EvolDir

February 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.

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

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Conferences

Bangkok MEEGID Nov30-Dec4

30/12/05

MEEGID VIII Bangkok, Thailand. 30th November-4th December 2006. Preliminary announcement.

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, the Centre National de la Recherche Scientifique (CNRS; http://www.cnrs.fr/) and the Institut de Recheche 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.nl/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. 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 will be given to health problems of special interest to Thailand ande South-East Asia: avian flu, SARS, malaria, dengue.

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.

Wishing you a happy new year

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

BrockU OntEcolEthologyEvol May5-7

The Brock University Department of Biological Sciences is proud to be hosting the 2006 Ontario Ecology and Ethology (and sometimes Evolution) 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 is the first announcement of this conference to be held May 5 to May 7 2006. More information will follow and will be available at the conference website: www.oeec.ca. Please pass on this announcement and attached poster to relevant students and faculty in your department.

If any questions arise, please do not hesitate to contact us at oeec@brocku.ca.

We look forward to receiving abstracts from interested students.

Thanks very much,

2006 OEEC Organizing Committee

oeec@brocku.ca

Edmonton CanSocZool May2-6

The inaugural symposium of the newly created "Comparative Morphology & Development" section (CMD) of the Canadian Society of Zoologists (CSZ) will take place at the 45th annual CSZ meeting in Edmonton, Alberta, Canada (May 2 - 6, 2006).

INAUGURAL SYMPOSIUM: Development, Morphology, Evolution: The Triple Helix

Confirmed speakers for the May 4 symposium include:

Dr. Brian K. Hall, Dalhousie University "Penguins, Platypus, Peripatus and Polypterus: Embryos in Evolution"

Dr. Nick Butterfield, University of Cambridge "From Microbes to Morphology: The Cambrian Explosion and Origins of the Modern Biosphere"

Dr. Mark Q. Martindale, University of Hawaii "The Evolution of Morphological Complexity: Developmental Tails (sic) from an Anemone Embryo"

Dr. Phil Currie, University of Alberta "On the Shoulders of Giants: Development, Size and the Evolution of Tyrannosaurid Dinosaur Crania"

Dr. Mimi A. R. Koehl, University of California- Berkeley "Sniffing with Hairy Noses: Fluid Mechanics and Convergent Evolution of Odor Capture by Antennae"

REGISTRATION & CALL FOR ABSTRACTS

To register to attend this exciting symposium, or to submit an abstract for a talk to be given in one of the many related contributed paper sessions on Larval Biology, Biomechanics & Functional Morphology, Paleobiology, or Evolution of Development, visit the the CSZ 2006 Meeting web site:

http://www.biology.ualberta.ca/csz2006/index.htm
*** DEADLINE FOR EARLY REGISTRATION AND ABSTRACT SUBMISSION ***: Feb. 15, 2006

Don't miss this opportunity to attend the memorable, and historically significant launch of the Comparative Morphology & Development section of the CSZ.

RELATED EVENTS

A companion symposium sponsored by the Canadian Secretariat (http://www.ualberta.ca/~ipy/index.html) of the International Polar Year consortium will occur at the CSZ meeting on May 3:

Biology of the Canadian Artic II. Integrating across scales: From site-specific to regional and global processes

And don't forget that Edmonton is just a short drive from one of the most spectacular driving tours in North America, the Icefields Parkway (http://www.canadianrockies.net/icepwy.html) that runs from Jasper (http://www.pc.gc.ca/pn-np/ab/jasper/), past the Columbia Icefields and Lake Louise, to Banff (http://www.pc.gc.ca/pn-np/ab/banff/) through the heart of the world-famous Canadian Rockies.

So there are many reasons to attend the annual CSZ meeting this year!

THE COMPARATIVE MORPHOLOGY & DEVELOPMENT SECTION

The CMD section of the CSZ aims to promote and enhance interactions, dialogue and intellectual cross-fertilization among the many Canadian zoologists and paleontologists who work on morphology (functional or comparative), larval biology, development, and developmental evolution, and particularly those who work at the interfaces between development, morphology and evolution. An exciting aspect of this new section will be the involvement of paleontologists, which we hope will make the annual meetings attractive to a wide range of participants from inside and outside of Canada. We are actively working to make the new CMD section a welcome home for both zoologists and paleontologists interested in development, morphology or evolution, and we welcome participation by Canadians and non-Canadians alike.

To learn more about the goals, history, inaugural symposium, student awards and other activities of the CMD section, visit the section's web site:

http://www.biology.ualberta.ca/CMD/home.htm
STUDENT AWARD

Starting with the 2006 CSZ meeting, the CMD section will offer an attractive award (the Brian K. Hall Award in Comparative Morphology and Development of $300) for the best student presentation by a member of the CMD section. See http://www.biology.ualberta.ca/CMD/home.htm#awards for details. So students are encouraged to participate.

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http://www2.biology.ualberta.ca/palmer/palmer.html (biological asymmetries, software, course notes) Chair, Comparative Morphology & Development section, Canadian Society of Zoologists. For info. see: http://www.biology.ualberta.ca/CMD/home.htm rich.palmer@ualberta.ca

GordonResConference MolEvol Feb5-10

MOLECULAR EVOLUTION 2006 GORDON RESEARCH CONFERENCE

February 5 - 10, 2006 (Sunday evening - Thursday evening). Full program below.

Join us! Go to http://www.grc.org/application/apply1.cfm to apply. We are still accepting applications. We have an outstanding program (see below), and invite you to join us. Chip Aquadro and Billie Swalla

location: Crowne Plaza Hotel (formerly the Holiday Inn), Ventura, California Site information: http://www.grc.uri.edu/sites/ca/cp/cp.htm The Molecular Evolution Gordon Research Conference brings together leading junior and senior scientists from around the globe to discuss current research as well as emerging opportunities and challenges in molecular evolution. This years meeting has sessions on ancestral protein reconstruction, computational evolutionary genomics, microbial/viral diversity and evolution, evolution of body plans, sex chromosome evolution, adaptive evolution, evolution of novelty and gene regulation, molecular evolution of interspecific hybrids, and the evolution of the germ line. The meeting will be held at the Holiday Inn, Ventura California. This ocean-side location is located in the town of Ventura, and provides a wealth of opportunities to engage in scientific interaction and at the same time explore on foot the beaches, town, and adjacent hills. Whale-watching, winery tours, the Getty Museum and other attractions are nearby. We particularly encourage participants to present posters on their research, and there will be ample opportunities for discussion.

Join us! Go to http://www.grc.org/application/-apply1.cfm to apply. We are still accepting applications.

SUNDAY FEBRUARY 5 (evening)

ANCESTRAL PROTEIN RECONSTRUCTION Eric Gaucher (Foundation for Applied Molecular Evolution) “Ancestral sequence reconstruction as a tool to understand natural history: past, present and future directions”

Belinda Chang (University of Toronto) “Reconstructing ancestral visual pigments: the origins of rods”

Joe Thornton (University of Oregon) “The evolution of molecular complexity: evolution of steroid hormone/receptor interactions”

MONDAY FEBRUARY 6

COMPUTATIONAL EVOLUTIONARY GENOMICS Bret Larget (University of Wisconsin) Synopsis

Lior Pachter (University of California at Berkeley) “Parametric alignment and evolution of cis-regulatory elements”

Pavel Pevzner (University of California at San Diego) “Fragile versus Random Breakage Models of Chromosome Evolution”

Lindell Bromham (University of Sussex) “Tempo and Mode of Molecular Evolution”

MICROBIAL & VIRAL DIVERSITY AND EVOLUTION Peg Riley (University of Massachusetts) Synopsis

Lin Chao (University of California at San Diego) “Surviving Deleterious Mutations”

John Logsdon (University of Iowa) “Molecular voyeurism: using a meiosis detection kit to reveal hidden sex lives of eukaryotes”

TUESDAY FEBRUARY 7

EVOLUTION OF BODY PLANS Billie Swalla (University of Washington) “Developmental Genes Drive the Evolution of Body Plans”

Antonia Monteiro (University of Buffalo) “Different ways of spotting butterfly and moth wings”

Ken Halanych (Auburn University) “Phylogeny and evolution of Lophotrochozoa”

Elena Kramer (Harvard University) “Genetic mechanisms underlying innovation in floral organ identity”

SEX CHROMOSOME EVOLUTION Bernardo Carvalho (University of Rio de Janeiro) “Origin and Evolution of the Drosophila Y”

Jenny Graves (Australian National University) “Mammalian sex chromosome evolution”

WEDNESDAY FEBRUARY 8

ADAPTIVE EVOLUTION David Rand (Brown University) “The evolution of adaptive evolution”

Brian Lazzaro (Cornell University) “Evolutionary Genetics of Insect Immunity”

Stephen Wright (York University) “Testing for selection in domestic and natural plant populations”

Michael Nachman (University of Arizona) “Adaptive evolution in reproductive genes and the origin of reproductive isolation in mice”

EVOLUTION OF NOVELTY AND GENE REGULATION Doug Crawford (University of Miami) “Evolution of Gene Expression and Physiology”

Kevin White (Yale University) “Selection, drift and constraint: Gene expression evolution in Drosophila and primates”

THURSDAY FEBRUARY 9

MOLECULAR EVOLUTION OF INTERSPECIFIC HYBRIDS Chau-Ti Ting (National Tsing Hua University,Taiwan) “Speciation study in the era of genomics”

Dan Barbash (Cornell University) “Positive selection and hybrid lethality in Drosophila”

Rudy Raff (Indiana University) “Seeking a genic basis for radical evolutionary changes in morphology”

Toby Bradshaw (University of Washington) “Molecular genetics of species differences in monkeyflowers”

EVOLUTION OF THE GERM LINE Eric Haag (University of Maryland) “Peculiarities of the Germ Line and Their Impact on Molecular and Developmental Evolution”

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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

HarvardU Conflict May11-12

CALL FOR SUBMISSIONS

2nd Annual Harvard Mind, Brain and Behavior Graduate Student Conference War, The Cognitive Science of Conflict: Organismic and Social Perspectives Thursday May 11th and Friday May 12th Submission Deadline is March 1, 2006

Faculty Speakers include: Professor Sara M. Lewis (Biology, Tufts University) Professor Jeff W. Lichtman (Molecular and Cellular Biology, Harvard University) Professor Everett I. Mendelsohn (History of Science, Harvard University) Professor James H. Sidanius (Psychology, Harvard University)

Graduate students from the Mind, Brain and Behavior Initiative at Harvard are pleased to announce an interdisciplinary conference on War: The Cognitive Science of Conflict. The conference is for graduate students, and is intended to increase dialogue among students from a variety of disciplines, including (but not limited to) neuroscience, psychology, computer science, neurobiology, linguistics, organismic and evolutionary biology, biological anthropology, history of science, education, and philosophy.

We are soliciting graduate student contributions to this conference. We welcome presentations on research that aims to understand conflict from an Organismic Perspective (within organisms) or from a Social Perspective (between organisms). Graduate student presentations should be no more than 30 minutes (followed by approximately 20 minutes of discussion) and aimed at a non-specialist audience.

Please email an abstract of no more than 1000 words to mind_brain_behavior@yahoo.com. Please include a cover sheet with your name, institutional affiliation, email address, telephone number, the title of your presentation, the perspective of interest (organismic or social), and the discipline(s) you will represent. You may send the abstract and cover sheet as a Word document, plain text, or pdf file.

The deadline for submissions is March 1, 2006. Authors will be notified by March 21, 2006 of the status of their submissions.

A website with additional conference information will be available soon and linked to the main Harvard MBB website at http://mbb.harvard.edu/. Inquiries should be directed to mind_brain_behavior@yahoo.com. Please forward this call along to other graduate students. We look forward to your submission!

mpatten@oeb.harvard.edu mpatten@oeb.harvard.edu

London EvolEntomology Feb1

Royal Entomological Society Postgraduate Forum 2006

Call for oral and poster presentations from postgraduate research students

The forum is a friendly venue where young scientists can gain experience giving presentations in a conference setting, as well as networking with other researchers. We invite students working on any aspect of entomology to join. [For university students: this is an excellent opportunity to get credit points towards your degree]. Prizes for best poster and oral presentation will be awarded.

Confirmed invited postgraduate speakers are:

Alessandra Curtotti (Queen Mary) "Host biting preferences of British Culex p. pipiens vs Culex p. molestus and the risk of West Nile Virus in Britain " and

Nehal Saleh (Queen Mary) "Scent marking and foraging behaviour in bumblebees"

The conference will take place February 1, 2006 at 41 Queen's Gate, London. Deadline for registration and abstract submission is January 15, 2006. For more information visit: http://www.royensoc.co.uk/ or contact Mr Eligiusz Baumgart Email:eligiusz.baumgart@imperial.ac.uk or Ms Nehal Saleh Email: n.saleh@qmul.ac.uk.

Nehal Saleh PhD Candidate School of Biological and Chemical Sciences Queen Mary London E1 4NS UK

http://www.biology.qmul.ac.uk/research/staff/chittka/chittkalab/Team/Nehal.html Tel: 44 (0) 207 882 5555 Ext. 4169

Interested in giving a presentation for our discussion group? Everyone welcome! For more information please visit: http://alpha.qmul.ac.uk/~btw092/biolunch/index.htm n.saleh@qmul.ac.uk n.saleh@qmul.ac.uk

Marseilles 10EvolBiol

The registrations and abstract submissions for the 10th Evolutionary Biology Meeting at Marseilles are open. For more information see the web site http://www.up.univ-mrs.fr/evol-cgr/ best regards

– Pierre Pontarotti EA 3781 Evolution Biologique Université d'Aix Marseille I 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 Marseille http://www.up.univ-mrs.fr/evol-cgr/ Pierre.Pontarotti@up.univ-mrs.fr

Marseilles 10EvolBiol 2

Information about the 10th Evolutionary Biology Meeting at Marseilles:

A new session has been added: Probalistic models and statistic tools for concepts in evolution.

We remember you that registrations and abstract submissions for the 10th Evolutionary Biology Meeting at Marseilles are on line.

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.up.univ-mrs.fr/evol-cgr/ Or, contact us at egee@up.univ-mrs.fr

Nadège Bardiot

EA 3781 Evolution Biologique Université d'Aix Marseille I 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.up.univ-mrs.fr/evol-cgr/ egee@up.univ-mrs.fr

McGillU CSEE Apr3-4 2

SOCIÉTÉ CANADIENNE D'ÉCOLOGIE ET D'ÉVOLUTION

CONGRÈS INAUGURAL

Première annonce et appel de conférences affichées

Le Congrès inaugural de la Société Canadienne d'Écologie et d'Évolution aura lieu les 3 et 4 avril 2006, à Montréal, co-organisé par l'UQÀM et l'Université McGill. Le programme comprend une assemblée générale pour ratifier la constitution et élire les membres du comité exécutif et du conseil, un symposium regroupant des conférences invitées sur le thème de "l'importance de l'écologie et de l'évolution pour le Canada", ainsi qu'une réunion d'information sur les programmes de financement CRSNG Découverte et autres. Nous aurons également une session permettant aux participants de présenter des affiches.

Nous invitons toutes les personnes intéressées à participer à ce congrès. Merci de nous envoyer un message courriel à ecoevo@gmail.ca, incluant votre nom et affiliation. Le titre du courriel doit comprendre les informations suivantes: nom de famille-initiales-inscription. La date limite pour les inscriptions est le 1er février 2006.

Les frais d'inscription seront de $20 (membres-étudiant(e)s) ou de $40 (membres) ou de $80 (non-membres). Merci de faire parvenir votre chèque au nom d'"Aquasalmo R&D Inc" à Louis Bernatchez (Congrès), Département de biologie, Pavillon Charles-Eugène Marchand, Université Laval, Québec QC, G1K 7P4, Canada. Ces chèques sont déposés dans un compte que nous utilisons temporairement, en attendant que la Société soit officiellement constituée.

Nous encourageons tous les participants à présenter une affiche et espérons que ce premier congrès constituera une vitrine pour la recherche canadienne en écologie et évolution. Si vous souhaitez présenter une affiche, merci de suivre la procédure ci-dessous. La société est bilingue et toutes les présentations peuvent être faites en franais ou en anglais.

Des informations sur la Société et les modalités d'inscription sont disponibles sur notre site web www.ecoevo.ca. Nous vous enverrons en janvier un programme détaillé du congrès incluant le projet de constitution et la liste de candidats pour le comité et le conseil.

Instructions pour les affiches

Les affiches doivent présenter des travaux dans les domaines de l'écologie et de l'évolution. Nous encourageons également les projets interdisciplinaires, destinés à une plus large audience, ou qui explorent l'enseignement de l'écologie et de l'évolution en général.

Merci de suivre les instructions suivantes pour la soumission de votre résumé :

* Les affiche doivent être d'un maximum de 2.35 m de large x 1.15 m de haut (7.7 x 3.77 pieds). Des punaises seront disponibles pour installer votre affiche et seront le seul moyen de l'attacher.

Evaluation et acceptation des résumés * Les auteurs sont responsables de l'exactitude et de l'apparence de leur résumé. * Le résumé doit être basé sur des résultats nouveaux et non publiés. * Le résumé peut être soumis avant que toutes les analyses et conclusions de l'étude soient finalisées. Dans ce cas, il est important d'indiquer au moins les résultats préliminaires.

Soumission du résumé * Merci d'envoyer votre résumé par courriel à ecoevo@gmail.com, avant le 1er février 2006. Le titre du courriel doit comprendre les informations suivantes: nom de famille-initiales-inscription&résumé. * Un accusé de réception vous sera envoyé à l'adresse courriel indiquée dans votre message d'inscription. Si cette adresse est erronée vous ne recevrez pas d'accusé de réception. Un numéro de référence sera attribué à votre résumé. MERCI DE NE PAS PERDRE CE NUMÉRO QUI VOUS SERA DEMANDÉ LORS DE COMMUNICATIONS ULTÉRIEURES. * Vous serez informez par courriel si votre affiche a été sélectionnée pour présentation, avant le 1er mars 2006. NOTE: les personnes qui soumettent leur résumé le plus tôt possible, seront informées les premières. * Si vous rencontrez des difficultés durant la soumission de votre résumé, merci de nous contacter à ecoevo@gmail.com. Le titre du courriel devra faire mention de: nom de famille-initiales-problèmesoumission.

Préparation des résumés Les résumés doivent être soumis en document attaché (.txt) ou rich text (.rtf). Utilisez le format suivant pour préparer votre résumé: 1. Auteurs et Affiliations. 2. Adresse complète, incluant courriel valide, du premier auteur. 3. Titre et résumé: le titre ne doit pas dépasser 255 caractères (environ 15 mots). Ne pas taper le titre en lettres capitales ou en gras. 4. Texte du résumé: le texte ne doit pas dépasser

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

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MichiganStateU FuncGenomics May16-19

*** FIRST ANNOUNCEMENT ***

2nd INTERNATIONAL SYMPOSIUM ON ANIMAL FUNCTIONAL GENOMICS May 16-19, 2006

Dear Colleagues:

We are pleased to announce that the Center for Animal Functional Genomics of Michigan State University will host the 2nd International Symposium on Animal Functional Genomics (ISAFG) on May 16-19, 2006. The Symposium will be held at the Henry Center on the campus of Michigan State University in beautiful East Lansing, Michigan.

The purpose 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 and animal models of disease. Featured areas of foci of the Symposium guest speakers and international delegates include Statistical Genomics, Bioinformatics and Data Mining, Animal Health, Reproduction, and Growth and Metabolism.

The 2nd ISAFG has been designed around 11 keynote lectures to be delivered by internationally renowned functional genomics scientists. In addition, selected abstracts will be presented orally by Symposium participants. All participants are welcome to bring posters highlighting preliminary or completed studies on gene expression profiling in animal model systems. A formal call for abstracts and details for Symposium presentations, registration, and hotel booking are now available on the Symposium's web site at http://www.isafg.msu.edu.

Please reserve May 16-19, 2006 on your schedules! We look forward to greeting you at Michigan State University. For more information please contact the 2nd ISAFG co-chairs,

Jeanne Burton (burtonj@msu.edu) Guilherme Rosa (rosag@msu.edu)

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Guilherme J. M. Rosa Assistant Professor Department of Animal Science Department of Fisheries and Wildlife

Michigan State University 1205-I Anthony Hall East Lansing, MI 48824-1225 USA

Phone: + 1 517 353-5102 Fax: + 1 517 353-1699 E-mail: rosag@msu.edu http://www.msu.edu/˜rosag/

Montreal Phylogenomics Mar16-19 Deadline extension

Subject: Deadline extension for phylogenomics conference Content: DEADLINE EXTENSION for the First International Conference on Phylogenomics conference

New deadline for early registration: February 1st 2006. New deadline for abstract submission for presentation: February 1st 2006

********* Conference announcement ******************

First International Conference on Phylogenomics Dates: March 16-19 2006 Location: Sainte-Adèle (near Montreal), Québec, Canada Web site: https://phylogenomics.bioinfo.umontreal.ca/meeting/ Organizers: Hervé Philippe and Mathieu Blanchette

Scope: This conference aims to reunite experts focusing on two distinct aspects of phylogenomics: the use of genome data inferring species phylogeny and the use of phylogenetic approaches to gain insights into gene functions. The methods developed for phylogenetic inference (especially the models of sequence evolution) are quite advanced and could benefit to function prediction. Similarly, the knowledge of the accurate species phylogeny increases the quantity of functional information that can be extracted. Conversely, knowledge of gene function and the other selective constraints is primordial to improve tree reconstruction methods. This conference will create synergy between these two phylogenomic communities, bridging the gap between there respective scientific endeavors. A special issue of BMC Evolutionary Biology will be dedicated to the conference, allowing contributors of the conference to submit their manuscripts.

Invited speakers: * Ford Doolittle Dalhousie University, Canada * Jonathan Eisen, The Institute for Genomic Research, USA * Brian Golding, McMaster University, Canada * Nick Goldman, EMBL-EBI Cambridge, UK * Richard Goldstein, National Institute for Medical Research, USA * Jotun Hein, University of Oxford, UK * Mark Pagel, University of Reading, UK * Eduardo Rocha, Université Paris 6, France * Andrew Roger, Dalhousie University, Canada * Michael Sanderson, University of California, USA * Adam Siepel, Cornell University, USA * Yves van de Peer, Ghent University, Belgium

Important dates: Deadline for early registration: February 1st 2006. Deadline for abstract submission for presentation: February 1st 2006 Deadline for manuscript submission (accepted abstracts only): March 1st 2006

Mathieu Blanchette <blanchem@mcb.mcgill.ca>

OriginOfLife Stockholm May8-11

CONFERENCE: ORIGIN & DISTRIBUTION OF LIFE IN THE UNIVERSE - A Nordic Perspective

Royal Swedish Academy of Sciences Stockholm, Sweden May 8-11, 2006

http://astrobiology.molbio.su.se The Swedish Astrobiology Network is pleased to announce the 2006 Nordic Astrobiology Conference, to be held at the Royal Swedish Academy of Sciences in Stockholm May 8-11, 2006.

The conference is sponsored by the Royal Swedish Academy of Sciences, the Swedish National Space Board, the Nordic Institute for Theoretical Physics (Nordita) and the Wenner-Gren Foundations. The conference will begin with an open public lecture by Dr. Chris McKay, and sessions based around the major conference themes will begin with Keynote presentations.

Geosciences: Chris McKay, NASA Ames Research Center, USA Aivo Lepland, Geological Survey of Norway

Space Sciences: Pascale Ehrenfreund, Leiden Univ, Netherlands Hans Rickman, Uppsala Astronomical Observatory, Sweden

Biological Sciences: Eors Szathmary, Collegium Budapest, Hungary Karsten Pedersen, Gothenburg University, Sweden

In conjunction with the conference, the journal Astrobiology will produce a special issue comprising peer-reviewed contributions from participants.

If you are interested in joining us in Stockholm, please register your interest at our website:

http://astrobiology.molbio.su.se There is no conference fee, and we are currently accepting abstracts for both oral and poster presentations. We welcome contributions in any of the three broad areas above and look forward to seeing you in Stockholm.

Please note: The deadline for registration & abstract submission is 31 March 2006. Also, we recommend that you book accommodation in good time. We have made a limited number of block bookings at hotels that are near the Royal Academy, but these will be filled on a first-come first-served basis.

Anthony Poole <ant@molbio.su.se>

SSEAnnualMeeting CallforSymposia

Call for Symposia Annual Meeting 2007

The 2007 annual meeting of the Society for the Study of Evolution will be held from June 18-23, 2007. The meeting will be hosted by Allan Wilson Centre for Molecular Ecology and Evolution Institute of Molecular BioSciences of Massey University in Aukland, New Zealand. The Council of the Society invites proposals for the two Society-sponsored symposia to be held in conjunction with the meeting. Symposium proposals should include: (1) a synopsis of the symposium theme (about one page); (2) a tentative list of speakers, including institutional affiliations, and topics; and (3) a rationale for the symposium explaining why this topic and this group of speakers are particularly appropriate for a Society-sponsored symposium.

In evaluating symposium proposals, the Council will favor those proposals whose topics concern newly emerging fields, fields ripe for syntheses, and fields different from those that have been included in recent Society symposia. The Council particularly encourages proposals that include young investigators and others traditionally underrepresented in Society symposia.

The Council will select only two proposals for half-day symposia at its meeting in June 2006. All proposers will be notified of the Council's decision in July. The Society provides partial travel support for organizers and participants in sponsored symposia. Details are available on request. To be assured of full consideration, proposals must be received at the following address by May 15, 2006:

Dr. Jessica Gurevitch, Executive Vice President The Society for the Study of Evolution Department of Ecology and Evolutionary Biology Stony Brook University Stony Brook, NY 11794-5245 USA e-mail: Jessica.Gurevitch@sunysb.edu <mailto:Jessica.Gurevitch@sunysb.edu> Proposals can be sent as paper copies by mail or as e-mail attachments in Word or RTF format.

Carey Madsen <careymadsen@bioscience.utah.edu>

SSEAnnualMeeting CallforSymposia 2

Information for SSE members regarding: -2006 Dobzhansky Prize Applications -Call for Symposia for 2007 SSE meeting in New Zealand

APPLICATIONS FOR THE 2006 THEODOSIUS DOBZHANSKY PRIZE

The Theodosius Dobzhansky Prize is awarded annually by the Society for the Study of Evolution to recognize the accomplishments and future promise of an outstanding young evolutionary biologist. The prize was established in memory of Professor Dobzhansky by his friends and colleagues, and reflects his lifelong commitment to fostering the research careers of young scientists.

Eligibility The candidate must have a Ph.D. (or equivalent) awarded no earlier than June 2003 and no later than 1st February 2006, and must be actively involved in research in the field of evolutionary biology. There are no other restrictions. Applicants do not have to be members of the Society for the Study of Evolution, but such membership is encouraged.

Nomination/Application.- Candidates may apply directly or may be nominated. Established researchers are encouraged to nominate outstanding young scientists who may be unaware of the existence and prestige of this prize. Each candidacy must be supported by the following materials detailing the candidates career to date: (1) a curriculum vitae, (2) a summary of research accomplishments, (3) a statement of research plans for the next 5 years, (4) pdf copies of three recent publications, (5) names and addresses of the three referees (including the nominating scientist where applicable) who have sent supporting letters. N.B.: THE THREE LETTERS OF REFERENCE ARE SENT SEPARATELY, BUT NO APPLICATION WILL BE CONSIDERED WITHOUT THESE LETTERS.

All application/nomination materials and letters of reference must be sent as PDF e-mail attachments. No file type other than PDF will be accepted. The deadline for receipt of all materials, including letters of reference, is

1 March 2006. All materials should be sent to the secretary of SSE (Dale H. Clayton) at the following email address:

careymadsen@bioscience.utah.edu

Award.- The Dobzhansky Prize is accompanied by a check for U.S. $5000, and will be awarded at the annual meeting of the Society for the Study of Evolution, 23-27 June 2006, in Stony Brook, New York. The recipient is expected to be present to receive the award and to give an oral presentation about his/her research. To facilitate attendance, the SSE provides funds to cover the costs of conference registration, accommodation during the conference, and expenses for travel to and from the conference. The recipient will be notified of the award by early May 2006.

Call for Symposia for Annual Meeting in 2007

The 2007 annual meeting of the Society for the Study of Evolution will be held from June 18-23, 2007. The meeting will be hosted by Allan Wilson Centre for Molecular Ecology and Evolution Institute of Molecular BioSciences of Massey University in Aukland, New Zealand. The Council of the Society invites proposals for the two Society-sponsored symposia to be held in conjunction with the meeting. Symposium proposals should include: (1) a synopsis of the symposium theme (about one page); (2) a tentative list of speakers, including institutional affiliations, and topics; and (3) a rationale for the symposium explaining why this topic and this group of speakers are particularly appropriate for a Society-sponsored symposium.

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Dr. Jessica Gurevitch, Executive Vice President The Society for the Study of Evolution Department of Ecology and Evolutionary Biology Stony Brook University Stony Brook, NY 11794-5245 USA e-mail: Jessica.Gurevitch@sunysb.edu Proposals can be sent as paper copies by mail or as e-mail attachments in Word or RTF format.

Scott Starr <sstarr@allenpress.com>

SaintLouisU MEEC2006 Mar17-19

The 26th annual Midwest Ecology and Evolution Conference (MEEC) 2006 to be held March 17-19th at Saint Louis University, St. Louis, MO.

MEEC is an annual, migratory conference organized by and for graduate students and post-docs. The conference is an excellent opportunity for students to network with others, learn about research being done in the Midwest, and present their own research in a relaxed and low-key environment. This year featuring keynote speaker Daniel Simberloff.

Registration is open! Please visit: www.wallace.slu.edu/meec2006 schutzmr@slu.edu schutzmr@slu.edu

SaltLakeCity MedicalBioinformatics Jun22-23

19th IEEE International Symposium on Computer-Based Medical Systems, CBMS 2006 Salt Lake City Utah, USA June 22-23, 2006

Special Track: BIOINFORMATICS and its MEDICAL APPLICATIONS https://www.cs.tcd.ie/Nadia.Bolshakova/CBMS_Bioinformatics06.html
CALL FOR PAPERS

Major computational challenges have been raised in the post-genomic era. Novel computational methods and approaches are required to acquire, store, organize, archive, analyse and visualize the large amount of biological and biomedical data. The goal of the track is to share ideas related to bioinformatics challenge among biological, biomedical and computer scientists. Authors are invited to submit original papers addressing any computational biology issue. Papers are invited (but not limited) to the following key themes: Biomedical Research Evolution and Phylogenetics Data Mining in Bioinformatics Microarray Analysis RNAi Analysis Sequence Alignment Pathways, Networks, Systems Biology Functional Genomics Visualization Protein Structure and Analysis Comparative Genomics Pattern Recognition Ontologies Software Systems Unlike workshops, where position papers and reports on initial and intended work are appropriate, papers selected for a special track should report on significant unpublished work suitable for publication as a conference paper. More information about the symposium, registration fees, venue can be found here: http://cbms2006.ece.byu.edu .

IMPORTANT DATES January 31, 2006 Submission of (6-page, maximum) paper March 1, 2006 Notification of acceptance April, 5, 2006 Final camera-ready paper due April, 8, 2006 Pre-registration deadline May 22, 2006 Hotel room reservations due You must pre-register to have your paper published in the proceedings. If you only plan to attend and are not submitting a paper, pre-registration is still strongly encouraged. This conference is space-limited, and registration may not be available on-site.

