, Lepidoptera etc.). Lack in determination knowledge is however not prohibitive, as parts of the determination work will be delegated and others can be learned. (2) A certain robustness for fieldwork, and a driving license. Climbing capabilities would be an important plus. (3) Methodological experience in designing both complex observational studies, as well as field experiments. (4) Experience in the appropriate statistics to analyze the results (spatially explicit, multivariate ..). (5) Experience in communicating research to the scientific public, focusing on conceptual advance rather than accumulation of details. Documented by a strong publication list. (6) A PhD or equivalent.

Please rapidly send applications, including CV, publication list, and major publications (if available also ad-

dresses of referees and statement of research interests) by email to Andreas Prinzing (andreas.prinzing@univ-rennes1.fr).

Please contact me if you have any questions.

Andreas Prinzing, Prof. Université de Rennes 1 Unité Mixte de Recherche CNRS 6553 ≪ Ecobio ≫ : Ecosystèmes - Biodiversité - Evolution Campus de Beaulieu, Bâtiment 14A 263 Avenue du Général Leclerc 35042 Rennes Cedex, France Tel : +33 2 23 23 67 12; fax: +33 2 23 23 50 26 andreas.prinzing@univrennes1.fr http://ecobio.univ-rennes1.fr/Fiches_perso/-Fiche.asp?pseudo=APrinzing http://ecobio.univrennes1.fr/Fiches_perso/Banque/publi1_APrinzing.doc Andreas Prinzing andreas.prinzing@univrennes1.fr/Fiches_perso/Banque/publi1_APrinzing.doc Andreas Prinzing andreas.prinzing@univrennes1.fr

UniCorkIreland NematodeGenomics

Post-doctoral C.elegans position available in the Genetics & Biotechnology Lab of Dr. Charles Spillane, University College Cork, Ireland. Website: www.ucc.ie/spillane Duration: 2 years (with possibility of extension), Salary in the region of 35,000 euros per annum. The research project sponsored by the Health Research Board is entitled 'Genetic and molecular dissection of mechanisms underlying trinucleotide expansions using C. elegans as a model organism'. The main focus of the project is to unravel mechanisms involved in expansion of DNA repeat tracts, which are recognized as a cause of several of human neurodegenerative diseases like Huntington Disease or Fragile X syndrome. Candidates should be highly motivated, willing to work on related nematode projects with postgraduate research students. Candidates with proven experience in C.elegans or other nematode molecular genetics, developmental genetics, & evolutionary genomics are particularly encouraged to apply. Apply by e-mail to c.spillane@ucc.ie for the position titled: C.elegans Post-Doctoral Researcher. Attach a cover letter, CV and complete contact information for 3 referees. Deadline: June 1st 2006.

"Spillane, Charles" < C.Spillane@ucc.ie>

VirginiaCommonwealthU Bioinformatics

Postdoctoral Fellow in Bioinformatics

Virginia Institute of Psychiatric and Behavior Genetics School of Medicine, Virginia Commonwealth University

A postdoctoral position is available in June or later in the Bioinformatics Laboratory at Virginia Institute of Psychiatric and Behavioral Genetics, Virginia Commonwealth University School of Medicine. Our research focuses on (1) single nucleotide polymorphisms (SNPs) in mammalian genomes and (2) bioinformatics projects in psychiatric genetics or pharmacogenetics (PGx). The successful candidate may work on our ongoing projects (e.g., genome-wide SNP data analysis, scoring algorithms for candidate genes or markers) or some other flexible projects, with the opportunity to join the research program in the Center for the Study

of Biological Complexity. The candidate will work in a dry lab environment. VCU was recently ranked No. 1 in high impact papers in Psychiatry, and among top 10 in The Scientist's Best Place to Work for Life Sciences Post Docs survey.

The university is located in Richmond, the state capital of Virginia, within 90 minutes from the mountains, the beach, and Washington, D.C. More information can be found at the website http://bioinfo.vipbg.vcu.edu/. Virginia Commonwealth University is an equal opportunity/affirmative action institution.

The qualified candidates should be highly motivated in research and have a Ph.D. in computational biology, molecular biology, or related. Experience in one of the programming languages (C/C++, Perl, SQL) is desirable. Experience in large-scale data collection and analysis is preferred, but not required. Applicants should send a CV, brief statement of research interests, and reference to: Zhongming Zhao (zzhao@vcu.edu).

