
E v o l D i r

April 1, 2005

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

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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Auckland SMBE05 Jun19-23 3

Don't miss March 10th deadline for SMBE YI <http://www.kumarlab.net/smbe/smbeyi05.htm> and March 15th deadline for abstracts for SMBE05 <http://www.mbe05.com/> (see 'call for papers' page)

Laura

—

Laura A. Katz, Associate Professor Department of Biological Sciences College Road Smith College Northampton, MA 01063 Phone: 413-585-3825 Fax: 413-585-3786 <http://www.science.smith.edu/departments/Biology/lkatz/>

ColoradoStateU EvolInfectDiseases May19-21

Dear All Apologies for cross-posting, but we would like to re-announce that we are proud to be hosting the Third Annual Ecology and Evolution of Infectious Diseases Conference, in conjunction with a modeling workshop, to be held in May 2005 at Colorado State Uni-

versity. The program is still under development, but a web page with further information can viewed at:

<http://rydberg.biology.colostate.edu/EEID2005/> The conference and workshop have funding from the National Science Foundation, so we will be accepting applications from post-docs and graduate students, both from the United States and internationally, for support of travel to Fort Collins. Application deadlines will be in early March, 2005, with decisions made shortly after.

Ecology and Evolution of Infectious Diseases Principal Organizer: Michael Antolin, Department of Biology and Program for Interdisciplinary Math, Ecology and Statistics (PRIMES), Colorado State University, Fort Collins, CO 80524 Workshop: May 14-18, 2005 Application of disease models to long-term population data Conference: May 19-21 Ecology and Evolution of Infectious Diseases: 3rd Annual Conference Organizing committee: Mike Antolin, Colorado State University Ottar Bjornstad, Pennsylvania State University Andrew Dobson, Princeton University Karen Garrett, Kansas State University Peter Hudson, Pennsylvania State University Mary Poss, University of Montana Les Real, Emory University David Smith, National Institutes of Health

Workshop focus: Advances in numerical and statistical models in infectious diseases have provided the opportunity for exploring how long-term population monitoring data can be analyzed in the context of disease dynamics. We will run a workshop in which graduate students and post-doctoral researchers will learn the major skills for analysis and modeling and then apply these to specific data sets. The workshop will be fo-

cused around two questions: 1) is it possible to test with models whether compensatory mortality caused by a previously undetected disease has influenced dynamics of a host population? 2) given a long-term population data set, which may or may not include disease prevalence, what observations or experiments would be needed to test hypotheses regarding infectious disease? We will recruit participants for this workshop by soliciting for graduate students and post-doctoral researchers who have access to long-term data sets they could bring with them to the workshop. The aim is to explore the data sets using a wide arsenal of analytical and statistical techniques. We plan to follow the model that has been developed in the PRIMES program at Colorado State University, where teams of graduate students with backgrounds and interest in ecology, mathematics, and/or statistics are grouped to solve analytical and biological challenges that arise. Thus, we hope to recruit graduate students and post-docs from statistics and applied mathematics to participate in the workshop, and certainly to attend the conference that follows. These students may not have access to long-term data sets, but would provide us with an opportunity to recruit applied mathematicians and statisticians into infectious disease research. We will use the experiences of the math and stats faculty in PRIMES at Colorado State to help in this recruiting effort. We hope to have 20 or more workshop participants, in addition to the researchers who will provide modeling and statistical expertise to the workshop participants. We expect that five additional participants will be graduate students or post-docs who are currently in the PRIMES program in Fort Collins. The researcher/faculty are: Mike Antolin, Ottar Bjornstad, Andy Dobson, Karen Garrett, Peter Hudson, Mary Poss, Les Real, David Smith.

Conference focus: This will be the third Ecology and Evolution of Infectious Disease conference and follows two previously successful meetings at Penn State and Emory. The conference will follow the workshop and build on the experience learnt from previous meetings. Essentially this will be a two day science meeting, aimed specifically at graduate students but limited in size to approximately 75 participants. The plan is to have talks presented mostly by graduate and post doctoral workers with a short but broad introduction from PIs. The conference will be organized around the following two areas, with two sub-areas subsumed under the first of them: 1.) Disease persistence and transmission: How do pathogens persist? i) the role of super-spreaders ii.) metapopulation dynamics 2.) Immune system dynamics: do they scale from the individual to the population level? i.) can within-host immune processes explain incidence, severity, and virulence? We plan to have each

area represented by more established researchers who can address theoretical, clinical, or empirical aspects of each area. Thus, we

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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>

Fairbanks Evol05 Jun10-14 2

The annual meetings of the The American Society of Naturalists <<http://www.amnat.org/>>, Society of Systematic Biologists <<http://systbiol.org/>>, and Society for the Study of Evolution <<http://lsvl.la.asu.edu/-evolution/>> are scheduled for 10-14 June 2005 in Fairbanks, Alaska, at the University of Alaska Fairbanks.

Online conference and talk/poster registration is now available.

The conference web site can be accessed at: <http://www.evolution05.uaf.edu/> Online registration for pre-and post-conference tours also is now available.

There will be three tours offered, one to the Permafrost Tunnel on the afternoon of 10 June and two more to the Bonanza Creek LTER Site and Toolik Field Station starting on 15 June.

Tour registration can be accessed at: <http://www.evolution05.uaf.edu/tours.cfm> PLEASE BE AWARE OF THE FOLLOWING DEADLINES:

*The last day for talk/poster registration is 31 March 2005. Registration must be completed online before talk/poster submission. Talk/poster registration is available only online.

*The last day for discounted early registration is 30 April 2005. Conference fees will increase by \$50 after this date.

*Campus housing is almost full. Single rooms and Cutler apartments are sold out, but double rooms are still available.

OTHER HIGHLIGHTS:

*Information about travel to Alaska, hotels, and on-campus lodging can be found on the web site.

*The request form for on-campus lodging can be found at: <http://www.evolution05.uaf.edu/lodging.cfm>

*Lodging for additional days on-campus following the

conference may be available. If you want your room for extra days, please request these dates on the campus housing registration form.

*The request form for vendor and exhibitor registration can be found at: <http://www.evolution05.uaf.edu/exhibits.cfm> *Sign up to receive conference updates by email on the web site at: <http://www.evolution05.uaf.edu/signup.cfm> 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 WWRB fax (907) 474-6967 email: fnkgm@uaf.edu

Fairbanks Evol05 Jun10-14 3

THE LAST DAY TO REGISTER TALKS AND POSTERS FOR THE 2005 EVOLUTION CONFERENCE IS 31 MARCH 2005—NOW 1 WEEK AWAY!

The annual meetings of the The American Society of Naturalists <<http://www.amnat.org/>>, Society of Systematic Biologists <<http://systbiol.org/>>, and Society for the Study of Evolution <<http://lsvl.la.asu.edu/evolution/>> are scheduled for 10-14 June 2005 in Fairbanks, Alaska, at the University of Alaska Fairbanks.

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*The last day for discounted early registration is 30 April 2005. Conference fees will increase by \$50 after this date.

*Campus housing is now sold out, but a wait list is available.

OTHER HIGHLIGHTS:

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*The request form for on-campus lodging can be found at: <http://www.evolution05.uaf.edu/lodging.cfm>

*Lodging for additional days on-campus following the conference may be available. If you want your room for extra days, please request these dates on the campus housing registration form.

*The request form for vendor and exhibitor registration can be found at: <http://www.evolution05.uaf.edu/exhibits.cfm> *Sign up to receive conference updates by email on the web site at: <http://www.evolution05.uaf.edu/signup.cfm> 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 WWRB fax (907) 474-6967 email: fnkgm@uaf.edu

Fairbanks Evol05 Jun10-14 Undergrads

DIVERSITY AT SSE/SSB 2005:

Call for applications for undergraduates of diverse backgrounds to attend the 2004 meeting of the Society for the Study of Evolution/Society of Systematic Biologists *** and ***

Call for volunteer mentors for this program from graduate students, postdocs and faculty.

In 2001, 14 undergraduates of diverse backgrounds received funding from a pilot NSF- Undergraduate Mentoring in Environmental Biology (UMEB) grant to attend the annual meetings of SSE/SSB in Knoxville, Tennessee, present posters, and interact with graduate student, postdoc and faculty mentors. The program has since supported undergraduates attending the 2003 meeting in Chico, California and the 2004 meeting in Fort Collins, Colorado.

The program will take place again at the 2005 meeting this June in Fairbanks, Alaska and we are now accepting applications. The application deadline is April 1, 2005. Applications will consist of a title, author line and abstract of the poster to be presented by the undergraduate; a one or two paragraph (no more than 1 page) statement of academic interests and career goals and of how attending the Evolution meetings will help

meet these goals; and one letter of recommendation from the undergraduate's research advisor. All materials should be submitted as pdf files and emailed to Rich Kliman at rmkliman@cedarcrest.edu. Applications will be accepted only from students registered or very recently graduated from U.S. institutions, including Puerto Rico (i.e., having finished classes during the winter or spring semesters before the meeting) and traveling to the meeting from within the US. Students demonstrating a need for funds to attend SSE/SSB will be given preference, and will be selected so that as a group, they will increase cultural diversity among undergraduates at Evolution meetings.

In addition to applications from undergraduates, we hope to receive email notices to rmkliman@cedarcrest.edu from graduate students, postdocs and faculty who wish to serve as undergraduate mentors for the meetings. Duties will include meeting with a pair of undergraduates in the program, attending and demystifying a half-day of talks with them, joining them for a meal, introducing them to colleagues and in general befriending them in ways that make evolutionary biology seem like a welcoming discipline. No costs for travel, housing or registration are covered. Please spread the word about this very rewarding activity.

Contact one of the program PIs or organizers for more information:

Scott V. Edwards, Harvard University (sedwards@fas.harvard.edu) Richard Kliman, Cedar Crest College (rmkliman@cedarcrest.edu) Elizabeth Zimmer, National Museum of Natural History, Smithsonian (zimmer@lms.si.edu)

SELECTION CRITERIA for participating undergraduates:

Students will be selected so that:

- a) As a group, attending students must increase cultural diversity among undergraduates at Evolution meetings.
- b) Students and faculty demonstrating a need for student funds to attend SSE will be given preference. Those students without access to travel funds from their institutions or their research advisor's research budget will be chosen over those that have significant support.
- c) Students must be registered undergraduates or very recent graduates (i.e., having finished classes during the winter or spring quarters (semesters) before the meeting).
- d) All students will be encouraged to attend the entire meeting to maximize their participation and to mini-

mize travel costs by spanning a Saturday overnight stay. Thus travel schedule will be for arrival on 9 June 2005 and departure on 15 June. Students selected for the award will make travel arrangements through a designated travel agent working with this program.

FloridaStateU FormFunction Mar17-20

Sponsored by the William H. and Lucyle T. Werkmeister Endowment Fund

FORM AND FUNCTION IN BIOLOGY PROGRAM
March 17-20, 2005 Florida State University * All sessions to be held in 204 Longmire

Thursday March 17 (2005) Session I (1 pm to 6 pm)-including a tea break * Richard Richards (University of Alabama): "Functional Analysis and Character Transformation" * Roger Sansom (Texas A & M): "Accounting for natural selection and developmental constraints" * Jane Maienschein (Arizona State University): "Form and Function start with the Egg" * Jorge Wagensberg (Museum of Natural History, Barcelona, Spain): "Rebellion of the Forms: what perseveres when uncertainty functions as a constraint" * Matt Day (Florida State University): "The Form of a Godly Mind: Phrenology, Evolution and Nineteenth-Century Theories of Religion" Dinner for all participants and attendees: (7:30) Location: 651 E. 6th Ave. Tallahassee, FL 32303

Friday March 18 Session II (9am to 1pm)-including a coffee break * Rudy and Elizabeth Raff (Indiana University): "Evolution in the light of embryos: origins of novel features" * Gunter Wagner (Yale): "Avian Digit Homology: experimental results and ontological implications" * Jason Robert (Arizona State University): "Form and function in stem cell biology" * Paul Brakefield (Leiden University): "Using selection experiments on *Bicyclus* butterflies to explore developmental constraints" Lunch: (1pm-2pm) Session III (2pm to 6 pm)-including a tea break * Peter Wainwright (University of California at Davis): "Form-function relationships and the evolution of biological diversity" * Joe Travis (Florida State University): "Convergence and Idiosyncrasy in Adaptation: Looking at Form and Function Matches at Different Biological Levels" * David Krakauer (Santa Fe Institute): "The Varieties of Form and Function" * Manfred D. Laubichler (Arizona State University): "Goethe vivat! The problem of form in theoretical biology" Dinner

Party for Speakers and Chairs only: (7:30pm) Location: TBA

Saturday March 19 Session IV (9am to 12pm)-including a coffee break * Steven Orzack (The Fresh Pond Research Institute): "Assessing natural selection and phylogenetic inertia as explanations of form and function" * Karl Niklas (Cornell University): "The pitfalls of deducing function from organic form and environmental context" * Roger Thomas (Franklin and Marshall): "Animal Skeletons: Laws of Form and the Appearance of Design" Lunch: (12:00pm-1:00pm) Session V (1pm to 3 pm)-including a tea break * Ron Amundson (Hawaii University): "Epigenetics confounds any definitive assignment of proper functions to body parts, and thereby serves civil rights" * Vassiliki B. Smocovitis (University of Florida): "No Agreement to Separate: G. Ledyard Stebbins and Developmental Genetics, 1959-1973" Boat Ride at Wakulla Springs (3:30pm)-transportation provided Barbeque for all participants and attendees: (7:30) Location: chez Ruse-651 E. 6th Ave. Tallahassee, FL 32303 Sunday March 20 Session VI (9am to 12pm)-including a coffee break * Frederick Davis (Florida State University): "Archie Carr and the Evolution of Cichlid Diversity: Musings on Rubrism, Buttheadness, and Isolation" * David Castle (Guelph University): "Form and Function in Agricultural Biotechnology" * Zac Ernst (Florida State University): "The function of intuition"

for registration email or call: Michael Ruse mruse@mailers.fsu.edu 850 644 4128 Charles Alt cja03d@fsu.edu Karen Foulke kfoulke@mailers.fsu.edu 850 644 0967

- Steven Orzack

The Fresh Pond Research Institute 173 Harvey Street
Cambridge, MA. 02140 617 864-4307

www.freshpond.org orzack@freshpond.org

GhentU StatGenetics May17

The Center for Statistics of Ghent University is organizing a one-day symposium on Statistical Genetics to be held in Ghent (Belgium) on May 17, 2005. The goal of this symposium is to bring together statisticians, data analysts, bio-information scientists and computational biologists from universities, research institutes and industry and to bring them in contact with the newest developments in statistical genetics. Leading

experts in this field will discuss different themes, including pharmacogenetics, genetic association analysis, marker-assisted plant breeding and micro-array analysis.

Invited speakers: Balding, David (Imperial College London, U.K.) Goldstein, David (University College London, U.K.) Hospital, Frederic (INRA, UMR de Genetique Vegetale, France) Lange, Christoph (Harvard School of Public Health, U.S.A.) Storey, John (University of Washington, U.S.A.) van Eeuwijk, Fred (Wageningen University & Research Centre, The Netherlands) Moerkerke, Beatrijs (Ghent University, Belgium) Vuylsteke, Marnik (Flanders Institute for Biotechnology, Belgium)

Details of the scientific program, as well as guidelines for registration are available on the symposium web site: <http://cvstat.ugent.be>. Registration will be opened on March 21. The number of participants is limited and hence early registration is strongly encouraged.

I look forward to meeting you at the symposium! Sincerely,

Stijn Vansteelandt.

Stijn Vansteelandt Phone. ++32 9 2644776 Ghent University Fax. ++32 9 2644995 Dept. Applied Mathematics and Computer Science Krijgslaan 281, S9 B-9000 Gent, Belgium

Center for Statistics: <http://cvstat.ugent.be>
Master in Statistical Data Analysis: <http://www.mastat.ugent.be>

Stijn Vansteelandt <Stijn.Vansteelandt@ugent.be>

JagiellonianU Cracow ExperimentalEvol Aug15-20

10th congress of the European Society for Evolutionary Biology, Jagiellonian University, Cracow, Poland from 15 to 20 August 2005

We would like to encourage applications for the following symposium:

'Testing evolutionary theory - the role of ecology in evolution'

Abstract: Evolutionary theory has refined greatly in recent years, particularly regarding the role of ecology. Concurrently, new methods and empirical sys-

tems allow testing this theory, the recent application of non-invasive molecular techniques to field and lab populations being especially instrumental. This symposium covers recent empirical studies in life history evolution and adaptive diversification using very different systems and methods: from microbes to vertebrates, from “evolution in a bottle” to populations with extended pedigrees, from natural to anthropogenic selection. Bringing biologists from these diverse fields together will stimulate testing evolutionary theory in exciting new ways.

Organisers: Martijn Egas, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam (egas@science.uva.nl) Tom van Dooren, Institute for Biology, Leiden University (vdooren@rulsfb.leidenuniv.nl) and Bruno Ernande, Laboratoire Ressources Halieutiques, IFREMER (Bruno.Ernande@ifremer.fr)

Invited speakers: David Coltman, Department of Animal and Plant Sciences, University of Sheffield Maren Friesen, Center for Population Biology, University of California Esben Olsen, Department of Biology, University of Oslo

See: <http://www.eko.uj.edu.pl/eseb/> for further details and registration.

Martijn Egas

Martijn Egas, assistant professor Institute for Biodiversity and Ecosystem Dynamics, <http://www.science.uva.nl/ibed> Department of Population Biology, <http://www.science.uva.nl/ibed/research/Research.Fields/pb/index.en.html> University of Amsterdam

P.O. box 94084 tel: 00 31 20 525 7748 1090 GB Amsterdam fax: 00 31 20 525 7754 email: egas@science.uva.nl

Martijn Egas <egas@science.uva.nl>

Krakow ESEB2005 GenomicsSymposium Aug15-20

Genomic approaches towards tracing adaptive evolution - a special symposium in ESEB 2005

Organizers: D. Tautz (Germany) & C. Schlötterer (Austria)

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 candidate genes towards analyses on the genomic scale. This new approach offers the potential of identifying genes subjected to selection without the need of a priori information about putative candidate genes.

This symposium will be held in the ESEB 2005 meeting in Krakow 15-20.8.2005, and it is sponsored by European Society for Evolutionary Biology (ESEB). Selected contributions from this symposium will be published in the Journal of Evolutionary Biology which has recently expanded its editorial board and welcomes more contributions from the field of molecular evolution (<http://www.blackwellpublishing.com/journal.asp?ref10-061X&site=1>).

Invited speakers in this symposium include:

Justin Borevitz, University of Chicago, USA: Microarrays for mapping and expression analysis: Toward the genetic determinants of light response adaptation in Arabidopsis and Aquilegia Antony M. Dean, University of Minnesota, USA: The Selective Cause of an Ancient Adaptation Emmanouil (Manolis) Dermitzakis, Sanger Institute, UK: Selective constraint and adaptive evolution of conserved non-coding sequences in the human genome Adam Eyre-Walker, University of Sussex, UK: Rates of adaptive evolution in bacteria, flies and humans Brandon Gaut, University of California at Irvine, USA: The impact of artificial selection on the maize genome Tony Long, University of California at Irvine, USA: The Genetic Architecture of Complex Traits Jose M. Ranz, University of Cambridge, UK: Patterns of divergence during the evolution of the eukaryotic transcriptome Christian Schlötterer, Veterinärmedizinische Universität Wien, Austria: Potentials and pitfalls of demography in hitchhiking mapping studies Diethard Tautz, Universität zu Köln, Germany: A systematic screen for adaptive trait genes in the house mouse

For more information about ESEB 2005 meeting, see: <http://www.eko.uj.edu.pl/eseb/> Juha Merila <juha.merila@helsinki.fi>

Oslo HennigSociety July25-29 Registration

24th meeting of the Willi Hennig Society

25-29 July 2005 in the mountains north of Oslo, Norway
 **REGISTRATION AND ABSTRACT SUBMISSION
 IS NOW OPEN**

See http://folk.uio.no/victoraa/Frontpage_files/-slide0001.htm - DEADLINE for registration and abstract submission is 1 July 2005.

Links are available on the above web site for preliminary meeting details and registration prices, direct registration and payment, and abstract submission via document template, the latter to be emailed as an attachment to victor.albert@nhm.uio.no.

This conference on PHYLOGENETIC BIOLOGY (both theoretical and empirical) will be held at the Quality Fagernes Hotel (see <http://www.choicehotels.no/html/en-gb72665.jsp> for site information).

Single or double rooms with full pension are available, as are cheaper options for students in youth hostel bookings with or without full pension. Rates are available with or without transportation from and to Gardermoen International Airport, Oslo.