SUBMISSION PROCEDURES FOR PAPER No hard-copy submissions are being accepted. Electronic submissions of original technical research papers will only be accepted in PDF format. File size is limited to 2 MB. Use a maximum of six A4 pages, including figures and references. Include one cover sheet, stating the track title (Special Track on Bioinformatics and its Medical Applications), paper title, authors, technical area(s) covered in the article, corresponding author's information (telephone, fax, mailing address, e-mail address), and your preference for oral or poster presentation. Author names should appear only on the cover sheet, not on the paper. Submit your manuscript no later than January 31, 2006. Authors will be notified of acceptance by March 1, 2006 after a review process by three independent experts. Each accepted paper to the Special Track on Bioinformatics and its Medical Applications will be published in the conference proceedings by IEEE CS Press, conditional upon the author's advance registration. Papers that were not accepted by the Program Committee of the track can be considered for publication as regular submissions by the General Program Committee of IEEE CBMS 2006. Please note that the format of IEEE CBMS 2006 proceedings will be the IEEE Computer Science Press 8.5x11-inch format. Submission is encouraged in this format. For more details please see the website of IEEE CBMS 2006: (http://cbms2006.ece.byu.edu/how.html#submission). All submissions will be done electronically via the CBMS web submission system.

TRACK CHAIR Nadia Bolshakova -Trinity College Dublin, Ireland

TRACK PROGRAM COMMITTEE Francisco Azuaje University of Ulster, Northern Ireland Nadia Bolshakova Trinity College Dublin, Ireland Fernando Martin-Sanchez Institute of Health "Carlos III", Spain James McInerney National University of Ireland Heather Ruskin Dublin City University, Ireland For further questions, please contact Nadia.Bolshakova@cs.tcd.ie

– Dr. James O. McInerney, Bioinformatics Laboratory, Department of Biology, National University of Ireland, Maynooth, Co. Kildare, Ireland. P: +353 1 708 3860 F: +353 1 708 3845 E: james.o.mcinerney@nuim.ie – Take a look at our website — http://bioinf.nuim.ie/ james.o.mcinerney@nuim.ie james.o.mcinerney@nuim.ie

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UAlabama SEEC2006 Mar3-5

The 3rd annual 2006 Southeastern Ecology and Evolution Conference will be held at the University of Alabama from 3-5 March.

http://seec.ua.edu SEEC is a fun and stress-free meeting for undergraduate, graduate, and post-doctoral researchers in the environmental and life sciences to discuss their current research and meet new colleagues from across the Southeast. You do not have to present a talk or poster to attend the conference and we welcome all interested students to join us and learn. Similar meetings are held for the Northeast (NEEC), and the Midwest (MEEC).

SEEC will feature talks by Drs. Leslie Rissler (University of Alabama), Lorne Wolfe (Georgia Southern University), and Anne Yoder (Duke University). Other notable occurrences include a Friday and Saturday night social, and the return of the ever-popular SEEC raffle.

Early registration is due by January 31, 2006 and costs $20. Late registrants will be charged an additional $5 fee. Abstracts for posters and oral presentations are due by January 31, 2006 with late abstracts being accepted on a first-come first-serve basis until all available slots are filled.

Check out the website for more information.

rissler@bama.ua.edu rissler@bama.ua.edu

UAlabama SEEC2006 Mar3-5 2

Hi Everyone! This is a reminder that SEEC 2006 registration is due in two weeks, Jan 31, 2006. You can find more details at www.seec.ua.edu. Please email seec2006@gmail.com for any questions!

Thanks,

SEEC 2006 committee

seec2006@gmail.com

UAlaskaAnchorage Sticklebacks Jul30-Aug4

CONFERENCE: The Fifth International Conference on Stickleback Behavior & Evolution University of Alaska Anchorage July 30th - August 4th, 2006 http://fish.uoregon.edu/sb/stickleback2006 We are pleased to announce 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 wcresko@uoregon.edu

UWarwick GeneticsSoc Mar28-31

'Meiosis and the causes and consequences of recombination'

A Joint Meeting Of The Biochemical Society And The Genetics Society

28th- 31st March 2006, University of Warwick

Abstract deadline January 25th 2006

Early-bird registration deadline February 28th

Sessions

Hotspots: distribution and characterisation

Gene conversion and crossing over

Chromosome dynamics in meiosis

Meiotic drive

When mammalian meiosis goes wrong

Confirmed speakers

Sally Otto (University of British Columbia), Tom Petes (University of North Carolina), Scott Keeney (Memorial Sloan-Kettering Cancer Center), Gil McVean (University of Oxford), Christine Mezard, (Institut National de la Recherche Agronomique, Versailles), Nicolas Galtier (CNRS, Montpellier), Matt Whitby (university of Oxford), Rhona Borts (University of Leicester), Michael Lichten (National Cancer Institute, Bethesda), Zac Cande (Berkley), Harry Scherthan (Max-Planck-Institut fur Molekulare Genetik), Kim Nasmyth (IMP, Vienna), Alec Jeffreys (University of Leicester), Catherine Montchamp-Moreau (CNRS, Gif-sur-Yvette), Kelly Dawe (University of Georgia), Harmit Malik (Seattle), Pat Hunt (Washington State University), James Lupski (Baylor College of Medicine), Jan van Deursen (Mayo Clinic).

Meiosis and meiotic recombination are fundamental processes, the understanding of which has wide ranging implications across many disciplines not least of which is human fertility, mapping of human genetic traits and the origin genetic disorders such as Downs Syndrome. Meiosis and meiotic recombination has been the foundation of all genetic analysis since the discovery of linkage and its break down early in the last century. Unravelling its molecular mechanism has since challenged geneticists, biochemists and cytologists. Understanding the control of the initiation and distribution of recombination is of fundamental import to the design of studies aimed at mapping single and complex trait disorders in all organisms. Understanding the biochemistry of the DNA and DNA protein interactions is essential to understanding this complex process. The origin of sex, meiosis and recombination still puzzles evolutionary biologists. Great strides are occurring in each of these disciplines and this joint meeting between the Biochemical and Genetic Societies will bring together elements from all of these disciplines.

Further details and Registration is available online:

<http://www.biochemistry.org/meetings/-programme.cfm?Meeting_No=SA049>http:/-/www.biochemistry.org/meetings/-programme.cfm?Meeting_No=SA049 Brian Charlesworth <brian.charlesworth@ed.ac.uk>

Vancouver GeneticsofSpeciation Jul21-24

** FIRST ANNOUNCEMENT**

SYMPOSIUM ON GENETICS OF SPECIATION

Sponsors: The American Genetics Association and Molecular Ecology Date: July 21-24, 2006 Location: Vancouver, British Columbia, Canada Web site: http://www.theaga.org/agasymposium/-index.html Organizer: Loren Rieseberg

The last decade has witnessed a transformation in our understanding of speciation genetics. This conference will attempt to synthesize what we know and to suggest promising avenues for further research. The meeting will include invited and contributed talks, as well as poster and discussion sessions to encourage greater involvement of symposium participants. Funds are available for student/postdoc travel and registration to promote broad participation.

The symposium will be held at the University of British Columbia, Vancouver, which is next to the Pacific Ocean and the coastal mountains. Time will be set aside Sunday afternoon (July 22) so that symposium participants can enjoy the Vancouver area.

We hope you will attend.

Invited Speakers:

Allen Orr (Key Lecture) Rochester, USA

Richard Abbott St. Andrews, UK Keith Adams Vancouver, Canada Nick Barton Edinburgh, UK Louis Bernatchez Quebec City, Canada Salvatore Cozzolino Naples, Italy Michael Doebeli Vancouver, Canada Sergey Gavrilets Knoxville, USA Scott Hodges Santa Barbara, USA Darren Irwin Vancouver, Canada Chris Jiggins Edinburgh, UK Mark Kirkpatrick Austin, USA Leonie Moyle Bloomington, USA Mohammed Noor Durham, USA Bret Payseur Madison, USA Katie Peichel Seattle, USA Naomi Pierce Boston, USA Daven Presgraves Rochester, USA Dolph Schluter Vancouver, Canada Kerry Shaw College Park, USA Willie Swanson Seattle, USA John Willis Durham, USA Chung-I Wu Chicago, USA Sara Via College Park, USA

Loren Rieseberg <lriesebe@indiana.edu>

VenturaCA MolEvol Feb5-10

MOLECULAR EVOLUTION 2006 GORDON RESEARCH CONFERENCE

February 5 - 10, 2006 (Sunday evening - Thursday evening)

Crowne Plaza Hotel (formerly the Holiday Inn), Ventura, California Site information: http://-www.grc.uri.edu/sites/ca/cp/cp.htm Chair: Chip Aquadro, Co-Chair: Billie Swalla

The Molecular Evolution Gordon Research Conference brings together leading junior and senior scientists from around the globe to discuss current research as well as emerging opportunities and challenges in molecular evolution. This years meeting has sessions on ancestral protein reconstruction, computational evolutionary genomics, microbial/viral diversity and evolution, evolution of body plans, sex chromosome evolution, adaptive evolution, evolution of novelty and gene regulation, molecular evolution of interspecific hybrids, and the evolution of the germ line. Speakers and discussion leaders represent some of the leaders in experimental and computational/statistical approaches to understanding both the pattern and process of molecular evolution and the molecular basis of diversity. The meeting will be held at the Holiday Inn, Ventura California. This ocean-side location is located in the town of Ventura, and provides a wealth of opportunities to engage in scientific interaction and at the same time explore on foot the beaches, town, and adjacent hills. Whale-watching, winery tours, the Getty Museum and other attractions are nearby. All scientists with an interest in molecular evolution and comparative genomics are encouraged to apply to attend the conference. We particularly encourage participants to present posters on their research, and there will be ample opportunities for discussion.

Join us! Go to http://www.grc.org/application/-apply1.cfm to apply. We are still accepting applications. We have an outstanding program (see below), and invite you to join us. Chip and Billie

SUNDAY FEBRUARY 5

4:00 pm - 9:00 pm Arrival and check-in

6:00 pm Dinner

7:30 pm - 9:30 pm ANCESTRAL PROTEIN RECONSTRUCTION

Discussion Leader: Eric Gaucher (Foundation for Applied Molecular Evolution) “Ancestral sequence reconstruction as a tool to understand natural history: past, present and future directions”

7:40 pm - 8:25 pm Belinda Chang (University of Toronto) “Reconstructing ancestral visual pigments: the origins of rods”

8:25 pm - 8:35 pm Discussion

8:35 pm - 9:20 pm Joe Thornton (University of Oregon) “The evolution of molecular complexity: evolution of steroid hormone/receptor interactions”

9:20 pm - 9:30 pm Discussion

9:30 pm - 11:00 pm Welcome Reception

MONDAY FEBRUARY 6

7:30 am - 8:30 am Breakfast

9:00 am - 12:30 pm COMPUTATIONAL EVOLUTONARY GENOMICS

9:00 am - 9:10 am Discussion Leader: Bret Larget (University of Wisconsin) Synopsis

9:10 am - 9:55 am Lior Pachter (University of California at Berkeley) “Parametric alignment and evolution of cis-regulatory elements”

9:55 am - 10:05 am Discussion

10:05 am Coffee Break 10:15 am Group Photo

10:35 am - 11:20 am Pavel Pevzner (University of California at San Diego) “Fragile versus Random Breakage Models of Chromosome Evolution”

11:20 am - 11:30 am Discussion

11:30 am - 12:15 pm Lindell Bromham (University of Sussex) “Tempo and Mode of Molecular Evolution”

12:15 pm - 12:25 pm Discussion

12:30 pm Lunch

1:30 pm - 4:00 pm Free Time

4:00 pm - 6:00 pm Poster Session I

6:00 pm Dinner

7:30 pm - 9:30 pm MICROBIAL & VIRAL DIVERSITY AND EVOLUTION

7:30 pm - 7:40 pm Discussion Leader: Peg Riley (University of Massachusetts) Synopsis

7:40 pm - 8:25 pm Lin Chao (University of California at San Diego) “Surviving Deleterious Mutations”

8:25 pm - 8:35 pm Discussion

8:35 pm - 9:20 pm John Logsdon (University of Iowa) “Molecular voyeurism: using a meiosis detection kit to reveal hidden sex lives of eukaryotes”

9:20 pm - 9:30 pm Discussion

TUESDAY FEBRUARY 7

7:30 am - 8:30 am Breakfast

9:00 am - 12:30 pm EVOLUTION OF BODY PLANS

9:00 am - 9:10 am Discussion Leader: Billie Swalla (University of Washington) “Developmental Genes Drive the Evolution of Body Plans”

9:10 am - 9:55 am Antonia Monteiro (University of Buffalo) “Different ways of spotting butterfly and moth wings”

9:55 am - 10:05 am Discussion

10:05 am Coffee Break

10:35 am - 11:20 am Ken Halanych (Auburn University) “Phylogeny and evolution of Lophotrochozoa”

11:20 am - 11:30 am Discussion

11:30 am - 12:15 pm Elena Kramer (Harvard University) “Genetic mechanisms underlying innovation in floral organ identity”

12:15 pm - 12:25 pm Discussion

12:30 pm Lunch

1:30 pm - 4:00 pm Free Time

4:00 pm - 6:00 pm Poster Session II

6:00 pm Dinner

7:30 pm - 9:30 pm SEX CHROMOSOME EVOLUTION

7:30 pm - 7:40 pm Discussion Leader: TBA Synopsis

7:40 pm - 8:25 pm Bernardo Carvalho (University of Rio de Janeiro)

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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

Wernigerode Germany Apomixis Jun27-Jul2

First Announcement: 3rd International Apomixis Congress

The third international conference on Apomixis will be held from June 27 to July 2, 2007. The meeting will be organized by the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK; www.ipk-gatersleben.de) within the context of its yearly "Gatersleben Research Conference" series, and will be held in the city of Wernigerode, which is located in the beautiful Harz Mountains in central Germany.

We plan to have a series of plenary lectures and sessions covering the following topics:

Meiosis and Apomeiosis Embryogenesis and Parthenogenesis Endosperm Development Polyploidy and Aneuploidy Population Genetics Expression Profiling Genetic Engineering Epigenetics

If you are interested in attending, please send me an email and I will send you a brochure and more detailed information in the next few months.

Best wishes, Tim (sharbel@ipk-gatersleben.de)

Dr. Tim Sharbel Apomixis Research Group Dept. of Cytogenetics and Genome Analysis Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstraße 3, D-06466 Gatersleben Germany Apomixis Group Webpage http://www.ipk-gatersleben.de/en/02/04/05/index.html IPKWebpage www.ipk-gatersleben.de tel: +049 (0)39482 5608 fax: +049 (0)39482 5137

GradStudentPositions

Dublin MolEvolBioinformatics

Location: Dublin, Ireland

Application deadline: 28 Feb 2006

Project Title: Gene gains, losses and relocations during vertebrate evolution

Description: A Ph.D. position starting in October 2006 is available in the lab of Dr. Aoife McLysaght in the Genetics Dept. of Trinity College Dublin. This project is sponsored by Science Foundation Ireland as part of their prestigious President of Ireland Young Researcher's Award (awarded to Aoife McLysaght in 2005). The project will eventually employ three Ph.D. students and one postdoctoral fellow working together.

The project will involve examination and statistical analysis of vertebrate genome data using bioinformatics methods. Candidates for the Ph.D. position are expected to have a good honours Bachelor's degree (at least grade 2.1 or equivalent) in molecular biology, bioinformatics or related discipline. Experience in molecular evolution and bioinformatics/computer programming are desirable.

For more details of the project, look under "Research" on the lab website http://www.gen.tcd.ie/molevol To apply: Send a complete CV (including grades), a description of your research achievements and interests, and the names of at least two referees.

Aoife McLysaght Smurfit Institute of Genetics Trinity College Dublin 2 Ireland

[e] aoife.mclysaght@tcd.ie [t] +353-1-6083161 [f] +353-1-6798558 [w] www.gen.tcd.ie/molevol mclysaga@tcd.ie mclysaga@tcd.ie

InstZoologyLondon Biodiversity

NERC PhD Studentship in measuring global trends in Biodiversity

Institute of Zoology, Zoological Society of London

Title of Project: Assessing the effectiveness of parks in maintaining biodiversity

Supervisors: Professor Georgina Mace (Institute of Zoology, principal supervisor), Dr Jonathan Baillie (Institute of Zoology, second supervisor), Dr Andrew Balmford (Department of Zoology, University of Cambridge, University supervisor).

Project outline: Which species are parks protecting? Are parks effectively maintaining populations of wild species? Are the population trends of species inside and outside of parks significantly different? Does the legal status or management type of parks have any bearing on population trends? What kinds of species benefit from which management structures? How do these trends vary across biomes? Addressing these questions will help to define the value of parks in conserving biodiversity and will aid in identifying the most effective strategies for the future. This information will also form the basis for a suite of important indicators that will inform conservationists and policy makers on the effectiveness of protected areas. Such indicators have been requested by the Convention on Biological Diversity (CBD) to aid in measuring progress towards the CBD target of reducing the rate of biodiversity loss by 2010 [1].

The studentship will focus on all African parks classified by IUCN into one of seven categories (IUCN classes Ia-VI) [2-3], representing different levels of protection. Distribution maps of all African mammals, birds, and amphibians will be used to explore which taxonomic groups are best represented in the African park systems. The data will also be explored by biome. This will follow a similar method to the Global GAP analyses [4], but with recently reviewed maps and a clear regional focus on Africa. This initial exercise will help to form a baseline from which protected area coverage for these three groups can be measured over time. All available population trend information will be collected for African species, both inside and outside of parks. This will be gathered from the Living Planet Index, IUCN SSC specialist groups, published literature, Government ministries/parks agencies, and from surveys carried out by conservation organizations. Methods similar to that of the Living Planet Index [5] will then be used to assess trends of species in protected areas from 1970 to the present. Multilevel generalized linear modeling will then be used to explore whether there is a relationship between population trends, over a given time period, and the type of park management/level of protection, whether species are inside or outside protected areas, as well as examining how these patterns vary across biomes. This will form the basis for a series of indices that can continue to be used to asses the effectiveness of African parks in conserving biodiversity.

CASE partner: the UNEP/WCMC

1] Balmford, A. et al. 2005. The convention on biological diversity's 2010 target. Science 307(5707), 212-213.

2] WCMC, 2003: World database on Protected Areas., IUCN-WCPA/UNEP-WCMC.

3] WDPA, 2003: World Database on Protected Areas. I.-W. UNEP-WCMC

(ed.)Washington DC, USA.

4] Rodrigues, A.S.L., S.J. Andelman, M.I. Bakarr, L. Boitani, T.M. Brooks, R.M. Cowling, L.D.C. Fishpool, G.A.B. da Fonseca, K.J. Gaston, M. Hoffmann, J.S. Long, P.A. Marquet, J.D. Pilgrim, R.L. Pressey, J. Schipper, W. Sechrest, S.N. Stuart, L.G. Underhill, R.W. Waller, M.E.J. Watts, and X. Yan, 2004: Effectiveness of the global protected area network in representing species diversity. Nature, 428(6983), 640-643.

5] Loh, J., Green, R.E., Ricketts, T., Lamoreux, J., Jenkins, M., Kapos, V., Randers, J. 2005. The Living Planet Index: using species population time series to track trends in biodiversity. Philosophical Transactions of the Royal Society B 360, 289-295.

For further details, contact Jonathan Baillie (Tel: 020 7449 6632; E-mail: Jonathan.baillie@ioz.ac.uk).

jo.Keogh@ioz.ac.uk jo.Keogh@ioz.ac.uk

InstZoologyLondon SparrowPopGenet

NERC PhD Studentship in Wildlife Epidemiology

Institute of Zoology, Zoological Society of London

Title of Project: Is disease a significant factor implicated in the UK House Sparrow (Passer domesticus) population decline?

Supervisors: Dr Andrew Cunningham, (Institute of Zoology, principal supervisor), Professor Malcolm Bennett, (University of Liverpool, University supervisor).

Senior IoZ Supervisor:

CASE partner: Royal Society for the Protection of Birds

Significant reductions in house sparrow populations have occurred across England over recent decades, particularly affecting the south east of the country. The BTO/JNCC/RSPB Breeding Bird Survey highlights the severity of population decline within London of 71% between 1994 and 20021. A number of possible explanations for the population decline have been proposed. These include reduction in food availability (insect prey for nestlings, seed/grain for fledglings and adults), increased predator density (domestic cat (Felis catus), sparrowhawk (Accipiter nisus)), reduced nest site numbers, the effects of pollution and infectious disease2. The importance of disease (infectious or non-infectious) as a potential factor contributing to avian population declines is increasingly recognised. In North America, research on the house sparrow in recent years has focussed on the viral encephalitides, particularly West Nile virus3. However, there is a paucity of knowledge of the disease status and population health of this species in the UK. A recent BTO report2 on the topic concludes that disease is a largely unexplored factor in terms of the species population dynamics in the UK and emphasises the need for further research.

The studentship will take advantage of an existing RSPB project researching factors affecting the distribution, abundance and demography of house sparrows in Greater London. This includes the ringing of sparrows and their repeated capture throughout the project duration, allowing serial monitoring of individuals. Detailed information, including body weight, biometrics, reproductive status and evidence of moult will be collected from these individuals. Monitoring of breeding success, diet and individual survival rates will be performed. In addition, the proposed research will:

1. investigate causes of mortality and population health of the house sparrow

2. compare the health status between populations of stable and declining house sparrows

3. contrast population health between the feeding trial and control groups

4. evaluate the relationship between disease status and the probability of individual survival.

This research combines the benefits of clinical examination and sampling of live birds with post mortem examinations from well-characterised study groups. In addition to the controlled London-based study, use will be made of the Garden Bird Health initiative (a national garden bird disease research project co-ordinated by the IoZ) for investigation of causes of mortality of house sparrows elsewhere. This work will help identify priority pathological conditions for investigation during the controlled study and will indicate if disease findings from the controlled study can be extrapolated nationally.

ildlife Epidemiologythe format.

not for yours of course. I will need your formal project outline soon (tomorrow?), see the webReferences:

1. Raven, M.J., Noble, D.G., & Baille, S.R. (2002) The Breeding Bird Survey 2002. BTO Research Report 334. British Trust for Ornithology, Thetford.

2. Crick, H.Q.P., Robinson, R.A., Appleton, G.F., Clark, N.A., Rickard, A.D. (2002) Investigation into the causes of decline of Starlings and House Sparrows in Great Britain. BTO Research Report No 290.

3. Rappole, J.H., Hubalek, Z. (2003) Migratory birds and West Nile virus. Journal of Applied Microbiology 94 Suppl:47S-58S.

CASE partner: Royal Society for the Protection of Birds

For further details, contact Andrew Cunningham (Tel: 020 7449 6674; E-mail: andrew.cunningham@ioz.ac.uk).

jo.Keogh@ioz.ac.uk jo.Keogh@ioz.ac.uk

KelloggBiologicalStation GK12

Graduate Fellowships Available The KBS GK-12 Program

The Kellogg Biological Station (KBS) of Michigan State University is pleased to announce the new establishment of a GK-12 graduate fellowship program supported by a 3-yr grant from the National Science Foundation. This program will team students pursuing PhD???s in ecology at KBS with K-12 science teachers in rural districts of southwest Michigan. Our goals include enriching K-12 science instruction by promoting and nurturing inquiry-based science teaching while providing our graduate students the opportunity to improve their teaching skills and help address the critical national need to improve K-12 science education. GK-12 Fellows may use this experience to supplement or substitute for traditional graduate teaching experience while they pursue their research training towards a PhD in ecology, evolutionary biology, or related field.

Major elements of the KBS program are: (1) Classroom partnerships in which a GK-12 fellow works with a teacher at a district's high school or middle school approximately 15 hrs/wk. Fellows will co-teach and additionally help teachers introduce inquiry activities related to Ecological Literacy into their classrooms and districts. (2) A one week summer teaching institute for fellows, teachers, and mentors, led by MSU College of Education faculty, that will focus on providing inquiry-based approaches to learning for understanding and educational leadership. (3) School-year workshops comprised of science inquiry and teaching components designed to support classroom efforts to incorporate inquiry-based learning in secondary science teaching.

GK-12 Fellows may be supported for up to two years while they work on their dissertation research at KBS, under the supervision of KBS faculty. Stipend support is $30,000/year, plus benefits, including tuition. Support for other years is available through KBS faculty sponsors and departmental, college and university sources. Students interested in the GK-12 program should contact potential KBS faculty sponsors, listed at www.kbs.msu.edu/faculty .Further information about KBS is available at www.kbs.msu.edu, and for further information about the GK-12 program please see www.kbs.msu.edu/gk-12. MSU is an affirmative-action, equal-opportunity institution.

– Jeff Conner Professor Kellogg Biological Station and Department of Plant Biology Michigan State University 3700 East Gull Lake Drive, Hickory Corners, MI 49060 e-mail: connerj@msu.edu http://www.kbs.msu.edu/-Faculty/Conner/Index.htm Phone: 269-671-2269 FAX: 269-671-2104

A Primer of Ecological Genetics by Conner and Hartl (www.sinauer.com/detail.php?id 20)

Jeff Conner <connerj@msu.edu>

KentStateU CircadianClockEvol

One graduate student position (preferably Ph.D.) is available immediately in my laboratory to study microevolution of the circadian clock system in Drosophila melanogaster under long-term acute environmental stress. Applicants should have a background in evolution (theory and molecular genetic laboratory experience) and respective analyses of DNA sequence data.

The position will be fully funded for 4 years (including fees and stipend) with possible extension up to 5 years and should commence in spring or summer 2006.

You may find additional information about my research on my web page (see in the signature).

If interested, please send ASAP (i) a CV with the names and contact details of two referees and (ii) a cover letter explaining your interests and motivation for the position to Dr. Dvornyk from whom further details can be obtained.

Volodymyr Dvornyk

Dr. Volodymyr Dvornyk, Assistant Professor Cunningham Hall, Room 245 Department of Biological Sciences Kent State University P.O. Box 5190 Kent, OH 44242-0001

Tel.: (330) 672-3625 Fax: (330) 672-3713 E-mail: vdvornyk@kent.edu Web: http://dept.kent.edu/biology/-Dvornyk/ "It can't be ever, because it can be never!" (A.P. Chekhov)

Volodymyr Dvornyk <vdvornyk@kent.edu>

NorthwesternChicagoBotanicGarden PlantConservation

Northwestern University and the Chicago Botanic Garden team up to offer a Master[1]s degree in Plant Biology and Conservation

The Program in Plant Biology and Conservation focuses on preparing students for future leadership positions in plant conservation and the botanical sciences. The program offers a Master of Science degree through The Graduate School at Northwestern University and research experience with scientists at the Chicago Botanic Garden. Advanced courses are taught by professors and scientists affiliated with both institutions. Application deadline for Fall admission is April 15, 2006. Please call the program director at 847-467-1266 or visit our webpage for more information. http://www.wcas.northwestern.edu/biosci/-graduate/masters.html nzerega@chicagobotanic.org

QueensUBelfast HoneyBeeViruses

PhD position in molecular evolution (host-parasite coevolution using viral pathogens of honey bees).

A full-time PhD position will become available in spring 2006 to work on the molecular evolution of viral pathogens of honey bees (Apis mellifera) in the labs of Dr. Robert Paxton/Dr Joachim de Miranda (www.qub.ac.uk/bb/people/paxton/paxton.html) and Prof. Ingemar Fries (www.entom.slu.se/eng/staff/-Ingemar_Fries.htm). Arguably the major threat to honeybees and beekeeping worldwide is their debilitating viruses, transmitted by parasitic Varroa mites. The doctoral research will form is part of a larger European project on the genetics and evolution of disease resistance in honey bees (acronym Bee Shop, currently under negotiation). Laboratory work for the advertised PhD position will be based with Dr. Paxton in Belfast (UK), where the student will be registered, and fieldwork will be with Prof. Fries in Uppsala (Sweden). Applicants should have a background in virology and/or evolution (theory and molecular genetic laboratory experience) and be willing to work with honey bees, in addition to a good BSc and/or MSc in a relevant field of biology. The position will be fully funded for 3 years (including fees and stipend) and should commence in spring or summer 2006. We particularly encourage applications from citizens of the new accession states to the European Union and from females. If interested, please send by 28 February 2006 (i) a cv with the names and contact details of two referees and (ii) a cover letter explaining your interests and motivation for the position to Dr Paxton (r.paxton@qub.ac.uk) from whom further details can be obtained.

Robert Paxton <r.paxton@qub.ac.uk>

RothamstedRes AdaptiveDivergence

Development of new computational strategies for identifying genomic regions which have undergone adaptive divergence between populations.

As partially isolated populations each adapt, under natural selection, to their local environmental conditions, so the genotype composition of these populations will diverge at regions of the genome which contribute to these local adaptations. Thus the process of adaptive divergence leaves a genetic signature which it is sometimes possible to detect (in outcrossing species at least) against the noisy background of divergence generated by mutation and random drift. There is a need for improved Bayesian methods to make the best use of the information provided by genotype data from multiple populations in order to identify these genomic regions.

This is a BBSRC CASE Studentship, which attracts a minimum annual stipend of 14,800 British Pounds.

The student will be based at Rothamsted Research. For further information, visit http://www.rothamsted.bbsrc.ac.uk (click on Careers/PhD Studentships)

BBSRC studentships are only available to UK nationals. For full details of BBSRC eligibility criteria please visit the above link.

For enquiries about the project, please contact Dr Kevin Dawson.

E-mail: kevin.dawson@bbsrc.ac.uk

"kevin dawson (RRes-Roth)" <kevin.dawson@bbsrc.ac.uk>

StAndrewsU PlantSystematics

I would be grateful if you could bring the following PhD studentship to the attention of any suitable student who is interested in conducting research for a PhD in the area of plant systematics and evolution. Best regards. Richard.

PHD STUDENTSHIP AT ST ANDREWS UNIVERSITY AND THE SCOTTISH CROP RESEARCH INSTITUTE

Application of a novel snoRNA marker system in plant systematics and evolution

Applications are invited for a PhD studentship jointly funded by St Andrews University and the Scottish Crop Research Institute (SCRI) that will be available from 1 October 2006. The project will focus on the utility of small nucleolar RNA (snoRNA) markers in plant systematics and evolution with particular emphasis on their use in studies of species identification, relationships, hybridization and polyploidization. The project will be supervised by Professor Richard Abbott (St Andrews), Dr Joanne Russell and Professor John Brown (SCRI), with inputs and involvement from Dr Pete Hollingsworth of the Royal Botanic Garden Edinburgh (RBGE). Research will be conducted mainly at SCRI and St Andrews with occasional periods spent at RBGE. Appropriate training will be provided in molecular, taxonomic and evolutionary components of the research. Applicants should have graduated or expect to graduate in 2006 with a first or upper second class honours degree (or equivalent) in a relevant biological subject. Applications including a CV should be submitted to one of the following from whom further particulars may be obtained.

Professor Richard Abbott, Mitchell Building, School of Biology, St Andrews University, St Andrews, Fife, KY16 9TH (rja@st-and.ac.uk)

Dr Joanne Russell, SCRI, Invergowrie, Dundee, DD2 5DA (Joanne.Russell@scri.ac.uk)

– Professor Richard Abbott Mitchell Building, School of Biology University of St Andrews St Andrews, Fife KY16 9TH UK Tel. 01334 463350 Fax. 01334 463366 Email. rja@st-and.ac.uk

Richard Abbott <rja@st-andrews.ac.uk>

UCincinnati Evolution

The Department of Biological Sciences at the University of Cincinnati is welcoming M.S and Ph.D. student applicants to join an active group conducting research in ecology, evolution and behavior. Of particular note is a growing group of faculty studying integrative behavior:

http://bioweb.ad.uc.edu/faculty/buschbeck/-behaviorposter/behaviorposter3.htm The Department offers competitive stipends for graduate students and provides several mechanisms to help students fund and complete research projects. Applications are accepted on a continuing basis. For fall admission applications should be submitted before Feb. 1. Please share this information with prospective graduate students in your department. More information is available at:

http://bioweb.ad.uc.edu/general.asp?subject=grad Ken Petren ken.petren@uc.edu University of Cincinnati

ken.petren@uc.edu

ULaval SalmonidEvolGenomics

We are currently looking for a Ph.D. candidate that would be involved in our ongoing research program aiming at elucidating the physiological and genomic bases of hybrid heterosis (hybrid vigour) in the brook charr (Salvelinus fontinalis). The research program is based on a mutidisciplinary approach that integrates i) the quantification of hybrid vigour for several adaptive traits that can also be important for aquaculture, ii) the comparative analysis of gene expression profiles by means of a 16000 cDNA microarray and RT-PCR, and iii) the endocrine basis for this regulation. More specifically, the Ph.D. candidate will be responsible for testing at the gene expression level two alternative hypotheses generally invoked for explaining heterosis. First, the dominance hypothesis implies that the expression of partially deleterious recessive alleles observed in parental forms will be masked in the hybrid progeny. In contrast, the overdominance hypothesis predicts that the combination of divergent alleles at a given locus will result in increased performance in the hybrid progeny.