Zhongming Zhao, Ph.D. Bioinformatics Lab @ VIPBG Dept. Psychiatry and CSBC Virginia Commonwealth University Phone: (804) 828-8129 Fax: (804) 828-1471

zzhao@vcu.edu zzhao@vcu.edu

WorkshopsCourses

Academic job workshop at SSE2006	UAzores IslandEvol
Barcelona Genomics Jun19-3069	UBologna GenomeEvolEukaryotes Sept17-227
FaroPortugal EvolEcol Sep11-1569	UCLA StatGenetics Aug21-25
FaroPortugal EvolEcol Sep11-15 269	UWales WildlifeForensics Sep9-15
KristinebergSweden LifeHistory Jul17-2870	UWashington StatGenetics
PortoPortugal PopSizeEstimation Aug30-Sep270	-

Academic job workshop at SSE2006

SSE, SSB and ASN are pleased to announce a free workshop for graduate students and post-docs at the Evolution 2006 meeting at Stony Brook University. Lorne

Wolfe and Daniel Promislow will run a workshop entitled "Survival of the Fittest: How to Get a Job in Academia" on Saturday, June 24 from 12:00 - 1:30 PM. This interactive presentation is designed to help fledgling biologists best position themselves to obtain the optimum academic position. Wolfe and Promislow will cover such topics as 1) the various types of academic positions available; 2) how to prepare a compelling application packet; and 3) what to do during the

interview; and 4) how to prepare a winning job seminar. The three societies have kindly agreed to provide a free pizza lunch to all participants. However, interested students and post-docs are requested to pre-register by May 15th.

If you wish to attend, please e-mail Daniel Promislow (promislow@uga.edu) and put "Job Lunch" in the subject heading.

Barcelona Genomics Jun19-30

Please, visit the Web page http://bioinformatica.uab.es/genomics for detailed information on the 2nd International Postgraduate Course in Genomics, that will be held in the Universitat Autònoma de Barcelona from June 19 through June 30, 2006.

Note that registration is open until May 31, 2006. Do not delay registration as the maximum number of registered students is 20.

We are looking forward to see you in Barcelona! Alfredo Ruiz

Alfredo Ruíz Panadero < Alfredo.Ruiz@uab.es>

FaroPortugal EvolEcol Sep11-15

ADVANCED COURSE ON DESIGN AND ANALYSIS OF ECOLOGICAL EXPERIMENTS September 11-15 2006, at the University of Algarve, Faro, Portugal

Presented by: Professor A.J. Underwood and Dr M.G. Chapman Centre for Research on Ecological Impacts of Coastal Cities, University of Sydney, NSW 2006, Australia

Registration (with payment) deadline: June 2, 2006 Cost: 500 euros, includes course materials and coffee breaks (accommodation and meals not included)

Site for registration and information on lodging: http://www.ualg.pt/ccmar/maree/education Course outline:

1. Revision and Development of Alternative Designs for

Complex Experiments of Fixed and Random Factors Typical biological experiments; Revision of The General Linear Model; Calculations of Sums of Squares; Multiple comparisons; Cornfield Tukey Rules; Multiple comparisons; Post-hoc pooling Practical Exercises Evaluation of alternative designs to test complex hypotheses

- 2. Correlations and Regressions Revision of regression and correlation Partial linear regressions One-Factor Analysis of Covariance (a sequence of 3 linear models) Practical Exercises Partial/multiple regression Analyses of Covariance, comparisons across more than 2 samples
- 3. Asymmetrical analyses of variance and Environmental Monitoring Asymmetrical analyses of variance Environmental monitoring: BACI (Before/After, Control/Impact designs) Beyond BACI designs to identify pulse and press disturbances How to deal with no ³Before data² Practical Exercises Asymmetrical analyses of variance for tests of fixed effects in experimental manipulations; How to construct ³Beyond_BACI analyses² from analyses of variance tables Problem solving with/without ³Before data²
- 4. Analyses of variances Identification of hypotheses about variances; Extraction and use of components of variation Practical Exercises Tests of hypotheses using components of variation
- 5. Power in experimental design Power analysis: Fixed and random factors Practical Exercises Calculating power for fixed and random factors; effects of sample size, variance and number of levels of factors on calculations of power in different experiments
- 6. Additional topics (lectures and/or practical classes): Quantification of problem-solving Logics of experimental tests of hypotheses Hypotheses about multivariate measures: tests using multifactorial designs

eserrao@ualg.pt

FaroPortugal EvolEcol Sep11-15 2

ADVANCED COURSE ON DESIGN AND ANALYSIS OF ECOLOGICAL EXPERIMENTS September 11-15 2006, at the University of Algarve, Faro, Portugal