Contributed presentations are invited either within the symposia topics or on any area within phylogenetic biology. All poster presentations are welcome. The Willi Hennig Society strongly encourages participation from students and postdocs on their developing research, either theoretical or empirical. There are several cash student prizes that will be awarded.

Victor A. Albert Professor, Botanical Garden

Natural History Museum University of Oslo P.O. Box 1172 Blindern NO-0318 Oslo, Norway

Visiting address: Sars' gate 1, NO-0562 Oslo

+47 48224268 (or +47 22851698; +47 22851824 fax)
http://folk.uio.no/victoraa/index_files/slide0002.htm
 "Victor A. Albert" <victor.albert@nhm.uio.no>

Oslo Hennig Society WebSite CORRECTION

CORRECTED WEB SITE

24th meeting of the Willi Hennig Society

http://folk.uio.no/victoraa/Frontpage_files/-slide0003.htm 25-29 July 2005 in the mountains

north of Oslo, Norway

**REGISTRATION AND ABSTRACT SUBMISSION
 IS NOW OPEN**

----- DEADLINE for registration and abstract submission is 1 July 2005. -----

Our apologies!

Victor A. Albert Professor, Botanical Garden

Natural History Museum University of Oslo P.O. Box 1172 Blindern NO-0318 Oslo, Norway

Visiting address: Sars' gate 1, NO-0562 Oslo

+47 48224268 (or +47 22851698; +47 22851824 fax)

http://folk.uio.no/victoraa/index_files/slide0002.htm

"Victor A. Albert" <victor.albert@nhm.uio.no>

Queens College Oxford EEFG Gordon Jul31-Aug5

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

When: Jul 31 - Aug 5, 2005

Where: Queen's College, Oxford, UK

Organizers: Chair - Thomas Mitchell-Olds (tmo@ice.mpg.de) Vice-Chair - Greg Wray (gwwray@duke.edu)

Conference web site: <http://www.grc.org/programs/-2005/evolut.htm> Confirmed Speakers:

Joy Bergelson Paul Brakefield Enrico Coen Anthony Dean Caroline Dean Scott Edwards Justin Fay Jeff Feder Dan Hartl Jennifer Hughes Bill Jeffery Henrik Kaessman Laurent Keller Carol Lee Trudy MacKay Martin Parniske Katie Peichel Derek Smith Joe Thornton Cynthia Weinig Sue Wessler Tom Whittham Patricia Wittkopp Mariana Wolfner

Finally, we want to thank dozens of colleagues who

suggested potential speakers. Your advice and suggestions have been fundamentally important for preparing a very exciting conference. We hope you can join us in Oxford!

Thomas Mitchell-Olds <tmo1@duke.edu>

Strasbourg Measuring Natal Dispersal Aug19-23

Hi all

I would like to bring the following workshop to your attention:

Title: Measuring natal dispersal: current approaches and future challenges Location: Strasbourg, France Conference: 6th meeting of the European Ornithologists' Union Date: 19 - 23 August 2005 Abstract: Natal dispersal, the movement of an individual from its birthplace to the site of first reproduction, is a key process with many causes and consequences for individuals, populations and communities. Despite its importance, our knowledge of dispersal is at best limited for most species. Obtaining reliable estimates of dispersal rates, distances and timing is notoriously difficult, mainly because of great logistic challenges. These include limitations of surveys to a few study plots mainly due to time and money constraints, difficulties in recording long-distance dispersal, and incomplete correlation between movements of individuals and gene flow among subpopulations. The aims of this workshop are to get an overview of currently used methods and techniques and to discuss the potential of new approaches in the study of natal dispersal. Researchers are encouraged to present their (new) methods for studying natal dispersal. We aim at bringing together as wide a range of topics as possible, including for example studies using genetic methods, radio-tracking or observational approaches as well as probabilistic techniques. We also hope that this workshop will increase the interest in and will stimulate new research programs on natal dispersal.

For further details, please visit: <http://vogelwarte.mpg.de/EOU05.Info.html#Symposia>
<http://vogelwarte.mpg.de/EOU05.Info.html> Hope to see you there!

Gilberto

Dr. Gilberto Pasinelli Senior Research Associate Zoological Institute University of Zurich Winterthur-

erstrasse 190 CH-8057 Zurich

Tel ++41 1 635 49 82 Fax ++41 1 635 68 21
gpasi@zool.unizh.ch

http://www.zool.unizh.ch/Research/Ecology/-Researchgroups/ReedBunting_en.html http://www.zool.unizh.ch/Research/Ecology_en.html http://www.zool.unizh.ch/index_en.html Gilberto Pasinelli
<gpasi@zool.unizh.ch>

Switzerland Sexual Size Dimorphism Aug21-26

THE EVOLUTION OF SEXUAL SIZE DIMORPHISM Workshop organized by Wolf Blanckenhorn, Tamas Szekely & Daphne Fairbairn 21-26 August 2005, Switzerland

<http://www.bath.ac.uk/bio-sci/szekely/workshop/SSD%20Workshop2%20webmod.htm>

We are organizing an international Workshop on sexual size dimorphism (SSD) at the Centro Stefano Franscini Conference (CSF) Center on Monte Verità, near Locarno in southern Switzerland.

The objectives of the Workshop are to - bring together researchers working on various aspects of SSD; - overview the pattern of SSD in major animal and plant taxa; - investigate the function and mechanisms of SSD.

Our main goal is to adopt a truly interdisciplinary approach, and encourage all participants to go beyond his/her specific research field.

We have invited a group of internationally renowned researchers to the Workshop. In addition, we have space for approximately 35 researchers including post-graduate students and post-docs.

The scientific program will consist of about 10 half-hour plenary lectures given by invited speakers. There will further be contributed short oral and poster presentations, and discussion in groups. We welcome post-docs, MSc and Diploma students, and PhD students. Participants are expected to attend the entire 5-day workshop, and their number is limited to 60.

The cost of the Workshop will be approximately 950 Swiss Francs (about 650 Euro or 800 US\$) that includes registration fee, accommodation and all meals. For postgraduate participants the Association for the Study of Animal Behaviour (ASAB) has generously

provided support to defer travel cost, and the CSF has generously provided support to defer the cost of room and full board on a competitive basis. Furthermore, we shall apply for Swiss National Fund funding to defer the travel cost for delegates from Eastern European countries. To qualify for this support, please contact Wolf Blanckenhorn.

Abstract submission and registration deadline: 31 April 2005

Please note that if space is limited applicants offering a presentation will be preferred. One participant is expected to present only one oral paper or poster. Instructions for payment and detailed travel information will soon be available on the web site.

If you are interested in attending, please email the following details to our conference e-mail address: congres2@zoolmus.unizh.ch

1. Full name including title

Gender

2. Institution & Department

3. Contact mailing address including street address, city and postcode

Phone Fax Email

4. Proposed presentation

Type of presentation (Talk/Poster)

Title of presentation

Authors including the presenting author (*)

Abstract (max. 250 words)

Keywords (5)

Special technical needs

The Workshop is generously funded by The Centro Stefano Franscini, the Swiss Zoological Society, the Ethological Society and the Zoological Museum of Zurich.

Best regards,

Wolf Blanckenhorn wolfman@zoolmus.unizh.ch Tamas Szekely T.Szekely@bath.ac.uk Daphne Fairbairn daphne.fairbairn@ucr.edu

sium Thursday, 14th of April 2005, University of Amsterdam, The Netherlands. <http://staff.science.uva.nl/~peijnenb> Marine-dwelling organisms are usually imagined to be part of huge populations, characterized by almost unlimited interchange. This is especially true for free-living critters in the plankton that may travel wherever the water current takes them. Allopatric divergence and speciation are therefore not expected to play a major role at the spatial scales at which they typically act in other habitats. Nonetheless, species diversity and levels of population genetic structuring are often unexpectedly high. This symposium reviews the observed patterns for pelagic as well as benthic organisms and discusses recent theories on the possible causes for these.

The symposium is organized on the occasion of the PhD defense of Katja Peijnenburg and will consist of presentations by a diverse group of internationally renowned as well as up-and-coming scientists, and will include a poster session.

The event is free of charge and open to all. However, we do ask for you to register by sending an email to Pieterella Luttkhuizen (luttkhuizen@science.uva.nl). Participants are encouraged to bring posters.

Confirmed speakers are: Nancy Knowlton (University of California, USA) Colomban de Vargas (Rutgers University, New Brunswick, USA) Matthew Hare (University of Maryland, USA) Jeanine Olsen (University of Groningen, Netherlands) Katja Peijnenburg (University of Amsterdam, Netherlands) Galice Hoarau (University of Groningen, Netherlands) Gregory Maes (University of Leuven, Belgium)

For registration and further questions, please send an e-mail to luttkhuizen@science.uva.nl.

The organisers, Pieterella Luttkhuizen, Katja Peijnenburg, Steph Menken, and Jef Huisman. University of Amsterdam, Institute for Biodiversity and Ecosystem Dynamics, the Netherlands.

“Katja T.C.A. Peijnenburg”
<peijnenburg@science.uva.nl>

UCSD GenomesEvolving Apr15-16

UAmsterdam MarinePopStructure Apr14 2

Genomes Evolving Symposium April 15-16, 2005 University of California, San Diego

Final announcement: One-day Structure@Sea Sympo-

On April 15 and 16, 2005, UCSD Biological Sciences

will host a symposium on Evolutionary Genomics. Our distinguished panel of speakers will examine diverse topics in evolution and genomics research, including theoretical and comparative evolutionary genomics, bioinformatics, and functional genomics.

Featured Speakers include:

Doris Bachtrog, UC San Diego Patricia Beldade, UC Irvine Michael Eisen, UC Berkeley Brandon Gaut, UC Irvine Alex Kondrashov, NCBI Michael Lynch, Indiana Rasmus Nielsen, Copenhagen Allen Orr, Rochester Daven Presgraves, Cornell Molly Przeworski, Brown Patricia Wittkopp, Michigan

Registration for the symposium is free. However, because of limited space, it is necessary to register to guarantee admittance to the symposium.

Please visit the website <http://genomesevolving.ucsd.edu/> for more information.

We look forward to seeing you there.

Organizers: Peter Andolfatto Doris Bachtrog Hopi Hoekstra

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UPaulCezanne Plant Conservation Sep29-Oct2

First Announcement on EVOLDIR

International Symposium Mediterranean plant conservation in a changing world

29 September - 2 October 2005 Hyeres Var, France

Organizers :

Institut Méditerranéen d'Ecologie et de Paléocécologie (IMEP, UMR CNRS 6116), Université Paul Cézanne (Aix-Marseille III). & Conservatoire Botanique National Méditerranéen de Porquerolles

Abstract :

The Mediterranean Basin represents one of the 34 “hotspots” of biodiversity, primarily because of its richness in plant species and the high rates of endemism it contains. However this region has been subject to long term and intense human impacts, and may be severely affected by future modifications to the environment associated with global change. The conservation of Mediterranean plant diversity in this changing world thus constitutes a key issue for conservation

biologists and landscape managers. The main objective of this symposium is to evaluate effective conservation solutions to the apparent dilemma of conserving plant diversity in a region where it is likely to become both more vulnerable and more variable in space and time. Twenty years after the seminal synthesis edited by C. Gómez-Campo in 1985 (Plant conservation in the Mediterranean area), and on the 25th anniversary of the Conservatoire Botanique National Méditerranéen de Porquerolles, this conference will provide a new assessment of the plant conservation status of the circum-Mediterranean flora. The focus of the conference will be on recent progress, with the additional aim of bringing to light gaps in our knowledge worthy of future attention. The emergence, and rapid development, of several new disciplines (e.g. conservation genetics, phylogeography, landscape ecology, and ecological modeling) have led to several conceptual and practical advances whose integration provides a standpoint from which to assess the conservation of plant biodiversity in the Mediterranean Region. The presentation of synthetic overviews, accompanied by the results of more focused innovative projects in this conference will contribute to the development of new perspectives for a dynamic approach to the conservation of the Mediterranean flora within the framework of the Global Strategy for Plant Conservation.

Program

29th September : - Session 1 Evaluation of conservation strategies in different regions around of the Mediterranean basin The purpose of this session is to assess the current state of our knowledge concerning (i) the rare and threatened species of the Mediterranean flora (existence of red lists, data bases and catalogues of protected plants), (ii) protected areas (status and purposes) and (iii) conservation actions that have begun in different regions of the Mediterranean Basin. Talks will be selected to cover the different biogeographical regions of the Mediterranean Basin (northern shores of the western Mediterranean, north-east Africa, the Balkans, Turkey and the Middle-East)

- Session 2 Major threats and their consequences for the Mediterranean flora This session will examine the major causes of rarefaction and threats of extinction in the Mediterranean flora. The different elements of global change (landuse change and habitat fragmentation, climate change and invasive species) will be examined. A priority will be given to the effects of these environmental changes on the distribution and population dynamics of narrow endemic, rare and protected species.

30th September : - Session 3 New advances in the bi-

ological and ecological plant conservation This full-day session will be centred on recent conceptual progress in plant conservation and its application to the Mediterranean flora. Two half-day sessions are programmed. In the first, the use of phylogeographic and genetic data for the identification of evolutionary significant units for the conservation of geographically peripheral, ecologically marginal or fragmented populations The potential role of a metapopulation approach will be considered here. In the second part of this session, studies of the ecological processes associated with species interactions, demography and ecogeographical plant differentiation will be covered in order to illustrate the importance of a spatially oriented approach to conservation ecology.

1st October : - Session 4 Experimental programmes of conservation and restoration The final session will provide a more practical viewpoint on conservation issues for Mediterranean plants. In this session cases studies of conservation and restoration will be presented with the aim being to cover a variety of situations and problems in the Mediterranean region This will allow for the emergence of practical guidelines for future projects of habitat and species conservation.

2nd October : Field excursion.

Scientific committee:

Responsible : Dr Frédéric Médail, email:
f.medail@univ.u-3mrs.fr

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UToronto EGLME Apr30 2

Eastern Great Lakes Molecular Evolution Meeting

SECOND ANNOUNCEMENT

Saturday, April 30, 2005 University of Toronto Koffler Institute for Pharmacy Management 569 Spadina Ave Toronto, Ontario

The 2005 Eastern Great Lakes Molecular Evolution Meeting will be held on Saturday, April 30, 2005, at the Koffler Institute for Pharmacy Management at the University of Toronto, in Toronto, Ont. Registration, coffee, and poster setup will begin at 8:30 A.M., with the talks will end around 5 PM, and will be followed

by a reception/poster session. We are pleased that the following speakers have agreed to give a talk a:

Carlos Bustamante (Cornell) Andy Clark (Cornell) Brian Golding (McMaster) Paul Hebert (Guelph) Jeff Lawrence (Pittsburgh)

Further information, registration and abstract submission can be found at <http://bbc.botany.utoronto.ca/-EGLMEM/> In addition to the invited speakers, there will be a selection of shorter contributed talks. Contributed talks will be selected from submitted abstracts, and will be of 12 - 15 minutes duration. Selection will be made by the organizing committee based on the submitted abstract, with attention given to timeliness and general interest of the work. An effort will be made to have as many labs represented as possible. Abstracts must be submitted by March 30, 2005. Individuals submitting requests to give talks will be informed by April 11, 2005, as to whether they have been selected to give a talk. Those not chosen for talks will be strongly encouraged to present a poster on their work. Posters will be available all day, with a mid-day poster session set aside.

Please feel free to duplicate and distribute copies of this notice and the registration form to anyone interested in attending the meeting, particularly students and faculty who are new to these meetings or to the field of molecular evolution. A schedule and additional details on the meeting will be distributed by email no later than April 22nd to all those who preregister. It will also be posted at: <http://bbc.botany.utoronto.ca/EGLMEM/registrants.html>

Information about traveling to Toronto, maps of the Toronto campus, and descriptions of research and educational activities at the University of Toronto can be found on the University of Toronto Home Page and related pages: <http://www.utoronto.ca/-toronto.htm> <http://www.osm.utoronto.ca/map/> <http://www.utoronto.ca/> If you have any questions, please contact: David Irwin Department of Laboratory Medicine and Pathobiology e-mail: david.irwin@utoronto.ca phone: 416-978-0519 Fax: 416-978-4108

Belinda Chang Department of Zoology e-mail: changb@zoo.utoronto.ca phone: 416-978-3507 FAX: 416-978-8532

David Guttman Department of Plant and Microbial Biology e-mail: david.guttman@utoronto.ca phone: 416-978-6865 FAX: 416-978-5878

Allan Baker Royal Ontario Museum e-mail: allanb@rom.on.ca phone: 416-586-5520 FAX: 416-585-5553

GradStudentPositions

Ifremer France EvolBiol	13	ULeicester EvolImmunology	20
InstZool London EvolBiol	14	UMunich EvolFuncGenomics	20
MaxPlanckBerlin ComputationalBiol	15	UOslo EvolMycology	21
OxfordU LateralTransfer	16	UOxford CercozoaEvol	21
OxfordU LateralTransfer 2	17	UOxford CercozoaEvol 2	22
OxfordU LateralTransfer 3	17	UTromso EvolSperm	23
Stockholm PlantEvolSyst	18	Uppsala EvReprSystems	23
UCanterbury EvolAnimalCommunication	18	YorkU EvolGenomics	24
UGroningen EcolEvol	19	ZurichETH EvolBiol	24
ULausanne 2 SocialEvol	19		

Ifremer France EvolBiol

Available PhD position at the French Research Institute for Exploitation of the Sea (Ifremer) in collaboration with the Centre for Ecological and Evolutionary Synthesis (CEES), University of Oslo - deadline April 1st.

The French Research Institute for Exploitation of the Sea (Ifremer) and the Centre for Ecological and Evolutionary Synthesis (CEES) proposes a doctoral scholarship to University candidates or engineers with a Master degree or equivalent. The scholarships are attributable for a period of 3 years, out of which approximately 18 months are to be spent at each of the two institutions. This research position is offered within one of the 29 themes proposed by Ifremer (see below) and is titled "Effects of the color of environmental noise on the persistence of marine exploited populations: a comparative approach among various ecosystems" (number 14). The procedure for application and a brief description of the thesis project is given below. For further information, please contact Nils Chr. STENSETH (n.c.stenseth@bio.uio.no or Jean-Marc FROMENTIN (Jean.Marc.Fromentin@ifremer.fr).

These scholarships are attributable for a period of max-

imum 3 years following a yearly evaluation of the results. They are obtainable by students who prepare their thesis in one of Ifremer's laboratories or in one of the laboratories of the collaborative Universities of Ifremer.

The proposed research subjects should correspond to one of the themes that are prioritized by the establishment and contribute to this research. The subjects and their corresponding scientific goals are indicated in the table that can be found at

www.ifremer.fr/francais/actual/bourses/affiche-bourses-2005.pdf . The scholarship, who corresponds to a monthly payment of 1380 ??? (1820 USD brut - 18 months spent at Sète, France) and from 2930 ??? (3860 USD - 18 months spent in Oslo, Norway) (not cumulative with other scholarships), are obtainable after an evaluation of the application from the Commission of scholarships at Ifremer. It is planned that 12 subjects for co-financed thesis and that the subjects in totality will be financed at Ifremer. The partners of Ifremer are territorial collectives, research institutes, industrial enterprises, professional organizations etc...

An application including a detailed CV and a letter of motivation must be sent to Nils Christian Stenseth (n.c.stenseth@bio.uio.no) before March 25th (preferably before).

The research projects are to be constituted in collaboration with the scientific correspondents, and the final

application including the papers are to be sent in 4 copies to Ifremer before April 8th 2005.

Description of research theme number 14: Effects of the color of environmental noise on the persistence of marine exploited populations: a comparative approach among various ecosystems.

Reception laboratories

??? Ifremer-IRD, Centre de Recherche Ahlieutique Mediterraéen et Tropical, BP 171, 34203 Sète Cedex, France ??? CEES, Dept. of Biology, University of Oslo, P.O. box 1050, Blindern, 0316 Oslo, Norway. See web page: <http://www.cees.no/> Duration: 3 years

Objectives and Originality:

The objectives of the study are to: (i) determine the properties of the marine physical environments of several exploited populations, using environmental databases such as COADS and (ii) model the variability in abundance of marine populations and evaluate the importance of environmental impacts. The approach will be data-oriented and will be mainly based on time series analyses.

The originality of this work will be related to the systematic description of the environmental stochasticity of different ecosystems (e.g., continental shelves versus open ocean) of various oceans (cold to temperate or tropical seas). The originality will also be within its extensive comparative approach, i.e., among various environments and species of various trophic levels (i.e., top predator versus small pelagic). The purpose of such extensive comparison work would be to answer to the following key questions:

??? Do all marine environments exhibit similar reddened noise (in reference to Vasseur & Yodzis 2004)?
 ??? Can we characterise similarities/differences among key marine systems? ??? What are the different effects of diverse environmental noises on exploited marine populations? ??? Do all the populations transform or integrate similarly the signature of environmental and climate noise? ??? What is the importance of life history traits, trophic level, and area in the response of the populations? ??? How can fisheries impact on population modify population responses to environmental noise?