We are primarily looking for a candidate with strong laboratory expertise in functional genomics, a solid theoretical background in evolutionary biology, as well as expertise in management and analysis of large data bases. The chosen candidate is expected to be enrolled in our P.D. program by May 2006.

To apply, please send a cover letter describing your research interests, a complete CV and names of three references by e-mail to Louis.Bernatchez@bio.ulaval.ca

To learn more about

Quebec : <http://www.quebecregion.com/f/>http://www.quebecregion.com/f/ Universite Laval : <http://www.ulaval.ca/>http://www.ulaval.ca/ The Biology department : <http://www.bio.ulaval.ca/accueil.aspx?tabindex=0&tabidY>http://www.bio.ulaval.ca/accueil.aspx?tabindex=0&tabidY

The Canadian Research Chair in Conservation Genetics of Aquatic Resources <http://www.bio.ulaval.ca/louisbernatchez/>http://www.bio.ulaval.ca/louisbernatchez/ Louis Bernatchez

Titulaire de la Chaire de recherche du Canada en conservation génétique des ressources aquatiques

Département de biologie Pavillon Charles-Eugène Marchand Université Laval, Quebec QC G1K 7P4 Canada

Tél: 418 656-3402 Fax: 418 656-2043 Couriel: Louis.Bernatchez@bio.ulaval.ca Web: http://www.bio.ulaval.ca/louisbernatchez/

Louis.Bernatchez@bio.ulaval.ca

ULaval SalmonidEvolGenomics2

We are currently looking for a Ph.D. candidate that would be involved in our ongoing research program aiming at elucidating the physiological and genomic bases of hybrid heterosis (hybrid vigour) in the brook charr (Salvelinus fontinalis). The research program is based on a mutidisciplinary approach that integrates i) the quantification of hybrid vigour for several adaptive traits that can also be important for aquaculture, ii) the comparative analysis of gene expression profiles by means of a 16000 cDNA microarray and RT-PCR, and iii) the endocrine basis for this regulation. More specifically, the Ph.D. candidate will be responsible for testing at the gene expression level two alternative hypotheses generally invoked for explaining heterosis. First, the dominance hypothesis implies that the expression of partially deleterious recessive alleles observed in parental forms will be masked in the hybrid progeny. In contrast, the overdominance hypothesis predicts that the combination of divergent alleles at a given locus will result in increased performance in the hybrid progeny.

We are primarily looking for a candidate with strong laboratory expertise in functional genomics, a solid theoretical background in evolutionary biology, as well as expertise in management and analysis of large data bases. The chosen candidate is expected to be enrolled in our P.D. program by May 2006.

To apply, please send a cover letter describing your research interests, a complete CV and names of three references by e-mail to Louis.Bernatchez@bio.ulaval.ca

To learn more about

Quebec : <http://www.quebecregion.com/f/>http://www.quebecregion.com/f/ Universite Laval : <http://www.ulaval.ca/>http://www.ulaval.ca/ The Biology department : <http://www.bio.ulaval.ca/accueil.aspx?tabindex=0&tabidY>http://www.bio.ulaval.ca/accueil.aspx?tabindex=0&tabidY

The Canadian Research Chair in Conservation Genetics of Aquatic Resources <http://www.bio.ulaval.ca/louisbernatchez/>http://www.bio.ulaval.ca/louisbernatchez/ Louis Bernatchez

Titulaire de la Chaire de recherche du Canada en conservation génétique des ressources aquatiques

Département de biologie Pavillon Charles-Eugène Marchand Université Laval, Quebec QC G1K 7P4 Canada

Tél: 418 656-3402 Fax: 418 656-2043 Couriel: Louis.Bernatchez@bio.ulaval.ca Web: http://www.bio.ulaval.ca/louisbernatchez/

Louis Bernatchez <Louis.Bernatchez@bio.ulaval.ca>

ULouisianaLafayette OctocoralGenetics

I have a position available for a student interested in studying genetic variation in deep-sea octocorals. Many deep-sea coral species have broad distributions spanning Atlantic and Pacific Oceans, but little is known about their dispersal and gene flow, or intraspecific variation. Over the past several years we have accumulated a number of samples from hard substrates between 1000 - 2400 meters depth. These will form the core of a project to study genetic variability, biogeography and systematics. Octocorals have been shown to have very low rates of mutation in the mitochondrial genome, and this project will involve developing novel nuclear markers for use at different systematic levels, including intraspecific analyses.

In addition to an available research assistantship in my lab, the University of Louisiana at Lafayette will be awarding up to five University Fellowships and Board of Regents Doctoral Fellowships to students entering the doctoral program in Environmental and Evolutionary Biology in fall 2006. Fellowships are funded for three to four years and carry stipends of $13,900/9 months-$22,000/per year with waivers of tuition and most fees. University Fellows are assigned limited teaching responsibilities; there is no teaching requirement for Board of Regents fellows. To be eligible for these fellowships, applicants must be a US citizen or have a degree from a US institution.

For more information about the biology graduate program visit http://www.ucs.louisiana.edu/ ~ pll6743/-biogradstudies.htm. The Department of Biology has approximately 25 faculty members and 70 graduate students (http://biology.louisiana.edu/). Areas of strength include ecology, conservation biology, evolution, and marine/coastal biology.

If you are interested in this opportunity, please contact me for additional information.

Scott France –

Scott C. France france@louisiana.edu Department of Biology University of Louisiana at Lafayette P.O. Box 42451 Lafayette, LA 70504

Office: (337) 482-6320 Lab: (337) 482-6494 FAX: (337) 482-5834 http://www.ucs.louisiana.edu/ ~ scf4101/ france@louisiana.edu france@louisiana.edu

ULund EvolMolSyst

The University of Lund announces the following vacancy:

POSTGRADUATE SCHOLARSHIP in Biology, within the discipline of Genetics (Evolutionary Molecular Systematics), with placement at the Department of Cell and Organism Biology, Faculty of Science.

Reference Number: 29

Starting Date: As soon as possible

Project Description:

Production and analysis of EST (expressed sequence tags) and cDNA sequences for studying the evolution of vertebrates.

Our group works on various aspects of molecular phylogeny and systematics of vertebrates. Over the last years we have successfully resolved several branches in the vertebrate tree using the data from more than 120 completely sequenced mitochondrial genomes. However, there are still many unresolved issues in the vertebrate tree that could not be resolved with significant support yet. Therefore, we plan to produce, collect and analyze data from nuclear sequences. Data from databases will be complemented by own EST or cDNA data in order to include sequences from species that are not available from databases but which are important to the phylogenetic question. The project is well-funded and all necessary equipment, generous lab space as well a large tissue and cell culture collections are available.

Qualifications:

The applicant should have interest and some knowledge in database search, sequence collection, alignment and/or phylogenetic reconstruction algorithms and may be able to program own scripts and tools to facilitate the data collection and analysis. A genuine interest in vertebrate evolution, phylogenetic analysis and bio-molecular methods, preferentially cDNA libraries and/or EST sequencing will be helpful to manage own projects. It is therefore advantageous to have worked on one or several of these fields during exam work, summer jobs and/or courses. In addition to the analytical work there will be the opportunity to produce own data. The lab-work will include cell culture, RNA isolation, cDNA library construction, and EST sequencing.

If you are interested in this project please send us a short description of your research interest and your computer skills, a CV, the names of two references, a copy of your exams work.

The complete advertisement and all application formalities can be found on:

http://www.biol.lu.se/cellorgbiol/postgrad/-vacant.html Feel free to contact me for further information.

Cheers

Axel Janke

–

Dr. Axel Janke Lund University Department of Cell and Organism Biology Genetics Division of Evolutionary Molecular Systematics Sölvegatan 29 S-223 62 Lund Sweden

http://phylo.gen.lu.se/ Email: axel.janke@cob.lu.se Tel.: +46/46/222 7849 FAX: +46/46/147874

axel.janke@cob.lu.se

UMelbourne popgenetics

PHD POSITION PEST SNAIL POPULATION GENETICS AND REPRODUCTION

Mediterranean white and conical snails (Cernuella virgata, Theba pisana and Cochlicella spp.) are significant pests of grain crops in coastal regions of southern Australia. Existing control methods, including burning of stubble prior to sowing crops, cabling to dislodge snails from aestivation sites, biological control (parasitoid of conical snails only) and chemical control have been only partially successful. A method of snail control that reduces our reliance on chemical pesticides and is species-specific would be highly desirable. The current project will investigate the genetic structure of the pest snail populations and reproductive strategy, in order to determine the suitability for future genetic control methods. The project is a joint venture between CSIRO, The University of Melbourne and the Grains Research and Development Corporation. The PhD student will be based at the University of Melbourne Department of Genetics and will receive training in field work, molecular techniques and population genetics. The student will be required to undertake field work in South Australia and this necessitates a valid Drivers Licence. The PhD student will have a bachelors degree with honours in biological science (specifically genetics). This is a full-time scholarship with a maximum of 3 years funding available, contingent on satisfactory progress. The stipend is valued at $25,000 per annum. To obtain further information contact Dr Belinda Appleton (b.appleton@unimelb.edu.au) or Dr Rod Mahon (Rod.Mahon@csiro.au) Applications including a curriculum vitae citing relevant studies and/or experience, a short statement of research interests, the names and addresses of three professional referees, and a copy of an official academic record/transcript should be forwarded as soon as possible to Dr Belinda Appleton, Department of Genetics, The University of Melbourne, Parkville, Victoria, 3010, or via email b.appleton@unimelb.edu.au.

b.appleton@unimelb.edu.au

USouthDakota EvolStalkEyedFlies

Graduate Research in Evolutionary Physiology of Stalk-Eyed Flies

I have an opening for a Ph. D. graduate student interested in research on the performance and fitness consequences of elaborate secondary sexual characters in insects using stalk-eyed flies as a model. Stalk-eyed flies provide the ideal model system to test for costs and tradeoffs related to male ornamentation. All species in this extraordinary family display exaggerated head morphology, with eyes and antennae displaced at the end of long stalks, and interspecific variation in eye span can be more than ten-fold. Furthermore, all available evidence indicates that eye stalks are critical sexual signals used in both male-male competition and female choice. This study will examine the effects of elongated eye stalks on flight performance and survivorship of stalk-eyed flies to assess whether these effects run counter to the effects of sexual selection. The position is part of an NSF-funded CAREER project in the laboratory of John Swallow (http://www.usd.edu/-~jswallow/index.html), Biology Department, University of South Dakota. Opportunities exist to develop a PhD research program that cover a variety of related issues (flight performance, flight energetics, predation avoidance) but I am particularly interested in finding someone to be involved in a series of mesocosm predation studies. Support will be a combination of Teaching and Research Assistantships. If interested please contact John Swallow (jswallow@usd.edu) Assistant Professor, Department of Biology, University of South Dakota, Vermillion, SD 57069, USA. Information regarding our graduate program and the application process can be found at the following web site: http://usd.edu/biol/graduateprogram.cfm

John G. Swallow

Assistant Professor Department of Biology University of South Dakota 414 E. Clark Street Vermillion, SD 57069 USA

Phone (605) 677-6176 Fax (605) 677-6557 http://www.usd.edu/~jswallow/

"Swallow, John G." <John.Swallow@usd.edu>

USussex EvolBiol

The University of Sussex has a number of a PhD opportunities in Evolutionary Biology to work with either

Adam Eyre- Walker (a.c.eyre-walker@sussex.ac.uk) on the process of mutation, the rates and fitness effects of new mutations or the rate of adaptive evolution.

Joel Peck (j.r.peck@sussex.ac.uk) on theoretical studies of the evolution of altruism, and related issues. Among these related issues are the conditions for effective group selection, the possibility of selection at the level of ecological communities, the major transitions in evolution, and the meaning of "information" in biological systems."

or

David Waxman (d.waxman@sussex.ac.uk) on the theoretical population genetics of quantitative traits, evolutionary adaptation, the behaviour and evolution of social insects, and the evolution of transposable elements.

Funding is potentially available for either UK or EU students and may last up to 4-years. Additional information can be found at http://www.lifesci.sussex.ac.uk/CSE/. Informal applications need to be received by friday feb 10th by any one of the above.

UWindsor EvolEcol

Graduate positions are available in fish sensory ecology/evolution ? Two graduate assistant positions are available in the laboratory of Dr. Dennis Higgs (http://www.uwindsor.ca/HiggsLab.htm) at the University of Windsor beginning September, 2006. One of the two positions will be in collaboration with Dr. Daniel Heath (http://cronus.uwindsor.ca/units/glier/genetics/lab.nsf) on the evolution of hearing, using advanced techniques in electrophysiology and DNA sequencing. The second assistantship is in the area of auditory behaviour and ecology. Assistantships will be at the Master?s or Ph.D. level, dependent upon interests and abilities of applicants. Some knowledge and appreciation of sensory ecology and evolution is required but training in electrophysiology, sequencing, and/or behavioural analysis will be provided. Interested parties should contact Dr. Higgs at dhiggs@uwindsor.ca with a statement of interest and a curriculum vitae.

dheath@uwindsor.ca

UWindsor FishSensoryEcolEvol

Graduate student positions are available in fish sensory ecology/evolution ? Two graduate student positions are available in the laboratory of Dr. Dennis Higgs (http://www.uwindsor.ca/HiggsLab.htm) at the University of Windsor beginning September, 2006. One of the two assistantships will be in collaboration with Dr. Daniel Heath (http://cronus.uwindsor.ca/units/glier/genetics/lab.nsf) on the evolution of hearing, using advanced techniques in electrophysiology and DNA analysis. This position will require travel for onsite electrophysiology. The second assistantship is in the area of auditory behaviour and ecology. Assistantships will be at the Master?s or Ph.D. level, dependent upon interests and abilities of applicants. Some knowledge and appreciation of sensory ecology and evolution is required but training in electrophysiology, sequencing, and/or behavioural analysis will be provided. Interested parties should contact Dr. Higgs at dhiggs@uwindsor.ca with a statement of interest and a curriculum vitae.

Daniel Heath Great Lakes Institute for Environmental Research University of Windsor 401 Sunset Ave Windsor, Ont, Canada N9B 3P4

E-mail: dheath@uwindsor.ca Phone: (519) 253-3000, Ext 3762 Fax: 971-3616

dheath@uwindsor.ca

UWindsor FishSensoryEvol

Graduate student positions are available in fish sensory ecology/evolution ? Two graduate student positions are available in the laboratory of Dr. Dennis Higgs (http://www.uwindsor.ca/HiggsLab.htm) at the University of Windsor beginning September, 2006. One of the two assistantships will be in collaboration with Dr. Daniel Heath (http://cronus.uwindsor.ca/-units/glier/genetics/lab.nsf) on the evolution of hearing, using advanced techniques in electrophysiology and DNA analysis. This position will require travel for onsite electrophysiology. The second assistantship is in the area of auditory behaviour and ecology. Assistantships will be at the Master?s or Ph.D. level, dependent upon interests and abilities of applicants. Some knowledge and appreciation of sensory ecology and evolution is required but training in electrophysiology, sequencing, and/or behavioural analysis will be provided. Interested parties should contact Dr. Higgs at dhiggs@uwindsor.ca with a statement of interest and a curriculum vitae.

dheath@uwindsor.ca

UmeaU SpatialPopEvol

PhD position in spatial population ecology I am looking for a PhD-student to participate in the “Spatial heterogeneity, functional responses and predator-prey dynamics”, financially supported by the Swedish Research Council.

Why are there so many species? This question is motivated by the finding that simple models and model systems are fragile - species extinctions are ubiquitous- and increasing the realism by including more species tend to make systems even more unstable. Many ecologists believe that the answer is that spatial heterogeneity stabilizes ecological systems. The objective of the project is therefore to increase our understanding of how spatial heterogeneity affects predator-prey dynamics. This is done by applying and developing a new theoretical tool, moment approximation, which can be used to investigate how population dynamics are influenced by spatial heterogeneity. The project includes testing a predator-prey model based on moment approximation, developing empirical models of the relationship between predator-prey covariance and population densities, and studying the relationship between covariance and density dynamics in published models and empirical data sets. The project has an emphasis on mathematical and statistical models but will also include predator-prey experiments in the lab. The project is intellectually challenging but will likely yield publications in top-ranked journals.

More information at my webpage: www.emg.umu.se/-personal/goran_englund.htm The application should include a short description of your research interests and why you are interested in the position, CV, copies of certificates from higher education, copies of publications including Bachelors/Masters thesis, and updated contact information for reference persons. Further information can be obtained from Dr. Göran Englund email: <mailto: goran.englund@emg.umu.se> goran.englund@emg.umu.se. Send your application, quoting appropriate reg.no 313 4666-05, to Umeå University, The Registrar, SE-901 87, Umeå, Sweden, no later than February 20, 2006.

* Göran Englund * Department of Ecology and Environmental Science * Umeå Marine Sciences Centre * Umeå University, 901 87 Umeå, Sweden * Phone: +46 90 786 9728, FAX: +46 90 786 6705 * E-mail: Goran.Englund@emg.umu.se * Homepage: http://-www.emg.umu.se/sve/personal/goran_englund.htm *

UppsalaU EvolFuncGenomics

Graduate position: at the Department of Evolutionary Functional Genomics

One PhD student position is available at the Department of Evolutionary Functional Genomics at Uppsala University. A major focus of the department is the genetic basis of plant adaptation, combining information on gene function from model organisms with studies of variation in adaptive traits in different species. The aim is to identify genes that affect variation in traits such as flowering time and growth rhythm. Our strategy is to integrate traditional ecological and phylogeographic studies with genomics and population genetics, at both theoretical and experimental levels.

The successful applicant will take part in a project on evolutionary functional genomics in Capsella. We are currently working on the common weed, Capsella bursa-pastoris, and also on its rarer relatives Capsella rubella and Capsella grandiflora. Several evolutionary interesting questions are / will be addressed within this project, for example: What is the genetic background of flowering time variation in Capsella and is it different among species? Which evolutionary forces shape DNA sequence variation at adaptive loci? What is the origin of the tetraploid Capsella bursa-pastoris? What is the population history of the three species? Why is the tetraploid Capsella bursa-pastoris more successful and widespread than the other species?

We are looking for an applicant with a strong interest in evolutionary genetics. A master or equivalent in genomics, genetics or a related subject is required and experience in molecular genetics (for example DNA sequencing, QTL mapping or RNA work), bioinformatics or theoretical genetics is an advantage.

The position is for four years. There is also the possibility to teach 10% and thus increasing the time to four and a half years.

The application should include curriculum vitae, degree certificate, a short description of the applicant and his / her experience, references and if requested the applicant should send his/her master thesis.

For further information contact: Anna Palmé, +46 (0)18-471 64 10, anna.palme@ebc.uu.se or Ulf Lagercrantz, +46 (0)18-471 64 18, <mailto:Ulf.Lagercrantz@ebc.uu.se>Ulf.Lagercrantz@ebc.uu.se
Departmental home page: <http://www.genetik.uu.se/>http://www.genetik.uu.se/
Union representatives: Anders Grundström, SACO-rådet, tel 018-481 53 80, Carin Söderhäll, TCO/ST, tel 018-471 19 96 and Stefan Djurström, SEKO, tel 018-471 33 15.

Send your application to: Registrator, UFV-PA 2006/93, Uppsala Universitet, Box 256, 751 05 Uppsala or fax 018-471 2000 no later than February 21 2006. If the application is sent by fax the original papers should be sent to the Registrator within a week of the deadline.

anna.palme@ebc.uu.se anna.palme@ebc.uu.se

UppsalaU PlantEvol

PhD student position in Plant Ecology at the Evolutionary Biology Centre, Uppsala University, Sweden

We seek a PhD candidate with a keen interest in population biology and the ecology and evolution of local adaptation in plants. The PhD student will join the research group of prof. Jon Agren and will work in a project exploring the functional and genetic basis of local adaptation in the outcrossing model plant Arabidopsis lyrata. The project is based on a combination of field experiments designed to identify the targets and agents of selection on morphology and phenology, and quantitative and molecular genetic approaches to identify the genetic basis of adaptive differentiation. It focuses on potentially adaptive characters such as resistance to herbivory, flowering time, and flower morphology. Problems addressed include (a) to what extent is population differentiation maintained by selection? (b) to what extent can selection on morphological and phenological characters be attributed to variation in the abiotic and biotic environment, respectively? (c) What is the genetic basis of plant adaptation? The exact profile of the PhD project will be settled together with the supervisor.

The successful candidate should have a masters or honors thesis in ecology or a related field. Experience from work in population ecology or population genetics is an advantage. Proficiency in English is a requirement.

Applications should include a brief description of undergraduate training, research interests and research experience, and a motivation of why the position is of interest. It should further include Curriculum vitae, an authorized copy of the undergraduate degree, and the names and contact information (address, email address, and phone number) of two-three referees. Relevant publications (including BSc/MSc thesis) should be enclosed.

The candidate will receive her/his postgraduate training within the postgraduate school at the Evolutionary Biology Centre (see http://www.ebc.uu.se/index_eng.htm). The postgraduate training comprises four years of full time studies. The successful candidate will receive a postgraduate fellowship the first year (14400 SEK/month) and a postgraduate position year 2-4 (18700-20900 SEK/month). The position can be combined with up to 20% of teaching asssistantship, which will then prolong the position accordingly. Tentative starting date: 1 April 2006.

Please, feel free to contact Prof. Jon Agren (phone +46 18 471 2860, jon.agren@ebc.uu.se) for more information.

Applications, quoting the reference number UFV-PA 2006/197 should arrive no later than February 15, 2006 at the Registrars office, Uppsala University, Box 256, SE-751 05 Uppsala, Sweden.

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

UtahStateU Evol

The College of Natural Resources at Utah State University is pleased to offer PhD Quinney Fellowships in all areas of Natural Resources Management, Ecology and Evolution. Fellowships pay $20,000 per annum for up to five years. For application details, please go to www.cnr.usu.edu <http://www.cnr.usu.edu/> and click on the Quinney Phd link on the right side of the page.

Professor Todd A. Crowl Director of Research & Graduate Education College of Natural Resources

“Todd A. Crowl” <tacrowl@cc.usu.edu>

VrijeU MolEcoEvol

Graduate position Molecular Ecotoxicology (f/m) Full working hours

Vacancy number: 1.2005.00247

The department of Animal Ecology, which is part of the Faculty of Earth and Life Sciences, Vrije Universiteit Amsterdam (The Netherlands), has a vacancy for a PhD student.

Job description

The student will conduct a research project entitled: Stress-based expression profiles in soil arthropods, which is part of the program Assessing the living soil. An ecogenomics approach to explore and unlock sustainable life support functions of soils. Genomic tools will be used to characterize and evaluate biological functions of the living soil. The aim is to link expression profiles with characteristics of the soil, in particular with the degree and type of pollution. Eventually this will lead to the development of a rapid microarray-based method of soil diagnosis. The aim of this Ph.D. project is to provide an understanding at the gene expression level of inhibition of Folsomia candida reproduction, growth and survival by soil contaminants. Firstly, the invertebrate soil quality chip will be used to study transcription profiles of springtails exposed to clean soils from different environments to create a normal operating range (NOR) of the F. candida transcriptome. Subsequently, effects of soil contaminants (metals, PAHs, oil) on the F. candida NOR will be investigated. The data will give more insight in the molecular consequences of sub lethal effects and will contribute to the development of a new framework for the diagnosis of ecological quality of soils.

Requirements

Molecular biologist with an interest in ecotoxicology;

Experience in statistical analysis of gene expression data is an advantage;

Good social skills necessary for working in the laboratory with colleagues.

Particularities

The appointment will be fulltime for an initial duration of 12 months. After satisfactory completion the appointment will be extended to a total duration of 4 years. Visit our website <http://www.vu.nl/-vacatures>www.vu.nl/vacatures for a review of working conditions at the VU.

Salary

The gross salary will be 1.877 Euro a month (first year) gradually increasing to $\neg 2.407, -amonth(fourthyear)$.

Additional information

About 75% of the time is devoted to research, the remaining 25% to education and assistance in courses. The education program is organized by the national research school on Environmental Science (SENSE). Applicants may request the complete project description from Désirée Hoonhout, tel +31-20 59 87004. Further information can be obtained from Dr. D. Roelofs, tel +31-20 59 87078, e-mail: <mailto: dick.roelofs@ecology.falw.vu.nl> dick.roelofs@ecology.falw.vu.nl, or Prof.dr. N.M. van Straalen, tel: +31-20 59 87070.The project will start by March 1st 2006.

Applications

Written applications should be addressed before February 1st to the Vrije Universiteit, Dr. J.M.R.M. Neutelings, Managing Director, Faculty of Earth and Life Sciences, De Boelelaan 1085, 1081 HV Amsterdam, The Netherlands (the vacancy number should be mentioned on the letter and on the envelop) or e-mail to: <mailto: %20falw-vacature@falw.vu.nl> falw-vacature@falw.vu.nl.

Dick Roelofs

Vrije Universiteit, Animal Ecology Room H-147 Phone: +31-20-5987078

dick.roelofs@ecology.falw.vu.nl

Jobs

Albany CuratorOrnithology

New York State Museum/NY State Education Department

SENIOR SCIENTIST (ZOOLOGY), SG-22 Curator of Ornithology

Location: Albany, NY Salary: $53,080*

The New York State Museum seeks applicants for a permanent curatorial and research position of Senior Scientist (Zoology), Grade 22, Ornithology. Duties include, but are not limited to, the following:

Conduct independent and interdisciplinary collections-based research on the birds in and beyond New York State; curate and augment the Museum's ornithology collection; seek funding for field and laboratory research and collections programs through competitive grants and other outside sources; prepare research results for presentation at professional conferences, public programming events, peer-reviewed publication, and exhibitions; communicate research to the Museum's diverse audiences, including outreach to groups not traditionally represented in other museum audiences; and develop public programs. The applicants' research program should be in evolution, molecular systematics, ecology, zoogeography, or natural history.

MINIMUM QUALIFICATIONS: Ph.D. in one of the biological sciences and two years of research experience in ornithology.

Preferred candidates will have experience in care and management of ornithology collections, a record of research and peer-reviewed publications, and a record of participating in regional and national scientific conferences. Candidates should demonstrate the ability to obtain outside funding through grants and/or other sources.

*Leads to a maximum salary of $65,502 based on annual performance advances.

CONDITIONS OF EMPLOYMENT: This will be a provisional appointment pending a new Civil Service examination.

APPLICATION DEADLINE: Qualified candidates should send a resume, a list of three references, a statement of research interests, and letter of interest by February 17, 2006 to:

Ms. Gayle Bowden Director, Human Resources Management Box NC-124 NYS Education Department 89 Washington Avenue, Room 528 EB Albany, NY 12234 Fax (518) 486-5631 E-mail: ncrowley@mail.nysed.gov

Jason R. Cryan, Ph.D. Director, Laboratory for Conservation and Evolutionary Genetics New York State Museum 3140 Cultural Education Center Albany, NY 12230 Phone: (518) 486-2008 E-Mail: jcryan@mail.nysed.gov FAX: 518-486-2034

Lab Website: www.nysm.nysed.gov/lceg/ NOTE ON SENDING ATTACHMENTS: The NY State Education Department's e-mail system blocks delivery of messages with some types of attachments (e.g., .zip and .exe files). If you are sending me such an attachment, please change the file extension to ".sed" and tell me about the change in the text of your message.

Jason Cryan <JCRYAN@MAIL.NYSED.GOV>

DalhousieU EvoDevo

As advertised in "Science"

Position in Biology: Developmental Biology Department of Biology Dalhousie University

The Department of Biology at Dalhousie University invites applications for a full-time probationary tenure-track position at the rank of Assistant Professor in Developmental Biology. The appointment will be effective 1 July 2006. Candidates must have a Ph.D. degree and demonstrated excellence in research potential. Preference will be given to applicants who use molecular techniques, have postdoctoral experience and demonstrate high teaching ability. The successful candidate will be expected to develop an internationally recognized, externally funded research program, teach undergraduate and graduate courses and supervise honors students and graduate students at the M.Sc. and Ph.D. levels.

Applications, including curriculum vitae, statements of research and teaching interests, and letters from three referees, may be submitted in confidence to:

Dr. M.O. Johnston Chair of Developmental Biology Search Committee Department of Biology Dalhousie University Halifax, Nova Scotia B3H 4J1 Canada

All correspondence will be acknowledged. Applications will be accepted until 28 February 2006.

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. Dalhousie University is an Employment Equity/Affirmative Action employer. The University encourages applications from qualified Aboriginal people, persons with disabilities, racially visible persons, and women.

– M.O. Johnston Professor Dept. of Biology Dalhousie University 1355 Oxford St. Halifax, Nova Scotia, CANADA B3H 4J1 Tel. (902) 494-8005 or 3515, Fax (902) 494-3736

Lab Website http://biotype.biology.dal.ca/~mjohnst/index.html Mark.Johnston@Dal.Ca Mark.Johnston@Dal.Ca

France PermanentResearcher

Dear all

This is to inform you about an attractive job offer in France the yearly announcement of researcher positions financed by the French Funding Organization Centre National de la Recherche Scientifique (CNRS). These are *life-time 100 % research* positions offered in an international competition to excellent candidates. The web page is http://www.sg.cnrs.fr/drhchercheurs/concoursch/default-en.htm. Posts are available, for instance in Biodiversity, evolution and biological adaptations: from macromolecules to communities, and Biological systems modelization, bioinformatics. The deadline, regrettably, is January, 16.

THE TYPES OF POSTS (see also http://www.sg.cnrs.fr/drhchercheurs/concoursch/chercheur/default-en.htm, http://www.sg.cnrs.fr/drhchercheurs/concoursch/informer/default-en.htm, http://www.sg.cnrs.fr/drhchercheurs/concoursch/pdf/guide-en.pdf): There are chargés de recherche, 2nd and 1st degree, and directeurs de recherche, 2nd and 1st degree, i.e. Associate Scientists after dissertation and after 4 years of experience, and Senior Scientists after 8 years or 12 years of experience, respectively. According to my experience already the Chargés de Recherche are actually free to do what they want within an overall, very large disciplinary category (there are some 40 categories defined for all sciences together). Directeurs are of course expected to, finally, develop leading roles. This may mean becoming leader of a team as proposed and agreed upon by the Research Unit (Unité Mixte de Recherche, UMR) and to search for extramural funds, which are scarce in France. Experience in such leading functions is thus an important plus for an application to a directeur post. And of course publications. Even though strange things are happening, multiple first or senior authored publications per year with an overall impact of 4 or more seem to be useful, but its open end. For Chargé, 2nd degree, several good publications from the PhD are probably needed.