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- 2. Correlations and Regressions Revision of regression and correlation Partial linear regressions One-Factor Analysis of Covariance (a sequence of 3 linear models) Practical Exercises Partial/multiple regression Analyses of Covariance, comparisons across more than 2 samples
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- 4. Analyses of variances Identification of hypotheses about variances; Extraction and use of components of variation Practical Exercises Tests of hypotheses using components of variation
- 5. Power in experimental design Power analysis: Fixed and random factors Practical Exercises Calculating power for fixed and random factors; effects of sample size, variance and number of levels of factors on calculations of power in different experiments
- 6. Additional topics (lectures and/or practical classes): Quantification of problem-solving Logics of experimental tests of hypotheses Hypotheses about multivariate measures: tests using multifactorial designs

eserrao@ualg.pt

KristinebergSweden LifeHistory Jul17-28

Marine Summer Course 2006

Analysing Biodiversity & Life History Strategies

* This course will deal with the latest methods in biodiversity research, including genomic approaches, DNA barcoding and molecular tools in developmental studies, presented by invited teachers, all internationally known experts in their fields. Hands-on experience with animals will be combined with possibilities to work with modern analytical techniques like phylogenetic analysis, sequence analysis, fluorescence and confocal laser scanning microscopy * Open to PhD students and post docs; both to members of the MGE network and to non-members * The MGE Network pays for everyone's course fee (including lunches, coffees, excursion and farewell dinner) and the accommodation for the PhD students. Everyone pay for their own travel. * July 17-28, 2006, Kristineberg Marine Research Station (www.kmf.gu.se < http://www.kmf.gu.se/>), Sweden * Deadline for applications extended to the 1st of May, 2006 * Information and application forms can be found at the MGE website (www.marine-genomics-europe.org http://www.marine-genomics-europe.org/, go to Training & Education).

Ulrika Hjelm Training and Education Programme Manager

NoE Marine Genomics Europe

Matthias Obst <matthias.obst@kmf.gu.se>

PortoPortugal PopSizeEstimation Aug30-Sep2

^{*}Conservation Genetics Data Analysis Course: *

*Recent Approaches for Estimation of Population Size, \ast

Structure, Gene flow, Parentage, & Selection Detection

/30 August to 2 September, 2006, Porto, Portugal/

Objective: To provide training in conceptual and practical aspects of data analysis for the conservation genetics of natural and managed populations. Emphasis will be on interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers and top-researchers to help develop the next generation of conservation geneticists, and to identify developments needed to improve data analysis approaches. This course will mainly cover analysis of allele frequency data (not DNA sequence data), including coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

* *

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 25 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students near the end of their degree program).

* *

Course/Workshop Format: For each subject, we provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-45 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and housing together of instructors and students in the same location will allow for extensive exchange and facilitate learning.

Instructors/Speakers: Fred Allendorf, Mark Beaumont, Peter Beerli, Albano Beja-Pereira, Daniel Falush, Adam Jones, Gordon Luikart, Karen Martien, Mark Miller, Scott Mills, Mike Schwartz, David Tallmon, and Robin Waples.

* *

*Location: *The course will be held in the facilities at

CIBIO (Center for Investigation of Biodiversity and Genetic Resources; http://cibio.up.pt/) on the Campus for Agricultural Sciences in the rural village of Vairão, just north of Porto, and a few kilometres from the Atlantic coast and the airport. Vairão is an ancient village whose origins can be traced back to the Roman Period (the Roman village Valeriani).