Such a topic is very broad and needs to be restricted to a given set

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InstZool London EvolBiol

NERC Funded PhD Studentships 2005

Applications are invited from graduates or final year students who have, or expect to have a First or Upper Second Class Honours Degree in a relevant subject, for projects based at the Institute of Zoology. The studentships will be available from October 2005. Full funding of £12,000 pa (outside London) or £14,000 pa (within London) + Fees is available to UK students, EU students are eligible for fees only.

A list of available projects is given below. For more information please click on the project titles. The Institute will award approximately 2 studentships from this list. For more information regarding the applications please contact the appropriate IoZ supervisor.

To apply for one of the awards, please send a cover letter and CV and the names and full contact details of two referees. Please state clearly in your cover letter which project you are applying for.

Send your application to the principal IoZ supervisor by the 11th March 2005.

NERC PhD Studentship in Biodiversity and Macroecology Institute of Zoology, Zoological Society of London Title of project: Sexual selection and extinction in birds Supervisors: Dr Peter Bennett (Institute of Zoology, principal supervisor), Dr John Ewen (Institute of Zoology, second supervisor), Prof Ian Owens (Department of Biology, Imperial, University supervisor). Project aims: Does sexual selection drive extinction? If so, how does it operate? Does the evolution of extravagant or exaggerated traits heighten extinction risk due to the costs of producing and maintaining them, or does sexual selection result in another form of specialisation, dooming species to extinction in the face of rapid anthropogenic change? These questions are highly controversial, with some current theory and evidence providing support for the role of sexual selection in extinction, while other studies reject the argument. Much of this confusion arises because different studies use different indices of the intensity of sexual selection, and different phylogenetic, ecological and geographical scales of analysis. This study will attempt to resolve this confusion by performing a series of new tests of how sexual selection might influence extinction risk in birds. Specifically by - i) examining variation

on a global scale, within major realms, in hotspots of threatened species, and in detail within the avian clade - the honeyeaters Meliphagidae; and ii) by developing a range of detailed indices of the intensity of sexual selection appropriate to the scale of analysis. For further details, contact Peter Bennett <people/bennett.htm> (Tel: 020 7449 6673; E-mail: peter.bennett@ioz.ac.uk <mailto:peter.bennett@ioz.ac.uk>).

NERC PhD Studentship in Behavioural and Evolutionary Ecology Institute of Zoology, Zoological Society of London Title of project: Kin discrimination in the multiple-queen ant *Leptothorax acervorum* Supervisors: Dr Andrew Bourke (Institute of Zoology, principal supervisor), Dr Seirian Sumner (Institute of Zoology, second supervisor), Dr William Foster (Department of Zoology, University of Cambridge, University supervisor). Project aims and methods: Kin selection theory predicts favourable treatment of relatives (kin discrimination) in social groups, but whether this occurs is controversial. In social insects, early studies failed to find unequivocal within-colony kin discrimination [e.g. 1], but more recent work suggests that it exists [2]. However, no study has demonstrated clear within-colony kin discrimination in favour of sexuals (queens and males), which is the critical prediction. Confirming or refuting this prediction would therefore represent a major advance in our understanding of a fundamental evolutionary theory. Using the multiple-queen (polygynous) ant *Leptothorax acervorum* as a model system, this studentship will test the hypothesis of within-colony kin discrimination favouring related sexuals.

L. acervorum represents an excellent system for this work because it is common, easily collected in the field, and readily kept and observed in captivity. In addition, previous work led by the principal supervisor has established seven polymorphic microsatellite loci for *L. acervorum* and provided extensive knowledge of colony kin structure and demography, as well as queen and worker behaviour [e.g. 3-8]. We therefore know that related queens in polygynous colonies share reproduction, with the result that workers tend adult queens and sexual larvae of differing relatedness to themselves. This provides a natural context for the evolution of within-colony kin discrimination. The student will perform a series of laboratory experiments involving behavioural observations, controlled manipulations and microsatellite genotyping to test the hypothesis of within-colony kin discrimination.

The student will receive training in evolutionary biology, behavioural

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MaxPlanckBerlin ComputationalBiol

The International Max Planck Research School for Computational Biology and Scientific Computing is a joint graduate program of the Free University of Berlin and the Max Planck Institute for Molecular Genetics, Berlin.

Applications are invited for a PhD program in the fields of Computational Biology and Scientific Computing. The PhD program is designed as a 3-year program starting in October. Scientific research will be accompanied by an interdisciplinary training in English with the main focus on formal sciences. Applicants to the PhD program should have a Master's degree or diploma in bioinformatics or scientific computing. Students with a degree in life sciences or theoretical sciences will also be accepted, if they are able to show profound knowledge in the complementary field. Students with a Bachelor degree that have the necessary background in Bioinformatics or Scientific Computing can apply for a 2-semester grant for a preparatory program. They can attend one of the two Master programs offered by the Free University and have the chance to join the PhD program thereafter.

PhD fellowships are funded with approximately 975 Euros (or BATIIa/2 level) and fellowships for Master students with approximately 715 Euros per month.

For further details and application procedure see <http://www.imprs-cbsc.mpg.de> A poster can be downloaded from <http://www.imprs-cbsc.mpg.de/download/poster2005.pdf> CLOSING FOR APPLICATIONS: April 1st, 2005.

Contact: Hannes Luz c/o Max Planck Institute for Molecular Genetics | Tel: +49 30 8413 - 1154 Computational Molecular Biology | Fax: +49 30 8413 - 1152 Ihnestrasse 73 | Email: luz@molgen.mpg.de D-14195 Berlin, Germany | www.imprs-cbsc.mpg.de hannes luz <luz@molgen.mpg.de>

OxfordU LateralTransfer

Oxford University: Protozoan Molecular Evolution 3 year NERC-funded DPhil position supervised by Professor T. Cavalier-Smith FRS in the Department of Zoology Starting 1 October 2005. Open to UK citizens and to EU residents. Please apply very soon.

THE PROJECT: Evolution, gene discovery, and lateral gene transfer in the ecologically most important soil Protozoa: Cercozoa

A major advance in understanding eukaryote evolution during the past 3 years has been the recognition that protozoa belonging to the phylum Cercozoa (established only in 1998 by Cavalier-Smith), together with Foraminifera and Radiolaria, constitute Rhizaria, one of five major supergroups forming the eukaryote evolutionary tree. Understanding the evolution, physiology, and ecology of this major branch of the tree of life is severely limited by the complete absence of any genome project for it. To help fill this major gap the student would sequence thousands of genes from cDNA libraries of about five phylogenetically ill-resolved and ecologically diverse cercozoan classes, and analyse them bioinformatically and phylogenetically. Cercozoa, as the only culturable rhizarians, are the best rhizarian targets for gene discovery by large-scale cDNA sequencing.

BACKGROUND Thirteen protozoan phyla with very distinctive body plans are now recognised, but only three or four play really major roles in all habitats (Amoebozoa, Ciliophora, Cercozoa, and to a lesser extent Euglenozoa). Recent work using environmental rRNA library screening and intensive culturing of the latter two phyla in my laboratory has shown that Cercozoa comprise thousands of species, many belonging to previously undetected major clades. Cercozoa now has 10 classes, representing huge morphological diversity, including testate, filose, and reticulate amoebae, flagellates, algae, and organisms previously classified as heliozoa, radiolaria, and even fungi. High levels of cercozoan diversity have been found in most environments sampled; some appear to be restricted to marine environments, others to non-marine, while some strains appear to flourish in both. In many microbial communities Cercozoa appear to be among the most abundant predators. They commonly eat bacteria and unicellular fungi, but are also known to digest larger organ-

isms, and the phylum includes at least two parasitic classes. Some unicellular strains can form large, reticulate, multinucleate plasmodia, the function of which is unclear. It is thus probably the most diverse but least studied of all protozoan phyla and thus the scope for exciting novel discoveries is immense. There is already an extensive EST project under way in a Canadian Laboratory for Bigeloviella, the best-studied representative of the only photosynthetic (exclusively marine) class (Chlorarachnea) in the phylum, which retained the plastid and miniaturised nucleus of an engulfed green alga. Our new project would be the first major and broad molecular study of any heterotrophic rhizarians. Our lab provides an excellent environment for this research as there would be a second student and a postdoctoral researcher (David Bass) also working on Cercozoan evolution and ecology, with much opportunity for exchange of ideas and mutual help.

AIMS 1. To quantitate gene transfer from food bacteria into cercozoan genomes (about 1% in Amoebozoa).

2. Discover genes associated with different aspects of the diverse lifestyles exhibited by Cercozoa.

3. Determine whether these heterotrophs have any genes supporting the theory of a photosynthetic ancestry of all Cercozoa.

4. Construct multigene trees to settle the evolutionary relationship of the major classes of Cercozoa and to test the theory that Rhizaria are sisters of excavates.

5. To follow up one or more of the likely unexpected discoveries of the sequencing projects in accordance with the student's developing interests and preferences using whatever methods are most appropriate.

REFERENCES Cavalier-Smith, T. & Chao, E. E. (2003). Phylogeny and classification of phylum Cercozoa (Protozoa). *Protist* 154, 341-358. Cavalier-Smith, T. (2003). Protist phylogeny and the high-level classification of Protozoa. *Eur. J. Protistol.* 39, 338-348. Bass, D. & Cavalier-Smith, T. (2004). Phylum-specific environmental DNA analysis reveals remarkably high global biodiversity of Cercozoa (Protozoa). *Int. J. Syst. Evol. Microbiol.* 54, 2393-2404. Nikolaev, S. I., C. Berney, et al. (2004). "The twilight of Heliozoa and rise of Rhizaria, an emerging supergroup of amoeboid eukaryotes." *Proc. Natl Acad. Sci. U S A* 101: 8066-8071.

Applicants should have a strong interest in bioinformatics and computer analysis of sequence data, as this forms the core of the project. An interest also in one or more of molecular evolution, microbial/protozoan ecology, biodiversity or biochemistry would be an advantage. Students interested in other aspects of



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

OxfordU LateralTransfer 2

Evolution, gene discovery, and lateral gene transfer in the ecologically most important soil Protozoa: Cercozoa

This notice of a graduate position was recently posted with incomplete application procedure details - the url of the graduate prospectus was missing. A summary of the project is re-stated below, along with the amended instructions. Apologies for this.

A major very recent advance in understanding eukaryote evolution has been the recognition that protozoa belonging to the phylum Cercozoa (established only in 1998 by Cavalier-Smith), together with Foraminifera and Radiolaria, constitute Rhizaria, one of five major supergroups forming the eukaryote evolutionary tree. Understanding the evolution, physiology, and ecology of this major branch of the tree of life is severely limited by the complete absence of any genome project for it. To fill this major gap the student would do high-throughput sequencing of thousands of genes from cDNA libraries of ~5 phylogenetically ill-resolved and ecologically diverse cercozoan classes, and analyse them bioinformatically and phylogenetically. Cercozoa, as the only culturable rhizarians, are the best rhizarian targets for gene discovery by large-scale cDNA sequencing.

ENQUIRIES TO: Professor T. Cavalier-Smith FRS.
EMAIL: tom.cavalier-smith@zoo.ox.ac.uk

APPLICATION PROCEDURE General information, application instructions, and application closing dates are given in the University of Oxford Graduate Prospectus (<http://www.admin.ox.ac.uk/gsp>). For entry in October 2005, complete applications must arrive by 18 March 2005 (3rd gathered field).

David Bass <david.bass@st-catherines.oxford.ac.uk>

OxfordU LateralTransfer 3

Oxford University: Protozoan Molecular Evolution 3 year NERC-funded DPhil (=PhD) studentship supervised by Professor T. Cavalier-Smith FRS in the Department of Zoology, starting 1 October 2005. Open to UK citizens and to EU residents having or about to obtain a good first degree in an appropriate biological or biochemical field.

Please apply very soon.

THE PROJECT: Biodiversity, population structure, and ecology of sarcomonad Cercozoa (Protozoa) This project is on the environmental adaptiveness of different genotypes of soil protozoa and the related question whether they are mostly sexual or mostly asexual. Cercozoa, established only in 1998 by Cavalier-Smith, is quantitatively the most abundant phylum of soil protozoa, as they include filose testate amoebae, numerous groups of zooflagellates (phagotrophic heterotrophic flagellates) naked reticulose amoebae and many organisms that are both flagellate and amoeboid (e.g. sarcomonads); the latter two body types especially seem to be particularly characteristic of and adaptively suited to living in soil and sediments. This project will focus on sarcomonad zooflagellates (heteromitids and Cercomonas), as they are the most widespread and abundant phagotrophic flagellates in soil, where they are major predators on bacteria, and easy to grow in the lab; they also occur widely in freshwater and some Cercomonas are marine. Molecular methods will be used to pioneer study of the ecology and population structure of specific genetic lineages of sarcomonads, primarily in soil, and to clarify their systematics and evolution more generally. The primary focus of this project is the role of sarcomonads in soil community ecology - in particular to provide the first evidence for the adaptiveness of individual genotypes for phagotrophic predatory soil protozoa.

The student will use rDNA sequencing, quantitative PCR, and DNA hybridization to study the qualitative and quantitative distribution of different selected Cercomonas ribotypes among habitats, through the seasons, and across environmental gradients, and for selected subclades expand the ribotype database and seek correlations with morphology. S/he will also do large-scale chaperone Hsp90 gene sequencing for cultures of the most abundant ribotypes of Heteromita, Bodomor-

pha and Cercomonas to determine whether they are haploid or diploid and whether they are sexual or asexual. If they are sexual the 18S rRNA and Hsp90 sequences of closely related genotypes can be used to define biological species boundaries and will provide genetic tools for comparing the ecology of sister species. The student will make use of our numerous existing cultures of Cercomonas, add to them considerably, and generate many more for heteromitids. BACKGROUND Soil and aquatic sediment ecosystems centrally involve decomposer food webs in which microbes are of major importance for biogeochemical cycles and where protozoa are the dominant consumers of bacteria. Of the 13 protozoan phyla with very distinctive body plans now recognised, only three or four play really major roles in all habitats (Amoebozoa, Ciliophora, Cercozoa, and to a lesser extent Euglenozoa). Recent work using environmental rRNA library screening and intensive culturing of the latter two phyla in my laboratory has shown that Cercozoa comprise thousands of species, many belonging to previously undetected major clades. Cercozoa now has 10 classes, representing huge morphological diversity, including testate, filose, and reticulate amoebae, flagellates, algae, and organisms previously classified as heliozoa, radiolaria, and even fungi; one of these, the sarcomonads, consists primarily of biciliate flagellates that glide on surfaces and can often form a wide variety of pseudopods during feeding. High levels of cercozoan diversity have been found in most environments sampled; some appear to be restricted to marine environments, others to non-marine, while some strains appear to flourish in both. In many microbial communities Cercozoa appear to be among the most abundant predators. They commonly eat bacteria and unicellular fungi, but are also known to digest larger organisms, and the phylum includes at least two parasitic classes. Some unicellular strains can form large, reticulate, multinucleate plasmodia, the function of which is unclear. It is thus probably the most diverse but least studied of all protozoan phyla and thus the scope for exciting novel discoveries is immense. Our recent molecular phylogenetic studies provided tools that now make detailed study of their ecology possible for the first time despite their taxonomy still being relatively chaotic and very ill-developed. Our lab provides an excellent environment for this research as there would be a second student and a postdoctoral researcher (David Bass) also working on Cercozoan evolution and ecology, with much opportunity for exchange of ideas and

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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>

Stockholm PlantEvolSyst

Three PhD studentships in Plant evolution / Plant Systematics are available at the Department of Botany at Stockholm University

Applications are welcome until April 1, 2005 To: Prefekten Botaniska institutionen Stockholms universitet SE-10691 Stockholm Sweden

Two of these studentships are connected to ongoing projects at the Bergius Foundation of the Royal Swedish Academy of Sciences:

1. Evolution within Ixoroideae (Rubiaceae) and 2. Allopolyploidy within Potentilleae (Rosaceae) and its relevance for diversity and evolution

More info: http://www.bergianska.se/-index_forskning.php?vidare=forskning_doktorander.html

Also see: <http://www.botan.su.se/> Torsten Eriksson Bergius Foundation Department of Botany SE-10691 Stockholm

Torsten Eriksson <Torsten.Eriksson@bergianska.se>

UCanterbury EvolAnimalCommunication

Ph.D. Scholarship in Animal Communication at the University of Canterbury

We are seeking a Ph.D. student to study mechanisms of social communication in archaic New Zealand frogs (genus *Leiopelma*). These frogs are "living fossils" that have remained virtually unchanged over the past 200 million years and never evolved bioacoustic signalling systems. *Leiopelma* are extremely long-lived, do not stray far from small home ranges, and repeatedly interact with the same individuals. These conditions foster the formation of complex social networks, which might be structured through chemical signalling. The project takes an integrative approach and makes use of microsatellite analyses to investigate genetic relatedness, chemical methods to characterise the signals, and field studies to examine how communication occurs in

natural populations. For further background, see Behavioral Ecology 15 (1): 88-93 (2004).

The scholarship is supported for three years by the Marsden Fund (Royal Society of New Zealand) and includes a \$19,000/year tax-free stipend, full international tuition/fees, and generous support for research expenses.

The University of Canterbury has a strong programme in behaviour, ecology, and evolution, as well as excellent facilities in chemistry and molecular genetics. The programme is directed by Bruce Waldman (School of Biological Sciences) and John Blunt (Department of Chemistry).

The deadline for applications is 15 April 2005. For further information, please contact us. To apply, send your Curriculum Vitae, a letter detailing your experience and career goals, and contact details for three referees to:

Dr Bruce Waldman School of Biological Sciences University of Canterbury Private Bag 4800 Christchurch New Zealand

Voice: +64 3 364 2066 FAX: +64 3 364 2590 Web: www.biol.canterbury.ac.nz Email: Bruce.Waldman@canterbury.ac.nz

Bruce Waldman <bruce.waldman@canterbury.ac.nz>

UGroningen EcolEvol

International Top Master's Programme in Ecology and Evolution

The Centre for Ecological and Evolutionary Studies at the University of Groningen (Netherlands) offers a new Master's programme in ecology and evolution. This "Top Master's Programme Evolutionary Biology" provides an intense training in modern research techniques and is therefore an optimal preparation for a subsequent PhD programme. In order to guarantee an excellent teacher-student ratio, the number of positions is limited to 15. The programme is highly selective and aimed at the brightest and most ambitious students from all over the world. All students admitted will receive a scholarship for the two-year Top Master's programme and potentially an additional four-year scholarship for a subsequent Ph.D. programme. The deadline for application is 15 April 2005. For more information visit www.rug.nl/biol/evobio or contact

Franz J. Weissing Professor of Theoretical Biology Centre for Ecological and Evolutionary Studies University of Groningen Kerklaan 30 9751 NN Haren The Netherlands tel: +31-50-363-2131 fax: +31-50-363-3400 email: f.j.weissing@rug.nl URL: www.rug.nl/biol/theobio Franjo Weissing <F.J.Weissing@biol.rug.nl>

ULausanne 2 SocialEvol

PhDs in social evolution

Two PhD positions are available to study social evolution in insects at the Department of Ecology and Evolution, University of Lausanne, Switzerland.

Our group studies the structure, function and evolution of insect societies. We are particularly interested in the causes and consequences of social structure variation in ants. The PhD positions are part of a new project in which we propose to study the link between social structure and dispersal, as well as the impact of social structure variation on the resolution of genetic conflicts among colony members. The project will involve a combination of field experiments, laboratory experiments and genetic analyses (microsatellites, SNPs and mtDNA sequencing). The primary model system will be *Formica selysi*, with possible extensions to other insect species.

The two PhD studentships are funded by the Swiss National Science Foundation for a period of 3 years. The Department of Ecology and Evolution in Lausanne provides a lively and stimulating environment for research. It harbours vigorous research programs in behaviour, ecology and evolution, and has excellent facilities for molecular genetics and genomics.

For more information on the department, research groups and publications, please look at: http://www.unil.ch/dee/page5090_en.html http://www.unil.ch/dee/page7000_en.html <http://www.unil.ch/dee/page9051.html> Information and applications:

Michel Chapuisat Department of Ecology and Evolution Biology Building University of Lausanne 1015 Lausanne Switzerland

Tel. +41 21 692 41 78 Fax +41 21 692 41 65

Michel.Chapuisat@unil.ch

ULeicester EvolImmunity

Research council funded PhD studentship Opening a blackbox in evolutionary immunology. Parasites are ubiquitous and affect a wide array of host characteristics at all levels of biological organization. Consequently, understanding their relationships has important ramifications for a variety of scientific fields.