THE PROFILES If you go to http://gestionoffres.dsi.cnrs.fr/fo/offres/default-en.php you will find a number of posts offered in the sections 29 (Biodiversity, evolution and biological adaptations: from macromolecules to communities), 44 (Biological systems modelization, bioinformatics), and also 20 (Continental Surfaces and Interfaces, which includes vegetation). But note that by further clicking on the numbers given to the jobs (e.g. N29/02) you will find that the Chargé positions (Associate Scientists) in sections 29 and 20 are focused to quite restricted fields of research. This is where science politics comes into play.

THE RECRUITMENT Directeur (Senior scientists) posts are told be more difficult to obtain for someone that comes from outside the French system. A so-called poste rouge is often recommended in advance, a funding for half a year within the host institution. Even for demanding a Chargé position, advance visits in the host lab may be appreciated. Obviously, this is hardly possible anymore for the deadline 16 January 06. A visit to the lab after having submitted the application seems to be very much expected in all cases. Generally, French institutions *do not* reimburse candidates the travel costs to visit labs or to come to interviews etc.. Yes, this is a shame. I hope we have some funds here at Rennes, but this is not sure.

After having applied *all* candidates will be invited to a presentation and an interview in Paris in spring 2006 (see http://www.cnrs.fr/comitenational/calend/printe06/cprint06.pdf). Travel costs will *not* be reimbursed by the CNRS, and on the level of host Units funds may be scarce, too. Presentations and interviews can be in English, French is possibly a plus.

I personally could offer help in putting together an application for qualified candidates with a project willing to choose University of Rennes 1 and to work here on the interface between ecology and phylogeny preferably of plants or, alternatively, on the diversity and diversification of arthropods in the canopy. The host lab here is the UNITE MIXTE DE RECHERCHE ECOSYSTEMES , BIODIVERSITE , EVOLUTION with particular expertise in mechanisms of speciation, life history evolution, and adaptation, expertise at the interface between macroevolution and macroecology, expertise in ecophysiology, landscape ecology and soon also behavioral ecology. It is a large institution with

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

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IPK Germany PlantGeneFlow

Hi,

I have a six month internship position from the "The International Association for the Exchange of Students for Technical Experience"

http://www.iaeste.org/network/index.html The position will begin in April/May 2006, and will involve both flow cytometric analyses of apomictic (asexual reproduction through seed) seed production, and molecular genetic analyses (microsatellite) of plants in the North American genus Boechera (wild relative of Arabidopsis). I am looking for someone who has basic molecular biology skills who also likes to work with computers, since many of our analyses are automated. Knowledge of German would be helpful, but is not required.

The candidate must be registered at a university, but you should also contact your local IAESTE office for more details on any restrictions (see above link).

The IPK is a large and well-endowed research center located about 2 hours southwest of Berlin, in the foothills of the beautiful Harz Mountains.

Please don't hesitate to contact me if you have any questions, or would like to apply.

Best wishes, Tim

Dr. Tim Sharbel Apomixis Research Group Dept. of Cytogenetics Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstraße 3, D-06466 Gatersleben Germany Email: sharbel@ipk-gatersleben.de

Apomixis Group Webpage http://www.ipk-gatersleben.de/en/02/04/05/index.html IPKWebpage www.ipk-gatersleben.de tel: +049 (0)39482 5608 fax: +049 (0)39482 5137

IowaStateU Genetics

Lush Endowed Chair in Animal Breeding and Genetics - IOWA STATE UNIVERSITY

The Department of Animal Science at Iowa State University invites applications for the Lush Endowed Chair in Animal Breeding and Genetics, which will be filled at the level of Associate or Full Professor level. This newly established Lush Endowed Chair will be an integral part of the Animal Breeding and Genetics group of 15 faculty at Iowa State University (http://www.ans.iastate.edu/section/abg/), which builds on the legacy of Jay Lush and is further enhanced by multiple collaborating faculty in related disciplines through the Center for Integrated Animal Genomics (http://www.ciag.iastate.edu/) and interdisciplinary graduate programs in genetics (http://www.genetics.iastate.edu), bioinformatics and computational biology (http://www.bcb.iastate.edu), and statistics (http://www.stat.iastate.edu).

Candidates should be recognized international scientists in Animal Breeding and Genetics or related fields and are expected to lead a competitive research and education program of international stature at Iowa State University. Applicants should submit a complete resume and names and contact information of three references to Dr. Maynard Hogberg, Chair, Department of Animal Science, 1221 Kildee Hall, Iowa State University, Ames, IA 50011- 3150, (tel: 515-294-2160; fax: 515-294-6994; e-mail: hogberg@iastate.edu). Applications will be accepted until March 1, 2006, or until a suitable candidate has been found. Iowa State University is an Equal Opportunity/Affirmative Action Employer. Women and minorities are encouraged to apply.

fjanzen@iastate.edu

Kastanienbaum ResTech

We are looking for an active, well-organized person to work 50% for the molecular lab in the Aquatic Ecology & Evolution Department located at EAWAG Limnological research centre in Kastanienbaum.

General responsibilities will include managing the purchasing, accounting and invoicing of supplies, maintaining databases and tissue collections, overseeing lab duties, assisting in student training. Specific responsibilities will be standard molecular lab work (e.g. DNA isolation, PCR, sample preparation for sequencing, editing sequence data and scoring fragment markers).

The ideal applicant will have had experience in managing a genetics laboratory (i.e., maintenance of laboratory equipment, facilities and frozen tissue collections, and purchasing of supplies and equipment) and in the application of molecular genetic methods (including PCR, microsatellites, AFLP and DNA sequencing using capillary sequencers).

Tidiness, attention to detail, good organizational skills and ability to manage people are a must.

Pre-requisite is an M.Sc. in a molecular biology field or a minimum of a B.Sc. in a related field with at least one year of experience in a molecular biology or molecular systematics environment, with working knowledge of standard molecular lab protocols. Our lab uses molecular markers for population genetics and phylogenetics of speciation and ecological differentiation of aquatic organisms, predominantly fishes. Current research group size is 2 or 3 senior researchers and/or postdocs, 4 PhD students and a fluctuating number of MSc students that use the molecular lab. For further details, see our website at http://www.fishecology.ch/ . This is a 12 months position, potentially renewable for several years.

Please apply by email with a letter expressing interest, your CV and names of three references sent to Michelle.Sidler@eawag.ch. Applications must be received by January 31, 2006, but applications will be considered until the post is filled. Start date is expected to be no later than March 1, 2006. Inquiries should be made to Dr Vicky Schneider (vicky.schneider@eawag.ch) or Prof. Ole Seehausen (ole.seehausen@aqua.unibe.ch).

ole.seehausen@eawag.ch ole.seehausen@eawag.ch

MaxPlanck Inst Ornithology EvolGenetics

Job Announcement

Evolutionary Geneticist

A full-time position is available at the Max Planck Institute for Ornithology to work in the research group Behavioural Ecology and Evolutionary Genetics. We are looking for a highly motivated scientist who is interested to participate in an ongoing research program aimed at identifying the genetic basis of variation in behaviour and sexually selected ornaments. We expect a profound knowledge of the analytical and laboratory skills required to use a candidate gene approach on a variety of questions related to avian behavioural ecology. Our current research focuses on reproductive behaviour, including timing of reproduction, effects of inbreeding, mate choice, the evolution of promiscuity, avian personalities and avian olfaction.

We offer a highly stimulating, international environment, outstanding research facilities including a fully equipped molecular laboratory, technical assistance, and superb logistic support. The working language is English. The position does not require teaching, but teaching is encouraged via existing contacts and collaboration with the University of Munich (LMU).

Applicants should have finished their PhD. Selection will be based on experience, motivation and the potential to integrate in the ongoing research program. The position will be filled as soon as a suitable candidate has been found. The position is initially for two years, with an option to become permanent.

The salary will be according to German public service rules and includes social security benefits. The Max Planck Society is an equal opportunity employer and encourages disabled persons to apply. It also aims at increasing the number of female staff members in fields where they are underrepresented, and therefore encourages women to apply.

Candidates should send a curriculum vitae and a statement of past research and relevant experience to the (email) address below. To ensure full consideration, applications should arrive before February 15, 2006. Informal enquiries can be made to Bart Kempenaers (b.kempenaers@orn.mpg.de).

Heike Gorny Max Planck Institute for Ornithology Postfach 15 64 D-82305 Starnberg (Seewiesen) Germany E-mail: gorny@orn.mpg.de Phone: +49-(0)8157-932-232 Fax: +49-(0)8157-932-400

Bart kempenaers <b.kempenaers@orn.mpg.de>

RiceU LabFieldTech

Job, Lab/Field Technician

Two newly established labs at Rice University are looking for a shared technician, to start immediately or by March 1, 2006. Duties will include both labwork and fieldwork examining the ecology and evolution of plant-animal and plant-microbe interactions. Candidates should have B.A./B.S. in biology and some hands-on experience in field and/or lab biology. Training will be provided, but experience with DNA techniques (PCR, sequencing) and/or microbial methods (endophytic or mycorrhizal fungi) is a bonus. The position is classified as full-time, temporary (6-24 months). Salary is in the range $1600-$2080 per month depending on experience. This position would be an excellent fit for someone planning on graduate study in ecology & evolutionary biology, as there will be the opportunity to gain experience in a number of research areas and to coauthor papers. Please send a resume and contact information for three references by email (kwhitney@rice.edu) or by post (K. Whitney/J. Rudgers, Dept. of Ecology and Evolutionary Biology, MS 170, Rice University, Houston TX 77251-1892).

kwhitney@rice.edu kwhitney@rice.edu

SanJuanPR GenomicsFacilitiesManager

We are looking for a person with established managerial and technical skills to help integrate and expand the Sequence and Genotyping Facility (http://dnaseq.hpcf.upr.edu/files/sequencing.html) located at the University of Puerto Rico-Rio Piedras, in the city of San Juan. The person will be hired under the Alliance for the Advancement of Biomedical Research Program (AABRE) (http:// aabre.hpcf.upr.edu/). Key duties and responsibilities include: (1) Maintaining molecular and computer equipment associated with core Sequencing and Genotyping. Equipment includes MegaBASE 1000 DNA sequencer, Li-Cor NEN Global DNA Analyzer System, and Odyssey Infrared Imaging System, and various key support equipment.

(2) Running centralized Laboratory Information Management System (LIMS) that includes a web-based interface for data archiving, dissemination, manipulation, and analysis for genomics core facilities.

(3) Running yearly workshops designed to train postdoctoral researchers, students, and technicians on ma-

jor equipment and emerging research techniques.

(4) Coordinating with the manager of the Bioinformatics Satellite laboratory and researchers at the High Performance Computing Facilities (HPCf) on the development of critical database resources for genomic research.

(5) Coordinating with biological and biomolecular science researchers to identify and secure funding avenues for infrastructure improvements in genomics and bioinformatics in Puerto Rico.

(6) Facilitating grant writing and project development.

Salary Range: $22,000-$35,000 (including benefits) depending on qualifications. Position has an initial appointment of four years, with opportunities for continued support. Senior personnel are encouraged to apply. The University of Puerto Rico is an equal opportunity/affirmative action employer. Applications from minorities and women are encouraged.

The University of Puerto Rico-Rio Piedras: UPR-RP is the oldest and largest campus of the UPR system. It has an active and growing research community in molecular genetics with a developing emphasis on genomic/functional genomic research. Key areas of research include neurobiology, development, evolutionary genomics, phylogenetics, and behavior.

Contact: Send CV and covering letter to W. Owen McMillan, Department of Biology, University of Puerto Rico-Rio Piedras, P.O. Box 23360, San Juan, PR, 00931. E-mail: wmcmill@rrpac.upr.clu.edu.

Questions may also be addressed to:

Jason T. Rauscher, Ph.D. Assistant Professor Department of Biology University of Puerto Rico, Rio Piedras P.O. Box 23360 San Juan, PR 00931-3360 tel: 787 764 0000 (ext. 7764) e-mail: rauscher@evoandes.net

rauscher@evoandes.net

TennesseeStateU EvolEcol

Job Title Assistant/Associate Professor Tenure Track - Biological Sciences

Job application online at: http://www.tnstate.edu/- Use pull-down menu (I want to ...) Position Number 007271

Teach undergraduate major and graduate courses in ecology, biostatistics and area of expertise. Establish an externally funded ongoing research program and direct undergraduate and graduate students' research projects. Minimum Qualifications/Experience Required is a Ph.D. degree in biology or related field with two or more years of postdoctoral experience. Also required is evidence of commitment to teaching with demonstrated research capability in ecology or environmental science and experience with advanced statistical methodology and modeling. Special Instructions to Applicants Please scan a copy of your doctorate transcript into the system. If you have problems attaching any of your documents, please call the Human Resources Office at 615-963-5285. Job Close Date 02-28-2006 Job Category Faculty Requisition Number 0195 Benefits Tennessee State University offers an excellent benefits package. Regular full-time employees are eligible to participate in a major medical/health plan, dental plan and disability plan; and accrue sick and/or vacation leave. In addition, several educational programs are available for employees of the University.

Thanks once again.

Phil Ganter

Phil Ganter <pganter@tnstate.edu>

TexasStateU PlantBiologist

Plant Biologist

The Texas State University Department of Biology invites applications for a tenure-track plant biologist position at the assistant professor level. An earned Ph.D. is required and a research program involving the application of field and molecular techniques to the conservation and management of plant populations, a record of extramural funding, and postdoctoral research and teaching experience are preferred. Salary and start-up packages are competitive. To apply, submit by mail a statement of teaching and research interests, curriculum vitae, unofficial transcripts, copies of up to four published papers, and contact information for four references to: Dr. David E. Lemke, Chair, Plant Biologist Search Committee, Department of Biology, Texas State University-San Marcos, San Marcos, TX 78666. Review of applications begins on March 1, 2006 and will continue until a suitable candidate is identified. Please visit http:// <http://www.bio.txstate.edu>www.bio.txstate.edu for a full description of the position and the Department's programs and faculty. Texas State is an Equal Opportunity Employer and is committed to increasing diversity in faculty and administrative positions. –

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 E-mail: gabor@txstate.edu

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

UBerne MolGeneticsTech

We are looking for an active, well-organized person to work 50% as a molecular genetics technician in the EAWAG and University of Berne Aquatic Ecology & Evolution Department located at EAWAG Limnological research centre in Kastanienbaum.

General responsibilities will include managing the purchasing, accounting and invoicing of supplies, maintaining databases and tissue collections, overseeing lab duties, assisting in student training. Specific responsibilities will be standard molecular lab work (e.g. DNA isolation, PCR, sample preparation for sequencing, editing sequence data and scoring fragment markers).

The ideal applicant will have had experience in managing a genetics laboratory (i.e., maintenance of laboratory equipment, facilities and frozen tissue collections, and purchasing of supplies and equipment) and in the application of molecular genetic methods (including PCR, microsatellites, AFLP and DNA sequencing using capillary sequencers).

Tidiness, attention to detail, good organizational skills and ability to manage people are a must.

Pre-requisite is an M.Sc. in a molecular biology field or a minimum of a B.Sc. in a related field with at least one year of experience in a molecular biology or molecular systematics environment, with working knowledge of standard molecular lab protocols. Our lab uses molecular markers for population genetics and phylogenetics of speciation and ecological differentiation of aquatic organisms, predominantly fishes. Current research group size is 2 or 3 senior researchers and/or postdocs, 4 PhD students and a fluctuating number of MSc students that use the molecular lab. For further details, see our website at http://www.fishecology.ch/ . This is a 12 months position, potentially renewable for several years.

Please apply by email with a letter expressing interest, your CV and names of three references sent to Michelle.Sidler@eawag.ch. Applications must be received by January 31, 2006, but applications will be considered until the post is filled. Start date is expected to be no later than March 1, 2006. Inquiries should be made to Dr Vicky Schneider (vicky.schneider@eawag.ch) or Prof. Ole Seehausen (ole.seehausen@aqua.unibe.ch).

ole.seehausen@eawag.ch ole.seehausen@eawag.ch

UCaliforniaRiverside EvolEcol

Faculty Position ? Assistant Professor Evolutionary Ecology University of California, Riverside

The Department of Biology seeks applications for a position at the level of Assistant Professor in the general area of evolutionary ecology. We are interested in individuals who are strongly quantitative, working to link data with theory. Taxonomic focus and system are open, but preference will be given to candidates who work in the areas of coevolution, metapopulation dynamics or interspecies interactions, and whose research complements some aspect of existing college strengths in ecology, evolution, physiology, behavior, paleobiology and genetics. The successful candidate will be expected to establish and maintain a vigorous research program, have a strong commitment to excellence in teaching in the graduate program in Evolution, Ecology and Organismal Biology, and in the undergraduate programs in Biology and Biological Sciences. There will also be an opportunity to participate in other programs, such as the Graduate Program in Genetics, Genomics, and Bioinformatics or to be affiliated with the Center for Conservation Biology.

Interested individuals should submit the following: (1) a curriculum vitae, (2) a statement of research and teaching interests, (3) samples of relevant publications, and (4) have three letters of recommendation sent to:

Chair, Evolutionary Ecology Search Committee Department of Biology 1208 Spieth Hall University of California, Riverside Riverside, CA 92521

For additional information about the UCR campus, the College of Natural and Agricultural Sciences, and the Department of Biology, visit our web sites (http://www.ucr.edu/ ;http://www.ucr.edu/ ;http://-www.biology.ucr.edu/). The University of California is an Affirmative Action/Equal Opportunity employer.

David Reznick (david.reznick@ucr.edu)

UCollegeDublin SummerRes

Dear all,

Applications for the 2006 summer undergraduate research programme are now open.

Full funding is available for 12 international students to attend a new summer research programme in Dublin (10 week course). Apologies for cross-postings; please circulate widely! If you know of any students who are qualified to apply for this summer's programme, please pass on the information below.

Cheers,

Julia

Collections-based Biology in Dublin Undergraduate Research Experience and Knowledge Award (UREKA) CoBiD is the joint programme for teaching and research linking University College Dublin and the National Museum of Ireland (Natural History Division). The UREKA award provides funding for students currently completing their first degree to join CoBiD researchers in a ten-week summer programme in Dublin. Collections-based Biology in Dubin (CoBiD) provides an exciting research environment, with experience both in high quality laboratories in the science departments in University College Dublin, and important international research centre in the National Musuem of Ireland (Natural History) collections in Dublin city centre. The CoBiD- UREKA summer programme is a ten-week intensive research course for undergraduate students. Diverse research projects are offered, with topics ranging from systematic biology including traditional and molecular techniques to ecology and population genetics. Students will work side-by-side with curators and senior scientists and will be involved in all aspects of collections-based research including collection and curation of specimens, experiments and analysis, participation in field expeditions, and dissemination of scientific results through oral presentation and publication.

The CoBiD summer school programme is funded by Science Foundation Ireland, and is open to students of any nationality.

Term dates: 12 June - 18 August 2006

Requirements * registered as an undergraduate student; expecting to complete a first degree no sooner than December 2006. * proficiency in English (written and spoken) * willingness to work hard, and ability to work independently * strong interest in the project of choice * career goals in organismal biology

To apply, you must complete the application form (available from the UREKA website) and submit it as an email attachment. You must also arrange for a seperate letter of recommendation to be sent by e-mail recieved directly from your reference.

All materials must be recieved by: Sunday 12 March

Research Projects | avian phylogeny | evolution of fossil crocodiles | mayflies and climate change | evolution of genomic imprinting | carboniferous coral “reefs” | evolution in mammalian sensory perception | resource partitioning in inshore fish | marine host-parasite evolution | plant evolution and extinction |

For more information, including project descriptions see www.ucd.ie/ureka/ or e-mail ureka@ucd.ie

– Julia Sigwart Collections-based Biology in Dublin http://www.ucd.ie/zoology/museum/ ureka@ucd.ie

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ULausanne Evolution

Junior Group leader in Ecology and/or Evolution at the Department of Ecology and Evolution, University of Lausanne, Switzerland

The Department of Ecology and Evolution at Lausanne University, Switzerland, (http://www.unil.ch/dee) invites applications for a junior group leader position (Maitre assistant) in the field of Ecology and/or Evolution. We are seeking a highly motivated young scientist with a post doctoral experience, a strong publication record, and the will to develop an independent research group within the department. Scientists from any area of Ecology and/or Evolution are encouraged to apply, be they field biologists, experimentalists, theoreticians, bioinformaticians, molecular biologists or genomicists. The position is for a maximum of four years and annual salary ranges from 85’000 to 146’000 CHF (54’800 to 94’000 Euros).

Applicants will be expected to develop an externally funded and internationally recognized research program. Teaching duties include a 14 to 28 hours advanced graduate course in the applicant’s research area, as well as taking part in the organisation of undergraduate practicals.

The department of Ecology and Evolution has a long track record of excellence in research. It is made of over 20 research groups in the field of ecology, evolutionary biology, behaviour, population genetics and genomics. The Department is currently home to 20+ post-docs and 40+ PhD students from many different countries and more than half of these are externally funded by Swiss and European research grants.

The University of Lausanne (http://www.unil.ch) provides excellent facilities, a lively intellectual and social environment and is beautifully located in Switzerland at the shore of Lake Geneva.

To apply for the position or for more information, please send a CV with a list of publications as well as the name of two referees (no later than the 17th of February, 2006) by email to:

Francoise Pham francoise.pham@unil.ch

DEE, Biophore UNIL-Sorge CH-1015 Lausanne Switzerland

For informal inquiries, please contact Jérôme Goudet (jerome.goudet@unil.ch) or Laurent Keller (laurent.keller@unil.ch).

jerome.goudet@unil.ch jerome.goudet@unil.ch

UMichigan EvolGeneticsTech

Research technician job

We are looking for an active and well-organized person with relevant research experience to work as a laboratory manager and research technician in the laboratories of Chris Dick and Paul Berry in the Department of Ecology & Evolution Biology at the University of Michigan. Our research involves use of DNA markers for phylogeny reconstruction and population genetic analyses of tropical plants.

The applicant should ideally have experience with DNA sequencing, PCR, DNA cloning and DNA fragment (microsatellite and AFLP) analyses. Managerial responsibilities include purchasing, accounting and invoicing of supplies, maintaining databases and tissue collections, and assisting in student training.

The candidate should minimally have a B.Sc. in a biology field with research experience in molecular biology. Post-doctoral applicants are encouraged to apply. Salary range is $24,000 to $38,000 depending on level of experience. This is a 12-month position, potentially renewable for several years.

Please apply by email with a letter expressing interest, your CV and names of three references to Chris Dick (cwdick@umich.edu). Applications should be received by January 31, 2006. Start date is expected to be no later than March 1, 2006.

For more information on the Berry and Dick labs, please visit the following web site: (http://www.lsa.umich.edu/eeb/research/researchareas/systematics/)

Christopher W. Dick Assistant Professor, Ecology and Evolutionary Biology Assistant Curator, University Herbarium University of Michigan 830 North University Ave 2009 Natural Science Building Ann Arbor, MI 48109-1048

Office phone 734-764-9408

Christopher Dick <cwdick@umich.edu>

UOxford OrganismalPlantBiol

Department of Plant Sciences : University of Oxford Sherardian Professorship of Botany (in ORGANISMAL PLANT BIOLOGY) Closing Date: Monday, March 06, 2006

Applications are invited for the above post, tenable from 1 October 2006, or such later date as may be arranged. Following a recent review of the biosciences the University is now investing in the future of the Plant Sciences in the form of this proleptic appointment (and a second Chair in cellular/molecular plant biology).

The chair is one the most prestigious in their subjects in the UK, and it is the intent of the University to appoint an individual of the highest calibre.

Further Details

The Sherardian Professorship was established in 1734, and the post is now to be filled in anticipation of the retirement of Professor H.G. Dickinson in September 2009. The successful candidate will have an international research reputation in ORGANISMAL ASPECTS OF PLANT BIOLOGY.

Selection Criteria

The successful candidate will also have evidence of dynamic, forward-thinking and feasible future research plans; the ability to produce, and communicate effectively, lectures for undergraduate and graduate students; experience of raising funds from outside bodies to run a major research group; managerial and organisational expertise, including experience of developing academic strategy and of financial management; and the ability to contribute effectively to ensuring the long-term development of the subject, and to maintaining interest in the subject in Oxford and its wide recognition outside.

The Department of Plant Sciences

The Department of Plant Sciences at the University of Oxford is devoted to teaching and research in plant science. The research interests range from systematics, forestry and ecology to cell, molecular biology and biochemistry (see www.plants.ox.ac.uk). It has 26 University lecturers and senior fellows, c.45 postdoctoral research workers and c.35 graduate research students, and is responsible jointly with the Department of Zoology for teaching some 300 undergraduate students reading the Honour School of Biological Sciences.

General Conditions

A non-stipendiary fellowships is attached to the post at Magdalen College, Oxford.

How to Apply

Separate further particulars, including details of how to apply, are available from: http://-www.admin.ox.ac.uk/fp/wd7-016.shtml (Sherardian Professorship of Botany) or from the Registrar, University Offices, Wellington Square, Oxford OX1 2JD (Tel: 01865 270200). The closing date for applications for each post is Monday 6 March 2006.

Informal enquiries may be directed, in the first instance, to Chris.Leaver@plants.ox.ac.uk or John.Pannell@plants.ox.ac.uk

John R. Pannell Department of Plant Sciences University of Oxford Oxford OX1 3RB United Kingdom

http://dps.plants.ox.ac.uk/external/staff/-staff_detail.asp?key=JP&frompg=people&bctext=-Academic

tel. +44-(0)1865-275145 fax. +44-(0)1865-275074

John Pannell <john.pannell@plant-sciences.oxford.ac.uk>

USouthernCalifornia MolComputationalBiol

As seen in the 27 January issue of Science:

FACULTY POSITIONS IN MOLECULAR AND COMPUTATIONAL BIOLOGY University of Southern California

The Molecular and Computational Biology Section of the Department of Biological Sciences in the College of Letters, Arts and Sciences at the University of Southern California (USC) invites applications for multiple open-rank tenure-track Faculty Positions. We are seeking outstanding colleagues who use modern molecular, genetic and/or computational approaches to address fundamental biological questions in diverse model systems that enhance and complement our current research strengths. Our program is undergoing significant expansion, including recent occupancy of a new molecular and computational biology research building.

Disciplines of major interest include, but are not limited to, cell and developmental biology; computational biology and bioinformatics; plant molecular biology; neurobiology; evolutionary biology; systems biology.

Review of applications will begin immediately. Please send curriculum vitae, statement of research objectives, and three letters of recommendation to e-mail: msearch@usc.edu For additional information about our program, visit our website: http://www.usc.edu/-dept/LAS/ biosci/mcb/

USC is an Affirmative Action/Equal Opportunity Employer

magnus@usc.edu magnus@usc.edu

UTasmania AntarcticPopGenet

The Institute of Antarctic and Southern Ocean Studies (University of Tasmania, Australia) is looking for a population geneticist to work in some area of Antarctic biology. Applications are invited for appointment to this position, which will be offered as a full-time, 5 year contract with the successful appointee being required to take up duty early in 2006. The appointee will be required to undertake original research in an area of Antarctic molecular biology. While all areas of molecular biology will be considered, preference will be given to candidates prepared to work in the area of population genetics. Applicants must have had practical experience working in a molecular laboratory but it is not necessary that they have previously worked in Antarctica.. The position also requires the appointee to contribute to the undergraduate and postgraduate teaching and supervision programs of the institute.

The appointment will be at Academic Level B and will have a total remuneration package of up to A$83,520 per annum (comprising salary within the range A$60,542 - A$71,385 plus 17% superannuation). The University offers excellent employment benefits and a pleasant working environment. The position is funded jointly with the Australian Antarctic Division. The Institute of Antarctic and Southern Ocean Studies is a multidisciplinary research and teaching institute with an international reputation in polar science. Research strengths cover many areas of Antarctic life sciences, physical sciences and social sciences. The institute has a large postgraduate program comprised of approximately 60 PhD students and coordinates undergraduate and honours programs. For further information about the position please contact the Director of IASOS, Professor Andrew McMinn, on telephone (03) 6226 2980, fax (03) 6226 2973 or email andrew.mcminn@utas.edu.au. A Job Application Package for this position can be accessed and downloaded from the Human Resources website at the following address: www.admin.utas.edu.au/hr/jobs Prof Andrew McMinn Director, Institute of Antarctic and Southern Ocean Studies University of Tasmania

Ph (03) 6226 2980 FX (03) 6226 2973

Andrew McMinn <andrew.mcminn@utas.edu.au>

UTulsa EvolPlantViruses

Assistant Professor: Plant Virologist

The Department of Biological Science at the University of Tulsa seeks to appoint a tenure-track Assistant Professor with expertise in the ecology and evolution of plant viruses, a position funded by a state NSF EPSCoR initiative. The successful candidate will develop an independent, extramurally-funded research program in plant viral ecology and evolution and train undergraduate and graduate students. A Ph.D. degree and postdoctoral experience are required. The position begins 15 August 2005. Start-up funds and support for lab personnel (two years for Postdoc or Technician) will be provided.

The University of Tulsa is a private, comprehensive university with a strong commitment to research and teaching. The Department of Biological Science has a faculty of fourteen and offers BS, MS, and Ph.D. degrees. To apply, send curriculum vita, statement of research and teaching interests, reprints, and three letters of reference to Mark Buchheim, Search Committee Chair, Department of Biological Science, The University of Tulsa, 600 S. College Ave., Tulsa, Oklahoma 74104. Review of applications has been re-opened will continue until the position is filled.

The University of Tulsa is an Equal Opportunity/Affirmative Action Employer.

– Mark Buchheim, Ph.D. Department of Biological Science The University of Tulsa Tulsa, OK 74104-3189 918-631-3833 (O) 918-631-3797 (L) 918-631-2762 (FAX)

Mark Buchheim <mark-buchheim@utulsa.edu>

VirginiaCommonwealthU Bioinformatics

The Center for the Study of Biological Complexity and the School of Engineering at VCU invite applications for a tenure eligible Assistant Professor to Professor level position in computational bioinformatics. The successful candidate will hold a Ph.D. in Computer Science or related field and is expected to develop a program of externally funded research. Interests should include algorithm development, interpretation, and scientific visualization of multi-scale/multi-dimensional biological datasets, database architecture and algorithm design, simulation of complex biological systems, or other relevant areas of computational biology and bioinformatics. The successful candidate will participate in teaching within the VCU's comprehensive new Bioinformatics Program.

The successful applicant will join the Center for the Study of Biological Complexity (www.vcu.edu/csbc/) in VCU Life Sciences, and the School of Engineering as part of our effort to integrate Life Sciences and Engineering. The School of Engineering, launched in 1996 and now enrolling over 1000 students, is home to the new department of Chemical and Life Science Engineering, Computer Science and Biomedical Engineering. The Center is an academic think tank that promotes integrative and interdisciplinary approaches to biological and biomedical research. The Center houses VCU's high performance computing facilities, including hardware, software, databases and support for bioinformatics, modeling and scientific visualization. The Center also maintains state of the art resources for genomic, proteomic and pharmacogenomic research, and houses students in VCU's programs in bioinformatics and systems biology.

Send a statement of research and teaching interests, curriculum vitae, three references and supporting documents by March 1, 2006, to Gregory A. Buck, Center for the Study of Biological Complexity, Virginia Commonwealth University, P.O. Box 842030, Richmond, Virginia 23284-2030, by e-mail at buck@mail2.vcu.edu.

VCU is an equal opportunity/affirmative action employer. Women, minorities and persons with disabilities are encouraged to apply

Zhongming Zhao, on behalf of Gregory Buck

Zhongming Zhao, Ph.D. Assistant Professor Dept. Psychiatry and Center for the Study of Biological Complexity Virginia Commonwealth University PO Box 980126 Richmond VA 23298-0126 Phone: (804) 828-8129 Fax: (804) 828-1471 Email: zzhao@vcu.edu

WashingtonDFWOlympia SciTech

We have an immediate opening for a Scientific Technician 3 with the Washington Department of Fish and Wildlife Genetics Lab in Olympia, WA.