Registration and cost: For detailed informahttp://cibio.fc.up.pt/congen will be available on 30 April; in the meantime enquiries contact albanobp@mail.icav.up.pt for <mailto:albanobp@mail.icav.up.pt> gordon.luikart@mso.umt.edu). Accommodations and meals are included in the registration fee. Cost: \$US 1,000 per person will cover all meals, lodging, transportation to and from the airport, and a visit to Gerês National Park and the World Heritage City of Porto. Up to two reduced-cost scholarships will be available for candidates with no funding.

Application and criteria for acceptance: /Deadline/ for application is */15 June/, 2006*. Applicants must provide a brief description of their research interests, career goals, and what they would like to learn from this course. Priority will be given to persons with their own data to analyze (for example graduate students near the end of their degree program). The applicants should submit a brief summary (<200 words) about the current state of their work, the hypotheses or questions addressed, the genetic markers used, and study species. To apply for scholarship support, candidates should also send their CV, a cover letter explaining why they should receive the scholarship, a cost estimate for their flight (round trip) to Porto, and a phone number where they can be reached for a brief interview. **

Albano Beja-Pereira <albanobp@fc.up.pt>

UAzores IslandEvol

Dear EvolDir members,

Here is the announcement of the MSc course in Island Ecology and Evolution, University of the Azores, 2006.

The MSc course in Island Ecology and Evolution, is one of a suite of 5 MSc courses run within Department of Biology, University of the Azores. This second edition of this MSc will focus Marine Invertebrates and will have international reach. In this unique programme, students are inducted to the University and

School via an introductory course consisting of orientation through site tours, excursion and a welcome social event and 8 weeks of intensive international teaching courses. Classes will be offered during June-July of 2006, by local, national and internationally recognized experts as guest teachers.

For more information check out the website: www.meie.uac.pt and/or contact:

Dr. Ana Cristina Costa Biology Department University of the Azores. Email: accosta@notes.uac.pt Phone: +351296250466

We would be very pleased if you could pass this information to possibly interested people.

Kind regards,

António Pagarete.

apereira@science.uva.nl

$\begin{array}{c} \textbf{UBologna GenomeEvolEukaryotes} \\ \textbf{Sept 17-22} \end{array}$

SUMMER SCHOOL "GENOME EVOLUTION IN EUKARYOTES (GEE)" , 17-22 September 2006

Dear EvolDir Members,

We are please to announce the first Summer School "Genome Evolution in Eukaryotes (GEE)" organized by the University of Bologna, and to be held in the University Residential Centre of Bertinoro (Ravenna - Italy) from 17th to 22nd of September 2006.

We are also pleased to inform you that the GEE website is now on line at www.gee.unibo.it. Genomics is a young science that moved its first steps mostly within medicine and diagnostics. In the last few years, however, Genomics has also gained a major role in the investigation of most of the "big questions" of Biology, such as the enlightening of mechanisms of Life, as well as the reconstruction of Life Evolution on Earth.

The possibility to re-analyze genomes in an evolutionary framework emerged only recently, together with the increasing number of sequenced organisms. Indeed, Genomics is now embodying the Evolutionary Biology ideas because, without an evolutionary approach, most of the obtained molecular data cannot be deeply understood. As a matter of fact, from the linkage of these two disciplines, a new science is now arising: the Evolutionary Genomics.

This School will be just within this context: the discussion of clue data of Genomics in a evolutionary framework will be the base of the teaching activity, and all analyzed genomic compartments will be examined in relation to their implication for the beginning and evolution of Life on Earth.

Chosen Teachers are among the best in their relative research fields. Moreover, Teachers come from 6 countries and 3 continents: this will give the School a strong international connotation. We really believe that the School represents a precious occasion for young scientists to discuss and expand their skills on the abovementioned topics. Official language of the School will be English.

Registration to the Summer School is now open. This school is reserved to Graduates, PostDocs as well as researchers that perform biological research activity in any Academic or Non-Academic structure around the world. Candidates must submit their CV to Dr. Barbara Mantovani (barman@alma.unibo.it) before 30th of June 2006. A maximum of 30 applications will be accepted. Organizing Committee will give priority to students who will better benefit from the courses because of the contiguity of their research activity.

Please be so kind to help us advertising the Course in your Department/Structure and among your colleagues. In the website you can also download a program of the School to distribute.