The interaction between the bumblebee and its trypanosomal gut parasite *Crithidia bombi* has become one of the central models for the study of the evolutionary ecology of immune systems 2. However, so far this system has been considered as a black box. For our understanding of the system to develop, more must be known about the specifics of the host parasite relationship.

This studentship will delve into the mechanisms of their interactions. What is the actual pathology of *C. bombi*? Its fitness effects on bumblebees are well known 3, 4 but what tissues or processes are actually damaged? On the host side, many details are now known about the insect immune system⁵, but what components of this system are used by the bumblebee to defend against this gut parasite 6? And what is the basis of the well-known specificity between different strains of *Crithidia* and individual bumblebee colonies².

Previous studies have shown that *C. bombi* can artificially infect *Drosophila*⁷. One exciting possible research direction is to use the candidate gene approach⁸ to transfer knowledge from this artificial system into *C. bombi*'s natural host, the bumblebee.

Many parasites, including important species that affect humans and livestock, must survive the harsh environment of insect guts to complete their life-cycle. Hence, understanding how insects protect themselves against such parasites has immediate practical implications.

At a minimum, applicants should have or expect to receive an upper second class honours degree in biology or a related discipline. Send your CV (including names of academic referees) and a one page statement on why you feel this project is right for you directly to Eamonn Mallon (ebm3@le.ac.uk <mailto:ebm3@le.ac.uk>, www.le.ac.uk/bl/ebm3/homepage.html <<http://www.le.ac.uk/bl/ebm3/homepage.html>>). The deadline for applications is 10th of May 2005 with the studentship starting September/October.

1 Lipa, J.J. and Triggiani, O. (1980) *Acta Protozoologica* 27, 287-290

2 Schmid-Hempel, P. (2001) *Naturwissenschaften* 88, 147-158

3 Brown, M.J.F., Loosli, R. and Schmid-Hempel, P. (2000) *Oikos* 91, 421-427

4 Brown, M.J.F., Schmid-Hempel, R. and Schmid-Hempel, P. (2003) *Journal of Animal Ecology* 72, 994-1002

5 Leclerc, V. and Reichhart, J.-M. (2004) *Immunol Rev* 198, 59-71

6 Brown, M.J.F., Moret, Y. and Schmid-Hempel, P. (2003) *Parasitology* 126, 253-260

7 Boulanger, N. et al. (2001) *Insect Biochemistry and Molecular Biology* 31, 129-137

8 Fitzpatrick, M.J. et al. (2005) *Trends in Ecology & Evolution* 20, 96-104

Dr. Eamonn Mallon Room 217 Department of Biology University of Leicester University Road Leicester LE1 7RH UK Telephone: 0116 2523482 Fax: 0116 2523330

Eamonn Mallon <ebm3@leicester.ac.uk>

UMunich EvolFuncGenomics

PhD Student Position - Evolutionary/Functional Genomics

A PhD student position is available in the laboratory of John Parsch at the University of Munich (LMU). The position is part of a project funded by the German Science Foundation (DFG) to study the evolutionary and functional genomics of *Drosophila* gene expression. The work will be primarily experimental and will include microarray analyses and the generation of transgenic *Drosophila*. Applicants should have a master's degree or equivalent in biology or a related field. In addition, previous laboratory experience in molecular biology and/or *Drosophila* genetics is desired. The University of Munich has a strong, interactive group in evolutionary biology, including theoreticians and experimentalists working on both plant and animal systems. We have an international group and the everyday working language is English. The department of biology is housed in the new, state-of-the-art BioCenter on the University of Munich High-Tech campus. More information is available on the web at:

<http://www.zi.biologie.uni-muenchen.de/institute/zi-abtln/evolutionsbiologie>

Interested candidates should send a CV, statement of research experience, and contact information of two potential referees per email to:

parsch@zi.biologie.uni-muenchen.de

Applications will be reviewed beginning May 1, 2005.

The University of Munich is an Equal Opportunity/Affirmative Action Employer and has an affirmative action policy for the disabled.

Prof. Dr. John Parsch Department of Biology II University of Munich Grosshaderner Str. 2 82152 Planegg-Martinsried Germany

UOslo EvolMycology

PhD position in evolutionary biology (mycology) at the Department of Biology, University of Oslo, Norway.

A 3-year PhD position in evolutionary biology (mycology) is currently being offered at the Dep. of Biology, University of Oslo, Norway (<<http://www.biologi.uio.no/>>www.biologi.uio.no). The position relates to the research project "Evolution of mating type and vegetative incompatibility genes in fungi: The dry rot fungus *Serpula lacrymans* as a model species". The project is a collaboration between researcher at the University of Oslo and at the Agricultural University of Uppsala, Sweden. The project is funded by the Research Council of Norway and the PhD position will be based at the University of Oslo, Norway.

The research project to which the position is linked includes evolutionary, phylogeographic and population genetic studies of fungi using the basidiomycete *Serpula lacrymans* and allied taxa as model organisms. One important aim is to explore evolutionary processes that influence the mating and vegetative incompatibility systems in fungi. Studies within the project will include a combination of molecular laboratory work and culturing of fungi, in addition to some field work. The PhD plan of the appointed candidate will be affected by the candidate's interests and competence within these fields and there will be considerable scope for the student to develop their own interests. Knowledge of the Norwegian language is not required.

Qualifications of importance in assessing candidates include:

- Motivation - Educational background - Practice with basic molecular techniques (PCR, DNA sequencing, etc.) - Experience in culturing fungi (or other microorganisms) - Good knowledge in evolutionary biology - Ability to work both independently and in a group - Experience in presenting scientific material - written and oral

The decision on whom to appoint will essentially consider the applicants' potential for conducting a successful PhD project of high quality. Short-listed candidates will likely be interviewed. Deadline for the receipt of applications is March 30. The starting date is flexible. The position is for three years within which the candidate appointed is expected to complete her/his PhD. The monthly starting salary is approx. EUR 2900.

For more information contact: PhD Håvard Kausrud, E-mail: haavarka@bio.uio.no

Application: Please submit three copies of: A letter describing your research interest and skills, CV, a copy of master thesis or equivalent, and contact information for three references to: The Faculty of Mathematics and Natural Sciences, v/Bente Schjoldager, P.O.Box 1032 Blindern, 0315 OSLO, NORWAY

haavarka@bio.uio.no haavarka@bio.uio.no

UOxford CercozoaEvol

Evolution, gene discovery, and lateral gene transfer in the ecologically most important soil Protozoa: Cercozoa

3 year NERC-funded DPhil (=PhD) studentship supervised by Professor T. Cavalier-Smith FRS in the Department of Zoology, starting 1 October 2005.

RE-POSTING: EXTENDED DEADLINE - NOW 27 MAY 2005.

A major very recent advance in understanding eukaryote evolution has been the recognition that protozoa belonging to the phylum Cercozoa (established only in 1998 by Cavalier-Smith), together with Foraminifera and Radiolaria, constitute Rhizaria, one of five major supergroups forming the eukaryote evolutionary tree. Understanding the evolution, physiology, and ecology of this major branch of the tree of life is severely limited by the complete absence of any genome project for it. To fill this major gap the student would do high-throughput sequencing of thousands of genes from C-DNA libraries of ~5 phylogenetically ill-resolved and

ecologically diverse cercozoan classes, and analyse them bioinformatically and phylogenetically. Cercozoa, as the only culturable rhizarians, are the best rhizarian targets for gene discovery by large-scale cDNA sequencing.

Aims:

1. Quantitate gene transfer from food bacteria into cercozoan genomes (~1% expected).
2. Discover genes associated with diverse cercozoan lifestyles.
3. Determine whether these heterotrophs have any genes supporting the theory of a photosynthetic ancestry for Cercozoa.
4. Construct multigene trees to settle evolutionary relationship among major classes of Cercozoa and test the theory that Rhizaria are sisters of excavate protozoa.
5. Follow up unexpected serendipitous discoveries of the C-DNA sequencing in accordance with the student's interests

General information, application instructions and application closing dates are given in the University of Oxford Graduate Prospectus (www.admin.ox.ac.uk/gsp). For entry in October 2005, applications must arrive by May 27th 2005, the closing date of the fourth 'gathered field'.

For more information about the project contact Professor Thomas Cavalier-Smith FRS, Department of Zoology, University of Oxford, South Parks Road, Oxford OX1 3PS, UK. E-mail: tom.cavalier-smith@zoo.ox.ac.uk, or contact the Graduate Office: Tel: +44 (0)1865 271286; fax: +44 (0)1865 310447.

Please inform Professor Cavalier-Smith directly if you are planning to submit an application, even if you have no specific queries about the project itself.

Open to UK citizens and to EU residents having or about to obtain a good first degree in an appropriate biological or biochemical field. For non-UK residents NERC can pay fees only, not living expenses. The University of Oxford is an Equal Opportunities Employer.

REFERENCES: Cavalier-Smith, T. (2003). Protist phylogeny and the high-level classification of Protozoa. *Eur. J. Protistol.* 39, 338-348. Cavalier-Smith, T. & Chao, E. E. (2003). Phylogeny and classification of phylum Cercozoa (Protozoa). *Protist* 154, 341-358. Bass, D. & Cavalier-Smith, T. (2004). Phylum-specific environmental DNA analysis reveals remarkably high global biodiversity of Cercozoa (Protozoa). *Int. J. Syst. Evol. Microbiol.* 54, 2393-2404.

David Bass <david.bass@st-catherines.oxford.ac.uk>

UOxford CercozoaEvol 2

Biodiversity, sex, and ecology of sarcomonad Cercozoa (Protozoa)

3 year NERC-funded DPhil (=PhD) studentship supervised by Professor T. Cavalier-Smith FRS in the Department of Zoology, starting 1 October 2005.

RE-POSTING: EXTENDED DEADLINE - NOW 27 MAY 2005.

Cercozoa (established by Cavalier-Smith, 1998), the most abundant phylum of soil protozoa, includes numerous zooflagellates and amoebae with long thin pseudopods adapted to creeping around soil particles. This project focuses on heteromitids and Cercomonas, the most widespread and abundant phagotrophic flagellates in soil, where they are major predators on bacteria, and easy to grow in the lab. Chaperone Hsp90 genes will be sequenced for cultures of the most abundant ribotypes of Heteromita, Bodomorpha, and Cercomonas to determine whether they are haploid or diploid and by seeking intragenic recombination determine whether they are sexual or asexual. If they are sexual the 18S rRNA and Hsp90 sequences of closely related genotypes will be used to define biological species boundaries and provide genetic tools for comparing the ecology of sister species. The student will use our numerous existing cultures of Cercomonas, add to them considerably, and generate many more for heteromitids. The environmental adaptiveness of different rRNA genotypes will be studied by rDNA sequencing, quantitative PCR, and DNA hybridization to study the qualitative and quantitative distribution of different selected Cercomonas ribotypes among habitats, through the seasons, and across environmental gradients, and for selected subclades expand the ribotype database and seek correlations with morphology.

General information, application instructions and application closing dates are given in the University of Oxford Graduate Prospectus (www.admin.ox.ac.uk/gsp). For entry in October 2005, applications must arrive by May 27th 2005, the closing date of the fourth 'gathered field'.

For more information about the project contact Professor Thomas Cavalier-Smith FRS, Department of Zoology, University of Oxford, South Parks Road, Oxford OX1 3PS, UK. E-mail: tom.cavalier-smith@zoo.ox.ac.uk

smith@zoo.ox.ac.uk, or contact the Graduate Office:
Tel: +44 (0)1865 271286; fax: +44 (0)1865 310447.

Please inform Professor Cavalier-Smith directly if you are planning to submit an application, even if you have no specific queries about the project itself.

Open to UK citizens and to EU residents having or about to obtain a good first degree in an appropriate biological or biochemical field. For non-UK residents NERC can pay fees only, not living expenses. The University of Oxford is an Equal Opportunities Employer.

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David Bass <david.bass@st-catherines.oxford.ac.uk>

UTromso EvolSperm

Position

A four-year PhD-position in evolutionary biology is open from approximately 1st of Mai at the University of Tromsø, Norway. Applicants must document knowledge about Evolutionary Biology equivalent to master level and should have experience from field-work in Behavioral Ecology. Applicants must also be willing to acquire knowledge about new methodology in cell-biology and immunology, and documented knowledge from these areas is an advantage. Specific knowledge about sperm cells is also an advantage, but not obligatory.

Project description

Mutations in the male germ-line are common and in highly monogamous species males may benefit from selecting against own, mutated sperm. This will, in turn, reduce a male's chance of fertilizing, but, on the other hand, prevent loss of DNA order down the family line. The importance of sperm selection by the male will be related to the intensity of sperm competition. That is, in species with high levels of sperm competition male selection against own sperm will impose high fitness costs and therefore be selected against. Conse-

quently, a lowered control of mutated sperm could explain the increased mutations rates - originating from the male germ-line - documented to co-occur with increased sperm competition. Identification of mutated sperm cells are most likely conducted by the immune system, which also surveys other somatic cells, and antibody coating of sperm cells are commonly observed in male vertebrates. The evolutionary framework outlined may explain some puzzling biological paradoxes, such as: why should the male, but not the female germ-line be non-self, why should stress and sex hormones be immunosuppressive and why do we observe the enormous sperm redundancy.

Practicalities

Application dead-line is 7th of April.

25% of the work-load (equivalent to 1 year) will be teaching in Life History Evolution.

Applications should include five copies of confirmed documents, including CV, and three copies of publications and manuscripts. These should be sent to:

Anne HInstitute for Biology University for Biology 9037
TromsøNorway Anne.Hoydal@ib.uit.no

Or

Ivar Folstad Ivar.Folstad@ib.uit.no

Uppsala EvReprSystems

PhD-student position in Evolutionary Genetics Department of Evolution, Genomics and Systematics, Evolutionary Biology Centre, Uppsala University, Sweden

We seek a highly motivated individual interested in pursuing a PhD degree in Evolutionary Genetics within a newly started research program on the evolution of reproductive systems in fungi.

Project description The differences in reproductive behaviour of organisms greatly affect patterns of genetic variation, and therefore the responses of populations to natural selection and other factors of evolution. Discovering why and how these characters evolve poses some of the most challenging problems in evolutionary biology. *Neurospora* is a eukaryote model system exceptionally suited as a subject for studies of the evolution of reproductive systems. The species of the genus exhibit the range of reproductive behaviour seen throughout fungi: obligately outbreeding, selfing, and a mixture of the two. This PhD-project aims at 1) identifying

genes and genetic mechanisms important for outcrossing in *Neurospora*, and investigating the evolutionary fate of these characters in selfing lineages; 2) Identifying trade offs in energy allocation as a potential driving force in the evolution of selfing taxa from their outbreeding ancestors.

The project will involve using molecular techniques such as DNA sequencing, quantitative PCR and whole genome microarrays, as well as statistical analyses. Although the general area of the work is already defined, there will be considerable scope for the student to develop their own interests and to influence the emphasis of their project within the broad area specified. The announced position is planned for four years. Requirements Applicants should possess a BSc or MSc degree in evolutionary genetics, microbiology, ecology, population genetics, or a related field, and should have a strong interest in using molecular methods to study key questions in ecology and evolution. General microbiology and molecular biology laboratory skills are a plus. Application Please submit your CV, a letter describing your research interest and skills, a copy of master thesis or equivalent, and contact information for two references to Hanna Johannesson (Hanna.Johannesson@ebc.uu.se), Department of Evolution, Genomics and Systematics, EBC, Norbyvägen 18D, SE 752 36 Uppsala, Sweden. The position remains open until a suitable candidate has been found.

The Evolutionary Biology Centre offers a superb interdisciplinary working environment located at the heart of Uppsala. Uppsala is located 40 minutes north of Stockholm by train, 20 minutes from Stockholms international airport.

Hanna Johannesson <Hanna.Johannesson@ebc.uu.se>

YorkU EvolGenomics

I am seeking graduate students interested in evolutionary and population genomics to join my lab in September 2005. Research in the lab is focused on the study of plant genome evolution and molecular population genetics. We are particularly interested in understanding the forces driving genome evolution, and in testing the role of natural selection at the genome level. Potential research projects include 1) investigating the effects of polyploidy on the evolution of transposable elements, 2) testing for the effects of gene expression level on molecular evolution, and 3) distinguishing the effects

of demographic history and positive Darwinian selection on patterns of genetic diversity. Research projects range from primarily lab-based collection and analysis of DNA sequence diversity data, to theoretical modeling and computer-based analysis of genome sequences. Further information about research in the lab can be found at <http://www.yorku.ca/stephenw> and information on York University's Biology graduate program can be found at <http://www.biol.yorku.ca/grad/> Interested students are asked to submit a CV, a copy of academic transcripts and contact information for three references to stephenw@yorku.ca by April 15, 2005.

Stephen I Wright, PhD Assistant Professor Department of Biology York University 4700 Keele St. Toronto, ON Canada M3J 1P3 Phone: (416) 736-2100 ext. 20213 Fax: (416) 736-5698 –

ZurichETH EvolBiol

PhD position in Evolutionary Biology

A 3-years PhD position is available in the group of Ecology and Evolution at the ETH in Zurich, Switzerland. We are looking for a motivated and independent student who is interested in fundamental aspects of evolutionary biology and is willing to employ modern molecular techniques.

The research project focuses on evolutionary aspects of phenotypic variation. We are interested in genetic and non-genetic sources of phenotypic variation and in how natural selection acts on these sources. The work will be primarily experimental, using evolution experiments with bacteria and viruses as well as genetic tools.

This work will contribute to an exciting new field at the interface between evolutionary biology and other biological disciplines, including molecular biology, bio-engineering, microbiology and systems biology. Candidates from any biological background are welcome to apply.

A Masters or equivalent is required. The ETH offers an international and stimulating research environment, with English as the official working language. Please send your application or informal requests for further information to Martin Ackermann (Martin.Ackermann@env.ethz.ch). See also <http://www.eco.ethz.ch/portraits/ackermann/> Martin Ackermann Ecology & Evolution ETH Zentrum NW Clausiusstrasse 25 8092 Zuerich Switzerland Tel.: +41 1 63

26928 Fax: +41 1 63 21271 www.eco.ethz.ch

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FloridaMusNatHist Bioinformatics

Although this job description was not written as such, it could be filled by a qualified postdoc interested in bioinformatics.

The Florida Museum of Natural History is currently recruiting an IT Expert that is responsible for the development of a biodiversity inventory tracking system. This project, called BioCorder, is funded for three years by the National Science Foundation (<http://www.flmnh.ufl.edu/biocorder/>). This programmer will work with other BioCorder biologists, programmers, and the Museum IT staff to develop a PHP/MySQL database infrastructure for bioinformatics. This database combines locally stored bioinformatics data (e.g., specimens, DNA sequences, images, etc.) with data stored in publicly available distributed databases (e.g., GenBank, PubMed, Ubio, ITIS, etc.) using a common user portal.

Experience with Perl, PHP, MySQL, Unix admin, Web Services, and database design is essential. A degree in Computer Science, Biology or Bioinformatics, or equivalent and 2 years work experience is preferred. Position requires the ability to communicate complex computer

science concepts to non-computer scientists, as well as excellent writing skills.

To view application instructions and complete an online resume, please visit (www.hr.ufl.edu/job/default.htm). Reference number for this vacancy is 32035, or you may search for title, IT Expert-FLMNH Mammals. Please apply by 3/24/05. If an accommodation due to a disability is needed to apply for this position, please call (352) 392-4621, or the Florida Relay System at (800) 955-8771 (TDD). An Equal Opportunity Institution.

If you have further questions regarding the position, please feel free to e-mail, dreed@flmnh.ufl.edu.