Duties: This position is responsible for processing samples and collecting microsatellite and other DNA data and to perform other lab functions/activities for the Genetics Lab. Works closely with Biologists, Scientific Technicians, and Research Scientists.

- Set up, conduct, and evaluate polymerase chain reaction (PCR) amplifications reactions; Monitor quality control of PCR products and sequencer data. - Use spreadsheet, database, and specialized computer software to perform laboratory functions and collect, process and archive data. - Operate DNA sequencers and other instruments to process samples and collect genetic data - Perform initial genotyping from electropherograms. - Extract DNA from a variety of source material. - Carry out some field collecting, sample processing and data collection, and lab maintenance.

Salary: $2607- $3318

To apply: Applicants need to obtain a copy of the knowledge, skills, and experience (KSE) exam and use it to complete the "exam" answer portion (part 9) of the State Job Application Form. If you are interested in this opportunity, please submit a state application including the KSE, resume, and cover letter describing how you meet the desirable qualifications and competencies to:

Joe Vidales (vidaljv@dfw.wa.gov) WDFW Personnel Office 600 Capitol Way North, Olympia, WA 98501-1091

Bulletin #459 closes January 26, 2006

Thank you for your interest, Denise

Denise K. Hawkins Fish Biologist/Geneticist hawkidkh@dfw.wa.gov Washington Department of Fish and Wildlife 600 Capitol Way N. Olympia, WA 98501 phone 360-902-2749 fax 360-902-2943 fax 360-902-2943

Other

ABI3100 standard problems

Dear All: im having some problems with the use of ABI3100. A week ago we started having problems to detect the last standard peaks. From 50 to 200 we detected, but not the bigest ones, and that makes impossible to name the alleles. We have changed absolutely every reactive and capillaries (we changed POP, formamide, standard and capillaries). Does anybody knows what is happening?

Thanks.

Andrea A. Merás ameras@iib.unsam.edu.ar

"Andrea A. Merás" <ameras@iib.unsam.edu.ar>

Allelic richness testing

Does anyone know of siftware for testing difference in allelic richness between two samples, preferably with a permutation test that resamples individuals as opposed to populations within sample (ie FSTAT)?

Cheers, Tim Jones

Dr. Tim Jones Cooperative Research Centre for Sustainable Production Forestry School of Plant Science University of Tasmania Private Bag 55 HOBART 7001 TASMANIA AUSTRALIA Ph (03) 62261827 Fax (03) 62262698 Ph (int) + 61 3 62261827

Tim Jones <tjones@utas.edu.au>

AnalysisContChar answers

Dear Colleagues,

below is a compilation of all replies received to my recent query re: comparative analysis of a categorical and a continuous character. I am currently exploring the "OUCH" option (though I'm not yet ready to endorse any one of the suggestions below over all others).

Thank you to all who replied!

Best wishes,

Rutger Vos

Steve Kembel

One thing that just struck me is that you might be able to use Hansen's method (Ornstein-Uhlenbeck process) which could estimate adaptive optima and drift of your continous variable for each of several multistate categorical variables, as well as allowing you to compare the relative strength of different models to explain variation in your continuous variables. I am not sure if this is totally appropriate for your particular question but I have seen these methods used to look at e.g.

relationships between habitat affinity (Êtegorical multistate) and various continuous variables for the classic Anolis data set. King and Butler describe and apply the method in a recent publication (Butler, M.A. and A.A. King, 2004. Phylogenetic comparative analysis: a modeling approach for adaptive evolution. American Naturalist 164:683-695.) and provide R code to estimate the relevant parameters in a package called OUCH (http:// quercus.biology.lsa.umich.edu/king/ouch/).

+Terry Ord++

If your dependent variable is continuous, you can still use independent contrasts by scoring each categorical trait as a dummy variable. You can also do this for likelihood methods, too. I use Emilia Martins' COMPARE, because it automatically calculates both independent contrast regression and phylogenetic general least square regression. However, if your multistate character is a scale measure, the only thing I know of is Pagel's MULTI-STATE approach, but I think that will mean you'll be forced to convert your continuous dependent into a categorical trait (which is never good). However, I'm not 100% certain on that, so check it out.

Richard Bailey

Alan Grafen's phylogenetic regression (see his website at Oxford Uni) is a sound method for comparing a continuous Y variable with categorical and other types of X variable in a multiple regression framework. You can also use any other type of Y variable (such as binary, but not categorical I don't think) that can be transformed to fit typical linear regression assumptions.

Rocio Perez-Barrales+

you may take a look to these software (probably you know them already!), I think you can study correlated evolution of continuos and discrete characters.

CAIC: PURVIS, A., AND A. RAMBAUT. 1995. Comparative analysis by independent contrasts (CAIC): an Apple Macintosh application for analysing comparative data. Computer Applications in Biological Sciences 11: 247251.

Martins, E. P. 2001. COMPARE. Computer programs for the statistical analysis of comparative data. Ver. 4.4. Available from the author at http://compare.bio.indiana.edu/. Dept. of Biology, Indiana University, Bloomington IN.

I think you can take a look to Mark Pagels web site as well. I am not sure but I do think he developed a program for continuous and discrete characters.

+Rachel Simmons

Would SIMMAP be useful for this?

http://brahms.ucsd.edu/simmap/simmap.html Dirk Albach+

I used the program Continuous by Mark Pagel http://www.rubic.rdg.ac.uk/meade/Mark/ to study the possible correlation of genome size (continuous character) with life history (Annual-perennial) and breeding system (selfing-outcrossing). It worked great for me.

++Thomas Broquet

I just used the GEE (generalized estimating equations) methodology developped by Paradis and Claude. I've been using it for a different purpose, but I think it may be a good approach for comparative analyses involving categorical characters. Have a look at their paper (reference below) and at the "Gee" and "Ape" packages to be used in the R statistical software. Within the "Ape" packages, try the function "compar.gee". I hope it will help. Paradis E. and Claude J. 2002. Analysis of comparative data using generalized estimating equations. Journal of Theoretical Biology 218: 175-185.

+Marguerite A. Butler+

Have you had a look at our OU method for Comparative Hypotheses (OUCH)? It is developed exactly with the situation in mind of a categorical and continuous character. Here is the citation:

Butler M.A. and King, A.A. (2004) Phylogenetic comparative analysis: a modeling approach for adaptive evolution. The American Naturalist 164(6):683-695.

I have a webpage explaining the motivation:

http://web.utk.edu/%7emhiga/ButlerLab.data/OUwork.html

— / —

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

Control region amplification

Dear Colleagues,

I am working on a population study in the beetle genus Pimelia and I would like to amplify the highly variable control region. Despite the many polymerases and primers, some of them matching 100%, I tried I couldnt get any amplification. For other markers such as COI and cytB I had no problems.

Could you please give some advice?

Thanks in advance,

Joan Pons

Dr. Joan Pons Unitat de Biologia Evolutiva, Facultat de Ciencies de la Salut i de la Vida, Universitat Pompeu Fabra C/ Dr. Aiguader 80, 08003 Barcelona, Catalonia, SPAIN Telephone: +34 93 5422947 Fax: +34 93 5422802 Email: joan.pons@upf.edu

Correlated Evol methods

Dear colleagues,

I am looking for a methodologically sound way of testing for correlated evolution between a categorical (multistate) character and a continuous character on a phylogeny. I am not sure what approach is appropriate, and whether there is a software package I can use for this purpose. I am soliciting your suggestions.

Thank you for any and all pointers,

Rutger Vos

–

Rutger Vos, PhD. candidate Department of Biological Sciences Simon Fraser University 8888 University Drive Burnaby, BC, V5A1S6 Phone: 604-291-5625 Fax: 604-291-3496 Personal site: http://www.sfu.ca/˜rvosa FAB* lab: http://www.sfu.ca/˜fabstar Bio::Phylo: http://search.cpan.org/˜rvosa/Bio-Phylo/

Creationism texts

Hello,

In the UK, Channel 4 has just screened a two part documentary presented by Richard Dawkins entitled 'the root of all evil?' which was about the perils of religious belief.

Having spent a brilliantly fun night out with colleagues last night discussing (among other things) creationism/evolution at length, I realise I have read no creationist texts and don't have a good enough handle on their arguments to be able to hold my own were I ever in Dawkins' position. Very naughty of me, really.

I had a quick look on Amazon but any reviews on anti-evolution texts seem to written by people who are somewhat biased and from Kansas or Texas.

I would therefore like to know the books on creationism/ID etc that evolutionists would recommend, so that I can arm myself in anticipation of getting into an argument with a creationist.

It hasn't happened yet, but always good to be prepared...

Thanks for your recommendations. Domino.

d.joyce@hull.ac.uk

Domino Joyce Evolutionary Ecology and Biodiversity Group School of Biological Sciences, University of Hull, Cottingham Rd, Hull HU6 7RX

Tel: 00 44 (0)1482 465542 Fax: 00 44 (0)1482 465458 E-mail: D.Joyce@hull.ac.uk

and sometimes: EAWAG, Limnological Research Center Seestrasse 79 6047 Kastanienbaum, Switzerland

Tel: 00 41 (0)41 3492200

Denatured EtOH

Recently our lab received a number of salmonid fin clips stored in denatured EtOH. We are hoping to be able to use these samples for microsatellite analysis, however we have had very poor results with samples stored this way in the past. We have tried both Chelex and Quiagen extraction methods on these samples but have thus far we've had no luck. I am wondering if anyone has had any luck with samples stored in denatured EtOH in the past and would appreciate any suggestions folks have.

Pat DeHaan patrick_dehaan@fws.gov

U.S. Fish and Wildlife Service Abernathy Fish Technology Center Conservation Genetics Lab 1440 Abernathy Creek Road Longview, WA 98632 TEL: 360-425-6072 x331 FAX: 360-636-1855

DobzhanskyAward Call for appl

Call for applications for the 2006 Theodosius Dobzhansky Prize

The Theodosius Dobzhansky Prize is awarded annually by the Society for the Study of Evolution to recognize the accomplishments and future promise of an outstanding young evolutionary biologist. The prize was established in memory of Professor Dobzhansky by his friends and colleagues, and reflects his lifelong commitment to fostering the research careers of young scientists.

Eligibility The candidate must have a Ph.D. (or equivalent) awarded no earlier than June 2003 and no later than 1st February 2006, and must be actively involved in research in the field of evolutionary biology. There are no other restrictions. Applicants do not have to be members of the Society for the Study of Evolution, but such membership is encouraged. Nomination/Application.- Candidates may apply directly or may be nominated. Established researchers are encouraged to nominate outstanding young scientists who may be unaware of the existence and prestige of this prize. Each candidacy must be supported by the following materials detailing the candidates career to date: (1) a curriculum vitae, (2) a summary of research accomplishments, (3) a statement of research plans for the next 5 years, (4) pdf copies of three recent publications, (5) names and addresses of the three referees (including the nominating scientist where applicable) who have sent supporting letters. N.B.: THE THREE LETTERS OF REFERENCE ARE SENT SEPARATELY, but no application will be considered without these letters. All application/nomination materials and letters of reference must be sent as PDF e-mail attachments. No file type other than PDF will be accepted. The deadline for receipt of all materials, including letters of reference, is 1 March 2006. All materials should be sent to the secretary of SSE (Dale H. Clayton) at the following email address:

careymadsen@bioscience.utah.edu

Award.- The Dobzhansky Prize is accompanied by a check for U.S. $5000, and will be awarded at the annual meeting of the Society for the Study of Evolution, 23-27 June 2006, in Stony Brook, New York. The recipient is expected to be present to receive the award and to give an oral presentation about his/her research. To facilitate attendance, the SSE provides funds to cover the costs of conference registration, accommodation during the conference, and expenses for travel to and from the conference. The recipient will be notified of the award by early May 2006.

Carey Madsen <careymadsen@bioscience.utah.edu>

Drosophila stocks needed

Does anyone have a Drosophila melanogaster stock of v ras or v alone or ras alone. Thanks for your help. Ron Woodruff –

R. C. Woodruff Distinguished Research Professor CoEditor-in-Chief , GENETICA Department of Biological Sciences Corner Merry and N. College Life Sciences Building Bowling Green State University Bowling Green, Ohio 43403 Telephone: 419-372-0376 Fax: 419-372-2024 email: rwoodru@bgnet.bgsu.edu

Ron Woodruff <rwoodru@bgnet.bgsu.edu>

EtBr camera setups

Hi,

I would like to get some feedback from anyone who knows about a good setup for using a regular digital camera for taking pictures of EtBr stained gels. I want to set up a regular digital camera with some sort of attachment that could fix it to the UV machine, and nothing more. Im trying to find n option to the expensive setting that this task usually requires.

If you know of any such settings please let me know @ grub0121@tc.umn.edu. I'll post the answers received later on.

Thanks

Karl Gruber <grub0121@tc.umn.edu>

Evol for the blind

Other:

I am a University lecturer in Evolutionary Biology and I currently have a registered blind student enroled on my Unit. Finding an evolutionary biology textbook for her is proving almost impossible. She does have some peripheral vision so she can read very large print (but not onscreen because it is very tiring). Has anyone come across this sort of problem before or has come up with a solution. An audio, CD ROM or DVD version of an evolutionary biology textbook would be the best solution but finding one is very very difficult.

Many thanks

Mark

Dr Mark A Culling School of Biological Sciences Centre for Ecology, Evolution and Conservation University of East Anglia Norwich Norfolk NR4 7TJ UK ++44 (0)1603 592947 m.culling@uea.ac.uk

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Gene names Greek mythology answers

Many thanks to all who responded, and/or expressed an interest in, the naming of genes after characters from Greek mythology. I cannot claim that the list is exhaustive but as I am now finding it very difficult, through trawling, to come up with new examples, I guess there are probably not so many more. I should like to start by thanking all those who responded (in no particular order): Sarah Cohen, Dmitri Petrov, Jeffrey Marcus, Diana Wolf, Jennifer Gleason, Andy Gardner, Tom Gilbert, Joe Williams, Karl Schmid, Louise Johnson, Diane Ramos, Kristie Mather, David de Lorenzo, Irene Till, Sergios-Orestis Kolokotronis, Roman Arguello, Etienne Patin, Nicole Riddle, Colin Meiklejohn, Jacek Szymura, Chung-I Wu, Hope Hollocher, Jean-Marc Reichart and (my brother) Greg.

Let me commence the run down with the gene that stimulated the original question, Medea, named after the woman who slayed her own children. A ?gene? called Medea exists in the beetle Tribolium (3). In this instance this is a selfish element that causes death of embryos not containing Medea via a maternal effect. So if a mother is heterozygous (+/-) and mates with a -/- father, the +/- progeny survive but the -/- ones die. The offspring killing activity is necessary for the spread of the + allele. In the case of the condition in Tribolium I called it a ?gene? as many selfish elements of this type are two loci in very tight linkage hence behaving effectively as one segregating type (allele). The Tribolium case I suspect was named in part by mythological reference but it is also a convenient acronym: Maternal-Effect Dominant Embryonic Arrest. There is also a Medea gene in Arabidopsis around which a mini-industry of naming after Greek myth has developed. It was rather embarrassing that I forgot about this as one of the workers in this field is all but 50 metres down my corridor (Rod Scott here in Bath).

Arabidopsis In the case of the gene in weed, a mutant version of the Medea genes acts possibly via imprinting or as a maternal effect to cause embryo mortality (1, 2). As a mutant copy from the father has no effect, the effect is specifically maternal killing of offspring, hence the Medea reference. Moving upstream, the gene Demeter in Arabidopsis is a regulator of Medea (4). Demeter in Greek myth brings forth the fruits of the earth, in particular she was the goddess of fertility and the growth of vegetation, protector of the earth and its resources, mother of cereals (where she gains her name from the Greek word “dimitriaka”) and primarily of grains. As the gene is necessary for seed develoment it seems very appropriate. Medea and Demeter are connected in myth as Medea?s arrival in Corinth had saved citizens from starvation, by sacrificing to Demeter and repeatedly appeasing the goddess. The gene Medea in turn regulates Pheres1(5, 6), Pheres being one of the two children killed by Medea. Like Medea in Tribolium, Artemis (7) in weed seems to derive its name also, at least in part, as an acronym: Arabidopsis Thaliana Envelope Membrane Integrase. If the myth was in the minds of the authors I couldn?t find any reference to the logic. From weed I have found one further putative connection, the gene Argonaute. The gene was named by reference to the squid-like appearance of the leaves of Arabidopsis mutants lacking AGO1 gene function(8). In this case the Greek connection seems to be one step removed. The scientific name of the paper nautilus, especially the largest species, Argonauta argo, is of mythical Greek origin. The argonauts were a group of Greek heroes that, led by Jason, travelled to Kolchis to gain the golden fleece. They were called that way, because their ship was the Argo. In Greek argonaut means “who travels on the Argo”. The squid?s discoverers probably mistook it’s sail-like flaps as a locomotive organ and thus drew the similarity to the mythical Argo. So the Argonaute gene looks to have no direct connection to myth, just to squid-like appearance.

Flies Despite this flurry in Arabidopsis, it seems, however, that the Drosophilists are most well acquainted with Greek myth. So far I have found 15 namings from Greek mythology. First there is the speciation gene Odysseus (9). Odysseus ordered the making of the Trojan Horse and rode inside along with other warriors. Chung-I Wu kindly explained that : ?The reason [for the naming] was somewhat silly. We were looking for something that could wreak havoc in a foreign territory. Odysseus hiding in a wooden horse is like the gene embedded in the introgression; the result was devastating.? Carrying on with the Odysseus connection, many of the Greek inspired names in flies are transposable elements. Some have expressed the opinion that this all started with D. virilis transposable elements being named after characters from the Odysseus (Ulysses, Penelope,

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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

Happy Birthday Jim Crow

Folks –

Wednesday, January 18 was the 90th birthday of James F. Crow of the University of Wisconsin. Apparently the birthday was celebrated in his department.

I have emailed him birthday wishes, as he was one of my early mentors (I did an undergraduate thesis with him in 1964). Here is a web page: http://www.genetics.wisc.edu/faculty/profile.php?id=102 which describes his career very well, and has his email address in case any of you are tempted to send birthday wishes yourself.

I would just add that some of his population-genetic contributions include 1. Being a pioneering early researcher on genetic loads, particularly in the 1956 Morton, Crow, and Muller paper, 2. His writings, particularly the 1970 Crow and Kimura textbook in theoretical population genetics 3. His role in the Crow and Kimura 1964 paper deriving the expected heterozygosity under the neutral theory 4. His role in encouraging the Japanese school of theoretical population genetics, including his long association with his Ph.D. student Motoo Kimura, his student Takeo Maruyama, and many others 5. His work with Kimura on a theoretical derivation of the advantage of sexual recombination under the theory of Fisher and Muller. 6. Facilitating the presence and work of Sewall Wright during Wright's last 33 years, when Wright was in active retirement in Crow's department.

This leaves out his work in many areas of genetics and his very widely used "Genetics Notes". On his web site is an impressive list of the many people who trained in his lab; it reads like a Who's Who of population genetics.

Jim continues to be active and, as always, interested in nearly everything genetic.

(Please feel free to copy this to other mailing lists)

—- Joe Felsenstein joe@removethispart.gs.washington.edu Department of Genome Sciences and Department of Biology, University of Washington, Box 357730, Seattle, WA 98195-7730 USA

Human migrations in Patagonia

Dear Evoldir members,

I will be grateful for information about recent DNA-based and other (linguistic, cultural) studies on the origins of Indians in the southern South America. There are two different groups of Indians in Patagonia - ones that are living along the western coast (canoe-Indians) and those that are inland (e.g. Mapuche Indians). Does anybody know about any DNA studies on possible different origins and different arrival times to South America in these two groups?

Thanks in advance.

Asta

*** Asta Audzijonyte Finnish Museum of Natural History & Department of Biological and Environmental Sciences University of Helsinki asta.audzijonyte@helsinki.fi

Asta Audzijonyte <asta.audzijonyte@helsinki.fi>

Hybridization GeneticDistance

Dear EvolDir,

I'm looking for case studies in which a number of related species (i.e. several members of a genus) have been hybridized and the occurrence of polyploidy vs homoploidy in the F1s been scored. Any species from any kingdom will be considered! Can anyone help? Best wishes, –mark

Mark A. Chapman <http://www.theburkelab.org/>

http://www.theburkelab.org/> Vanderbilt University Department of Biological Sciences VU Station B 351634 Nashville, TN 37235

mark chapman <mark.a.chapman@vanderbilt.edu>

Insect inspiration

In the Netherlands,Wageningen UR, Entomologie, will start next week a exibition : Insect - Inspiration. Information: www.wur.nl www.josevloon.cjb.net (look under "expositis" and "textielobjecten", i'm sorry it's only in Dutch, but the picutes will be nice)

Greeting , JosÃ© van Loon

josevloon@hetnet.nl

Madrid Volunteer FieldAssist

BIRD RESEARCH IN SPAIN: VOLUNTEER FIELD ASSISTANTS NEEDED

Our group (4 people) is studying several questions about the evolutionary biology of a population of spotless starlings (Sturnus unicolor) nesting in boxes in an oak wood 50 km. from Madrid. We are looking for field assistants with some field experience in bird ringing and observation. Work will involve capturing, measuring an ringing adult birds and nestlings, setting video cameras in nest-boxes and scoring behaviour from tapes and direct observation. Our fieldwork extends from late March to early July. We are willing to accept people that could stay for periods of at least two months within that time. We can offer free accommodation in our nearby field station as well as a weekly contribution towards food expenses.

If interested please contact Diego Gil (<mailto:dgil@mncn.csic.es>dgil@mncn.csic.es)

Diego Gil Departamento de Ecología Evolutiva Museo Nacional de Ciencias Naturales (CSIC) José Gutiérrez Abascal, 2 28006 Madrid Spain

Tel: 00 34 91 411 13 28, ext. 1285 Fax: 00 34 91 564 50 78 email: dgil@mncn.csic.es

Diego Gil <dgil@mncn.csic.es>

MarineEcology Call for Evol papers

CALL FOR PAPERS : SPECIAL TOPICS VOLUME

ECOLOGY AND EVOLUTION OF OF VENT, SEEP AND WHALE-FALL ORGANISMS

In the journal Marine Ecology an evolutionary perspective

Volume Guest Editors: Lisa Levin, Jim Barry, Horst Felbeck, Craig Smith, Craig Young Print ISSN: 0173-9565 Online ISSN: 1439-0485

Deadlines: Indication of Interest: No later than Jan 30, 2006 Please send a title and 1 paragraph abstract or description of the topic. Send to llevin@ucsd.edu; subject: MAE Special Topics Manuscript Submission Deadline: April 30, 2006 Please do not submit without prior notification and approval. Publication: Planned for Early 2007

Focus: We welcome any papers addressing ecology and evolutionary ecology of vent, seep, and WHALE-FALL organisms, from microbes to megafauna. Particularly welcome are studies that address hypotheses about adaptation, life-history tactics, species interactions, environmental regulation, and phylogenetic relationships. comparative studies that address multiple taxa, ecosystems or regions are also welcome..

Information about the journal: Marine Ecology (formerly Pubblicazioni della Stazione Zoologica di Napoli) publishes original contributions on the structure and dynamics of marine benthic and pelagic ecosystems and on the critical links between ecology and evolution of marine organisms.

The journal prioritises contributions elucidating fundamental aspects of species' interaction and adaptation to the environment through integration of information from various organizational levels (molecules to ecosystems) and different disciplines (molecular biology, genetics, biochemistry, physiology, marine biology, natural history, geography, oceanography, palaeontology and modelling) as viewed with an ecological and an evolutionary perspective. It encourages theoretical and speculative studies addressing the same issues in a section called Views, Comments and Ideas.

The journal particularly invites original research articles on "in situ" or laboratory-based research aimed at testing challenging hypotheses explaining adaptation of marine organisms to environmental constraints including biotic interactions. Papers are encouraged that present cutting-edge techniques or novel applications of methods addressing questions related to the journal's themes. Theme issues will appear annually.

For full guidelines for authors please visit: www.blackwellpublishing.com/mae ONLINE SUBMISSION: Please submit your paper at http://mc.manuscriptcentral.com/mae http://-mc.manuscriptcentral.com/mae

Micros capturing

Dear Evoldir,

I am in the process of developing microsatellites for a tropical tree species. For the microsatellite enrichment process I am going to use streptavidin-coated beads from Promega (Z5481). This is the first time I am using Promega beads. If you have used this bead for the same purpose, I would appreciate for sharing your experiences on follwing points:

1. Efficiency 2. Detail procedure of hybridization, microsatellite capturing and elution (because their technical note on that product mainly deals with mRNA isolation) 3. Difference in efficiecy level, if you have also used Dynabeads (Dynal).

Best regards,

Madhav Pandey mpandey71np@yahoo.com

Dr. Madhav PANDEY Visiting Research Scientist Forest Genetic Conservation and Biotechnology Research Division Department of National Parks, Wildlife and Plant Conservation 61 Phaholyothin, Chatuchak Bangkok, Thailand 10900 Tel: +6670761218 Fax: +6625799576 Email: mpandey71np@yahoo.com

mpandey71np@yahoo.com

NED dye substitution

Hi, does anyone know whether it is possible to substitute NED with some other dye when doing fragments analysis on ABI? I've read that it may work with TAMRA. Did anyone try such substitution? Any comments will be very helpfull...

thank you in advance tomasz

– Tomasz Wilk Institute of Environmental Sciences Jagiellonian University Gronostajowa 7 30-387 Krakow, Poland wilk@eko.uj.edu.pl

NSF plans and NIH funding

NSF REQUESTS COMMENTS ON STRATEGIC PLAN FOR BIOLOGY

The National Science Foundation has announced that it is beginning a process to develop the next NSF Strategic Plan. NSF is seeking input from the scientific community to help the Foundation develop the first draft of the new plan.

According to an NSF document, the Foundation uses its current plan (www.nsf.gov/publications/-pub_summ.jsp?ods_key=nsf04201 <http://-www.nsf.gov/publications/pub_summ.jsp?ods_key=-nsf04201>) "to guide NSF and stakeholders in a way that is responsive to the science and engineering community that we serve." NSF's intent is for the next plan covering the period of 2006-2011 to continue to serve this purpose by communicating NSF's strategic goals, objectives, priorities and strategies over this time period. Furthermore, federal performance and budget procedures require that the new plan comply with the priorities and strategies being drafted in the "National Science Board 2020 Vision for the National Science Foundation."

Comments from the science community should be submitted by 20 January 2006 through the website at www.nsf.gov/about/performance/input.cfm <http://-www.nsf.gov/about/performance/input.cfm> . NSF is particularly interested in feedback on the following questions:

1. Does NSF's current Strategic Plan effectively communicate NSF's roles and responsibilities as part of the science and engineering (S&E) community? If not, what is lacking and how can the next plan be improved?

2. What broad characteristics of the near- and long-term environment for S&E research and education should NSF consider and address in its next Strategic Plan?

HOUSE ADJOURNS WHILE SENATE FACES TOUGH BATTLE OVER ANWR

In a late night vote-a-thon, the House completed work Monday morning on the Defense Department appropriations and budget reconciliation bills, the two pieces of legislation they had to clear before adjournment. At 5:00 a.m. on 19 December the House successfully passed H.R. 2863, the $453 billion Department of Defense spending package. In addition to funding military operations in Iraq and Afghanistan, the bill clears the way for opening the Arctic National Wildlife Refuge (ANWR) to oil and gas drilling and includes language calling for a 1 percent across-the-board cut to discretionary spending, excluding Veteran's Affairs. After an additional hour of debate, the House passed S. 1932, the budget reconciliation bill, which cuts nearly $40 billion from the federal government in the next five years.

Fiscal conservatives and drilling proponents hailed the passage of the two bills; Representative Mike Pence (R-IN) called the combination a renewal of their "commitment to the principles of fiscal discipline and limited government." But many Democrats resented that they were forced to vote on ANWR in the must-pass Defense appropriations bill. "There is something especially outrageous about the willingness of majority party leadership to allow the Department of Defense bill, in a time of war, to be held hostage to totally unrelated special interest items," said Rep. David Obey (D-WI), the senior Democrat on the Appropriations Committee.

The Senate must now pass the spending bills before they can be signed into law. Media reports suggest this could be a tough battle, with Democrats threatening to filibuster the Defense appropriations bill starting Monday.

Last week Senators and Representatives reached a new deal on the Labor-Health and Human Services (HHS)-Education appropriations conference report, which was originally rejected in the House on 17 November. The House passed the deal last week after both chambers agreed to add $120 million for rural healthcare.

Under the new conference report, the Math and Science Partnerships (MSP) program in the Department of Education receives $184 million, $6 million less than the House-approved number, but $5.4 million and $5.5 million more than the Senate version and the FY 2005 level, respectively. Conferees from the House and Senate encouraged the MSP grantees "to incorporate advanced placement.staff development training into their math and science partnership projects to help teachers meet the highly qualified criteria under the No Child Left Behind Act."

For more information on NIH funding under the Labor-HHS-Education conference report, please refer to the 5 December 2005 AIBS Public Policy Report available at http://www.aibs.org/public-policy-reports/public-policy-reports-2005_12_06.h tml

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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

Negative fst

Hello, maybe someone can help me with a special problem concerning Fst- values.

I am working with the program Fdist2 in order to analyse the selection acting on two populations in different environments. My problem is now: I have found loci that have lower Fst- values than the 0.025-Quantile of the simulated distribution (neutral model simulated by Fdist), which has negative Fst- values in parts of heterozygosities up to 0.7 (because there is little differentiation between the populations). These loci have NEGATIVE Fst- values as well, which confuses me in interpreting them. Can I state that the loci are definitely below the 95%- envelope of the simulated distribution (and can be regarded as outliers), although negative Fst- values do not exist formally (for a differentiation cannot be negative), and only exist because of the way Fst is calculated? I would be very grateful for any help. Thanks! Cheers, Katharina Oetjen

oetjen@mpil-ploen.mpg.de oetjen@mpil-ploen.mpg.de

Negative fst answers

Hi everybody, as several people asked me to post the replies to my question about the negative fst- values, here they are... thanks to everybody who answered!

This was my question:

I am working with the program Fdist2 in order to analyse the selection acting on two populations in different environments. My problem is now: I have found loci that have lower Fst- values than the 0.025-Quantile of the simulated distribution (neutral model simulated by Fdist), which has negative Fst- values in parts of heterozygosities up to 0.7 (because there is little differentiation between the populations). These loci have NEGATIVE Fst- values as well, which confuses me in interpreting them. Can I state that the loci are definitely below the 95%- envelope of the simulated distribution (and can be regarded as outliers), although negative Fst- values do not exist formally (for a differentiation cannot be negative), and only exist because of the way Fst is calculated?

********** the answers:

Paul Sunnucks wrote:

I may not be following you, but in procedures that estimate (rather than calculate) FST, it is possible to get slightly negative values if the real value is small and the estimate happens to have a little error in the negative direction.

my reply:

as for the negative fsts, i know how they can appear. but i wondered if an estimated value of a locus can be regarded as being _lower_ than an expected one if both are negative. or would one rather say, as they are both negative, the “real” fsts are both zero, which means they are equal?

Paul:

if the 'real' value is negative but less so than the simulations, this would seem to imply one or more of: (1) the actual values are slightly positive but the real value is genuinely lower than the simulations (2) the simulations are downwardly biased (3) both are inaccurate representations of zero.

in other words, just because they are negative does not mean that the real values are zero - they could be a little positive. Not sure how you would distinguish, but nonetheless you would have to conclude that any effect was tiny and potentially of little biological significance.