Best wishes,

Dr. Marco Passamonti GEE Summer School Secretariat

mpassa@alma.unibo.it

UCLA StatGenetics Aug21-25

STATISTICAL GENETICS SHORT COURSE August 21 - 25, 2006 on the UCLA campus Los Angeles, California http://www.genetics.ucla.edu/courses/statgene We will hold a five full-day intensive workshop on state-of-the-art statistical genetics methods for detection of genetic loci for complex traits, either qualitative or quantitative.

Each day will include hands-on computer exercises using statistical genetics computer programs, especially Mendel, SimWalk, and FBAT.

We will cover the general theory behind the methods as

well as emphasize the practical aspects needed to give the best chances of success. The Course is designed to assist people who are actively studying the genetics of complex traits. Topics will include:

* Study Design and other data issues * Mistyping Detection * Haplotyping * Analysis of Qualitative Traits including: - Parametric Linkage Analysis - Non-Parametric Linkage (NPL) - Association Testing: Family-based Case/Control * Analysis of Quantitative Traits including: - Variance Component Analysis - Association Testing

Participants in the Course need no prior experience with these methods or programs, but should be "computer literate". Participants will be required to bring a laptop computer to run the analysis exercises.

The Course instructors are faculty from the Statistical Genetics Group of the UCLA Department of Human Genetics:

- 1. Kenneth Lange 2. Steve Horvath 3. Jeanette Papp
- 4. Janet Sinsheimer 5. Chiara Sabatti 6. Eric Sobel

The cost of the course, including all course materials and complete room and board, is:

US\$1000 for students from non-profit institutions, US\$1500 for all others from non-profit institutions, and US\$2500 for participants from for-profit institutions.

The course will be held 21-25 August 2006 in Los Angeles, California at the University of California. Accommodation and lectures will be in DeNeve Plaza on the UCLA campus.

For more information, including the simple application process, please visit http://www.genetics.ucla.edu/courses/statgene. Undergraduate and Master's Student Session August 19 - 20, 2006

We will also hold a two-day introductory session, "Introduction to Gene Mapping of Complex Traits", for competitive undergraduate and Master's students to attend before participating in the general session.

Accepted students will receive a full scholarship for both sessions of the course, which includes room and board, as well as a travel allowance. Students need not bring a labtop computer if they don't have access to one.

Applicants for this student session must be US citizens or permanent residents; proof of status may be required. Students from disadvantaged and underrepresented groups are especially encouraged to apply.

For more information, please visit http:/-

/www.genetics.ucla.edu/courses/statgene> . Janet@mednet.ucla.edu Janet@mednet.ucla.edu

UWales WildlifeForensics Sep9-15

Wildlife DNA Forensics Training Course 9-15th September 2006 Wildlife DNA Services University of Wales, Bangor, UK We would like to announce that registration is now open for our training course in Wildlife DNA Forensics. The seven-day course combines lectures and practical sessions to provide participants with the skills to apply population genetic tools to the investigation of wildlife crime. Organised by Wildlife DNA Services, the course is aimed at laboratory researchers and technicians interested in investigating issues such as the illegal trade in animals, plants and their derivatives, poaching and animal welfare crimes. Participants will learn how to conduct all aspects of a forensic investigation from evidence handling and validation through to species, population and individual identification. For further info follow the link at the bottom of this page: http://www.wdnas.com/forensics_training_courses.html Or contact Rob Ogden (rob-ogden@wdnas.com) – Dr. Rob Ogden Project Manager Wildlife DNA Services 9th Floor Alun Roberts Building University of Wales Bangor, LL57 2UW UNITED KINGDOM T: +44 1248 388 479 F: +44 1248 388484 www.wdnas.com den@wdnas.com

UWashington StatGenetics

The deadline for scholarship applications for the Summer Institute in Statistical Genetics is April 21, 2006.

The early registration deadline is May 22, 2006.

Details at http://www.biostat.washington.edu – Bruce S. Weir Professor and Chair, Department of Biostatistics University of Washington Seattle, WA 98195-7232 Phone (206) 221-7947. Fax (206) 543-3286.

Bruce Weir

bsweir@u.washington.edu>

Instructions

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 LATEX files, Excel files, etc. ...plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

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. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating 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 LATEX do not try to embed LATEX or TEX in your message (or other formats) since my program will strip these from the message.