Best Regards, David Reed

David L. Reed, Assistant Curator of Mammals Florida Museum of Natural History University of Florida Dickinson Hall, Museum Rd & Newell Dr. Gainesville, FL 32611 (352) 392-1721 ext. 220 (voice) (352) 846-0287 (fax) e-mail: dreed@flmnh.ufl.edu <http://www.flmnh.ufl.edu/mammals/>

**InstZoologyLondon
ConservationGenet**

SENIOR RESEARCH FELLOW IN CONSERVATION GENETICS (GBP 37,558 to GBP 45,885 plus GBP 2,962 pa. London weighting) The Institute of Zoology (IoZ), based in Regent's Park, London, is the research division of the Zoological Society of London (ZSL). Through our research partnership with the Department of Zoology, University of Cambridge, we pursue our mission as a national centre for conservation biology. We seek to appoint a Senior Research Fellow to lead a research programme in conservation genetics. We are particularly keen to develop research programmes in environmental and ecological genomics, but will also consider suitable candidates in other areas of population or wildlife genetics. The appointment can be made at any point from senior lecturer to professorial level, depending on relevant research experience. The successful applicant will have an outstanding record of achievement and excellence in areas relevant to the Institute of Zoology's mission, with high quality publications, an international reputation, demonstrated group-leadership abilities and evidence of sustained success in competitive science funding. Evidence of commitment to practical implementation of scientific work is desirable. Suitable candidates may be considered for appointment as an Affiliated Lecturer at the University of Cambridge. Informal queries should be directed to the Director of Science (Professor Georgina Mace) by email (Georgina.Mace@ioz.ac.uk). Candidates should submit a CV and an outline of research plans not exceeding 2 sides of A4, with details of three referees (including the current/most recent employer), to: Human Resources Dept., Zoological Society of London, Regent's Park, London NW1 4RY, UK or email hr@zsl.org by 24 March 2005.

w.jordan@ucl.ac.uk

KonradLorenzInst 2 Genetics

1. Genetics Laboratory Technician Position Konrad Lorenz Institute for Ethology of the Austrian Academy of Sciences, Vienna, Austria

We seek a highly organized and motivated genetics laboratory technician to assist with research projects in behavioral ecology and evolutionary biology (In particular, working with Dr. Dustin Penn and his group on the Major Histocompatibility Complex). Applicants should have excellent bench skills using molecular genetic techniques (especially, DNA extractions, PCR, microsatellite development and typing, AFLPs, auto-

matic sequencing, etc.). They should be independent, reliable, and responsible for general laboratory maintenance. The position requires working with other technicians, scientists, and assisting students; therefore, we seek someone who is friendly, and cooperative, as well as having excellent technical and organizational skills. German would be useful but it is not necessary as ours is an international institute that communicates largely in English. Salary depends upon experience, and the position is initially for two years, and it could eventually become permanent depending upon performance. Review of applications begins immediately and will continue until the position is filled, and the starting date is flexible. The position is open to women and men likewise.

The Konrad Lorenz Institute is located in the Vienna Woods, on the outskirts of Vienna (see our website: <http://www.oeaw.ac.at/klivv/>). There are other laboratories in Vienna that use genetic techniques, including the neighboring Research Institute of Wildlife Ecology (University of Veterinary Medicine). Vienna offers excellent public transportation, excellent schools, cultural activities, and outdoor recreation (<http://www.virtourist.com/europe/vienna/index.html>).

To apply, please send an application letter, a CV, and two letters of reference to the address below.

Mag. Teresa Schweiger, Secretariat Konrad Lorenz Institute for Ethology Austrian Academy of Sciences Savoyenstrasse 1a A-1160 Vienna, Austria Tel: +43 1 51581 2700 Fax: +43 1 51581 2800 T.Schweiger@klivv.oeaw.ac.at

2. POST-DOCTORAL POSITION: Behavioral Ecology/Evolutionary Biology Konrad Lorenz Institute for Ethology of the Austrian Academy of Sciences, Vienna, Austria

We seek a highly motivated and interactive scientist to collaborate with Dr. Dustin Penn and his group on research focused on the evolution of genetic polymorphisms at MHC and olfactory receptor loci (this includes work on sexual selection and chemosensory communication, as well as host-pathogen interactions). Other research topics at the institute include sexual conflict, sperm competition, and post-copulatory mate choice. Applicants must have a strong background in either molecular genetics or population genetics, and some statistical expertise is preferred. Scientists are expected to write grants and help obtain extramural funds. Good English skills are necessary (our institute operates bilingually, and English is widely spoken in Vienna). The position is open to men and women likewise. It is for two to three years, depending upon progress, and the salary depends upon experience. Review of ap-

plications begins immediately and the deadline is April 15, 2005.

The Konrad Lorenz Institute for Ethology of the Austrian Academy of Sciences is located in the Vienna Woods, on the outskirts of Vienna. We work with a variety of vertebrates, including humans, and have good facilities, especially for studying fish and birds (see <http://www.oeaw.ac.at/klivv/>). We also interact with a number of other research groups in Vienna (see <http://www.oeaw.ac.at/klivv/en/misc/links.html>). To apply, please send (1) a CV, (2) copies of 2-3 publications, (3) a brief statement of research interests, (4) letters of reference via e-mail or regular mail to the address below.

Mag. Teresa Schweiger, Secretariat Konrad Lorenz Institute for Ethology Austrian Academy of Sciences Savoyenstrasse 1a A-1160 Vienna, Austria Tel: +43 51581 2700 Fax: +43 51581 2800

T.Schweiger@klivv.oeaw.ac.at

Cheers,

Mag. Teresa Schweiger Secretariat Konrad Lorenz Institute for Ethology Savoyenstr. 1a A 1160 Vienna Tel: 01/51581-2700 Fax: 01/51581-2800

Teresa Schweiger <T.Schweiger@klivv.oeaw.ac.at>

LafayetteLA NOAA MarineMammalGeneticsTechs

The National Marine Fisheries Service is seeking two molecular genetics technicians to work in the Marine Mammal Molecular Genetics Lab in Lafayette, LA.

DNA Technician/Lab Manager National Marine Fisheries Service Lafayette, LA

We seek a highly motivated technician to join an active lab investigating population genetics and evolutionary histories of a variety of marine mammal species. The successful applicant will be highly organized, detailed, be able to work as an independent part of a team, and have considerable experience with a variety of standard molecular techniques (for example, DNA extraction, PCR, gel electrophoresis, DNA sequencing, microsatellites, etc.). Applicant must have experience running and maintaining a capillary-based automated DNA sequencer (ABI310 or 3100 preferable). Other responsibilities will include DNA sequencing and genotyping of marine mammal samples for ongoing studies

of population genetics. The successful applicant will be expected to work closely with other personnel and direct other technicians and students in common molecular techniques such as DNA extraction, PCR, sequencing etc. This is a full time contract position with the potential for annual renewal and a start date no later than May 1 2005. Salary is commensurate with experience. Applicants should be US citizens or have valid work visas. Qualified candidates should submit a letter of application describing qualifications for the position and reason for interest, CV, and letters from three references (email ok) to Patricia.Rosel@noaa.gov.

Molecular Technician National Marine Fisheries Service Lafayette, LA

We seek a highly motivated technician to join an active lab investigating population genetics and evolutionary histories of a variety of marine mammal species and to work on a project studying the population genetics of pilot whales. Applicants must have considerable experience with a variety of standard molecular techniques (DNA extraction, PCR, gel electrophoresis, DNA sequencing, microsatellites, AFLPs etc.) so that he/she can work with minimal supervision. Responsibilities include DNA extraction, sequencing and genotyping of pilot whale samples as well as database entry and archiving. Experience running an ABI capillary sequencer preferred. The position requires someone who is detail oriented and highly organized. This is a full time 2-yr contract position open immediately. Applicants should be US citizens or have valid work visas. Qualified candidates should submit (via email) a letter of application describing qualifications for the position and reason for interest, CV, and letters from three references (email ok) to Patricia.Rosel@noaa.gov.

patricia.rosel@noaa.gov

MaxPlanck Rostock LifeHistoryEvol

The Max Planck Institute for Demographic Research is seeking to expand further its activities in the field of Evolutionary Biodemography and is recruiting to PhD, Post-Doc, and Research Scientist level vacancies involving the

Mathematical Modeling of Life History Evolution

The successful candidates will complement an existing research team of 19 staff, including a number of recently recruited evolutionary ecologists, and will work

alongside a total of some 80 employees from diverse backgrounds engaged in a range of issues in demography. The team aims to gain a fundamental understanding of how age-specific demographic processes are shaped by evolution. We have ongoing projects on age-specific schedules of mortality, reproduction and growth, on the evolution of senescence, on reproductive effort, parental investment and intergenerational transfers, on environmentally-cued life-history choices, and on the costs of reproduction and the delayed effects of stress. We seek to advance our knowledge of these issues using a combination of theoretical modeling, analysis of existing databases, and a variety of field and laboratory based studies. We wish to complement our empirical studies with theoretical insights through the appointment of scientists engaged in the mathematical modeling of fundamental evolutionary processes. We are seeking able scientists from all levels with strong academic track records in quantitative disciplines. Those with backgrounds in mathematics or quantitative life history modeling are particularly encouraged to apply. Applications should be addressed to Executive Director, Prof. James W. Vaupel and should include a CV with a statement of academic interests and relevant experience, qualifications, a list of publications and the contact details of 3 referees. All material should be e-mailed to: math-evol.positions@demogr.mpg.de. See www.demogr.mpg.de for information. The Max Planck Society wishes to increase the share of women in areas where they are underrepresented, and strongly encourages women to apply. The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply. Math-Evol Positions, Attn. Prof. James W. Vaupel Max Planck Institute for Demographic Research Konrad-Zuse-Strasse 1, D-18057 Rostock, Germany E-mail: math-evol.positions@demogr.mpg.de

Dr. David L. Thomson Max Planck Institute for Demographic Research Konrad-Zuse Str. 1 D-18057 ROSTOCK Germany

Tel. +49 (0)381 2081 229 Fax. +49 (0)381 2081 529 E-mail: thomson@demogr.mpg.de Website: www.demogr.mpg.de "Thomson, David" <Thomson@demogr.mpg.de>

This posting went out to TDWG a couple weeks ago, but applications are still being accepted: ———

Collections Database Specialist

The Santa Barbara Museum of Natural History is seeking a database specialist to develop and implement an online database of specimen and taxonomic data on California beetles. Responsibilities will include enhancing an existing MS Access database, porting data to MS SQL Server, developing a web interface for secure database access, and applying biodiversity informatics community standard protocols (DiGIR, XML) to permit database interoperability with other online services. The position requires thorough understanding of relational databases, including MS Access and MS SQL Server, Structured Query Language, ODBC standards, the use of XML to transport data between database systems, protocols for providing database access online, and web page construction, including HTML, PHP, JavaScript, CSS, and web ready imagery.

This is a full time, temporary, NSF-funded position lasting up to one year. To apply send resume and description of qualifications, including URLs of online databases previously implemented to:

Human Resources - CDS Santa Barbara Museum of Natural History 2559 Puesta del Sol Rd. Santa Barbara, CA 93105

A more detailed job description is posted at:

www.sbnature.org/visitors/hr.php For additional information about the position email Dr. Michael Caterino at:

mcaterino@sbnature2.org

For more information on the California Beetle Project visit:

www.sbnature.org/collections/invert/entom/-cbphomepage.htm SBMNH IS AN EQUAL OPPORTUNITY EMPLOYER

– Michael S. Caterino Santa Barbara Museum of Natural History 2559 Puesta del Sol Rd. Santa Barbara, CA 93105-2998 USA Phone (805) 682-4711 Ext. 151 FAX (805) 563-0574

mcaterino@SBNATURE2.ORG

**SantaBarbaraMNH
DatabaseSpecialist**

SantaBarbaraMNH MuseumSchool

PALEONTOLOGY COLLECTIONS & TEACHING POSITION

The Santa Barbara Museum of Natural History is collaborating with a private school in an effort to create a “museum school” that endeavors to inspire in students a passion for science through hands-on engagement.

Students will work with collections and scientists on the full range of collections care and research activities that typically occur in natural history museums. In this context, we are looking for a dynamic paleontologist who, besides his/her research ambition, also has a genuine interest in working with high school students and fully engage them in his/her work.

The ideal candidate should have a Ph.D. or be very close to having finished his/her dissertation. Specialization within paleontology is open, though it would be helpful if the candidate could pursue some field research in the American West. The candidate should have a background and experience in collection management and curation.

The school is interested in recruiting quickly and looking for a candidate who would be available immediately or as soon as possible. Interested candidates should contact: Karl L. Hutterer, Executive Director, Santa Barbara Museum of Natural History, 2559 Puesta del Sol Rd., Santa Barbara, CA 93105. Phone: (805)682-4711, ext. 101. Fax: (805)569-3170. E-mail: khutterer@sbnature2.org.

————— posted by mcaterino@sbnature2.org

Saudi Arabia Conservation Genetics

Conservation Geneticist, King Khalid Wildlife Research Centre,

Kingdom of Saudi Arabia

The King Khalid Wildlife Research Centre (KKWRC) is managed by the Zoological Society of London (ZSL) under contract to the National Commission for Wildlife Conservation and Development in the Kingdom of Saudi Arabia. The Centre is located 70km north of Riyadh. The primary mission of KKWRC is to assist the Commission’s conservation work, and the Conservation Genetics laboratory is an integral part of that aim. The laboratory, established eight years ago, is equipped with an automated sequencer that allows analyses such as DNA sequencing and fragment analysis (microsatel-

lites and SSCP) to be conducted on-site.

The Geneticist is in charge of the laboratory and the genetics research carried out. Duties include: design and conduct molecular genetic studies in support of conservation programs for threatened and endangered fauna in Saudi Arabia; supervise a laboratory, including 2 technicians, that is shared with veterinary diagnostic and parasitology programs; train local staff in molecular genetics investigative techniques; conduct pedigree-based analyses of captive stocks of gazelles and make recommendations for captive-breeding programs; prepare written reports of analyses and publish results in peer-reviewed outlets.

Past and present projects in the laboratory include taxonomic assessment of the Saudi gazelle, phylogeography of Hamadryas baboons, genetic detection of pathogens of wildlife, defining conservation units for mountain gazelle, sand gazelle and Nubian ibex, assessing systematics and taxonomy of Arabian tahr, and investigating relationships between inbreeding and fitness among lineages of captive-bred gazelles. Potential exists for research on carnivores (particularly wolves, leopard, sand cat, wildcat, and caracal), raptors, and spiny-tailed lizards.

Required qualifications: candidates must have a PhD in biology, molecular biology, genetics or a closely related field. We seek an experienced professional but will consider well-qualified post-doctoral candidates. Candidates will have experience with laboratory procedures involved with molecular genetics studies, including primer design, PCR optimization, and data acquisition using an automated sequencer; knowledge of principles of phylogenetics, phylogeography, population genetics and pedigree analysis; experience with analysis of DNA sequence and microsatellite data, preferably in a conservation context; candidates must be able to read, write and speak English fluently, communicate effectively, both orally and in writing, and work as part of a culturally diverse team.

Additional desired qualifications: knowledge of principles of conservation biology, ecology and management of vertebrates; experience supervising laboratory technical staff; experience with forensic applications.

As an employee of ZSL, the successful candidate will have close links with geneticists and molecular ecologists at the Institute of Zoology (IoZ) (the research wing of ZSL: www.zsl.org/ioz), and there is the potential for collaborative projects between the successful candidate and postdoctoral fellows at IoZ.

The contract will be for one year initially, with the possibility of extension, beginning as early as mid-June.

The benefits include free accommodation, use of a vehicle, flights to and from Saudi Arabia at each end of the contract and a return flight each year. Annual leave (60 days).

Please send an application letter and CV to the Human Resources Department, Zoological Society of London, Regent's Park, London NW1 4RY (hr@zsl.org) For further information, contact Conservation Programmes, cp@zsl.org <mailto:cp@zsl.org>

Closing date: 5 April 2005

Registered Charity Number: 208728

Marcia Latty Senior HR Officer Zoological Society of London Regent's Park London NW1 4RY
Tel: 020-7449-6251 <<http://www.whipsnade.co.uk/-adoption/index.html>>

marcia.latty@zsl.org

Scotland Director Biomath

Director of Biomathematics & Statistics Scotland

BioSS is an internationally renowned group of statisticians, mathematicians, bioinformaticians and computing specialists.

BioSS undertakes research, training and consultancy work to underpin the work of eight scientific institutes, augmented by a range of research grants and contracts, and operates with an annual budget of circa £1.3M.

We seek to appoint as Director an exceptional individual with:

- * an international standing in applied statistics, biomathematics, bioinformatics or a related field;
- * experience of collaborations with subject-area scientists to solve problems in agriculture, the environment, food or health; and
- * the organisational skills to co-ordinate and develop a highly motivated, distributed, group of specialist staff.

See www.bioss.ac.uk for details of BioSS, the post and the attractive salary (£50K+) and benefits package.

Closing date for applications: March 25th 2005.

frank@bioss.ac.uk frank@bioss.ac.uk

SeaGrant Fellowships

Dear Brian,

I received the following from the New Jersey Sea Grant folks and thought it would be worth posting to Evoldir.

Thanks,

Gail

Dear SG Research Coordinators, California Sea Grant would appreciate your help distributing this fellowship program announcement to appropriate audiences in your networks. Thanks, Shauna

Shauna Oh Program Manager, Research & Education California Sea Grant College Program University of California, San Diego Scripps Institution of Oceanography 9500 Gilman Drive, Dept 0232 La Jolla, CA 92093-0232 (858) 822-2708 (858) 534-2231 fax shaunaoh@ucsd.edu <http://www.csgc.ucsd.edu> 2005 REQUEST FOR APPLICATIONS - SCIENCE FELLOWS PROGRAM California Bay-Delta Authority Science Program California Sea Grant College Program

The California Bay-Delta Authority (CBDA) Science Program, in cooperation with California Sea Grant, is seeking applications from highly qualified predoctoral students and postdoctoral researchers who are interested in a career in multidisciplinary, multi-institutional, field-based research in riverine and estuarine systems. For 2005, the Science Program is interested in research that addresses the three priority topics as outlined in the recent CBDA Science Program 2004 Proposal Solicitation Package (PSP): Water Operations and Biological Resources; Ecological Processes and Their Relationship to Water Management and Key Species; and Performance Assessment to Improve Tools and Implications of Future Changes.

ELIGIBILITY - Prospective Predoctoral Science Fellows, at the time of application, must be in or recently been admitted to a PhD program in natural resources, environmental sciences, coastal, aquatic or related studies at any accredited US institution of higher education. Prospective Postdoctoral Science Fellows must hold a PhD or complete a PhD before the starting date of the fellowship in a doctoral degree program in environmental sciences or in a related field from any accredited US institution of higher education. US citizenship or residency is required.

AWARD - The fellowship will provide support for up to three years for both predoctoral and postdoctoral fellows in the form of a grant/award that includes funds for a stipend (\$45,000/yr-postdoctoral; \$25,000/yr-predocotrual) and for research-related expenses (up to \$25,000/yr-postdoctoral; \$14,500/yr-predocotrual).

SELECTION - Selection will be made competitively from applications submitted to the California Sea Grant College Program by May 18, 2005. In 2005, approximately five postdoctoral and two predoctoral fellowships will be awarded to begin approximately by September 1, 2005.

APPLICATION/CONTACT - For complete details and application instructions, please refer to the CBDA Science Fellows Program - 2005 Request for Applications, on the Sea Grant web site: <http://www.csgc.ucsd.edu/EDUCATION/-SgEducationIndx.html> If you have specific questions or require additional information contact: CALFED-fellow@seamail.ucsd.edu

Dr. Gail M. Simmons Dean, School of Science The College of New Jersey P-105 Science Complex P.O. Box 7718 Ewing, NJ 08628 (609) 771-2724 voice (609) 637-5116 FAX simmons@tcnj.edu email

Gail Simmons <simmons@tcnj.edu>

UBern EvolGenetics

assistant professor in molecular ecological/evolutionary genetics

The Division of Aquatic Ecology and Macroevolution, a division of the Institute of Zoology/University of Bern and the Limnological Research Centre of the Swiss Federal Institute for Environmental Science (EAWAG), invite applications for an assistant professor/scientist in the area of molecular ecological genetics/evolutionary genetics/population genetics. The position is initially available for three years and can be renewed for a total of up to five years (non-tenure track).

We seek applicants with a record of excellent postdoctoral research in a relevant area of molecular genetics. The division investigates ecology and genetics of adaptive diversity, population divergence and speciation with a strong focus on freshwater fish as a model system. The successful candidate is expected to contribute a strong molecular genetic component to the research of the division, and to develop an independent

research program, partly supported by external funding, in ecological/evolutionary genetics of fish.

The successful candidate will have to participate in teaching in both BSc and MSc programs in the Institute of Zoology, beginning in fall 2005, and to supervise both undergraduate and graduate students. Scientific language of the lab is English, and teaching is in English too. Salary will be depending on age and experience.

The division of Aquatic Ecology and Macroevolution is a division both of the EAWAG and the Institute of Zoology. Its research facilities (the Fish Ecology and Evolution lab) are located at the Limnological Research Centre of the EAWAG in Kastanienbaum, about 1.5 hours from Bern and 20 minutes from Lucerne by public transport. Facilities include a molecular genetics laboratory with two 8-capillary CEQ8000 sequencers, a modern large tropical aquarium facility, cold water fish breeding and keeping facilities, outdoor experimental ponds, wetlab space and office space overlooking Lake Lucerne. Information on the group can be found at <http://www.fishecology.ch/> Information on other research areas in the Swiss Federal Institute for Environmental Science can be found at http://www.eawag.ch/-research_e/e_index.html Information on other research areas in the Zoological Institute can be found at http://www.zoology.unibe.ch/index_e.php Applicants should send (before March 31 2005) a CV, a publication list, a short (less than two pages) summary of past and future research interests, and the names and emails of three potential referees to Ole Seehausen, EAWAG Limnological Research Center, Seestrasse 79, CH-6047 Kastanienbaum, Switzerland. The application material should also be submitted in a single PDF-file to ole.seehausen@aqua.unibe.ch. For inquiries please contact Ole Seehausen at ole.seehausen@aqua.unibe.ch
ole.seehausen@eawag.ch ole.seehausen@eawag.ch

UEastAnglia EvolBiol

School of Biological Sciences - University of East Anglia, Norwich

Chair in Evolutionary Biology

We are seeking a world-class researcher to build on our strong standing in the field of Evolutionary Biology, through the appointment of a Chair.