Dr Paul Sunnucks Senior Lecturer in Zoology School of Biological Sciences Monash University, Melbourne Clayton Campus 3800 Victoria Australia ph + 61 3 9905 9593 fax + 61 3 9905 5613

email paul.sunnucks@sci.monash.edu.au

webpage: http://www.biolsci.monash.edu.au/staff/-sunnucks.html ************

I have no experience with the software you have used (Fdist?) but negative ESTIMATES of Fst values do not have to be a concern. Formally Fst can not be negative but when estimated from data, i.e. using the procedure by Reynolds, Weir and Cockerham (see Genetics 1983 and Evolution 1984), you can get negative estimates due to sampling error.

The common interpretation of such values is that if the TRUE Fst value would be 0, due to sampling error the ESTIMATE will be negative in 50% of the times (if the error has a symmetrical (i.e. normal) distribution...).

I hope this helps,

Best, Zoltán Bochdanovits

—–Original Message—– From: evoldir@evol.biology.mcmaster.ca [mailto:evoldir@evol.biology.mcmaster.ca] Sent: Thursday, January 05, 2006 7:03 AM To: z.bochdanovits@vumc.nl Subject: Other: negative fst-values

I see your point about the two negative estimates being equal or not. I think you are right to conclude that the “real” Fst's are both 0, hence equal...

Best, Zoltán

****

There is a correspondance between Fst and the kin selection coefficient of relatedness r, which can take negative values. For more on negative r see: Grafen (1985, Oxf Surv Evol Biol); Foster et al. (2001, Ann Zool Fennici); Gardner & West (2004, J Evol Biol). The latter is on my website <www.mast.queensu.ca/˜andyg>, and contains full references for the other two papers. For the link between r and Fst, see perhaps Francois Rousset's 2004 book.

Hope that's of some help.

Andy

****

I'm afraid, I haven't worked with fdist2 program, so I'm not very familiar with output and its interpretation. I have only worked with Fstat program to calculate Fst, which also sometime gives negative values for pairwise Fst between populations. This means that differentiation within population is higher than between populations, however values were never significant with Fisher's exact test.

Regards, Monika

email: mzavodna@purdue.edu

—–Original Message—– From: evoldir@evol.biology.mcmaster.ca [mailto:evoldir@evol.biology.mcmaster.ca] Sent: Thursday, January 05, 2006 1:12 AM To: mzavodna@purdue.edu

*************** It is possible to get negative values for F-statistics but it is mostly due to the way we estimate them. You are correct in saying they do not exist formally as there is no such thing as a negative variance. Usually

— / —

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

Pedigree reconstruction

Hi:

I am looking a software for pedigree reconstruction for use with wild and farmed populations from a broodstock management program. Probably the relationship among these population are very far and softwares for relationship from first order can‘t help me.

thanks in advance

Rodrigo Badilla Marine Biologist Chile

rodrigo.badilla@gmail.com

PopGen analyses

Dear All, I am looking to purchase a laptop (most probably a Mac machine that runs on Mac OS X Tiger) that will be used primarily for analyses of pop gen data (ARLEQUIN, DNASp, Migrate, IM, Mesquite, etc.). To date I have been a PC user, and I am concerned that I may pick up problems trying to use many of these programs on a Mac. Any advice on this matter would be much appreciated, Cheers, Mark de Bruyn Queensland University of Technology, Brisbane, Australia <markus.debruyn@gmail.com>

markus.debruyn@gmail.com

SNP study questions

Hi EvolDir Readers

I am doing a genomewide SNP analysis to determine population structure and phylogenetic trees. Some of my SNPs are linked, some on the same chr but very distant and then of course their are ones on seperate chromosomes. I've done a few analyses but want to try more programs. The analyses I did was on STRUCTURE, that was very nice because you can specify which markers are linked and how far they are from one another and specify that the phase is unknown. Furthermore I did neighbour joining trees based on fst values and also PC plots. All of this works very nice and results corresponds. Is there any other nice programs that anyone can suggest. Especially programs that can work with diploid data where you can specify if the markers are linked but unphased.

Another question: If I work with unphased haplotypes; are there a way that I can analyse them in PAUP, MEGA or PHYLIP without inferring the haplotypes first with a program like PHASE. Is there a way I can code the SNPs in the nexus file so that the PAUP will see the three genotypes say “AA; Aa; aa” as 1A ; 0.5A0.5a ; and 1aa. I find it a bit difficult to explain but what I basically want to say is their a way I can code it that the program will see the heterozygote as half of the one homozygote and half of the othe one?

Last question: Say I use the PHASE program to infer my haplotypes and do further analysis on these haplotypes, how does it influence the confidense of my results. Can I for instance use these haplotypes to infer coalessence times with a program like BATWING, or is that taking it a bit too far?

Thanks Carina Graduate student email: cschlebu@yahoo.com

Carina Maria Schlebusch <carina.schlebusch@nhls.ac.za>

Salmonid samples

Hi,

My research group is looking for DNA or tissue samples from as many different salmonid (including close outgroup) species as possible (beyond Atlantic salmon). If you can help us, please email me at liberles@uwyo.edu. Thanks for any assistance.

David Liberles

"David A. Liberles" <Liberles@uwyo.edu>

Scientific Artwork

Dear All,

Just got this. Sounds like an exciting new avenue for making research exciting to the public. Contact is Sim Bamford, sim@sim.me.uk

=========

Calling all researchers...

A new fringe to Edinburgh's International Science Festival will be happening this April. One of the events will be a gallery of artwork inspired by science research. Biological, Mathematical, Engineering - all fields are welcome!

If you'd like to you can put up an image or some data from your research and it may then act as inspiration and become part of that exhibition.

For more details:

www.ensight.org.uk Please do pass this message on to anyone whom you think would be interested.

Sim Bamford

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– Philipp Wesche Institute of Evolutionary Biology University of Edinburgh Tel.: 0131 650 8659 (office) http://www.philippwesche.org/

Software Arlequin ver3 01

A new version (3.01) of Arlequin is now available on

http://cmpg.unibe.ch/software/arlequin3 Compared to version 3.0, Arlequin 3.01 include some bug corrections and some additional features:

Bug corrections and modifications:

1. Minimum Spanning Tree Checkbox is now available for Genotypic data with known Gametic Phase. 2. Choice of how FST is computed is now available when computing pairwise distances, and it is synchronized with the choice of distance in the AMOVA panel. 3. "Search for shared haplotypes" is now available for Genotypic Data with known Gametic Phase. Arlequin also ouputs the list of haplotypes before the table of frequencies. 4. [[Mantel]] section was not recognized if located after a [[Structure]] section. 5. Improved conversion between GenePop and Arlequin formats. 6. "Diploid Data" option is now present when converting from Genepop to Arlequin. 7. Output of s.d. of the number of alleles was sometimes wrongly reported as zero in output of Fu's FS test. This is now corrected and annoying warning messages about " "No molecular diversity within a sample while performing Fu's test" have been suppressed in output file.

New features:

1. New editor of genetic structure allowing one to modify the current Genetic Structure directly in the graphical interface. 2. Computation of population-specific FST indices, when a single group is defined in the Genetic Structure. This may be useful to recognize population contributing particularly to the global FST measure. This is also available in the locus-by-locus AMOVA section.

– Laurent Excoffier Computational and Molecular Population Genetics (CMPG) Zoological Institute, University of Bern 6, Baltzerstrasse, CH-3012 Bern, Switzerland Tel: +41 31 631 30 31 Fax: +41 31 631 48 88 Email: laurent.excoffier@zoo.unibe.ch URL: http://cmpg.unibe.ch/people/excoffier.htm Laurent Excoffier <laurent.excoffier@zoo.unibe.ch>

Software CoMET

Evoldir,

This is an announcement that we've made new software available, called CoMET. CoMET is a Mesquite module for calculating the likelihood of different Brownian motion-based models of continuous character change on phylogenies. Thus the name CoMET (Continuous-character Model Evaluation and Testing).

The software require input of a phylogeny and continuous trait data. The models differ in assumptions about evolutionary “time”. Different models may suggest different modes of evolution (non-phylogenetic, punctuated, etc) for a continuous trait or traits. These models have been used to study the evolution of body sizes, vocalizations, and gene expression level in the references below.

CoMET is available for download at:

http://www.lifesci.ucsb.edu/eemb/labs/oakley/software/comet.htm Best wishes,

Todd Oakley

REFERENCES

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2. Mooers, A.O., Vamosi. S., and D. Schluter. 1999. Using phylogenies to test macroevolutionary models of trait evolution: sexual selection and speciation in Cranes (Gruinae). American Naturalist 154: 249-259.

3. Mooers, A.O., and D. Schluter. 1998. Fitting macroevolutionary models to phylogenies: an example with vertebrate body sizes. Contributions to Zoology 68: 3-18.

Todd Oakley, Assistant Professor Ecology Evolution and Marine Biology University of California-Santa Barbara Santa Barbara, CA 93106 USA (805) 893-4715

lab: http://www.lifesci.ucsb.edu/eemb/labs/oakley/ pubs: http://www.lifesci.ucsb.edu/eemb/labs/oakley/pubs/publist.html oakley@lifesci.ucsb.edu oakley@lifesci.ucsb.edu

Software Hickory v1 0 4

Hickory is free software providing Bayesian estimates of the within-population inbreeding coefficient (f), of differentiation among populations (Gst and theta), and of diversity within populations (Hs).

An attentive user of Hickory recently brought a serious bug to my attention. Calculations of Hs were being done incorrectly for co-dominant marker data. As a result, estimates of Gst were also incorrect.

Please note that the error affects *only* estimates of Hs from *co-dominant* marker data. It does not affect estimates of theta or f from co-dominant markers, nor does it affect estimates of any parameters from dominant markers.

I’ve compiled and uploaded a new version of Hickory (v1.0.4) for Windows and Linux. (We’re working on a version for OS X and hope to be able to announce it later this spring.) In addition to correcting the calculation of Hs for co-dominant markers, v1.0.4 has several small enhancements over earlier releases. See the documentation for details.

We encourage all users of Hickory to upgrade to this version. If you are a new user, please take the time to register on the registration page. By registering you ensure that you’ll receive an e-mail announcement when a new version is released.

Hickory is available from

http://darwin.eeb.uconn.edu/hickory/hickory.html
Kent

– Kent E. Holsinger kent@darwin.eeb.uconn.edu http://darwin.eeb.uconn.edu – Department of Ecology & Evolutionary Biology – University of Connecticut, U-3043 – Storrs, CT 06269-3043

TaqMan multiplex PCR

Dear EvolDir Members,

I have a colleague who is designing an experiment to compare abundance of fungi associated with pine roots. To compare biomass, his goal is to use quantitative PCR on extracted root tips to compare relative abundance with TaqMan (dual labeled probes with 5 fluorphore and 3 BHQ) probes on an ABI 7300. He is planning to compare using absolute quantification by comparing standards of known concentration along with his environmental root samples. Because I am not familiar with the ABI system, I was hoping that anyone with experience with optimization and TaqMan reactions could answer questions re: multiplexing, standard cycling parameters and optimization.

1. ABI recommends cycling parameters: 1 cycle at 50C, 2min, 1 cycle of 95C 10 min, 35-45 cycles of 92C 15 s, 60C 1 min. Is there any indication that adjusting the annealing temperature will increase sensitivity of detection (ie: lower threshold cycles?) We used Primer3 rather than the recommended ABI software to design TaqMan probes, therefore, we were not sure if the reactions are optimized at these annealing temps.

2. Standard reactions by ABI are 250 nmol of dual-labeled probe Is this standard concentration work for most reactions? With multiplexing?

3. Recommended volume is 25 ul reactions can this be reduced to 15 ul volumes?

4. Second, the ABI machine was calibrated to detect:

[6FAM], either [VIC, JOE] and [NED]

Other choices include: [ROX, HET, TET]

The experiment requires several reps and therefore, multiplexing would seriously cut down on the number of runs required. Has anyone multiplexed with any of the three combinations (listed above) or found better combinations? – Has anyone had success with multiplexing three probes and if so, which combinations were used? The ABI manual states that quantification is not 'reliable' with multiplex reactions.

5. Of course ABI recommends their Master Mix which is outrageously expensive. Bio-Rad has an equivalent master mix (IQ-Supermix) which is much cheaper as does Qiagen. Does anyone have any experience with these other master mixes?

Any help would be much appreciated.

Please respond to:

Sarah Bergemann UC Berkeley, ESPM sbergemann@nature.berkeley.edu

Sarah Bergemann <sbergemann@nature.berkeley.edu>

Wild Tribolium

Dear EvolDir,

Does anyone have a Tribolium castaneum stock recently set up from a wild sample (max 1 year, not bottlenecked)? Or where it is easiest to get them from?

Thanks for your help,

Losia Lagisz

Department of Animal and Plant Sciences, University of Sheffield, Western Bank, Sheffield S10 2TN, UK M.Lagisz@shef.ac.uk

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fastatoNETWORK fileconverter

Hi there

Does anybody know of a freely available program that converts fasta / nexus / mega / phylip etc. files to the *.rdf files used by the NETWORK program

Thanks Carina cschlebu@yahoo.com <mailto:cschlebu@yahoo.com>

PostDocs

BrownU EvolGeneExpression

Postdoctoral Position: Computational Approaches to the Evolution Of Gene Expression Signals

I am seeking a postdoctoral researcher interested in: 1)the evolution of non-coding signals 2)incorporation of large scale cross-species comparisons into sequence analysis 3)identification of functional SNPs

Some background in programming or quantitative analysis would be preferred To apply email CV and cover letter to: bioinformatics@brown.edu

MOLECULAR EVOLUTION: PRE-MRNA SPLICING The splice junctions in a pre-mRNA substrate are defined by some combination of several different types of sequence elements: splice sites, branch points, 3' splice site (3'ss), polypyrimidine tract, 5' splice site (5'ss), exonic and intronic splicing enhancers. The extent to which a particular type of splicing signal is used to define splice junctions varies across the tree of life. The minority of yeast genes that contain introns rely upon rigidly defined 5'ss, branch point and 3'ss to correctly specify intron/exon boundaries. In higher eukaryotes, the 5'ss and 3'ss of vertebrate introns contribute relatively little to the definition of the splice sites but additional types of sequence elements such as exonic splicing enahancers (ESE) or intronic splicing enhancers compensate for the low stringency of the splice site motifs. Although many of these auxiliary elements are poorly characterized, there appear to be species-specific differences in their use. One difference can be found in a cross species comparison of intronic splicing enhancers. Plants depend on U-rich intronic splicing enhancer elements, whereas the predominant mammalian intronic splicing enhancer is a G-triplet motif. This difference in sequence elements may represent a functional divergence as plant introns are processed with suboptimal efficiency in vertebrates. As ESEs overlap with the genetic code, they presumably evolve more slowly than intronic splicing enhancers. I would like to test this explicitly by first characterizing pre-mRNA processing signals in other species and then measuring their rate of evolution. If the protein coding function of exons restrains the evolution of ESEs then, conversely, the requirement to preserve ESEs function should places some restrictions on the ability of coding regions to evolve. The consequences of this restriction would be most severe in cases where a gene's function requires the coding sequence to have the potential to adopt a variety of sequences, as is the case for highly polymorphic or rapidly evolving genes. One line of research may include a search for mechanisms (e.g. stronger splice sites or a shift to intronic splicing enhancers) that reduce or eliminate the reliance on ESEs for correct pre- mRNA processing.

William_Fairbrother@brown.edu
William_Fairbrother@brown.edu

CNRS France EvolBiol

A few post-doc positions are available at CNRS for 2 years, starting in September or October 2006. Deadline for applications is June 2006. Two of them are in the field of evolutionary biology.

http://www.sg.cnrs.fr/drhchercheurs/Post_doc_2006/-default.htm One position is available in my own lab, on experimental evolution with mites :

http://www.k-projects.com/cnrs_postdocs/-public/departement_details.php?IdDpt=10&Dep=-SDV&NumOffre=8&Langue=en

Sincerely

Isabelle

Isabelle Olivieri Université Montpellier 2, cc 065 Institut des Sciences de l'Evolution Place Eugène Bataillon 34095 Montpellier cedex 05 France Fax : 33 (0) 4 67 14 36 22 Tel : 33 (0) 4 67 14 37 50 (/ 36 31) LAB http://www.isem.univ-montp2.fr/-GE/Metapopulations/MetaAccueil.php Master BGAE, spécialité EBE, parcours RPI : http://mon.univmontp2.fr/MBGAEEBERPI/ Ecole Doctorale : http:/- /www.univ-montp2.fr/ ˜ edbi/ olivieri@isem.univ-montp2.fr

ChicagoFieldMuseum TibetanPlants

Postdoctoral position in evolution, biogeography, and conservation of Tibetan flowering plants

The Botany Department at the Field Museum (Chicago, Illinois, USA) seeks applicants for a two-year postdoctoral position in a project funded by the MacArthur Foundation to conduct research and build capacity for biodiversity conservation in the eastern Himalaya. This collaboration with the Smithsonian Institution and the Kunming Insitute of Botany focuses on three nature reserves in southern Xizang (Tibet) where field trips will take place in the summers of 2006 â 2008. In the field, the position entails general collecting of vascular plant specimens and assisting in the training of local land managers, students, and others in field techniques. In Chicago, the successful applicant will conduct research on the evolution and biogeography of Tibetan plants at the Field Museum under the supervision of co-PI Dr. Richard Ree. Considerable flexibility in choosing a taxon or study question will be granted â the person could pursue an independent project, or take part in ongoing projects of the co-PI focusing on taxa such as Pedicularis and Corydalis in the greater Hengduan region. It is expected that the research will incorporate molecular data, to be generated in the Field Museum's Pritzker Laboratory, a modern and fully-equipped facility for molecular systematics.

In addition to research, the position entails various logistical and informatics-related duties, such as assisting the co-PI in managing a specimen database and developing a project web site, facilitating short-term visits by Chinese collaborators and trainees to Chicago, and helping arrange field trips. These responsibilities will take up about 30% of the time.

Botanists with an interest in temperate Asia, alpine plants, Northern Hemisphere biogeography, and/or biodiversity informatics are encouraged to apply. Previous field and laboratory experience is strongly preferred; GIS expertise is a plus. Starting date is flexible: as early as August 2006 (in time for the first field trip) is possible. Salary is $33,000 to $35,000 USD/year + full benefits for two years.

To apply, please email a cover letter, CV, and contact information for two references to the following address. For more information, contact:

Dr. Richard Ree Botany Dept., The Field Museum 1400 S Lake Shore Drive Chicago, IL 60605 USA

phone: 1-312-665-7857 e-mail: rree@fieldmuseum.org

rree@fieldmuseum.org

Dublin MolEvolBioinformatics

Location: Dublin, Ireland

Application deadline: 14 Feb 2006

Project Title: Gene gains, losses and relocations during vertebrate evolution

Description: A postdoctoral position starting in October 2006 is available in the lab of Dr. Aoife McLysaght in the Genetics Dept. of Trinity College Dublin. This project is sponsored by Science Foundation Ireland as part of their prestigious President of Ireland Young Researcher's Award (awarded to Aoife McLysaght in 2005). The project will eventually employ three Ph.D. students and one postdoctoral fellow working together.

The project will involve examination and statistical analysis of vertebrate genome data using bioinformatics methods. Candidates for the Postdoctoral Fellowship are expected to have completed a Ph.D. on or before October 2006 in the field of molecular evolution, comparative genomics, or related discipline. Experience in molecular evolution, statistical analysis and bioinformatics/computer programming are desirable.

For more details of the project, look under "Research" on the lab website http://www.gen.tcd.ie/molevol To apply: Send a complete CV (including grades), a description of your research achievements and interests, and the names of at least two referees.

Aoife McLysaght Smurfit Institute of Genetics Trinity College Dublin 2 Ireland

[e] aoife.mclysaght@tcd.ie [t] +353-1-6083161 [f] +353-1-6798558 [w] www.gen.tcd.ie/molevol mclysaga@tcd.ie mclysaga@tcd.ie

DukeU EvolPhilosophyBiol

Post-doctoral fellowship for Academic Year 2006-2007. The Duke Center for the Philosophy of Biology invites applications from philosophers and biologists for its NSF sponsored post-doctoral fellowship in the philosophy of biology. This fellowship is intended for junior faculty who can secure research leaves from their universities and/or who will have completed their Ph.D.s immediately before taking up the fellowship. In addition to their research, fellows will participate in the Center's faculty research seminar, help organize the annual philosophy of biology conference, and teach one graduate seminar on their area of special interest. Applicants should submit vita, list of references, one or more sample papers, and a statement describing the area of research to which the candidate proposes to devote their fellowship period. Electronic submission of documents is encouraged. Consideration of candidates will commence on 15 February. Send material to Robert Brandon, rbrandon@duke.edu, Department of Philosophy, Box 90743, Duke University Durham, NC, 27708

Thanks, Robert

Robert Brandon <rbrandon@duke.edu>

DukeU SocietalEvol

Post-doctoral Fellowship. Applications are invited from biologists (with a strong interest in philosophy) or philosophers (with training in biology) for a two-year post-doctoral position leading a study of possible universal principles of coloniality/sociality. The empirical component of the study is a search for the morphological, physiological, and behavioral correlates of the emergence of colonial associations generally (from bryozoans to bees to buffalo). The philosophical component is an analytical study of the possible correlates, leading to methods for operationalizing them. For a more detailed description of the project, see: www.biology.duke.edu/mcshealab. Funding for the position is expected but pending. Opportunity to join Duke Biology Dept, which has exceptional strength in evolutionary studies. Applicants should submit a CV, short statement of research interests, one or two sample papers, and names and e-mail addresses of three references. Electronic submission of documents is encouraged. Consideration of candidates will begin on 15 February. Start date is 1 July. Send materials to: Dan McShea, dmcshea@duke.edu, Dept. of Biology, Duke University, Box 90338, Durham, NC 27708.

Dan McShea

Dan McShea <dmcshea@duke.edu>

DukeU VertebrateBiogeography

NSF-Funded Postdoctoral Position available for the study of Malagasy Vertebrate Biogeography

Background:

The project will test the hypothesis that the geological complexity of western Madagascar, particularly its river drainage systems, has yielded a more complex pattern of species distributions and areas of micro-endemism than are found in the eastern regions of the island. The project aims to yield novel insights that will connect geological and geographic forces to patterns of vertebrate distribution and endemism. Madagascar has been designated as one of the most critical geographic priorities for conservation action, retaining less than 10% of the natural habitats that existed before human colonization. Field inventory activities, conducted by colleagues at the Field Museum of Natural History and the University of Antananarivo, will focus on the herpetofauna and mammals occuring at the survey sites. Phylogenetic and biogeographic analysis of these animals, each with unique life-history and dispersal characteristics, will be conducted to identify areas of high endemism potentially associated with underlying geological features, and also to test for the role that rivers have played in generating patterns of vertebrate diversity and distribution. The project will be a case study for the integration of field, lab, and geospatial analysis for understanding biogeographic patterns. The project also has a significant focus on capacity-building through the education and training of both American and Malagasy students.

Qualifications:

The successful applicant will be expected to have the necessary molecular skills to generate DNA sequence data for a number of vertebrate groups, as well as the appropriate phylogenetic and/or population genetic analytical skills to interpret the data. In particular, given that we will be focusing on many taxonomic groups at or below the species level, expertise in coalescent methods is highly desirable. The applicant should also have an enthusiasm for biodiversity studies and conservation, as well as a willingness to interact with and, on occasion, train Malagasy scholars. Field work is not an integral part of the position, though field possibilities may exist depending upon the skills and interests of the successful candidate. Finally, expertise or interest in bats is a plus. Conditions:

This position is funded for two years, with the possibility of a third year extension. Salary is competitive, and the position will carry full benefits. The position is open until filled, though ideally, the candidate will begin his/her duties by June, 2006.

To Apply:

Send current CV, publications, and list of references to:

Anne D. Yoder, Professor Departments of Biology & BAA Duke University, Box 90338 Durham, NC 27708 ph: 919-660-7275 anne.yoder@duke.edu http://www.biology.duke.edu/yoderlab/ Anne Yoder <anne.yoder@duke.edu>

EmoryU EvolColorVision

Dear Colleagues,

I am looking for Postdoctoral fellows who are interested in working on "Adaptive evolution of color vision in vertebrates." Candidates should have a strong background in molecular biology (construction and screening of genomic DNA or cDNA libraries, and molecular characterization of positive clones, including DNA sequencing) and strong interests in evolutionary biology. Please send CV to:

Shozo Yokoyama, Ph. D. Asa G. Candler Professor of Biology Department of Biology Emory University 1510 Clifton Road Rollins Research Center Atlanta, GA 30322 Tel:404-727-5379 FAX:404-727-2880 Email:syokoya@emory.edu

syokoya@emory.edu

INRA UParisXI MetabolicEvol

Post-doc in metabolic evolution

A postdoctoral position in metabolic evolution is immediately available in the group Fundamental Quantitative Genetics (INRA-University Paris XI-CNRS-INA PG) in Gif-sur-Yvette, France, in tight collaboration with the Laboratory of General Oenology, University Bordeaux 2, France. The position is for two years.

The project is part of a research program on the genetic and evolution of metabolic systems. The goal of this project is to search for new criteria of adaptive ability, using glycolysis and fermentation in yeast as a model system, and focusing on three levels of cellular integration: enzymatic, metabolic and cell growth. A collection of Saccharomyces cerevisiae strains from oenology, brewing and baker origins, will be analysed to evaluate if, and in which extent, human selection has affected concentrations of glycolytic and fermentative enzymes (and their possible correlations), the glycolytic flux value and cell growth. The analysis of the relationships between these different levels will allow the identification of enzymes which have possibly been targets of human selection, and which could be valuable indicators of adaptive ability in this species. Beyond the yeast model, this type of approach will shed light on evolutionary adjustment of a major physiological function, and evolution of regulation.

Applicants should have skills in evolutionary biology. Experience in microbiology, biochemistry and/or quantitative genetics is a plus. This position will be funded by the French Agence Nationale de la Recherche (ANR) for two years.

If interested, please contact Delphine Sicard and send your CV, list of publications, and the names of at least two references, by mid-February to : sicard@moulon.inra.fr.

Delphine Sicard, Université Paris-Sud. UMR de Génétique Végétale, INRA-UPS-CNRS-INA PG 91190 Gif-sur-Yvette, France http://www.moulon.inra.fr Delphine Sicard <sicard@moulon.inra.fr>

ImperialCollegeLondon BiodiversityHotspots

9 Month Postdoctoral Research Assistant in Biodiversity Hotspot Analysis

Applications are invited for a 9 Month Postdoctoral Research Assistantship as part of the Avian Diversity Hotspots Consortium. This NERC-funded consortium is a collaboration between Imperial College, Sheffield University and the Institute of Zoology (London). The overall aim of the consortium is to investigate the ecological and evolutionary basis of biodiversity hotspots, using birds as a model system. The successful candidate will collate a global database on the geographic distribution of bird species; identify biodiversity hotspots; and perform statistical analyses on the diversity and distribution of hotspots. Candidates should be interested in large- scale problems in ecology and evolution, have extensive experience of statistical modelling and management of large databases, and be willing to work collaboratively within a large team of researchers. Experience in GIS-based modelling, construction of interactive web pages, and avian biology may also be advantageous. This postdoctoral appointment is for 9 months and salary will be based on the RA1 scale, depending on age and experience. This position will be based in Ian Owens? Research Group at Imperial College?s Silwood Park field station, approximately 30 miles outside London. Regular travel to other consortium members and specialised libraries and museums will also be required.

The closing date for applications is 16 January 2006, or until post is filled.

Applications should be made by email to Mrs Diana Anderson (d.anderson@ic.ac.uk; Phone + 44 (0)207 59 42207; Fax: + 44 (0)207 5942339; Department of Biological Sciences, Imperial College at Silwood Park, Ascot, Berkshire SL5 7PY, UK) and should include a letter of application addressing the relevant criteria, a detailed CV and the names and addresses of at least three referees. Please state ?postdoctoral position? in the header of the email message.

– Prof. Ian P. F. Owens Division of Biology & NERC Centre for Population Biology Imperial College London Silwood Park Ascot, Berkshire SL5 7PY UK

http://www.imperial.ac.uk/people/i.owens Ian Owens <i.owens@imperial.ac.uk>

KelloggBiologicalStation EducationCoordinator

Postdoctoral Position W.K. Kellogg Biological Station Michigan State University GK-12 Fellowship Program Coordinator

A full time postdoctoral position to coordinate the new KBS GK-12 Graduate Fellowship Program, recently funded by NSF, is now available. The program will place eight graduate fellows in K-12 classrooms of southwest Michigan to build teaching skills and to promote the adoption of inquiry-based K-12 science teaching. The focus of the GK-12 program is inquiry-based teaching for ecological literacy. Elements of the program include Fellow-teacher classroom partnerships, a 1-week summer teaching institute, and school-year workshops. A more complete description of the program can be found at www.kbs.msu.edu/gk-12 . The successful applicant will coordinate project participants, help to organize science content and teaching workshops, and contribute to project leadership. Candidates should have a Ph.D. in ecology, science education, or a related discipline. Current funding from NSF's Directorate for Education and Human Resources covers a 3-year period. The position will also afford candidates the opportunity to pursue scholarly interests in their own primary discipline.

Further information about KBS, located in a mostly rural area 10 minutes north of Kalamazoo, midway between Chicago and Detroit, can be found at www.kbs.msu.edu . Interested candidates should submit to the address below a curriculum vita and statements of research and teaching interests (either separately or as part of a cover letter). Please also arrange to have 3 letters of reference sent to: Dr. G.P. Robertson, W.K. Kellogg Biological Station, Michigan State University, Hickory Corners, MI 49060. Electronic submission of all materials is encouraged to GK-12@kbs.msu.edu. MSU is an affirmative-action, equal-opportunity institution.

Jeff Conner <connerj@msu.edu>

LeidenU EvolAllometry

Three Year PostDoc Opportunity in Section of Evolutionary Biology, Institute of Biology, Leiden University, Leiden, The Netherlands

We have been awarded by the dutch N.W.O. a three-year PostDoc grant on 'The control and evolution of animal form' to follow-up our analysis of the evolution of allometry using our Bicyclus butterfly system. Please see the original paper last year in Science 307: 718-720, together with the summary-objectives from the grant itself that is reproduced below. Interested people should make contact with Paul Brakefield or Bas Zwaan (brakefield@rulsfb.leidenuniv.nl; zwaan@rulsfb.leidenuniv.nl) attaching a CV where appropriate.

Our team in Leiden includes Patricia Beldade. This project is part of a network of interacting projects all using tropical Bicyclus butterflies in a multidisciplinary research program in evolutionary genetics and evo devo. This network includes Tony Frankino whom established our interests in allometry and set up the original selected lines which will form part of the new project. The successful candidate would be expected to be able to start by June 2006. The group also works with Drosophila and two-spot ladybird beetles.

Summary with main objectives: Animal groups exhibit a spectacular diversity in the scaling relationships among different body parts or traits, and between these and overall body size; changes in such allometries among traits is clearly a major pathway by which morphology evolves. However, even with over a century of interest in the evolution of allometry, little is known about the mechanisms of change in scaling relationships. Developmental processes must play a central role in maintaining the functional scaling relationships among traits as well as in their evolution. To study both process and pattern in evolution we have initiated an integrated, broadly 'evo-devo' research program on allometry. In this project we will quantify allometry across species of Lepidoptera as previously examined experimentally in artificial selection experiments using the tropical butterfly Bicyclus anynana (e.g. for forewing size relative to hindwing size, or forewing size relative to body size). We will also perform a range of genetic, developmental and physiological experiments using individuals from our selected lines to unravel the underlying mechanisms of evolutionary change, and to explore the bases of observed patterns of bias in the evolution of the allometries in terms of how the individual traits contributed to changes their scaling relationships. A deeper understanding of the roles of proximate mechanisms in the evolution of such complex phenotypes is needed to build a predictive 'evo-devo' theory of trait evolution that can then be generalized to other organisms. This is the overall goal of our multidisciplinary project.