The School of Biological Sciences has achieved an excellent international reputation with wide research inter-

ests. It was graded 5 in the UK's Research Assessment Exercise and its teaching was also graded as "Excellent". The School is a prominent member of UEA's Centre for Ecology, Evolution and Conservation, which facilitates collaborations among 22 faculty members, including colleagues in the top-ranked School of Environmental Sciences. The University's strong research profile is further enhanced by new developments such as a School of Medicine with a joint Biomedical Research Centre, which will open in 2005. UEA is part of the Norwich Research Park, which includes the John Innes Centre, which has full genomic facilities, as well as the Institute for Food Research, which has first-rate proteomic facilities.

Applications are invited for the above position tenable from September 2005. Applicants should have an excellent international research record, including the use of molecular genetic techniques for studies of adaptation and evolution in populations and species of eukaryotic organisms. They will join an active group of molecular biologists, evolutionary geneticists, ecologists and conservation biologists, with state-of-the-art molecular ecology laboratories. The successful applicant will be expected to provide leadership in the field, establish a strong, well-funded research group and contribute to undergraduate teaching.

Information about the School and Faculty Research interests can be found at www.uea.ac.uk/bio/. Informal enquiries should be made to the Head of the School, Professor John Turner, Tel:+44-(0)1603-592782, email j.g.turner@uea.ac.uk).

Further particulars and an application form can be obtained from the Personnel Office, University of East Anglia, Norwich NR4 7TJ, UK (<http://www.uea.ac.uk/personnel/jobs>, email: Personnel@uea.ac.uk or answer phone: +44(0)1603 593493). Please quote reference number AC572. We will begin reviewing applications on 1 May 2005.

–

Brent Emerson Lecturer in Evolutionary Biology Centre for Ecology, Evolution and Conservation School of Biological Sciences e-mail: b.emerson@uea.ac.uk University of East Anglia ph: (44) 01603 592237 Norwich NR4 7TJ fax: (44) 01603 592250 ENGLAND mob: (44) 0795 121 8827

Brent Emerson <b.emerson@uea.ac.uk>

UHull 2 EvolBiol

The Department of Biological Sciences at the University of Hull, UK, is advertising 2 positions in molecular ecology and/or evolutionary biology.

The successful candidates will be expected to establish their own research programmes, although we anticipate they will also interact with the large group of evolutionary biologists already present. <http://www.hull.ac.uk/biosci/> *** Please note closing date is 8th April 2005 ***

PROFESSOR OF MOLECULAR ECOLOGY/ EVOLUTIONARY BIOLOGY (ref S01)

University of Hull, UK, Department of Biological Sciences

Applications are invited for the post of (full) Professor in the Dept of Biological Sciences (<http://www.hull.ac.uk/biosci>). The University of Hull has identified the Environmental Sciences as a core area of research strength. Strategic investment has been manifested through the creation of the Hull Environment Research Institute, and the allocation of £2.5M of funding for research infrastructures. The Department of Biological Sciences has particular research strength in the area of molecular ecology and evolutionary biology, with a group of over 30 researchers including 7 academic staff/independent research fellows. There are excellent facilities for molecular analyses, bioinformatics and maintenance of fish and aquatic invertebrates.

Candidates will have an international research reputation in an area of evolutionary biology or molecular ecology, indicated by a strong record of publication in high-profile journals and of leadership of a dynamic research group supported by grant income from competitive sources.

There will be a generous start-up package, including technical support and associated academic staff appointments. It is anticipated that the successful candidate will have an input into the appointment of the lecturer in molecular ecology/ evolutionary biology (below). Salary is negotiable, but will be no less than the JNC Professorial minimum, which was £43,513 in August 2004.

Further particulars are available from <http://www.hull.ac.uk/biosci/appointments/chair.html> Or by calling the Departmental office +44 (0)1482 465198

LECTURER IN MOLECULAR ECOLOGY/ EVOLUTIONARY BIOLOGY (ref S02)

University of Hull, UK, Department of Biological Sciences

Applications are invited for the post of Lecturer (=Assistant Prof) in the Dept of Biological Sciences (<http://www.hull.ac.uk/biosci>).

Candidates will work in an area of evolutionary biology or molecular ecology, and have a research programme capable of being published in high-profile journals and generating grant income from competitive sources.

It is anticipated that the successful applicant will interact productively with both the new Professorial appointment and the established group of researchers in molecular ecology/ evolutionary biology.

There will be a start-up package and a relatively modest initial teaching load.

Further particulars are available from <http://www.hull.ac.uk/biosci/appointments/chair.html> Or by calling the Departmental office +44 (0)1482 465198

Informal enquiries should be directed to

Dr Joerg Hardege (Head of Department) tel. 44(0) 1482 465187 j.d.hardege@hull.ac.uk

Prof George Turner (Professor of Evolutionary Biology); 44(0) 1482 466425 g.f.turner@hull.ac.uk

For further information and details of how to apply, tel: -44 (0)1482 465557, fax: 44 (0)1482 466660, email: science-recruitment@hull.ac.uk (quoting ref. S01 prof; S02 lecturer).

***** Closing date for applications 8th April 2005 *****

Additional information can be obtained from Mrs Gillian Dennison (Dept Secretary) 44(0) 1482 465198 g.dennison@hull.ac.uk Or <http://www.hull.ac.uk/biosci/appointments/chair.html> —

Dr David Lunt, Department of Biological Sciences, University of Hull, Hull HU6 7RX UK

Phone: +44 (0)1482 465514 Fax: +44 (0)1482 465458 Email: d.h.lunt@hull.ac.uk WWW: <http://www.hull.ac.uk/biosci>

UMaryland ReproductiveIsolation

Position: Faculty Research Assistant

Period: June 1, 2005 through May 31, 2006 (renewable)

Description: This is a full-time position to assist in the execution of NSF-sponsored research on reproductive isolation and postcopulatory sexual selection in stalk-eyed flies.

Duties and Responsibilities: Oversee lab operations. These include maintaining cultures of stalk-eyed flies, supervising one or two undergraduates who assist with making food, feeding, watering and cleaning population cages, collecting and managing data for various breeding experiments, placing orders for supplies, and occasionally assisting with graduate student and post-doc experiments.

Requirements: Bachelor's degree in the biological sciences and research experience, preferably with insects. Basic knowledge of spread sheets is essential. Familiarity with epifluorescent microscopy, PCR, and microsatellite genotyping using ABI DNA analyzers is desirable. Ability to interact well with undergraduate and graduate students, as well as postdocs, is essential.

Salary: \$27,262 per year

Health Insurance: Up to \$3000 supplement if enrolled in a University plan.

Send statement of interest, resume, transcript, and contact information for two references to:

Dr. Jerry Wilkinson Department of Biology University of Maryland College Park, MD 20742

Phone: 301-277-8854 fax: 301-314-9358 email: wilkinso@umd.edu

Deadline: Applications will be accepted until the position is filled.

Jerry Wilkinson <wilkinso@umd.edu>

UPoitiers EvolEcol

Professorship in Evolutionary Ecology of host-parasite

interactions

We seek to fill a permanent position of Professor in Evolutionary Ecology (senior researcher) in the joint research unit (UMR) GBPC (Population Biology and Genetics of Crustaceans, D. Bouchon) of the University of Poitiers (France).

The ideal candidate works in the field of evolutionary ecology of host-parasite interactions, which can also include the study of immune defences. Interest in using arthropods as a model and experience in molecular techniques is advantageous. We expect willingness to collaborate with others in the group and to contribute to its teaching commitments. The successful candidate will be expected to develop a strong research program in host-parasite interactions, possibly including emerging fields such as evolutionary consequences of endosymbionts or comparative genomics.

Starting date is September 2005. Applications must be sent before 31 March 2005

Additional information is available upon request from: Pr. Didier Bouchon Université de Poitiers Génétique et Biologie des Populations de Crustacés, UMR CNRS 6556 40 avenue du Recteur Pineau F-86022 POITIERS Cedex tel : +33 (0)5 49 45 38 95 fax : +33 (0)5 49 45 40 15 <http://labo.univ-poitiers.fr/umr6556> <mailto:didier.bouchon@univ-poitiers.fr>

didier.bouchon@univ-poitiers.fr

URennes Epigenetics

A tenure track position «Maitre de Conférences» (Associate Professor) for teaching and research is open in our group “Genome Evolution and Speciation” (UMR CNRS 6553) at University of Rennes 1 (western France), on “Ecological success, epigenetics and plasticity” (Position 67MCF 0537S of the French Ministry of Education). Research activity will include the exploration of epigenetic mechanisms, and eventually the role of transposable elements involved in the response to hybrid genome duplication (allopolyploid speciation) in successful invasive plant species, with the perennial grass *Spartina* (Poaceae) as a main (but not exclusive) model system. Experience in transcriptome analysis and bioinformatics is needed to develop microarrays. (See Ainouche M., Baumel A., Salmon A. 2004 - Biological relevance of polyploidy, ecology to genomics: *Spartina anglica* Schreb. a natural model

system for analysing early evolutionary changes that affect allopolyploid genomes. *Biological Journal of the Linnean Society* 82, 475-484., or Salmon A., Ainouche M., Wendel J.F. 2005 - Genetic and epigenetic consequences of recent hybridization and polyploidy in *Spartina* (Poaceae). *Molecular Ecology*, 14, 1163-1175). Teaching (in French) will include Evolutionary and Comparative Genomics, Bioinformatic Analyses and Plant Molecular Evolution. Experience on plant systems is preferable but is not a strict requirement. The successful applicant will work with an enthusiastic interactive group aiming to develop ecological genomic approaches in the Centre Armoricaire de Recherches en Environnement (CAREN) at Rennes. This position is opened to any citizen (preferably fluent in French) in section 67 of the CNU (Commission Nationale des Universités) “Ecology and population Biology” and should have been previously qualified by any section of the CNU relevant to the topic of the position (i.e. evolutionary ecology, molecular genetics, cell biology, biochemistry), according to the procedure requested by the French Ministry of Education (http://www.education.gouv.fr/personnel/enseignant_superieur/enseignant_chercheur/)

Additional information is available upon request from Malika.Ainouche@univ-rennes1.fr and applications must be sent before 31 March 2005.

M. L. AINOUCHE Evolution des Genomes et Speciation, Dpt Ecologie Evolutive UMR CNRS 6553 Eco-bio, Université de Rennes 1 Campus Scientifique de Beaulieu, Bat. 14A 35 042 Rennes Cedex France Ph. 33 (0)2 23 23 51 11 Fax 33 (0)2 23 23 50 47

malika.ainouche@univ-rennes1.fr

US FishWildlifeService FishGenetics

We are currently advertising for a GS 9/11 fisheries geneticist to work on endangered fish in the desert southwest. Position ID is

Job Announcement Number: DS-04-12-103820-FG. For more information contact Manuel Ulibarri 505.734.5910

FISHERY BIOLOGIST (GENETICS) SALARY RANGE: 40454 - 48947 USD per year OPEN PERIOD: Wednesday, March 02, 2005 to Tuesday, March 15, 2005 SERIES & GRADE: GS-0482-09/11 POSITION INFORMATION: Full Time Term WHO MAY BE CONSIDERED: U.S. Citizens

Dexter National Fish Hatchery and Technology Center is located in Southeastern New Mexico in the heart of Pecos River valley. It is approximately 18 miles south of Roswell, NM of UFO fame. The 640 acre facility has been renovated and is devoted entirely to the propagation, culture and research of threatened and endangered aquatic species. The general area is a rich farming district with numerous dairies dotting the surrounding countryside. The population density is typical of farming communities with a small town of approximately 1500 people. The school system is excellent (K-12) and most religious faiths are represented locally and within a 24 mile commute. The elevation is approximately 3,500 feet, average rainfall is 8 to 12 inches and average snowfall varies from a few inches up to two feet depending on the storm systems. The growing season is approximately 180 to 200 days.

<http://jobsearch.usajobs.opm.gov/getjob.asp?JobID=27770884>

Connie_KeelerFoster@fws.gov

USydney MolEcol

LECTURESHIP/SENIOR MOLECULAR ECOLOGY LECTURESHIP –

Applications are invited for a new position in molecular ecology at the School of Biological Sciences (University of Sydney).

For further detail, visit <http://www.usyd.edu.au/> and go to Positions Vacant.

All the best,

Lars – Dr Lars S Jermiin School of Biological Sciences Heydon-Laurence Building A08 University of Sydney New South Wales 2006, Australia

+61-2-9351-3717 (Ph) +61-2-9351-4119
 (Fax) lars.jermiin@usyd.edu.au [http://-www.bio.usyd.edu.au/~jermiin](http://www.bio.usyd.edu.au/~jermiin) [http://-](http://www.bio.usyd.edu.au/~jermiin)

UtahStateU AnimalPop

ASSISTANT PROFESSOR We are filling a tenure-track, 9-month, Assistant Professor position in Animal Population Ecology at Utah State University. We seek an individual studying the structure and dynamics of animal populations in terrestrial systems. The successful candidate will have strong quantitative skills and training in statistical, spatial and/or simulation modeling, and strengths in both theory and empirical field-based research. To apply, send a letter of application, a curriculum vita, statements of research interests/experiences and teaching philosophy/experiences, copies of pertinent publications, and three letters of reference to Chris Call, Search Committee, Department of Forest, Range, and Wildlife Sciences, Utah State University, Logan, UT 84322-5230, by surface mail or in PDF format by e-mail (cacall@cc.usu.edu). Review of applications will begin on March 31, 2005, and continue until the position is filled. See www.usu.edu/jobs (2-113-05) for full announcement. AA/EOE.

Mandi Jones <mandi.jones@usu.edu>

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ABIGeneMapper Alternative

Dear Evoldir members,

Does anyone know of an alternative software to ABI's GeneMapperTM? For now I'm forced to use the computer that is connected to the ABI sequencer to be able to process my samples (microsatellites). I would like to be able to analyze my samples on my desktop but the Stand-alone install of GeneMapper has too high demands on my computer for this to work.

All the best,

Jens

jc@vims.edu

ABIGeneMapper Alternative answers

Dear Evoldir members,

Thanks to all who responded to my questions regarding alternatives to ABI's GeneMapper. Below are some answers regarding these alternatives.

-Genographer (<http://hordeum.oscs.montana.edu/genographer/>)

-Genotyper & Genescanner

-STRand (<http://www.vgl.ucdavis.edu/informatics/-STRand/>)

-GeneMarker (<http://www.softgenetics.com/gm/-index.htm>) <<http://www.softgenetics.com/gm/-index.htm>> -Allele sampler

All the best,

Jens

jc@vims.edu

Analysis with Arlequin

Dear all,

We are trying to analyze a group of sequences with Arlequin and are finding a basic problem that we are hoping somebody may have encountered previously.

Some information about the data: -the data comes from direct sequencing of PCR fragments of a nuclear gene, from a diploid species. Therefore, the heterozygotes for a SNP appear with the degenerate code (R, Y, etc).

-We build the input with the different haplotypes found in each population

The problem: -we cannot get the program to interpret the degenerate code. The way things are going now, it dismisses any SNP position with a degenerate code

and therefore interprets all the haplotypes as being the same.

We tried changing several parameters with no luck. I am hoping we simply ignored a simple detail about this... but I could not find any specific information in the manual- both sequence examples provided in the program DO NOT include degenerate sequences.

Thanks for any help!

alex

Alexandre Rodrigues Caetano, Ph.D. Embrapa Recursos Genéticos e Biotecnologia Parque Estação Biológica Final Av. W/5 Norte, Brasília-DF C.P. 02372 70770-900 Brasil

Tel.: (55)-61-448-4778 Fax: (55)-61-340-3658

acaetano@cenargen.embrapa.br

<http://www.cenargen.embrapa.br/>

“Alexandre R. Caetano”
<acaetano@cenargen.embrapa.br>

-there are two basic ways to deal with the situation: (1) one can convert the sequence data into genotypes at the variable sites/SNPs and analyze the data that way, as genotypic data, phase unknown.

(2) there are ways to predict haplotypes from this type of data, which can then be inputted into arlequin, and other programs, as phase known haplotypes, etc. See Kidd et al. 2000 Am. J. Hum. Gen.

Many thanks to all of you who tried to help!

cheers,

alex

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<acaetano@cenargen.embrapa.br>

Analysis with Arlequin answers

Dear all,

We posted a couple of questions about using Arlequin to analyze sequence data from nuclear genes a few days ago. Many folks sent me several nice ideas and many others asked to know the answers I got. I figured it would be easier to just post what I thought was most significant:

Here is what I previously posted: >Some information about the data: >-the data comes from direct sequencing of PCR fragments of a nuclear >gene, from a diploid species. Therefore, the heterozygotes for a SNP appear >with the degenerate code (R, Y, etc). > >-We build the input with the different haplotypes found in each population

>The problem: >-we cannot get the program to interpret the degenerate code. The way things are >going now, it dismisses any SNP position with a degenerate code and therefore interprets all the >haplotypes as being the same.

The solutions/answers: -even though the manual says so, arlequin does not interpret sequence degenerate codes, at least for the type of data we have (diploid, unknown phase)

BAPS software users

I've received emails from BAPS sw users, who have been puzzled with certain aspects of the analysis done by the program. Unfortunately, the user manual has not been specific enough on some details, so I wish to make users aware of certain functionality. The text below is also added to the BAPS webpage. Best Jukka

An announcement to the users of BAPS software. The following important aspects concerning functionality were previously not clearly indicated in the manual.

Hint #1! You can fill as many K values into the BAPS 3.1 input window as you wish, e.g. like 200 hundred values. This option makes the sensitivity analysis based on many estimation runs with an equal K much simpler. The input field simply shifts to the right when it becomes filled. So the input could look like:

10 10 10 10 10 10 11 11 12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 etc.

What the program does for each K value (even the replicates of the same value) is to find the optimal partitions with k \leq K, it stores these internally, and the after all K values have been processed, it merges the stored results

according to the logml values. Even if small k values are considered a priori possible, they can have extremely bad fit compared to the larger values, in which case they are ignored in the results.

Hint #2! For those who have used Structure sw previously, the difference in the use of K may be confusing. Please, do not enter the $K=1$ into the field, since it is meaningless value for BAPS (the estimation algorithm of BAPS still considers $k=1$ to be a plausible number of clusters a priori).

The software is available at:

<http://www.rni.helsinki.fi/~jic/bapspage.html> corander@mappi.helsinki.fi

Bootstrapping loci individuals

I am wondering which bootstrap technique (individuals versus loci) is most appropriate for gauging confidence in the genetic differentiation between populations. I am reticent about bootstrapping over individuals as to me they do not appear to be independent (i.e. they are related). I would like to know which method is most appropriate for my needs (determining confidence in the relationships between populations), and also perhaps examples of where you would use each method.

My ruminations to date: I suppose both are valid (or else they wouldn't both be available in software by people much more learned than I), but it will depend on the question you ask.

Bootstrapping across individuals (which I am not entirely cool with since data points are not independent - they are related, at least to some degree, which will, to me anyway, will necessarily bias estimates in favour of differentiation) would enable you to gauge confidence in how well your samples support differentiation between populations. Taken this way, you assume that the distribution of genetic variation in your samples is representative of the populations as a whole.

In contrast, bootstrapping across loci gauges how well the genome supports differentiation. Here, obviously, you assume that your loci are representative of the distribution of differentiation between populations across the genome as a whole. A major potential problem here is that a handful of loci may be unlikely to accurately portray this distribution (but clearly this is an implicit problem with every population genetics study under the sun). The efficiency of bootstrapping when sample sizes

are small (i.e. a handful of loci) may be pertinent here, though I am not up on the bootstrapping literature.

You can imagine a locus that is quite unrepresentative may bias your results (e.g. 2 populations have a particular allele in high frequency, due solely to homoplasy). In that case, going the individual-route might be more appropriate as the real-variance is better approximated with the much larger sample size of individuals. At the other extreme, if you know your samples are good (for example, you have sampled all individuals), then bootstrapping loci would seem more appropriate to me as the variance due to sampling individuals is zero.

I guess the thing to do is bootstrap whichever sample distribution (individuals or loci) you think best approximates the variance of the respective real distributions (population or genome). It may very well be that both distributions are equally well approximated, and would therefore deliver similar bootstrap proportions.

Long story short, the two tests seem complementary. Despite reservations, I think I would report bootstrap proportions across individuals. I would defend this by saying that 1) I assume my microsatellites are representative because they are putatively randomly distributed across the genome, or 2) the results are true given the data used (which happens to also be the only data available), and are open to debate with new data. Any input on this problem would be greatly appreciated. Thanks. Joseph. (josephwb@umich.edu)

Joseph W. Brown Graduate Student, Mindell Lab Department of Ecology and Evolutionary Biology 3015 Ruthven Museums Building Museum of Zoology, Bird Division University of Michigan, Ann Arbor 48109-1079 Email: josephwb@umich.edu Fax: (734) 763-4080 Homepage: <http://www.ummz.lsa.umich.edu/students/josephwb/index.htm> Biology 162 Laboratory: <http://www-personal.umich.edu/~josephwb/Biol162/-Lab.html> Queen's Conservation Genetics Group: <http://biology.queensu.ca/~cgg> Queen's Conservation Genetics Group: <http://biology.queensu.ca/~cgg>

Bootstrapping loci individuals answers

I recently sent out a message asking whether bootstrapping across individuals or loci is appropriate for gauging the confidence in relationships between populations, but I see from some of the responses that my question

could have been posed better. I thank everyone who replied so far, but I'd like to restate the question.

I am working in a population genetics framework and have genotyped many individuals for each of several populations for a dozen microsatellite loci. I know which pairwise populations are significantly differentiated as determined through the non-parametric permutation approach of Excoffier et al. (1992). My initial query really had to do with constructing a population dendrogram showing the relationships between populations. The program POPULATIONS (Olivier Langella) offers bootstrapping across individuals or loci using 15 different differentiation metrics. My question, then, is which of these two options is most appropriate (or even if both are statistically valid). To reiterate, I feel reticent about bootstrapping across individuals because they are not statistically independent (they are related). Please read the former message (below) for more ruminations. Thanks. Joseph. (josephwb@umich.edu)

Initial query: I am wondering which bootstrap technique (individuals versus loci) is most appropriate for gauging confidence in the genetic differentiation between populations. I am reticent about bootstrapping over individuals as to me they do not appear to be independent (i.e. they are related). I would like to know which method is most appropriate for my needs (determining confidence in the relationships between populations), and also perhaps examples of where you would use each method.

My ruminations to date: I suppose both are valid (or else they wouldn't both be available in software by people much more learned than I), but it will depend on the question you ask.

Bootstrapping across individuals (which I am not entirely cool with since data points are not independent - they are related, at least to some degree, which will, to me anyway, will necessarily bias estimates in favour of differentiation) would enable you to gauge confidence in how well your samples support differentiation between populations. Taken this way, you assume that the distribution of genetic variation in your samples is representative of the populations as a whole.

In contrast, bootstrapping across loci gauges how well the genome supports differentiation. Here, obviously, you assume that your loci are representative of the distribution of differentiation between populations across the genome as a whole. A major potential problem here is that a handful of loci may be unlikely to accurately portray this distribution (but clearly this is an implicit problem with every population genetics study under the sun). The efficiency of bootstrapping when sample sizes are small (i.e. a handful of loci) may be pertinent here,

though I am not up on the bootstrapping literature.

You can imagine a locus that is quite unrepresentative may bias your results (e.g. 2 populations have a particular allele in high frequency, due solely to homoplasy). In that case, going the individual-route might be more appropriate as the real-variance is better approximated with the much larger sample size of individuals. At the other extreme, if you know your samples are good (for example, you have sampled all individuals), then bootstrapping loci would seem more appropriate to me as the variance due to sampling individuals is zero.

I guess the thing to do is bootstrap whichever sample distribution (individuals or loci) you think best approximates the variance of the respective real distributions (population or genome). It may very well be that both distributions are equally well approximated, and would therefore deliver similar bootstrap proportions.

Long story short, the two tests seem complementary. Despite reservations, I think I would report bootstrap proportions across individuals. I would defend this by saying that 1) I assume my microsatellites are representative because they are putatively randomly distributed across the genome, or 2) the results are true given the data used (which happens to also be the only data available), and are open to debate with new data. Any input on this problem would be greatly appreciated. Thanks. Joseph. (josephwb@umich.edu)

Joseph W. Brown Graduate Student, Mindell Lab Department of Ecology and Evolutionary Biology 3015 Ruthven Museums Building Museum of Zoology, Bird Division University of Michigan, Ann Arbor 48109-1079 Email: josephwb@umich.edu Fax: (734) 763-4080 Homepage: <http://www.umz.lsa.umich.edu/students/josephwb/index.htm> Biology 162 Laboratory:

— / —

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>

Consensus patterns

Dear all

We are working with protein interaction data and peptide-domain interactions obtained from high-throughput experiments. We would like to obtain for a list of peptides the consensus pattern.

I have found many useful websites where I can generate a profile from multiple sequence alignment but what would be really useful will be a tool where I can feed a list of short peptides (not aligned) and obtained a consensus (so the alignment is also done automatically in the moment I give the input).

I will keep searching, but in case you know of anything doing this I would be grateful if you could let me know.

Thanks in advance Best regards

Vicky Schneider M.V, Schneider Senior Curator MINT database, Cesareni Group, Department of Genetics Universita' di Tor Vergata, via della Ricerca Scientifica 00133 Roma, Italy Tel: +39 0672594916 FAX: +39 0672594766 biosearch@virgilio.it

biosearch@virgilio.it

D sechellia samples

I am a PhD student at Stanford and need strains of D.sechellia for my current study. Please let me know if you can contribute strains from your stocks

Thanks in advance, Yael

ysalzman@stanford.edu

DNA collection intheField answers

Hi all

Below are the replies to my request " I'm trying to find field manuals (web based preferably) relating to the collection of DNA samples (blood/tissue/feather/etc.) aimed at field workers or wildlife officers without no genetic or lab experience. Covering issues such as types of sample/storage media, maintaing DNA integrity, contamination etc. Also again at the non-genetic-specific experienced level relating to collecting wildlife samples for forensic purposes, including chain-of custody/evidence procedures etc. "

Thanks to everyone you replied for your help.

Tee

Hi,

I am not sure if you still need this, but here is a really good site: http://www.absc.usgs.gov/research/-genetics/dna_sampling_protocol.htm Thanks,

Suzanne

Dear Tee Felix Forest from SANBI passed onto me your email looking for a DNA bank manual. As it happens we are publishing one entitled 'DNA and Tissue banking for biodiversity and conservation', to be on sale in 6 months, watch this space! Vincent

Dr Vincent Savolainen Molecular Systematics Section Royal Botanic Gardens, Kew Richmond, Surrey TW9 3DS London UK Tel +44-(0)20-8332-5366 Fax +44-(0)20-8332-5310 Email v.savolainen@kew.org

You may find something on the American Museum of Natural History Ambrose Center's web site.

Best wishes, Lisa

Lisa M. Campbell, Ph.D. Administrative Curator Plant Research Laboratory The New York Botanical Garden Bronx, NY 10458 USA tel: 718.817.8168 fax: 718.817.8101

Dear Taylor. I can send you some notes (like a subject in word format), but it is in spanish. You can find on it the conservation of different kind of tissue, blood, feather, fe.ces, etc. Please, if you are interested tell it to me. Sorry, and good luck. Joaquin. Joaquin Munoz <quini@ebd.csic.es>

Dear Dr. Taylor,

Somebody once put a html version of a possibly relevant paper of ours on the web <http://www.csulb.edu/~zedmason/researchpapereg.htm>

Best regards,

Mike. Michael N Dawson

Dr Tiawanna Taylor School of Biological and Conservation Sciences University of KwaZulu-Natal Private Bag X01 Scottsville 3209 KwaZulu Natal South Africa

Email: taylort@ukzn.ac.za Tel: +27 (0) 33 260 6032

DNA from blood

Dear EvolDir members,

I have one question to submit to the group:

One proposes us to study DNA polymorphisms in an Ameridian population. Nevertheless, the sample is composed of glycerolized red cells. So do you think it is possible to rescue DNA from them, that for example had been adsorbed in the erythrocytes?

Your thoughts and opinions about this would be very helpful and highly appreciated. Thanks! Sincerely,

Stéphane MAZIERES

maziere@cict.fr

ESF PopGenet funding

Information on the new ESF Programme ConGen (Integrating Population genetics and conservation biology: merging theoretical, experimental and applied approaches) is now available at <http://www.esf.org/-congen>. The scope of this ESF Programme is to activate a multidisciplinary European network of scientists working on conservation genetics from different perspectives and at different levels: (i) experimental population genetics, (ii) theoretical and computational population genetics, and (iii) practical conservation genetics of captive and natural populations.

Congen announces a Call for Workshops and for Applications for Short Visit and Exchange Grants, deadline 15 March 2005:

(1) ConGen invites proposals from potential organisers of workshops to be held in 2005 on topics with a clear connection to the Programme. Priority will be given to workshops taking place in countries that financially support the Programme (Austria, Belgium, Croatia, Czech Republic, Denmark, Finland, Hungary, the Netherlands, Norway, Spain, Sweden and Turkey).

(2) ConGen is offering funding for a number of Short Visits (up to 15 days) and Exchange Grants (from 15 days to 6 months) related to the scientific objectives of the Programme. Priority will be given to applicants who come from or intend to visit countries that financially support the programme (Austria, Belgium, Croatia, Czech Republic, Denmark, Finland, Hungary, Netherlands, Norway, Spain, Sweden and Turkey).

Further information and access to the online application forms at the above address.

If you wish to be included in the ConGen email mailing list to receive regular updates on Programme activities, please send an email to jgoetz@esf.org.

For inquiries contact:

Mrs. Joanne Goetz (ESF office; Email: jgoetz@esf.org)

Kuke Bijlsma (chair; Email: r.bijlsma@rug.nl)

Volker Loeschke (co-chair; email: volker.loeschke@biology.au.dk)

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r.bijlsma@rug.nl <http://www.rug.nl/biologie/evogen>

====ESF programme ConGen now calls for Workshop Proposals

and Travel Grant Applications. Deadlines March 15, see <http://www.esf.org/congen>

====

r.bijlsma@rug.nl

Ernst Mayr passing

Ernst Mayr, perhaps the most influential evolutionist in the world during the 20th century, died on Thursday, February 3, 2005. He was well into his 100th year, enjoying good health until near the end. In hand were several more manuscripts that he would have published had he lived longer.

Mayr's influence was wide and deep. His two major works on evolution and systematics (Mayr 1942, 1963) are still read today. He was a constant innovator of systematic nomenclature (Mayr 1978). Mayr's books on the history of biology (Mayr and Provine, 1980, Mayr 1982), and on the philosophy of biology (Mayr 1988) had a major influence on both fields. Between Mayr and Richard C. Lewontin, Harvard's Museum of Comparative Zoology became the center of training for young historians and philosophers of biology.

Mayr was a forceful writer, and never hesitated to challenge his colleagues. Naturally, he had many detractors, whom he relished. His ideas endured much criticism from me, but he never wavered as a friend and advisor. The worst thing, he claimed, was being ignored. After

roundly criticizing the contributions of population genetics to evolutionary biology (Mayr 1959), Mayr later nominated Sewall Wright for the Balzan Prize, and attended the award ceremony in Italy when Wright won the prize. When Theodosius Dobzhansky published his *Genetics and the Origin of Species* in 1937, Mayr pointed out to him with glee that the figure of a cell division on the spine of the book had the chromosomes backward (Dobzhansky was an accomplished cytologist, and had not noticed).

Finally, no notice of his death has mentioned his prodigious production of correspondence over his lifetime. He answered nearly every letter that reached him, and initiated much correspondence. His influence through correspondence will have to be evaluated in the future and I predict it will be immense.

Best wishes to all on Evoldir, Will Provine

Mayr 1942. *Systematics and Origin of Species*. New York: Columbia University Press.

Mayr, 1959. Where are We? *Cold Spring Harbor Symposia of Quantitative Biology* 24, 1-14.

Mayr 1963. *Animal Species and Evolution*. Cambridge: Harvard University Press.

Mayr 1978. *Origin and History of Some Terms in Systematic and Evolutionary Biology*. *Systematic Zoology* 27, 83-88.

Mayr and Provine, eds. 1980. *The Evolutionary Synthesis*. Cambridge: Harvard University Press.

Mayr 1982. *The Growth of Biological Thought: Diversity, Evolution, and Inheritance*. Cambridge: Harvard University Press.

Mayr 1988. *Toward a New Philosophy of Biology: Observations of an Evolutionist*. Cambridge: Harvard University Press.

William Provine <wbp2@cornell.edu>

ErnstMayrAward SystBiol 2

ERNST MAYR AWARD IN SYSTEMATIC BIOLOGY

General Information. The Ernst Mayr Award is given to the presenter of the outstanding student paper in the field of systematics at the annual meetings of the Society of Systematic Biologists, as judged by the Ernst Mayr Award Committee. The award consists of

\$1000.00 and a set of available back issues of the journal.

Who is Eligible. Members of the Society who are students or have completed their Ph.D. within the last 15 months are eligible. Students wishing to participate should register and submit titles for the SSB Meeting in Fairbanks, Alaska (<http://www.evolution05.uaf.edu/>), and notify the current awards chair (Kelly Zamudio, krz2@cornell.edu) of your interest. Please include in your e-mail, your name and complete contact information, and a 400-word abstract of your talk (in the body of your e-mail text). Based on the submitted abstracts, the Mayr Awards committee (appointed by the Awards Chair) will select the best 15 for inclusion in the actual competition at the meetings, which will be held at a single venue in a separate session. Deadline for abstract submission is March 31, 2005, (same deadline for title submission for the Alaska meeting). Previous winners are not eligible.

Judging. Papers will be judged on creativity, quality, excellence of research, and quality of presentation. Abstracts should clearly indicate methods used, the relevance to systematics and the conclusions. Presentations focusing on other areas of biology (ecology, behavior, genetics, populations or molecular biology, etc.) that lack a strong systematics emphasis are not eligible.

Co-Authors. The paper may be co-authored. It is understood that the ideas, data and conclusions presented are primarily and substantially the work of the student presenting the paper and the intention is that person will be senior author on the published version of the paper.

Notification of Winner. The winner of the award will be announced during the banquet at the annual meetings, and an announcement will be published in *Systematic Biology*.

For details on this and other SSB Student and Researcher Awards please visit the SSB website: <http://-systbiol.org/> -

Kelly R. Zamudio Associate Professor Faculty Curator of Herpetology Dept. of Ecology and Evolutionary Biology E209 Corson Hall Cornell University Ithaca NY - 14853-2701

phone: (607) 254 4212 FAX: (607) 255 8088

<http://www.eeb.cornell.edu/zamudio/KZhome.html>
krz2@cornell.edu krz2@cornell.edu

Formalin DNA

Dear evoldir members, I would like to submit two questions to the group: (1) We are looking for a contact person in China, who could help us to obtain "Pseudorasbora parva" specimens from the Amur (and eventually other chinese rivers) for genetical purposes. (2) I am also interested to hear about (working) protocols for DNA extraction from formalized tissue. We obtained some samples from freshwater fish (caught about 4 months ago) that are fixed in formaline and afterwards have been put in ethanol. Is there any chance to get genetical information from these samples?? Does someone has experience with that? Kind regards, Dieter

– Dieter Anseeuw Katholieke Universiteit Leuven
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+32.(0)56.24.69.99 <http://www.kulak.ac.be/~danseeuw> Dieter.Anseeuw@kulak.ac.be

FrequencyData Fst

Dear colleagues,

I would like to perform Fst analysis as a genetic distance measure between populations but I have only the allele frequency data of 6 microsatellite loci, I also have differences in sample size for each locus. Does anybody know about a program able to analyze this kind of data?

Thanks for your help,

Pilar

pdelarua@um.es

Gambusia samples

Hello, I would be grateful if anyone would be able to

provide me with DNA or fin tissue/specimen (preferably in 95% ethanol) of both *Gambusia affinis* and *G. holbrooki* from natural localities (i.e USA mainly), the best sample should be around 30 specimens. If you know of anyone that might be able to help, I would also appreciate your help. Please contact me to the address given below. Thank you very much for your help!
Patrick

Patrick BERREBI UMR 5119 "Ecosystèmes Lagunaires" Equipe EFEP (Écologie Fonctionnelle et Évolution des Poissons) Université Montpellier II CC 093. Place E. Bataillon 34095 Montpellier Cedex 5 (France)

Tel. France 04 6714 3732 - International 33 4 6714 3732 Fax. France 04 6714 3719 - International 33 4 6714 3719 <<http://www.univ-montp2.fr/serveurs/-ecolog.html>> berrebi@univ-montp2.fr

Glycoside Hydrolases

Dear all

I am a PhD student and I've begun working with proteins, mainly glycoside hydrolases. Well, I've been trying to get all sequences available on computer data banks, but the tools for searching are not so efficient. So, does anybody know a tool I could use so I could type, for example: glycoside hydrolases and get all the sequences; or if I would type glycoside hydrolases family 5, I would get all sequences from family 5 not along with other sequences that contains in their names the number 5 or the word family. I am just not being able to find a constrain for the search.

It would be nice to receive some clues! Thanks
Emanuelle Corbi Correa yaraly@ig.com.br Brazil

Individual genetic distances

Hi there, I'm currently trying to finish my master's thesis and I've run into a problem with my analysis. I have microsatellite data for 9 loci for a single population that contains 1) bisexual species and 2) related unisexual hybrids. I want to generate a genetic distance matrix at

an individual level for my multi-locus genotype data, that will allow me to compare graphically the genetic relatedness between the hybrids and sympatric bisexuals. However, I can't seem to find a program that will allow me to generate a genetic distance matrix for genotype data at an individual level (as compared to a sub-population level through allele frequencies). I've hit a wall here and so if anyone can help me figure out how to do this analysis, I'd be super appreciative. Thanks so much in advance! Cadhla

Cadhla Ramsden M.Sc Candidate Department of Integrative Biology University of Guelph N1G 2W1 cramsden@uoguelph.ca

Kansas Evolution Hearings

Dear Colleagues,

You may be receiving calls or e-mails from the Kansas Department of Education offering you a free, all expense paid trip to Kansas to testify in hearings comparing evolution and "intelligent design". Though that is doubtless a terrific draw for any of us, especially in March, I would encourage you to please consider the views of the local pro-science group, Kansas Citizens for Science (www.kcfs.org). KCFS has been closely involved in this battle from the beginning and has been tracking the Board of Education's shifting attempts to have public hearings giving equal time to intelligent design and evolution.

KCFS expresses the view that the event to which you are being invited is a "Kangaroo Court", with science (and evolution) on trial, and that participation by members of the science and education communities will only hurt the cause of science education in Kansas.

Please read their views, posted here: <http://www.kcfs.org/standards05/Press.release.3-3-05.html>

The kernel of their position is that the hearings are a sham (not an opportunity to "defend science") that have been organized for political purposes. KCFS writes:

"KCFS asserts that the proposed hearings by the board committee not be held. First, the minority report (reason for the hearings) has received peer-review and found to be lacking. Despite opportunities to do so, Dr. Bill Harris, primary author of the minority report has refused to answer these challenges to his scientific credibility. We don't need additional comment when current

comment has not been answered. Second, Dr. John Marburger, White House science advisor has made it clear that the White House, the administrative branch of our government, considers evolution to be the cornerstone of modern biology and rejects ID as a science theory. Obviously he has failed to grasp the proposed definition in the Kansas minority report. Third, the hearings are a sham as we all know that Connie Morris and Kathy Martin ran for office on anti-evolution platforms. Steve Abrams introduced the creationist sub-standards which were approved in 1999. These are the three individuals who will act as the board committee judge and jury of the scientific credibility of evolution. Fourth, it is unclear whether these proposed hearings are to inform the board on matters of science, or inform the public at large. Either way, the hearings are a sham."

The KCFS has expressed its views in resolution form, at <http://www.kcfs.org/standards05/-KCFS.resolution.html> The key provision is their concern that "The science community should not put itself in the position of participating in a rigged hearing where non-scientists will appear to sit in judgment and find science lacking. Science should not give the anti-evolution members of the board the veneer of respectability when they take their predictable action. Let the board take responsibility for its actions without dignifying those actions with the appearance of academic rigor."

If you have any questions, feel free to get back to me, or to one of the KCfS members such as Jack Krebs, jkrebs@sunflower.com

More info on Kansas is on the NCSE web site, of course, at <http://www.ncseweb.org/pressroom.asp?state=KS> If you have accidentally accepted an invitation, kindly reconsider.