Our program is powerful because it will integrate work on both process and pattern to study morphological evolution by taking advantage of existing lineages of the model butterfly Bicyclus anynana that have novel allometries for ecologically relevant morphological traits. This research will provide crucial insights about the mechanisms that underlie evolution in the relative size of different body features. Our primary objectives are to:

1) use a broad 'evo-devo' approach to analyze the proximate (genetic, physiological and developmental) bases of the regulation of scaling relationships for a set of morphological traits in B. anynana;

2) determine if the observed biases in the contributions made by the individual traits to evolution in their scaling relationships share a common proximate basis;

3) determine whether understanding the proximate basis of trait integration and co-ordination during development resolves the striking difference between theoretical predictions of scaling relationship evolution and the results observed in our artificial selection experiments;

4) relate the male fitness consequences of changes in allometry to differences in male secondary sexual traits;

5) and with colleagues at Naturalis (RMNH), place the experimental work with B. anynana into a wider, comparative analysis of the evolution of the allometry within the butterflies.

http://biology.leidenuniv.nl/ibl/S6a/ and weblog of Patricia is http://biology.leidenuniv.nl/ibl/S6a/news/

"P.M.Brakefield" <brakefield@rulsfb.leidenuniv.nl>

McMasterU Astrobiology

The Origins Institute at McMaster University invites applications for postdoctoral fellowships in the general field of Astrobiology, to begin in September 2006. The OI has proposed up to a total of six post-docs as part of its new, interdisciplinary, astrobiology programme. These positions are subject to the availability of funds - to be announced in early April, 2006.

We seek to hire post-docs who have expertise in fields ranging from planetary science to evolutionary biology, as listed below. Astrobiology research programmes at the OI comprise three basic and related directions:

(1) The Conditions for Life; including the nature and formation of planetary systems; the timing and origin of habitable conditions (water, biomolecules, energy sources) on planets and moons, the origin of biomolecules that characterize pre-biotic conditions;

(2) The Origins of Life; including pre-biotic conditions, complexity and autocatalytic sets, habitats and energetics of early life, the nature of first cells; and

(3) Extremophiles; including terrestrial microbial life in extreme conditions, Mars analogue studies, as well as microbial life in the Arctic and Antarctic.

These programmes are collaborative efforts between OI members, as well as co-investigators across Canada and researchers at the NASA Ames Research Center in the US. The OI post-docs will benefit from a wide range of expertise in observational, experimental, theoretical and computational aspects of these problems - as well as the facilities with which to pursue them. These include the SHARCNET, state-of-the-art High Performance Computing facility (McMaster is a leading member of SHARCNET).

For more information about the OI and the astrobiology research programme, please see: http://origins.mcmaster.ca/jobs.html The positions will be offered for two years, and can be renewed for an additional year. Applicants should send a full Curriculum Vitae (including list of publications), a two page statement of research background and interests, and arrange to have three reference letters to arrive at the OI by March 31, 2006.

Applications and letters should be addressed to:

Prof. Ralph Pudritz, Director, Origins Institute, ABB 241, McMaster University, 1280 Main Street West, Hamilton, ON L8S 4M1, Canada. Re: OI Postdoctoral Fellowships

Inquiries about the competition should be sent to the OI secretary, Ms. Rosemary McNeice, at origins@mcmaster.ca. McMaster is committed to Employment Equity and encourages applications from all qualified candidates including women, aboriginal peoples, persons with disabilities, and members of visible minorities.

Origins@mcmaster.ca

NCStateU MolEvolGenet

North Carolina State University Molecular Evolutionary Genetics

We are looking for a postdoctoral candidate with training in evolutionary genetics and molecular biology who wants to investigate the evolution of sexual communication systems.

Background Information: Most night-flying moth species locate mates through production of, and response to, a very precise blend of two or more volatile chemical compounds. Within a population, females with atypical blends have been shown to be less attractive to males than females with the population's common blend. Similarly, rare males that respond to atypical blends have been found to be at a disadvantage in finding mates. The genes that control pheromone blend ratios have never been found to be linked to, or affect male response, so mutations that cause changes in each of the two components of communication are expected to arise independently. On a simple theoretical level, this type of sexual communication system is expected to be evolutionarily constrained because an individual with a mutation leading to an altered blend or response will be selected against, when rare. Even if the selective disadvantage to rare individuals with alleles for novel signals or responses is minimal, mass selection is not expected to increase their frequency in the population. Based on these assumptions it is difficult to account for the great diversification of chemical mixtures used in mate communication by over 10,000 moth species. We are investigating a number of potential evolutionary mechanisms that could have resulted in this diversification by dissecting the genetic underpinnings of selective mating in moths.

We are working with two sympatric moth species (Heliothis virescens and Heliothis subflexa) that have very distinct sex pheromone blends, do not mate in the wild, but can be induced to mate in the lab. We have mapped a number of Quantitative Trait Loci (QTL) that control production of specific female sex pheromone components and male response to these components. We have moved two specific QTL between species and tested their impacts on mating in the field. We have also identified a number of candidate genes that appear to be involved in male response to specific pheromone components.

We are now in a good position to test candidate genes and to determine the genetic and molecular basis for differences between the sexual communication systems of these two moth species. We are looking for a postdoc who has good training in molecular biology and wants to use this knowledge to answer questions about evolution of sexual communication systems.

North Carolina State University is a leading research institution with a strong commitment to the study of quantitative, molecular, and population genetics. The University is situated in Raleigh, NC and is within 30 miles of Duke University, UNC-Chapel Hill, NIEHS, an EPA research unit, and the Research Triangle Park.

For more details about our lab see: http://www4.ncsu.edu:8030/%7Efgould/

The successful applicant will participate in the interdepartmental Keck Program in Behavior Biology—http://www.cals.ncsu.edu/beh_bio/index.html

Send letters of inquiry to: Fred_Gould@NCSU.edu

TurkuFinland EvolFuncGenomics

Post-doctoral position in Evolutionary and Population Genetics, Turku, Finland.

A post-doctoral position is available in Craig Primmer's research group (see http://users.utu.fi/primmer for more details) at the University of Turku, Finland, as a part of the recently funded Finnish Centre of Excellence in Evolutionary Genetics and Physiology which also includes the research groups of Professor Juha Merilä (see http://www.helsinki.fi/biosci/egru/) and Professor Mikko Nikinmaa (http://www.sci.utu.fi/biologia/-fysiologia/nikinmaa_eng.htm).

The successful applicant will be expected to have the necessary molecular skills and scientific enthusiasm to contribute significantly to functional genomics aspects of two multi-disciplinary collaborative projects: - identification of genes involved in local adaptation in a wild grayling, Thymallus thymallus, study system (see Haugen & V2000; Koskinen et al. 2002 for background) - identification of genes involved in maintaining species barriers in Ficedula flycatchers (see Primmer et. al 2002; Sætre et al. 2003 for background).

In addition to playing a major role in these projects, the successful applicant will be encouraged to develop their own research program within the scope of the Centre of Excellence (including supervision of graduate students), and research funding will be provided to support this. A very limited amount of undergraduate teaching on research related topics will also be encouraged.

Researchers with previous post-doctoral experience in functional genomics (in any organism) and with the imagination and interest necessary to use their experience to address questions in evolutionary biology are especially encouraged to apply.

Informal inquires and applications should be addressed to Prof. Craig Primmer (craig.primmer@utu.fi). Applications should include a full CV, a statement of previous research and supervision experience as well as an outline current research interests and names and contact details of at least two referees. Review of applications will commence at the end of January 2006 with the preferred starting date being prior to April 2006. The position is initially available until the end of 2008. The salary range is 2200-2900 EUR per month, depending on the previous post-doctoral experience of the candidate.

Haugen, T. O. & V, L. A. (2000) Population differences in early life- history traits in grayling. Journal of Evolutionary Biology 13: 897-905

Koskinen MT, Haugen TO and Primmer CR. (2002) Contemporary fisherian life-history evolution in small salmonid populations. Nature 419: 826-830.

Primmer CR, Borge T, Haavie J, and Sætre G-P. (2002) Single-nucleotide polymorphism (SNP) characterization in species with limited available sequence information: high nucleotide diversity revealed in the avian genome. Molecular Ecology 11: 603-612.

Sætre G-P, Borge T, Lindroos K, Haavie J, Sheldon BC, Primmer CR, and Syvänen A-C. (2003) Sex chromosome evolution and speciation in Ficedula flycatchers. Proceedings of the Royal Society of London. Series B. 270: 53-59.

Craig Primmer

Professor of Genetics Division of Genetics and Physiology Department of Biology (Vesilinnantie 5) 20014 University of Turku FINLAND

tel. +358 2 333 5571 fax. +358 2 333 6680 craig.primmer@utu.fi http://users.utu.fi/primmer craig.primmer@utu.fi

UAlaska InternationalPolarYear

University of Alaska Presidential International Polar Year Postdoctoral Fellowship Program

The University of Alaska is pleased to offer 10 postdoctoral fellowships, starting during academic year 06-07, for a period of up to three years to cover the time frame of the fourth International Polar Year plus analysis and publication of results (see www.alaska.edu/-swacad/postdoc/). Starting salary will be US $50,000 plus full faculty benefits, plus $5000 per year travel and research allowance. Applications are due by 1 April 2006, and decisions will be announced by 1 May 2006.

Awardees will be expected to conduct research contributing to at least one of the six IPY themes (see www.ipy.org) with a focus on the Northern High Latitudes. In addition, applicants should clearly indicate how their research would benefit from the cultural, ecological, and geological diversity of Alaska. Awardees may choose to be stationed at any of the University main campuses (Fairbanks, Anchorage or Juneau; see www.alaska.edu) and will be hosted by a Department or Research Institute. Interested senior-level graduate students and recent PhDs are encouraged to contact UA faculty members regarding prospective research projects.

Information about Institute of Arctic Biology faculty and their research interests is available at http://www.iab.uaf.edu/ . HOW TO APPLY:

A complete Postdoctoral Fellowship application consists of the following items:

*A University of Alaska Job Application for this fellowship position (accessed by following the "visit the job posting" link below)

*A current CV or resume that shows educational background and work experience

*An official transcript and/or other official documents of your complete undergraduate and graduate school record (original or certified copies of transcripts must be sent via postal mail, electronic or non-certified copies will not be considered acceptable)

*At least three written recommendations from non-University of Alaska personnel. Recommendation forms are available for download from the link below. Separate letters of reference can be used if more convenient, but please provide a copy of the sheet entitled "Information for Letters of Recommendation," to each person writing a recommendation.

*Additional letters of recommendation, including from University of Alaska faculty, if you desire

*A synopsis of your doctoral dissertation (one page abstract)

*A statement (no longer than three pages double-spaced) that outlines your long-range career plans, how your postdoctoral research relates to IPY, and how an IPY postdoctoral tenure at UA would complement your existing experience and preparation.

To apply, visit the job posting (see www.alaska.edu/swacad/postdoc/) and follow the application instructions.

NOTE: Application Deadline is April 1, 2006

Address for all supplementary documents: Vice President for Academic Affairs and Research IPY Postdoctoral Fellowship Committee 202 Butrovich Building PO Box 755000 Fairbanks, Alaska 99775-5000

For questions or further information, please contact Craig Dorman, VPAA/R at the above address or by phone: 907.450.8018, Fax 907.450.8002, or e-mail: craig.dorman@alaska.edu

Kevin G. McCracken Institute of Arctic Biology & Department of Biology and Wildlife University of Alaska Fairbanks Fairbanks, Alaska 99775 office (907) 474-6419 Rm. 228 WRRB fax (907) 474-6967 email: fnkgm@uaf.edu http://mercury.bio.uaf.edu/~kevin_mccracken/

UBourgogne AvianLifeHistory

CNRS and UNIVERSITE de BOURGOGNE* *

Post-doctoral RESEARCHER IN

Oxidative stress and life-histories in birds

*26,000 **euros per annum*

A postdoctoral research assistant is required for a project entitled Oxidative stress, aging and longevity in birds, funded by a ANR grant to Bruno Faivre and Daniel Ricquier. The project aims to explore the molecular links between energetics and life-history traits in zebra finches. In particular, we wish to investigate the role of a class of mitochondrial transporters (avianUCP) as a regulatory mechanism of ROS production. The candidate should have a good background in evolutionary biology and a good skill for laboratory work (molecular and biochemical analyses). Although we wish to recruit a candidate with an aptitude for a lab-based work, she/he could also be involved in the experiments carried out on living birds. The post is available for up to 2 years, starting April 1^st 2006, and will be based in the Faculté Necker Enfants Malades (Ricquiers lab, Paris).

Further information can be asked to :

Bruno Faivre (bruno.faivre@u-bourgogne.fr <mailto:bruno.faivre@u-bourgogne.fr>)

Daniel Ricquier (ricquier@necker.fr <mailto:ricquier@necker.fr>)

Frédéric Bouillaud (bouillaud@necker.fr <mailto:bouillaud@necker.fr>)

Letters of application, including a CV, the names, postal and e-mail addresses and fax numbers of three academic referees, should be sent to: Bruno Faivre (bruno.faivre@u-bourgogne.fr <mailto:bruno.faivre@u-bourgogne.fr>).

Closing Date: *15 February 2006*.

Summary of the project

The study of patterns and processes underlying aging depends on two crucial questions addressed at two different levels. The first one investigates how natural selection shapes the pattern of aging currently observed. The second one focuses on the proximal physiological and molecular mechanisms that determine the fitness reduction with age. Among the proximal factors, the deleterious effects of internal damages caused by free radicals have received much attention. This idea is based on the observation that mitochondrial respiration produces harmful molecules called oxygen free radicals, or reactive oxygen species. Free radicals are very unstable molecules that are prone to react with other molecules, resulting in an oxidative chain reaction. They can cause deleterious effects on cellular integrity by damaging cellular membranes, peroxidizing lipids, oxidizing proteins or damaging DNA. Because free radical-induced damages accumulate during the lifespan, they have been suggested to be one of the major proximate causes of the age-associated decline in fitness. Birds are particularly interesting species for the study of aging. Indeed, they show particularly low aging rates and extended lifespan compared to mammals of similar size. This is puzzling, because birds have higher metabolic rates, internal temperatures, energy expenditure and circulating plasmatic glucose levels than mammals of similar size. To temper the negative effects of ROS, aerobic organisms have evolved a sophisticated antioxidant system relying on an arsenal of compounds which scavenge and quench free radicals. Therefore, the particularly high longevity of birds may be due to a low production of free radicals or to a high level of antioxydant defences, or both. This proposal attempts to merge the expertise of two disciplines: evolutionary biology and energetics.

Recent publications of the group on the topic

Alonso-Alvarez C., S. Bertrand, G. Devevey, J. Prost, B. Faivre & G. Sorci (2004). Increased susceptibility to oxidative stress as a proximate cost of reproduction. /Ecology Letters /7 :363-368.

Alonso-Alvarez C., S. Bertrand, G. Devevey, M. Gaillard, J. Prost, B. Faivre & G. Sorci (2004). Are carotenoids limiting resources? An experimental test of dose-dependent effect of carotenoids and immune activation on sexual signals and antioxidant activity. /American Naturalist/ 164 :651-659.

Arsenijevic D, Onuma H, Pecqueur C, Raimbault S, Manning BS, Miroux B, Couplan E, Alves-Guerra MC, Goubern M, Surwit R, Bouillaud F, Richard D, Collins S, Ricquier D. 2000. Disruption of the uncoupling protein-2 gene in mice reveals a role in immunity and reactive oxygen species production. /Nature Genetics/ 4:435-439.

Criscuolo F., Gonzalez-Barroso M., Bouillaud F., Ricquier D., Miroux B. et Sorci G. (2005) Mitochondrial uncoupling proteins : new perspectives for evolutionary ecologists. /American Naturalist /166 :686-699/./

Criscuolo F., Gonzalez-Barroso M., Le Maho Y., Ricquier D. and Bouillaud F. (2005). Avian uncoupling protein expressed in yeast mitochondria prevents endogenous free radical damage. /Proceedings of the Royal Society London B/ 272 : 803-810.

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Stéphane Garnier

Equipe Ecologie Evolutive UMR CNRS 5561 Biogéosciences Université de Bourgogne 6 Bd Gabriel 21000 Dijon - France

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UCDavis EvoDevo

Postdoctoral position

Intraspecific variation in developmental pathways.

Dear colleagues,

We are looking for an exceptionally capable and motivated postdoctoral fellow prepared to take the leading role in a study aimed at connecting variation in DNA sequences, developmental pathways, and adult phenotypes. The three-year, NSF-funded position can start as early as March 1, 2006. Experience in population genetics, bioinformatics, and analysis and management of large sequence data sets is a big plus.

The goal of this project is to understand how DNA sequence variation affects gene expression, and how differences in gene expression translate into phenotypic variation, using the Drosophila bric a brac (bab) locus as a model. The bab locus, which consists of two closely related transcription factors, is responsible for ~60% of genetic variation in female cuticular pigmentation in a natural population of D. melanogaster. bab also affects the development of other sexually dimorphic traits, including the sex comb, abdominal sternite bristles, and terminal filaments in the ovary. We will sequence the entire 200-kb bab genomic region from 100 isogenic lines and identify the SNPs and other molecular polymorphisms associated with phenotypic differences among lines. Simultaneously, population-genetic approaches will be used to understand the evolutionary forces that control the distribution of these polymorphisms in nature. We will then quantify the levels of bab transcripts in phenotypically divergent lines, and use this data to understand the impact of molecular polymorphisms and their interactions on gene expression and development. Finally, we will analyze DNA sequence and expression variation in the upstream regulators and downstream targets of the Bab transcription factors to understand how genetic variation is transmitted through developmental pathways. The ultimate goal of the project is to develop a predictive model that links molecular, developmental, and phenotypic variation in natural population.

The project involves a close collaboration between two labs: Artyom Kopp's (developmental genetics/ genomics/ evolution of development) and Sergey Nuzhdin's (quantitative molecular genetics and genomics). The research environment at UC - Davis will offer the postdoctoral fellow an excellent chance to interact and collaborate with many other people working in the fields of evolutionary genetics and genomics. Northern California, where Davis is located, offers a variety of recreational opportunities as well. More information about UC - Davis can be found in the links below. Kopp lab: http://www2.eve.ucdavis.edu/kopplab/ Nuzhdin lab: http://nlab.ucdavis.edu/node/view/177 Evolution and Ecology: http://www-eve.ucdavis.edu/ UCD Genome Center: http://www.genomecenter.ucdavis.edu/index_html.html College of Biological Sciences: http://www.dbs.ucdavis.edu/ City of Davis: http://www.ci.davis.ca.us/visitors.cfm If interested, please contact Artyom Kopp at akopp@ucdavis.edu – Artyom Kopp Section of Evolution and Ecology and Center for Genetics and Development University of California - Davis Davis, CA 95616 USA lab (530) 752-8328 office (530) 752-8657 fax (530) 752-9014 http://www2.eve.ucdavis.edu/kopplab/ akopp@ucdavis.edu

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UCaliforniaIrvine EvolInfectiousDisease

Postdoc: Epidemiology and Evolution of Infectious Disease University of California, Irvine

One or more Postdoctoral Scholar positions are available to develop computational analyses and mathematical models of infectious diseases. The project will be jointly supervised by Robin Bush and Steven Frank, with opportunity to interact with a diverse group of evolutionary geneticists and infectious disease biologists at the University of California, Irvine (http://ecoevo.bio.uci.edu). This position provides an opportunity to develop an independent line of research and to collaborate with our group on quantitative problems. Potential projects include computational analyses of molecular data, computational tools for inference, and dynamical models of epidemiology and evolution.

This position requires a Ph.D. and a record of published research in areas related to molecular evolution, epidemiology, computational or mathematical biology. We require computational experience and quantitative skills, including competence in at least one commonly used programming language. Positions are for two or more years, subject to review after one year. Review of candidates and applications will begin February 18, 2006.

Qualified candidates, including minorities and women, are strongly encouraged to apply. Applicants should submit a cover letter, a curriculum vitae, and the names, addresses and phone numbers of two references to:

Dr. Robin Bush Department of Ecology and Evolutionary Biology 359 Steinhaus Hall University of California, Irvine Irvine, CA 92697-2525 phone: 949-824-2243 fax: 949-824-2181 e-mail: rmbush@uci.edu

The University of California, Irvine has an active career partner program, is an equal opportunity employer committed to excellence through diversity, and has a National Science Foundation Advance Gender Equity Program.

rmbush@uci.edu rmbush@uci.edu

UCologne BiolInformation

Postdoctoral Position in Statistical Physics of Biological Information

The Institute for Theoretical Physics, University of Cologne (Germany), offers a postdoc position in biological physics in the newly established research group of Dr Johannes Berg.

We are looking for a highly motivated individual to work on the statistical physics of biological information. Current research topics include biological networks and sequences, and gene expression and its evolution. The position involves collaborations both with biologists and physicists. Applicants should have a strong background in computational biology or statistical physics.

The University of Cologne offers an excellent environment for research on the interface between physics and biology. The Institute for Theoretical Physics has a strong focus in statistical physics and hosts several groups working on biological systems. Joint projects between the Institute of Theoretical Physics and the Institute of Genetics exist within the recently established Collaborative Research Centre SFB680 “Molecular Basis of Evolutionary Innovations”.

For further details and application particulars see http://www.thp.uni-koeln.de/ ˜ berg/jobs.html Prior enquiries are most welcome.

Johannes Berg Tel.: +49 (0)221 470 4205 Universität zu Köln Fax.: +49 (0)221 470 5159 Zülpicher Straße 77 Institut für Theoretische Physik D-50937 Köln Germany

http://www.thp.uni-koeln.de/ ˜ berg Johannes Berg <berg@thp.uni-koeln.de>

UCork FunctEvoGenomics

Postdoc, UniCork.Ireland. FunctEvoGenomics

SFI Post Doctoral Fellow : Plant functional evolutionary genomics

We are seeking an enthusiastic & highly motivated Postdoctoral Fellow to join our multidisciplinary research team working on epigenetics and reproduction. Our group employs a combination of molecular biology, functional genomics, evolutionary bioinformatics and genetics to study basic and applied aspects of reproduction (www.ucc.ie/spillane). The successful applicant will work on an Science Foundation Ireland (SFI)-funded project on elucidating processes of evolutionary birth & death of genes, using the plant Arabidopsis as a model for functional evolutionary genomics. The 3 year project involves collaboration with Karl Schmid (Max Planck ICE, Jena), Ken Wolfe (Trinity College Dublin) and Dolores Cahill (National Centre for Proteomics, Dublin). The starting gross salary for the SFI Postdoctoral Fellow will be 33,000 euros per annum. We are seeking candidates that can effectively combine molecular evolutionary/bioinformatics analysis with molecular/genetics approaches. Candidates with proven experience in molecular evolution, population genomics, bioinformatics, plant developmental/molecular genetics & evolutionary genetics are particularly encouraged to apply. Applicants should send an e-mail outlining your research interest and motivations, including; (a) your C.V. (please list publications and experimental skills) & (b) contact details and e-mail addresses for 3 referees to:

Dr. Charles Spillane, Genetics & Biotechnology Lab, Biochemistry Dept & Biosciences Institute, University College Cork, Cork, Ireland. E-mail: c.spillane@ucc.ie

Deadline: 3rd February 2006 UCC is an equal opportunities employer

“Spillane, Charles” <C.Spillane@ucc.ie>

UDurham AncientDNA

The deadline for applications for the following post has now been set as 10 February, 2006.

Postdoctoral Research Associate Molecular Ecology/Ancient DNA:

Population Genetics of an Extinct Southern Elephant Seal Colony in the Ross Sea, Antarctica

A 2.5 year post is available for a joint position through the University of Durham (UK) and the University of Maine (US). Most work will be undertaken at the University of Durham in the UK starting in April 2006. The study will involve the amplification of DNA from 1000-6000 year old southern elephant seal samples from the Ross Sea. Molecular methods will be used to track demographic changes in this now extinct population over time, assess evidence for selection at target loci (in the context of climate change), assess population genetic structure in comparison with extant populations, and refine estimates of the mtDNA mutation rate for this species. The successful applicant will have skills in the amplification of ancient DNA, and experience with the use of coalescent models. Applicants should also have an understanding of the estimation of mutation rate by MCMC maximum likelihood methods. Durham has excellent facilities for work in molecular ecology and ancient DNA, including 5 automated sequencers and a high specification purpose-built ancient DNA lab.

Applicants should submit a cover letter outlining qualifications, a complete CV, three letters of recommendation, and up to three reprints to:

Dr. A. Rus Hoelzel School of Biological and Biomedical Sciences South Road, University of Durham Durham, DH1 3LE, UK email: a.r.hoelzel@dur.ac.uk

a.r.hoelzel@durham.ac.uk

UMaryland HumanEvolGenomics

Postdoctoral Positions in Human Evolutionary Genomics

Postdoctoral positions are available in a human population genetics laboratory in the Department of Biology at the University of Maryland at College Park for NIH and NSF funded research. Research foci in the lab include the study of African genetic diversity and population structure (we currently have an extensive set of samples from over 100 geographically and ethnically diverse African populations), human evolutionary history, the genetic basis of adaptation (including genotype/phenotype studies), the genetic basis of resistance against infectious disease (with a focus on malaria) and co-evolution of the human and Plasmodium falciparum genomes. Additional information about the Tishkoff lab can be found at http://www.life.umd.edu/biology/tishkofflab/ .

UMCP is located in a suburb of Washington D.C. with easy access to a number of research institutions in the Baltimore/D.C. area including NIH, the Smithsonian, TIGR, George Washington University and Johns Hopkins University. More information about the Biology Department and the Behavior, Ecology, Evolution, and Systematics (BEES) program at UMCP is available at http://www.life.umd.edu/biology/ and http://www.life.umd.edu/biology/

Candidates with either a strong molecular biology and/or statistical genetics background are encouraged to apply for the postdoctoral positions (computational and laboratory positions are available). Starting dates are flexible. Salaries are commensurate with qualifications and experience.

Please send curriculum vita and three letters of reference to Dr. Sarah Tishkoff, Dept. of Biology, Biology/Psychology Building #144, Univ. of Maryland, College Park, MD 20742 or e-mail to tishkoff@umd.edu. Applications should ideally be received by April, 2006.

Women and minority members are strongly encouraged to apply. The University of Maryland is an equal opportunity/affirmative action employer.

Sarah Tishkoff, Ph.D. Associate Professor Dept. of Biology Biology/Psychology Building Univ. of Maryland College Park, MD 20742 Tel: 301-405-6038 Fax: 301-314-9358 email: <mailto:tishkoff@umd.edu> tishkoff@umd.edu <http://www.life.umd.edu/biology/tishkofflab/> http://www.life.umd.edu/biology/tishkofflab/ **NOTE NEW E-MAIL ADDRESS LISTED ABOVE**

UMassachusettsAmherst DarwinFellow

DARWIN FELLOW

The Graduate Program in Organismic and Evolutionary Biology at University of Massachusetts Amherst announces a two-year POST-DOCTORAL FELLOWSHIP/LECTURESHIP. OEB draws together more than 80 faculty from the Five Colleges (University of Massachusetts Amherst and Smith, Hampshire, Mount Holyoke and Amherst Colleges), offering unique training and research opportunities in the fields of ecology, organismic and evolutionary biology. Our research/lecture position provides recent PhD's with an opportunity for independent research with an OEB faculty sponsor as well as experience developing and teaching a one-semester undergraduate biology course. Position subject to availability of funds. 1st year salary: $30,000. 2nd year salary: $32,000. Applicants in the area of collections-based research are particularly encouraged to apply.

To apply, send curriculum vitae, three letters of reference, statements of research and teaching interests, and letter of support from your proposed OEB faculty sponsor. A list of faculty and additional information is available at www.bio.umass.edu/oeb . For more information, see:

http://www.bio.umass.edu/oeb/oeb_darwin.html OEB Darwin Fellowship 319 Morrill Science Center 611 N. Pleasant Street University of Massachusetts Amherst Amherst, MA 01003 413-545-0928 darwin@bio.umass.edu Application review begins: 1/30/06 Start date: 8/13/06

The University of Massachusetts Amherst is an Affirmative Action/Equal Opportunity Employer. Women and members of minority groups are encouraged to apply.

Norman Johnson njohnson AT umass DOT edu

UMontpellier SturgeonConservation

Proposal for post doctoral Position

“Conservation of a highly endangered species, the west European sturgeon, Acipenser sturio L, 1758: strategies for reproductive crossbreeding of reared individuals” Key words: Acipenser sturio, endangered species, conservation ex situ, reproduction, physiology, genetics, assistance with decision-making, biology conservation.

Foreword: Following the previous proposition in 2005, an applicant was retained. After two months, the people resigned for private reasons. New candidates should sent a motivation letter, a provisional working schedule and a CV to Patrick.williot@cemagref.fr with copies to eric.orchard@cemagref.fr as well as paul.gontheir@cemagref.fr

Setting out the problem Context Most sturgeon populations throughout the world are under fairly serious threat, and some have even disappeared entirely (Birstein et al., 1997). The European Atlantic sturgeon, Acipenser sturio Linnaeus, 1758, is no exception to this trend. Whereas at one time it was present throughout Europe, from the Baltic Sea to the Atlantic, the Mediterranean, and the Black Sea, this species can now be found only in France (Ninua, 1976; Holcik et al., 1989; Elvira et al., 1991; Almaa & Elvira, 2000; Barannikova et al., 2000; Debus, 1995; Economidis et al., 2000; Fernandez Pasquier, 2000; Gessner, 2000; Mamcarz, 2000; Rochard et al., 1990; Williot et al., 2002 a). In 1982 it became a protected species throughout France. In spite of the status, the situation continues to deteriorate (Williot et al., 1997; 2002b; Rochard et al., 2001), Thus from the early 90s attempts have been made to constitute a small confined stock of fish (Williot et al., 1997, Williot et al. submitted). The number of individuals concerned is small for two reasons. This ancient population is very much dwindled and rearing methods are still uncertain. From the late 90s, the research programme on species conservation is shared with a German team (IGB Berlin) within a cooperation framework. A small batch of specimen artificially produced in 1995 was sent to Berlin in 1996 (Williot et al., 2000). The main objective behind constituting an ex situ stock is to increase the number of individuals of the species in order to protect it. How can we plan, organise, and carry out the best reproductive crossbreeding in order both to protect the species and maintain maximum genetic diversity in the offspring? Current state of knowledge The knowledge is limited. The best environmental and management conditions for rearing these animals are uncertain. The main uncertainty deals with water salinity, 3 levels are tested 0, 15 & 33. Other constraints and/or uncertainties are food, density and all other environmental conditions such as water temperature, light, photoperiod, shape of tanks. Many biological data are unknown, namely those related to breeding. There are sex determinism (genetically controlled with heterozygous female for Acipenser transmontanus and the hybrid bester after Van Ennennaam et al., 1999 and Omoto et al., 2005 respectively), sex ratio of reared juveniles, dynamics of sexual differentiation, and in general the whole gametogenesis. The first genetic investigations date from the end of the 1990s (Birstein et al., 1998; Ludwig and Kirschbaum, 1998). We therefore have our first genetic data on stock that was reared in 2000 (Ludwig et al., 2004). We have a first genetic map covering 6 microsatellites loci (alleles, degree of relation, heterozygote) and mitochondrial DNA. The genetic variability of these loci is weak, there is a considerable imbalance in the allelic frequencies, degrees of relationship are high, few individuals have rare alleles. All individuals have the same haplotype, which suggests that all the individuals analysed (recent animals, as opposed to museum samples) have a similar maternal line. The genetic variability of the current population in Gironde is less than for that in the North Sea, estimated from museum samples (Ludwig et al., 2004). Since these tests were carried out, a few individual fish have been added to the stock that we have in France. Recent samples were carried out and are currently analysed in Germany and Italy with different methods. Lastly, a quarterly endocrine monitoring has recently been put in place for the largest individuals. Proposals for work projects There are four parts: 1. Analysis of existing genetic data on two levels: - General data on A.sturio and 2 neighbouring species, Acipenser naccarii and Acipenser oxyrinchus (Ludwig et al., 2002; Holcik, 2000; Garrido-Ramos et al., 1997; Hernando et al., 1999; de la Heran et al., 2004). - Detailed analysis at individual level of animals currently kept in housing.

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UMontpellier SturgeonConservation 2

Sorry, My last message was a bit difficult to read. Here is a TXT version Yours

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PROPOSAL FOR POST DOCTORAL POSITION

“Conservation of a highly endangered species, the west European sturgeon, Acipenser sturio L, 1758: strategies for reproductive crossbreeding of reared individuals”

Key words: Acipenser sturio, endangered species, conservation ex situ, reproduction, physiology, genetics, assistance with decision-making, biology conservation.

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SETTING OUT THE PROBLEM Context Most sturgeon populations throughout the world are under fairly serious threat, and some have even disappeared entirely (Birstein et al., 1997). The European Atlantic sturgeon, Acipenser sturio Linnaeus, 1758, is no exception to this trend. Whereas at one time it was present throughout Europe, from the Baltic Sea to the Atlantic, the Mediterranean, and the Black Sea, this species can now be found only in France (Ninua, 1976; Holcik et al., 1989; Elvira et al., 1991; Almaa & Elvira, 2000; Barannikova et al., 2000; Debus, 1995; Economidis et al., 2000; Fernandez Pasquier, 2000; Gessner, 2000; Mamcarz, 2000; Rochard et al., 1990; Williot et al., 2002 a). In 1982 it became a protected species throughout France. In spite of the status, the situation continues to deteriorate (Williot et al., 1997; 2002b; Rochard et al., 2001), Thus from the early 90s attempts have been made to constitute a small confined stock of fish (Williot et al., 1997, Williot et al. submitted). The number of individuals concerned is small for two reasons. This ancient population is very much dwindled and rearing methods are still uncertain. From the late 90s, the research programme on species conservation is shared with a German team (IGB1 Berlin) within a cooperation framework. A small batch of specimen artificially produced in 1995 was sent to Berlin in 1996 (Williot et al., 2000). The main objective behind constituting an ex situ stock is to increase the number of individuals of the species in order to protect it. How can we plan, organise, and carry out the best reproductive crossbreeding in order both to protect the species and maintain maximum genetic diversity in the offspring? Current state of knowledge The knowledge is limited. The best environmental and management conditions for rearing these animals are uncertain. The main uncertainty deals with water salinity, 3 levels are tested 0, 15 & 33. Other constraints and/or uncertainties are food, density and all other environmental conditions such as water temperature, light, photoperiod, shape of tanks. Many biological data are unknown, namely those related to breeding. There are sex determinism (genetically controlled with heterozygous female for Acipenser transmontanus and the hybrid bester after Van Eenennaam et al., 1999 and Omoto et al., 2005 respectively), sex ratio of reared juveniles, dynamics of sexual differentiation, and in general the whole gametogenesis. The first genetic investigations date from the end of the 1990s (Birstein et al., 1998; Ludwig and Kirschbaum, 1998). We therefore have our first genetic data on stock that was reared in 2000 (Ludwig et al., 2004). We have a first genetic map covering 6 microsatellites loci (alleles, degree of relation, heterozygote) and mitochondrial DNA. The genetic variability of these loci is weak, there is a considerable imbalance in the allelic frequencies, degrees of relationship are high, few individuals have rare alleles. All individuals have the same haplotype, which suggests that all the individuals analysed (recent animals, as opposed to museum samples) have a similar maternal line. The genetic variability of the current population in Gironde is less than for that in the North Sea, estimated from museum samples (Ludwig et al., 2004). Since these tests were carried out, a few individual fish have been added to the stock that we have in France. Recent samples were carried out and are currently analysed in Germany and Italy with different methods. Lastly, a quarterly endocrine monitoring has recently been put in place for the largest individuals. PROPOSALS FOR WORK PROJECTS There are four parts: 1. Analysis of existing genetic data on two levels: - General data on A.sturio and 2 neighbouring species, Acipenser naccarii and Acipenser oxyrinchus (Ludwig et al., 2002 ; Holcik, 2000 ;

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UNebraska PopBiol

POPULATION BIOLOGY POSTDOCTORAL RESEARCH FELLOWSHIP

THE UNIVERSITY OF NEBRASKA-LINCOLN is seeking applications for a 2-year postdoctoral position in the Interdisciplinary Program in Population Biology.

A Ph.D. in Biology, Ecology, Evolution, Genetics, or Mathematics, and expertise in any aspect of population biology is required. Qualified candidates are required to contact a potential faculty advisor from the list of core faculty associated with the program to develop a 2-year research project. Information about the program and complete instructions for application can be found at http://popbio.unl.edu. Applications must include a CV, a 5-page research proposal, and a description of potential graduate seminars (synergistic activity plan). In addition, the applicant must arrange for three letters of reference (one of which must be from the proposed faculty sponsor). Applications and letters should be sent to:

Population Biology Fellowships Program School of Biological Sciences University of Nebraska-Lincoln 348 Manter Hall Lincoln, NE 68588-0118.

Applications should be received by 1 March 2006 in order to ensure full consideration. The salary range is in line with international standards for postdoctoral positions. We strongly encourage applications from women, and members of minority groups. UNL is committed to a pluralistic campus community through Affirmative Action and Equal Opportunity, and is responsive to the needs of dual career couples. We assure responsible accommodation under the Americans with Disabilities Act. For further information contact Alan C. Kamil at 402-472-6676 for assistance.

Diana Pilson <dpilson1@unl.edu>

UOxford CompEvolBiol

Applications are invited for a one year fixed-term postdoctoral research position starting immediately. The post is in association with the Evolutionary Biology Group and the Ancient Biomolecules Centre, Department of Zoology, at the University of Oxford. The position is to be entirely computer-based, and will involve the analysis of DNA sequences (both ancient and modern) with the aim to address broad evolutionary issues such as domestication, population genetics, and coalescent processes. Potential candidates should have an interest in phylogenetics and evolutionary biology. The successful candidate will have the freedom to define the exact scope of the project, although it should fit within the current research programme of the group. Experience with computer programming and/or statistical techniques is desirable, and the post could involve the development of new evolutionary models within our existing Bayesian MCMC software.

More information about research taking place in our groups is available from website: http://evolve.zoo.ox.ac.uk and http://evolve.zoo.ox.ac.uk abc.zoo.ox.ac.uk. Further particulars available by Tel: 01865 271190; E-mail: recruit@zoo.ox.ac.uk. Applications, including curriculum vitae, contact details of three referees and a description of your research achievements and interests, should be sent to the Personnel Office, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS quoting reference number: AT 06008. The closing date for applications is 10 February 2006.

For more information, please contact

Dr. Beth Shapiro Acting Director, Henry Wellcome Ancient Biomolecules Centre Oxford University, Depts. of Zoology and Statistics Oxford, OX1 3PS, UK +44 (0) 1865 281248

beth.shapiro@zoo.ox.ac.uk

VirginiaTech AngiospermMolSyst

A one year postdoctoral position with potential extension to two years is available in molecular systematics and evolution of angiosperms. The study focuses on using gene sequence information from representatives of angiosperm families to address current systematic and evolutionary problems in the group. The candidate is expected to have experience in molecular systematic laboratory methods and phylogenetic analyses. The starting date is preferably ASAP, but May or August dates are possible. Salary is negotiable. If interested, please contact Khidir Hilu (hilukw@vt.edu; Phone: 540-231-5407), or send a cover letter detailing your experience in the field, a current vita, and names and addresses of two references to: Khidir Hilu, Department of Biological Sciences, Virginia Tech, Blacksburg, Va 24061, USA

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Sincerely yours,

Khidir Hilu Professor of Biology

Department of Biological Sciences Virginia Tech Blacksburg, Va 24061 USA Phone: 540-231-5407 Fax: 540-231-9307 http://www.biol.vt.edu/faculty/hilu/ "Khidir W. Hilu" <hilukw@vt.edu>

WorkshopsCourses

Bloomington EvolComplexity June3

Workshop on the Evolution of Complexity

as a part of the Tenth International Conference on the Simulation and Synthesis of Living Systems: ALife X

June 3rd, 2006. Bloomington, IN, USA

Motivation

The evolution of complexity is a central theme in Biology. Yet it is not without any ambiguity. Complexity has been used to refer to different things. For instance, complexification has been interpreted as a process of diversification between evolving units or as a scaling process that is related to the idea of transitions between different levels of complexity. Other meanings of complexity have been introduced, both inside and outside the realm of Biology. What concerns most researchers is to get insight into the mechanisms that produce their notion of complexity.

The focus of this workshop will be on biological interpretations of complexity and the driving mechanisms: primarily we want the focus to be on evolutionary and related dynamics as mechanisms for producing complexity. Furthermore, we want to bring together historical and novel research in this context.

Questions to be addressed at the workshop include: - - What are the environmental constraints of complexity growth in living systems? - - What is the origin and role of developmental mechanisms in evolution? - - Are the principles of natural selection, as they are currently understood, sufficient to explain the evolution of complexity? - - What are the limits at different levels to the evolution of complexity, and which conditions could reduce evolved complexity? - - <Which models are | What language is> more appropriate to <understand | speak about> the evolution of complexity in living systems? - - How could complexity growth be measured or operationalised in natural and artificial systems? - - How can data from nature be brought to bear on the study of this issue? - - What are the main hypotheses about complexity growth that can actually be tested? - - Is it possible to <direct|manipulate> the evolution of complexity, or which benefits would bring its understanding?

Paper Submission:

Submitted papers should follow the format guidelines for the ALife X proceedings (http://www.alifex.org/submissions/). Papers should not exceed 6 pages in length and must be made in PDF format. The submissions will be made electronically at the workshop website. Submissions are open. Please use the submissions site. Papers will be judged by members of the Programme Committee by their relevance to the workshop and conference, originality, clarity of the presentation, and overall quality.

Important Dates:

Submission deadline: February 28th, 2006 Notification of acceptance: April 1st, 2006 Camera-ready papers due: April 15th, 2006 Workshop date: June 3rd, 2006

Workshop Structure:

The workshop will take place in Bloomington, IN, USA, on June 3, 2006, the first day of the conference. The aim is to have 2-4 invited speakers, and talks by the authors of groundbreaking contributions. We feel that it is important to have a discussion on the presentations and submissions at a workshop and hence will introduce a workshop format that achieves this goal.

Invited speakers (* indicates confirmed): Mark Bedau* Jim Crutchfield* Stuart Kauffman Ricard Sole

Proceedings:

Workshop proceedings will be published in a special volume distributed at the conference. (This volume will be different from the MIT press conference proceedings). Depending on the quality of submissions, a special issue of the Artificial Life journal may be created.

Programme Committee:

Lee Altenberg Mark Bedau Hugues Bersini John Bonner Dominique Chu Jim Crutchfield Bruce Edmonds Carlos Gershenson Mario Giacobini Franics Heylighen Tom Lenaerts Juan Julin Merelo Barry McMullin Melanie Mitchell Chrystpher Nehaniv Jorge Pacheco Tom Ray Jon Rowe Stanley Salthe Cosma Shalizi Peter Schuster Eros Szathmary Richard Watson

Organising Committee:

Carlos Gershenson Centrum Leo Apostel, Vrije Universiteit Brussel Krijgskundestraat 33. B-1160, Brussels, Belgium cgershenatvub.ac.be

Tom Lenaerts IRIDIA CP 194/6, Universit Libre de Bruxelles Av. Franklin Roosevelt 50. B-1050, Brussels, Belgium tlenaertatulb.ac.be

Websites:

Workshop: http://ecco.vub.ac.be/ECO/ Conference: http://www.alifex.org c.l.nehaniv@herts.ac.uk

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BodegaMarineLab AppliedPhylogenet Apr8-15

UC Davis WORKSHOP IN APPLIED PHYLOGENETICS at Bodega Marine Laboratory, Bodega Bay, California

April 8-15, 2006

sponsored by the

Center for Biosystematics and Bodega Marine Laboratory,

University of California, Davis

Introduction. Phylogenetic methods have revolutionized modern systematics and become indispensable tools in evolution, ecology and comparative biology, playing an increasingly important role in analyses of biological data at levels of organization ranging from molecules to ecosystems. The construction of phylogenetic trees is becoming a methodology that is well-defined, with broad agreement on the central issues and questions. A nearly standard set of topics is now taught as part of the curriculum at many colleges and universities. On the other hand, applications of phylogenetic methods to interesting problems outside of systematics is an area of special excitement, innovation, and controversy, and perspectives vary widely.

In April, 2006, for the seventh year, we will teach a workshop for graduate students interested in applying phylogenetic methods to diverse topics in biology. The one-week course will be an intensive exploration of problems to which modern phylogenetic tools are being applied, including topics in biogeography, ecology, conservation biology, phylogenomics, functional morphology, macroevolution, speciation, and character evolution. The course leads off with recent advances in phylogenetic methodology, and then turns to methods and tools that can be brought to bear to address these “applied” issues in the context of a given phylogeny.

The course will be held entirely at Bodega Marine Lab on the Northern California coast, which has extensive computing resources and on-site housing. The course format will involve equal parts of lecture, discussion, and training in software and internet tools. One afternoon during the week will be left free for field trips to local natural areas.

Specific Topics to be Covered in the first week

* Finding, evaluating and interpreting phylogenetic trees; phylogenetic databases * Recent advances in tree reconstruction: Bayesian inference; stochastic optimization strategies; divide-and-conquer methods * Analysis of character evolution–theory: parsimony, likelihood and Bayesian approaches; null models and statistical testing * Analysis of character evolution–form and function of complex character systems * Phylogenetic biogeography and phylogeography; coalescent methods for inferring migration rates and patterns * Phylogenetic comparative methods * Phylogenetic perspectives on biodiversity and conservation biology * Data mining of sequence databases for phylogenetic analysis * Estimation of divergence times from sequence data

Instructors for the workshop.

* Dr. H. Bradley Shaffer * Dr. Michael Sanderson * Dr. Peter Wainwright * Dr. Tom Near * Dr. Phil Spinks * Dr. Gordon Burleigh * Dr. Shelley McMahon * Dr. Justen Whittall * Dr. Rich Glor

Prerequisites. Students should have some familiarity with phylogenetic methods through previous coursework. Some experience with PAUP, PHYLIP, or other programs for phylogeny reconstruction will be assumed.

Admission and Fees. Students will be admitted based on academic qualifications and appropriateness of research interests. The course fee is $375. This includes room and board at BML for duration of the course (arriving April 8, leaving April 15).

Application Deadline. Applications are due by February 15, 2006. Please send a completed application form (available at http://ginger.ucdavis.edu/sandlab/ap.htm) and one letter of recommendation from your major advisor. We encourage applications to be sent via email as PDFs to pqspinks@ucdavis.edu. Sorry, but due to the limited size of the class, postdocs and faculty are discouraged from applying. Students will be notified via e-mail by February 28 of acceptance.

Send all application materials to

Dr. Phillip Q. Spinks Section of Evolution and Ecology 2320 Storer Hall University of California Davis Davis, CA 95616 email:pqspinks@ucdavis.edu

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Edinburgh MolEvol Jul17-21

BBSRC THEORETICAL GENETICS AND EVOLUTION SUMMER SCHOOL ON MOLECULAR EVOLUTION AND DIVERSITY 2006

Edinburgh, Monday July 17th 2006 (starting at 2pm)-Friday July 21st (ending at noon)

The BBSRC will be running a summer school (course) for Postgraduate and Postdoctoral researchers working on quantitative aspects of evolutionary biology, dealing with variation both within and between species. The course is intended for young scientists who take an ongoing and broad interest in molecular evolutionary biology, and wish to gain a greater understanding of quantitative and theoretical tools and approaches that will aid their interpretation of evolutionary data. The course will include plenary talks from experts in population genetics and molecular evolutionary analyses, including people who are working on developing methods, and people who are applying them to biological data from a range or organisms. There will be a few practical (computer) sessions, intended to help participants learn how to approach analyses of sequence and other types of data, and to think about how they can be used in studying biological questions. Those chosen for the course will be asked to present a short talk or a poster about their research project (or planned project).

Places on the course, and accommodation during the course, are free, but are limited to postgraduates and postdoctoral researchers who have not attended the course in previous years. Travel to Edinburgh is at your own expense.

Applications will be via a web site: http://www.biology.ed.ac.uk/public/conferences/molevoldiv2006/ and will ask for a talk or poster title and abstract as well as your name and supervisors name and your institution and department. Places are not restricted to BBSRC-funded students or post-docs. The deadline is March 31st 2006.

The Summer School will cover the following areas of micro- and macroevolution:

Theme A: Genetic diversity within populations The neutral theory and the coalescent Mutation Human minisatellites Genomic context and molecular evolution Theme B: Genetic variability between populations. Theme C: Macroevolution and variation between species Alignment of sequences Reconstruction of Phylogenetic Trees, Detecting natural selection from gene genealogies Gene families, Gene duplications in evolution Genome alignment: Theme D: Evolution of development Theme E: Evolution in microorganisms

Lecturers in 2006 will include: Nick Barton, Peter Keightley, Toby Johnson, Brian Charlesworth and Deborah Charlesworth (Edinburgh University) John Armour, John Brookfield, and Paul Sharp (University of Nottingham), Gil McVean (Oxford University) Michael Akam (Cambridge, Zoology) Timothy J.C. Anderson (Department of Genetics, Southwest Foundation for Biomedical Research, San Antonio) Jaap Heringa (Centre for Integrative Bioinformatics, Free University, Amsterdam) Susan Ptak (Max Planck Institute for Evolutionary Anthropology, Leipzig) >

– Professor Deborah Charlesworth Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Ashworth Lab., King's Buildings, West Mains Rd., Edinburgh EH9 3JT, UK

phone 131-650-5751 Fax: 131-650-6564

deborah.charlesworth@ed.ac.uk deborah.charlesworth@ed.ac.uk

Helsinki GenesUnderNatSel May15-19

EMBO practical course: "Statistical methods for identification of genes under natural selection"

Helsinki 15th-19th May 2006

Organizers: J. Corander & C. Schlötterer

The identification of genes subjected to natural selection has been one of the primary research interests in population genetics over the past decades. With the recent technological advancements and the availability of numerous fully sequenced genomes, the emphasis is shifting from the analysis of single genes towards genome scans for genes subjected to selection.

The course aims to train biologists with the fundamental techniques on how to use statistical methods for the identification of selected genes. Furthermore, we will also show how the statistical tests could be improved by the incorporation of available data from genome scans.

Participants of the course will be provided with the background of the statistical tests, they will be trained in the use of available statistical software packages, and finally they will have the opportunity to apply this knowledge to their own data.

Teachers: Mark Beaumont Jukka Corander Joachim Hermisson Christian Schlötterer Ziheng Yang

More information can be found at:

http://cwp.embo.org/pc06-02/ Christian Schloetterer <christian.schloetterer@vu-wien.ac.at>

MBL MolEvol Jul23-Aug4

Workshop on Molecular Evolution

http://workshop.molecularevolution.org/ Michael P. Cummings, Director

23 July - 4 August 2006 plus extended topics session 5 August - 11 August 2006

Application Deadline 1 March 2006

The Workshop on Molecular Evolution has been the finest course of its type in the world since it was started in 1988. The Workshop consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of molecular evolution. A distinguishing feature of the Workshop is a well-equipped computer laboratory with Linux workstations and servers for comparative analysis of molecular data. Authors and experts in the use of computer programs and packages such as Clustal W and Clustal X, FASTA, GCG, LAMARC, MrBayes, PAML, PAUP*, and PHYLIP provide demonstrations and consultations. This two-week program is designed for established investigators, postdoctoral fellows, and advanced graduate students with prior experience in molecular evolution and comparative genomics. Scientists with a strong interest in molecular evolution, systematics, and population genetics are encouraged to apply. Enrollment is limited to 60 students, and 15 students will be admitted to an extended topics session for the purpose of analyzing their research data sets. Many participants find the extended topics session to be especially useful.

Topics to be covered include:

* Databases and sequence matching: database searching: protein sequence versus protein structure; homology; mathematical, statistical, and theoretical aspects of sequence database searches * Phylogenetic analysis: theoretical, mathematical and statistical bases; sampling properties of sequence data; Bayesian analysis, hypothesis testing * Character analysis in a phylogenetic context: analysis of quantitative and discrete characters; hypothesis testing * Maximum likelihood theory and practice in phylogenetics and population genetics: coalescent theory; maximum likelihood estimation of population genetic parameters * Bayesian methods in phylogenetic analysis * Molecular evolution integrated at different levels: population biology; biogeog-

raphy; ecology; systematics and conservation * Molecular evolution and development: gene duplication and divergence; gene family organization; coordinated expression in evolution * Comparative genomics: genome content; genome structure; genome evolution * Transposable elements: types; history; evolutionary dynamics; as a major component of genomes

Partial funding support for the Workshop comes from the National Aeronautics and Space Administration (NASA).

Fee: $2000 (room and board at no additional charge), plus an additional $750 for the extended topics session.

Application Form at http://www.mbl.edu/education/-admissions/applications/ Further information at http://workshop.molecularevolution.org/ mike@umiacs.umd.edu

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MountainLakeBioStation courses

Dear Biologist,

The Mountain Lake Biological Station is pleased to announce its summer 2006 program. Our NSF REU-Sites program will be in its 14 year, and we'll offer five exciting field-based courses (2 and 4 week). See details below, and attached. Or visit our web site any time.

We appreciate any help you can lend posting or distributing this material to your colleagues and students. Thanks for your help.

If the attachments don't make it, here are the links: http://mlbs.org/download/MLBS_REU_Announce.pdf http://mlbs.org/download/MLBS_REU_Poster.pdf Best wishes and Happy New Year,

Eric Nagy Associate Director, MLBS

P.S. Apologies for any multiple copies of this mailing. Your email address may occur on more than one of the lists we use.

MOUNTAIN LAKE BIOLOGICAL STATION

<file:///www.mlbs.org>mlbs.org SUMMER 2006

The Mountain Lake Biological Station (University of Virginia) announces paid research opportunities for undergraduates and university-level credit courses in field biology. We offer students hands-on experience and training in a wide variety of biological field studies. Students are invited to join us for an exciting and unforgettable summer in a beautiful and stimulating teaching and research environment. Scholarships and financial aid for courses are available.

NSF-Funded Research Experience for Undergraduates (REU) Program <http://www.mlbs.org/-REU.html>mlbs.org/REU.html We match undergraduate students with visiting scientists for 10 weeks of advanced, independent research on a project of the student's own design. REU positions come with a "take home" stipend of $3,640. And the program covers all room and board expenses. Minority students are especially encouraged to apply. Deadline for receipt of applications is March 1.

Field Courses

<http://%20www.mlbs.org/courses.html>mlbs.org/-courses.html 1) Plant Biodiversity and Conservation May 30 - June 23 (4 weeks). The extraordinary diversity of the Southern Appalachians will serve as a backdrop to explore the world of plants.

2) Biology of Fungi June 26 - July 21 (4 weeks). An introduction to the biology of fungi, with emphasis on field identification and current experimental methods used to study fungal genetics, ecology and evolution.

3) Stream Ecology June 26 - July 21 (4 weeks). This course will focus on integrating principles of stream and watershed ecology as a means of gaining insight into stream dwelling organisms and their environments.

4) Ecology & Conservation of Freshwater Fishes July 24 - August 4 (2 weeks). An investigation of the ecology and conservation of freshwater fishes through a series of discussions, lectures, lab and field exercises.

5) Biodiversity in the Southern Appalachians July 24 - August 4 (2 weeks). This course will teach students how historical processes and current land-use patterns shape the compositions of ecological communities.

Our field station is located on a mountaintop in southwestern Virginia and is home to a lively research, teaching and social community. For details on these programs, full course descriptions, application material, and a list of research areas see our web page <http://mlbs.org/>mlbs.org University of Virginia, Mountain Lake Biological Station, PO Box 400327, Charlottesville VA 22904-4327, U.S.A., <mailto: mlbs@virginia.edu> mlbs@virginia.edu, +1-434-982-5486

Eric S. Nagy, Ph.D. Associate Director, Mountain Lake Biological Station Research Assistant Professor, Department of Biology University of Virginia / Mountain Lake Biological Station P.O. Box 400327 / Charlottesville, VA 22904-4327 USA street address: 485 McCormick Road / 238 Gilmer Hall tel: +1-

434-982-5486 (+1-540-626-5227 June-August) fax: +1-434-982-5626 (+1-540-626-5229 June-August) cel: +1-434-906-3122 eml: <mailto: enagy@virginia.edu> enagy@virginia.edu personal web page: <http://faculty.virginia.edu/nagy>faculty.virginia.edu/nagy MLBS web page: <http://www.mlbs.org/>mlbs.<http://www.mlbs.org/>org

enagy@virginia.edu

OhioStateU SpatialHeterogeneity Feb6-10

Workshop

Spatial Heterogeneity in Biotic and Abiotic Environment: Effects on Species Ranges, Co-evolution, and Speciation

Mathematical Biosciences Institute, The Ohio State University, February 6-10, 2006

Organizers: Sergey Gavrilets (University of Tennessee, Knoxville), John Thompson (University of California, Santa Cruz), Mark Kirkpatrick (University of Texas, Austin)

Webpage: http://mbi.osu.edu/2005/workshops2005.html Talks:

Roger Butlin “Adaptation to environmental gradients: observations on /Littorina saxatilis/ and a simulation” Ilkka Hanski “Spatially realistic models of metapopulation dynamics” Sylvain Gandon “Fluctuating epistasis (with or without coevolution) and the evolution of recombination in a metapopulation” Scott L. Nuismer “Polygenic traits and local adaptation in antagonistic interactions” Richard Harrison “Mosaic Hybrid Zones: Twenty Years After” Masakado Kawata “Speciation by sensory drive through the evolution of visual pigments along an environmental light gradient” Troy Day “Evolutionary change in spatially distributed populations: a kin selection perspective” Alan McKane “Stochastic models in biology and their deterministic analogs” Bob Holt “Reflections on demographic constraints and evolution in heterogeneous environments” Edmund D. Brodie III “Phenotypic mismatches across the geographic range of a predator-prey arms race” Craig W. Benkman “A coevolutionary arms race causes ecological speciation in red crossbills” Sergey Gavrilets “Dynamic patterns of adaptive radiation” Mark Kirkpatrick “Chromosome inversions, local adaptation, and speciation” Jane Hill “Evolutionary changes during climate-driven range expansion” Laurent Excoffier “The effect of spatial expansions on neutral molecular diversity” John N. Thompson “Coevolution, Geographic Ranges, and Speciation: Current Results and Unanswered Questions” Henrik Jeldtoft Jensen “The Tangled Nature model: a study of community structure, species area relation and and species diversity within a model of co-evolution” Jim Mallet “Speciation in sympatry: is it so difficult?” Jordi Bascompte “The spatial dimension of ecological networks” Richard Gomulkiewicz “Fixation of new mutations in spatially variable environments”

Sergey Gavrilets <gavrila@math.utk.edu>

RiodeJaneiro Phylogenies Mar13-19

Short lecture and practical course on “Advanced methods in reconstructing phylogenetic relationships” funded by the EMBO World Programme. Dates 13th to 19th March, 2006, Rio de Janeiro, Brazil. EMBO cover hotel accommodation and food, but NOT travel costs. For details of the course and how to apply see the course webpage: http://bioinf.ncl.ac.uk:16080/molsys/ .Or contact Prof. Martin Embley at martin.embley@ncl.ac.uk.

Dr. T. M. Embley Professor of Evolutionary Molecular Biology The Devonshire Building Division of Biology School of Biology and Psychology University of Newcastle upon Tyne NE1 7RU UK

Tel 0191 246 4804 Fax 0191 246 4998

New Lab Webpage:

http://www.ncl.ac.uk/microbial_eukaryotes/ Take a look at our Molecular Systematics course Web Page - it is also available in down-loadable (powerpoint) format:

http://bioinf.ncl.ac.uk/molsys Martin.Embley@ncl.ac.uk Martin.Embley@ncl.ac.uk

UEdinburgh QuantGenetics

MSc in QUANTITATIVE GENETICS AND GENOME ANALYSIS UNIVERSITY OF EDIN-

BURGH http://www.qgen.co.uk This full-time degree programme (12 months M.Sc./ 9 months Diploma) starts each September and provides a solid foundation in population and quantitative genetics together with experience in relevant statistical methodologies. It includes options in evolutionary genetics , human genetics and animal breeding. There is a growing need for individuals with these combined strengths to apply quantitative genetics theory to practical problems in both the biomedical and agricultural industries; and to undertake research on current problems in population genetics, genome analysis, and analysis of complex traits. This Masters course is an excellent platform for doctoral studies.

The course is based at the Institute of Evolutionary Biology http://www.biology.ed.ac.uk/research/-institutes/evolution/ with substantial input of teaching and research facilities provided by the Roslin Institute, Scottish Agricultural College, the Medical Genetics Section of the Department of Medical Sciences, and the MRC Human Genetics Unit. These are all internationally recognised centres for research in quantitative genomics and research training is an integral part of the course.

**STUDENTSHIPS AVAILABLE FOR SELECTED APPLICANTS **

The course has a number of scholarships open to UK applicants and other EU nationals. Details are at http:/-/www.qgen.co.uk. Studentships will be awarded on a competitive basis.

We welcome applications from able graduates (expected 2.1 or higher) in either

1. Biosciences, Genetics, Agricultural Sciences, Medicine or Veterinary Medicine who have an interest in, and aptitude for quantitative biology, or

2. Mathematics, Statistics or Physical Sciences who wish to apply theory to genetic problems.

Closing date for applications 31 March 2006 but earlier applications welcome.

The application form can be downloaded from the Postgraduate Office web pages at http://-www.postgrad.ed.ac.uk Informal enquiries and requests for further information to http://qgen@ed.ac.uk n.barton@ed.ac.uk n.barton@ed.ac.uk

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ULausanne HumanCooperation Mar9-10

This is the second announcement for a symposium on

THE NATURE OF HUMAN COOPERATION

March 9-10 2006

University of Lausanne, Switzerland

The program, some preparatory reading and access information are now on the website, please go to http://-www.unil.ch/dee/page25289_en.html . There is no registration fee, but participants should register through the website until February 22th 2006.

Invited speakers:

Samuel Bowles (Santa Fe Institute) Robert Boyd (University of California Los Angeles) Ernst Fehr (University of Zürich) Daniel Fessler (University of California Los Angeles) Herbert Gintis (Sante Fe Institute) Peter Hammerstein (Humboldt University Berlin) Karl Sigmund (University of Vienna) Joan Silk (University of California Los Angeles) John Tooby (University of California Santa Barbara) Robert Trivers (Rutgers University)

Organizers: Michel Chapuisat, Laurent Keller, Jacques Dubochet, Jérôme Goudet and Nicolas Perrin Secretary: France Pham, secretariat.dee@unil.ch, Tel + 41 (0) 21 692 41 60

Michel Chapuisat Department of Ecology and Evolution Biophore, Quartier Sorge University of Lausanne CH-1015Lausanne(Switzerland) Ph: +4121 6924178 / Fax: +4121 6924165 URL: http://-www.unil.ch/dee/page7000.html Michel Chapuisat <Michel.Chapuisat@unil.ch>

UWashington StatGenetics Registration

Online registration for the 11th Summer Institute in Statistical Genetics, now located at the University of Washington in Seattle, is now open 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 notifcation 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.