Reed A. Cartwright Lab Phone: (706) 542-1448 Doctoral Student Dept Fax: (706) 542-3910 Cell: (706) 248-4259 University of Georgia <http://www.dererumnatura.us/> Department of Genetics <http://scit.us/> C232 Life Sciences Bldg <http://www.pandasthumb.org/> Athens, GA 30602-7223 <http://www.georgiascience.org/> Cuiusvis hominis est errare, nullius nisi insipientis in errore perserverare. – Cicero

MHC differentiation

Dear people,

We try to analyse population differentiation using genomic copies of the MHC (Major Histocompatibility Complex). Because there are many duplicated genes in our species (guppies), we cannot assign alleles to loci. Therefore, Fst and genetic distance measures (Dm and Ds) seem inappropriate.

Are there established methods to analyse these data?

Thanks in advance!

Domino Joyce and Cock van Oosterhout

email: c.van-oosterhout@hull.ac.uk email:
d.joyce@hull.ac.uk

– Dr. Cock van Oosterhout University of Hull
Hull HU6 7RX, UK Tel.: +44(0)1482 465505
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465458 <http://www.microchecker.hull.ac.uk> C.Van-
Oosterhout@hull.ac.uk

Microsat electrophoresis

Dear Colleagues, I intend to analyse fish samples using microsatellite silver staining method. It is very appreciate if you give advices to buy good electrophoresis cell (vertical box). Best wishes Binh Thai

Binh Thai PhD Research Student School of Ecology and Environment Deakin University P.O. Box 423 Warrnambool, Victoria, 3280 AUSTRALIA Phone: 03 5563 3569, 0431 745 873 Fax: 03 5563 3462 e-mail: tbt@deakin.edu.au

Binh Thai <tbt@deakin.edu.au>

Microsat electrophoresis answers

Dear Colleagues, I posted my question about selecting Microsatellite electrophoresis few weeks ago. Thank you very for your suggestions.

We silver stain microsatellite loci, and have been doing this for a number of years. The gel rigs we use are from Biorad, we have two sizes of gel but the most user friendly are the short fat gels (38 x 30 cm) onto which you can load 96 samples plus controls. The gels are

very easy to use. The power packs are also Biorad, but this is probably because we got a good deal on them. Then we use pre-measured silver staining reagents from Promega, which probably isn't the cheapest way of doing things but having everything pre-measured is a huge time saver. Hope this helps Jo

I used a Hoefer SE660 vertical gel for analysing human derived tetranucleotide loci in baboons (see <http://www.hoeferinc.com/product.asp?ProdID=32>). This system allows you to run four gels simultaneously and up to 100 lanes. I got very clean results using 1mm thick 8% non-denaturing acrylamide (29:1 acrylamide:bisacrylamide) gels which were then stained with silver. Ive attached a picture as an example the alleles closest together differ by 1 repeat unit. I also tried to look at dinucleotide loci (this time from gazelles), but I found these more difficult to resolve because the alleles were closer together and there were more stutter bands than with the tetranucleotide loci. An alternative might be to consider a Spreadex gel. These are preformed gels and run on a horizontal system and can be stained with SYBR green. Never used them myself but other people say they are very good. They are probably significantly more expensive than acrylamide. The Elchrom site is found at <http://www.elchrom.com/public/index.php?article=144>. Good luck and I hope that this helps. Please feel free to contact me again if you need any more info. Cheers Rob.

During my phd I used big slab gels (the old sequencing rigs) I would attach the gel to one of the plates using some sigma product which i could find in an old lab note book if you need it. Anyways the protocol for this method at least the actual silver staining part is in Morgan et al 2003 J heredity which is attached. This protocol worked very well for my needs, but given the cheapness of dye labeled primers I might do a cost benefit analysis before you spend tons of money on silver staining chemicals. I guess that all hinges on you having access to a sequencer or gel scanner. Hope this helps. Ted

I am working with microsatellites in Mexico on seagrasses. I am using the electrophoresis set of Biorad (Sequigen GT) it is a bit expensive, but it works fine. I am using the 38 x 50 cm gels, and load them 2 times. this gives me (if lucky), results of 120 samples. To estimate size I use 10 bp ladder of invirtogen!

Hope this will help.

Yours,

Kor-jent

Hi I use the OWL Scientific vertical rigs. The S3S model. 18002425560. When you order it you get two

sets of plates. I use these rigs more than BWR because the buffer tends to leak from top to bottom on those. If you are using silver staining they plates work pretty well with the promega silver sequence staining reagents... I never seem to have much trouble with it. Lee Dear Binh, I'm using Biorad Sequigen. It's just wonderful :-). It uses large amount of buffer but thanks to it there are almost no smiles on gel. In my opinion the best set is 30x38 with 0,4mm spacers (thinner gels have problems with reaching the desired temperature in prerun). If you're going to analyse large sets of samples I advise you to buy 100 Shark Tooth Comb. I'm silver staining on longer plate as it's easier to manipulate - don't forget to change the picture form the camera as the samples are in reverse order. You could also load it in reverse order :) Good luck! Maciek

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Binh Thai <tbt@deakin.edu.au>

Phenotypes Genes

Dear All, I have a question about gene variation in relationship to phenotype diversity that needs your help to clarify:

If two species are different in phenotype (say fruit color red vs. blue) and they hybridize in nature. The hybrids show differences in fruit color phenotypes (say some have red fruits, some have blue and some have a mosaic of red and blue). For a gene contributes to the color difference, do we expect to see an association or correlation between the fruit phenotypes and gene sequences in the hybrid populations? Whereas no such correlations should be observed for a gene that has nothing to do with the fruit color? Is this correct?

If you observe a correlation between the phenotypes and the sequences of a gene regulates the pathways of the pigments synthesis, could you infer that difference in the gene is potentially linked to the difference in the phenotypes?

Your thoughts and opinions about this would be very helpful and highly appreciated. Thanks! Sincerely, Jenny Xiang

—

Jenny Xiang <jenny_xiang@ncsu.edu>

Phenotypes Genes answers

Dear All, Some colleagues asked me post the responses of my question. Here they are. Different messages are separated by a line of symbols. Thanks to all who responded. -Cheers! -Jenny

#####

I think the key idea you are struggling towards is that of QTLs - quantitative trait loci.

You can detect such loci by following the co-inheritance of DNA markers and traits such as colour in crosses. You might even detect the loci that are involved in the trait with much work.

You could do a literature with the term qtl in it.

For example on the scirus.com site. I had a first shot at it for you. See here

<http://www.scirus.com/srsapp/search?q=qtl+cross++lines+colour&ds=jnl&g=s&t=al> l

\$\$\$\$\$

This is regarding your query on the evolution directory. This is an interesting question! One would expect association (linkage disequilibrium, LD) between the gene locus and the trait if the gene indeed controls the trait. If the genetic architecture of the trait is not too complex, this association might be detectable in natural hybrid populations. However, there are other factors as well that can cause LD in hybrid populations, and you would have to control for these. E.g.: (1) In both experimental and natural hybrid populations, the crossing of two species induces LD between many or all loci in the genome, and these associations are expected to decay in subsequent generations. (2) Persistent genetic structure (population subdivision) in the hybrid population also causes LD across the genome. (3) Selection that favors particular gene combinations (epistatic selection) can do the same. So one would have to control very carefully for these factors. If they are all taken into account, it may be possible to interpret associations between genes and traits in natural hybrid populations.

There is some recent literature on this topic, please let me know if you need some references. I also worked on this topic myself a little in the recent past, and I have a project running that addresses these questions in tree

hybrid zones.

#####

You'd need to be extremely cautious about making that assumption. If the hybrids are variable in their status (e.g. some F1s, some B1 to either parental species, some advanced-generation intercrosses and introgressions), one would expect to find associations between fruit color and almost any gene in the genome. For example, in this circumstance, red-fruited hybrids would on average carry a higher proportion of the red-fruited species genome than blue-fruited hybrids, so red fruit would show an association with almost any allele that is at substantially higher frequency in the red-fruited species than in the blue-fruited species. Such associations would be strong evidence for linkage only if (a) all the hybrids were of the same generation (e.g. F2); or (b) the population were a hybrid swarm many generations old that has undergone random mating among the hybrids and no mating with the parental species. In (a) you could still get association due to linkage with a causative gene on the same chromosome, similar to linkage mapping. In (b) the region of linkage disequilibrium would be much smaller but would still probably encompass more than a single gene. Thus, even in these situations, I'd only treat allele-phenotype associations as evidence for causation if the gene were a functional candidate.

If the status of the hybrids is variable or unknown, it may still be possible to test associations by controlling for ancestry; e.g. using Pritchard's STRUCTURE program, but this would require scoring a genome-wide set of markers to provide data on ancestry. Anyway, good luck!!

\$\$\$\$\$

Before making any inferences with regards the role of your candidate "red vs blue" gene a degree of verification needs to be carried out. If you did find sequence polymorphisms that cosegregate with fruit colour then this is an indication that the gene controls the phenotype, however could be due to genetic linkage. Tests can be carried out in a number of ways - QTL mapping will show if the gene/trait are linked, however isn't concrete proof. You could grow up an F2 of, say, 10000 plants and (if single gene control) genotype the 2500 reds and 2500 blues to check the sequence polymorphism cosegregates (ie bulk DNA from 50 reds, pcr and cut with an enzyme that cuts the 'red' gene. anything that isn't cut is a 'blue gene' in a red plant. And the same for blue plants/red genes. Ultimately introducing the blue gene into a red plant and vice versa is the acid test. An interesting paper showing strong correlation between DNA polymorphism and phenotypic variation

is Thornsberry et al (2001) Nature genetics 28:286 Also, it seems increasingly that developmental processes are controlled by transcription factors and these TFs may not show sequence polymorphism (eg

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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>

Relation s migration answers

Many thanks to all those who responded to my question concerning the the relationship between 's' and rate of migration of an allele. The original question, plus a list of responses is given below:

My cursory conclusion were (remembering that this was just to write a paragraph in a review) were

Rate of migration (over geographic distance) can get confused with migration (proportional exchange between subpopulations), so its probably best to use 'wave of advance' or 'rate of spread' for the former. Its a bit clumsy, and probably not the way non-specialist would use it, but it is at least unambiguous.

There is nothing technically wrong with Fishers' equation or approach.

These papers use simulation to look at rate of spread in sub-populations: Slatkin, M. (1976). The rate of spread of an advantageous allele in a subdivided population. In "Population genetics and ecology" (S. Karlin and E. Nevo, Eds.), pp. 767-780, Academic Press, London. Slatkin, M. and Charlesworth, D. (1978). The spatial distribution of transient alleles in a subdivided population: a simulation study. Genetics 89: 793-810.

An excellent, accessible review is Morjan, C. L. and Rieseberg, L. H. (2004). How species evolve collectively: implications of gene flow and selection for the spread of advantageous alleles. Molecular Ecology 13: 1341-1356.

Anyone more interested should look at the models of ecological invasion as analogous processes

*****original question*****

I have two questions concerning the relationship between the selective advantage of an allele and the rate at which it migrates over geographic distance [for those

of you interested in the background: we can model or measure the selective advantage associated with alleles conferring drug resistance in malaria, so have estimates of 's', but the alleles appear to occur very rarely and have subsequently migrated around the world].

Intuitively there must be a positive relationship but has it been quantified? On the basis that Fisher/Haldane/Wright sewed up most of population genetics in the 1920s to 1940s I tried there and was not disappointed:

Fisher, R. A. (1937). The wave of advance of advantageous genes. *Ann.Eugen* 7: 355-369.

who found that rate of advance was proportional to the square root of 's'. This paper appears to be cited only rarely (at least in this context; it is used a lot in chemistry as a basis of diffusion of reactions) so my first question is whether it was flawed, overlooked, or was simply superseded by later work?

My second question pertains to island and stepping stone models: has anyone investigated the relationship between 's' and migration rate from these models? Apologies if they have, but I haven't located it because most of the work looks at more complex questions like maintenance of clines, genetic variability etc.

I realise I could probably do it myself using stepping models but there is the (non-negligible) risk I would get it wrong, it is unnecessary if it has been done already, but most importantly I just need to cite the result in a review and don't want to have to prove it in an appendix.

As a technical point, malaria is haploid so we need not worry about dominance.

Thanks to those who can comment.

Regards,

Ian.

*****Responses from Evoldir (in order of receipt)

Dear Ian,

I am not sure if I am exactly replying to your question, but you could probably get some idea from two of our publications if you look them carefully.

1. Vogl et al. 2003 *Genetics* 165: 1385-1395 2. Das et al. 2004 *Genetics* 168: 1975-1985 3. Baines et al. 2004 *Genetics* 168: 1987-1998.

In Baines et al. we have dealt with the migration of the selected allele with an experimental setup and also found evidence of cline of haplotypes across latitudinal transects.

Best wishes,

Aparup

Dr. Aparup Das, Faculty Fellow Population Genomics and Evolution Laboratory Department of Biology Poornaprajna Institute of Scientific Research Post Box No. 18, Devanahalli BANGALORE - 562 110, INDIA Tel: +91-80-27647333 (O), 27647555 (lab) Fax: +91-80-27647444 E-mail: aparup@poornaprajna.org; adas@uni-muenchen.de Homepage: <http://www.poornaprajna.org/aparup.htm> Ian Hastings

Fisher's Wave of Advance work has not been ignored. It has frequently been revisited by mathematicians, who love to ring changes on it.

It is mentioned (and a simplified derivation given) in my course notes which are available on the web: <http://evolution.gs.washington.edu/pgbook/pgbook.html> (see pages 158-159).

It is also covered, I think, in Warren Ewens's recent book (2003). I think I cited it in my 1976 Annual Review of Genetics review of migration work.

I wouldn't call over 800 citations in the literature being ignored or overlooked.

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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>

Removing branch lengths

Dear evolutionists,

Does anybody know any program that can remove the branch length values from a tree file? I have hundreds of trees that need to be reformatted for other analyses.

Thank you very much for your considerations.

Tuo

Tuo Shi Environmental Biophysics and Molecular Ecology Institute of Marine and Coastal Sciences Rutgers University 71 Dudley Road, New Brunswick, NJ 08901 Phone: (732)-932-6555 x332 Fax: (732)-932-4083

Tuo Shi <tuoshi@imcs.marine.rutgers.edu>

SPAGeDi 1.2

Dear evoldir members,

I wish to announce the release of a new version of the program SPAGeDi available at: <http://www.ulb.ac.be/sciences/ecoevol/spagedi.html>

SPAGeDi (Spatial Pattern Analysis of Genetic Diversity) is primarily designed to characterize the spatial genetic structure of mapped individuals and/or mapped populations using genotype data of any ploidy level (assuming polysomic inheritance in case of polyploids). SPAGeDi runs on PC under Windows 9x or later versions.

It can compute various statistics describing relatedness or differentiation between individuals or populations by pairwise comparisons, and analyze how these values are related to geographical distances, 1) in a way similar to a spatial autocorrelation analysis, 2) by linear regressions (the slopes of these regressions can be used to obtain indirect estimates of gene dispersal distances parameters such as neighborhood size). SPAGeDi can also treat data without spatial information, providing global estimates of genetic differentiation and/or matrices of pairwise statistics between individuals or populations. Data from dominant markers such as AFLP or RAPD can also be treated to estimate pairwise kinship or relationship coefficients between individuals.

The statistics computed include F_{st} , R_{st} , D_s (Nei's standard genetic distance), and $(\Delta\mu)^2$ (Goldstein and Pollok 1997) for analyses at the population level and, for analyses at the individual level, pairwise kinship, relatedness and fraternity coefficients (with different estimators for each) as well as Rousset's distance between individuals and a kinship analogue based on allele size. Jackknife over loci gives approximate standard errors. Permutations of locations, individuals or genes provide ad hoc tests of spatial structure, population differentiation or individual inbreeding, respectively. A new allele size permutation test also allows to check whether microsatellite allele sizes carry a relevant information about genetic structure.

In addition, the actual variance of the statistics can be estimated following the method of Ritland (2000), providing a measure necessary for marker-based inference of the heritability or Q_{st} of quantitative traits.

What's new in SPAGeDi ver 1.2?

Compared to the previous version 1.1, there are several major improvements in this version :

1) SPAGeDi 1.2 proposes new statistics (e.g. N_{st}) to characterize differentiation among populations using ordered alleles, i.e. considering the phylogenetic distance between alleles (or haplotypes), as proposed by Pons and Petit (Genetics, 1996). Specific permutation tests permit to assess whether the allele phylogeny contributes to the differentiation pattern, testing for the occurrence of phylogeographic patterns.

2) SPAGeDi 1.2 proposes an estimator of the mean kinship coefficient between populations (G_{ij}) closely related to the autocorrelation of population allele frequencies (Barbujani 1987, Genetics).

3) SPAGeDi 1.2 proposes a new estimator of the relationship coefficient between individuals (Li et al. 1993, Human Heredity).

4) SPAGeDi 1.2 can consider specific reference allele frequencies (to specify in a file) to compute relatedness coefficients between individuals.

5) SPAGeDi 1.2 includes an iterative procedure to estimate gene dispersal parameters from isolation-by-distance patterns by regressing pairwise kinship coefficients on distance over a restricted distance range (this requires an estimate of the effective population density), following Vekemans and Hardy (2004, Mol Ecol).

6) SPAGeDi 1.2 provides better error messages and the most common errors when preparing data files are systematically listed in a file called error.txt. Empty lines in data files are now allowed. Problems when entering instructions with the keyboard under Windows 2000 and latter versions have been solved.

Reference: Hardy, O. J. and X. Vekemans (2002). SPAGeDi : a versatile computer program to analyse spatial genetic structure at the individual or population levels. *Molecular Ecology Notes* 2: 618-620.

Olivier Hardy

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<http://www.ulb.ac.be/sciences/ecoevol/index.html>

Olivier Hardy <ohardy@ulb.ac.be>

SSB ForeignTravelAwards

SSB Travel Award for Foreign Scholars

SSB is pleased to announce the availability of awards for scholars from developing countries to attend workshops and courses in systematics, or to visit a molecular lab for training. The emphasis of this program is the transfer of knowledge to the scholar's home country. This means that the student should currently be in their home country, or have definite plans to return in the near future. Courses such as the Molecular Evolution Workshop at Woods Hole and the applied Systematics Course at Bodega Bay are examples of courses that are appropriate for this funding, in addition to other equivalent opportunities. Support for attending a course will be contingent on admission to the course through the normal admissions process.

A complete application includes: 1) a justification of the course or planned visit, and a description of how this will provide appropriate training (1 page max). 2) a letter detailing how the knowledge acquired will be transferred to the country of the scholar's origin (1 page max) 3) applicant's CV

The entire application should be no more than two pages long, not including the curriculum vitae. Application deadline is March 31 of each year.

Requests should be sent by e-mail to Dr. Kelly R. Zamudio, SSB Award Committee Chair, Cornell University, at krz2@cornell.edu. If possible, applicants are encouraged to use pdf format for all documents.

For details on this and other SSB Student and Researcher Awards please visit the SSB website: <http://systbiol.org/> krz2@cornell.edu krz2@cornell.edu

SSB Graduate Student Awards

SSB Graduate Student Research Awards in Systematic Biology

The Society of Systematic Biologists (SSB) announces its annual Graduate Student Research Award competition. The purpose of these awards is to assist students in the initiation (first two years) of their systematics projects and in the collection of preliminary data needed by them to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Applicants may be from any country, but must be members of SSB, and are ad-

vised to join the Society as soon as possible to facilitate their applications (see <http://systbiol.org/>). Previous awardees may not re-apply, but other previous applicants are encouraged to re-apply. Awards will range between \$1,000 and \$2000 and up to six awards will be made.

All applications materials this year must be in electronic format. Applicants and their recommenders are strongly encouraged to use pdf format, rather than Word or some other application, to minimize difficulty transferring files. We strongly recommend that applicants send all materials (except letters of reference) in a single pdf file; for this you will need to use functions in Adobe Acrobat or similar application. Letters of recommendation should be sent by the referees in pdf format or in the text of an e-mail; please include the full name of applicant in letters of recommendation.

Applicants must submit 1) a curriculum vitae (one page) 2) brief research proposal including objectives, methods, significance, and schedule (max. three single-spaced pages including literature cited and any figures and tables) 3) budget and budget justification (1 page) 4) and arrange for two letters of recommendation; one letter must be from the student's current graduate advisor.

The research proposal must clearly state the current stage of the proposed research and the current year and status of the student. Please include e-mail contacts for the applicant in the application itself. Both Masters and Ph.D. students are eligible. Systematics is interpreted broadly to include questions below and above the species level, molecular and morphological approaches, and issues of pattern and process. Funding is not limited to any particular aspect of research, but rather is available for field, museum/herbarium, and/or laboratory work.

Please email all application materials and queries to: Dr. Kelly Zamudio krz2@cornell.edu Cornell University Department of Ecology & Evolutionary Biology

To be considered for this year's award, application materials, including letters of recommendation, must be received electronically no later than March 31, 2005.

For details on this and other SSB Student and Researcher Awards please visit the SSB website: <http://systbiol.org/> -

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SSB MiniPEET awards

SSB Mini-PEET Award

SSB is pleased to announce the availability of four awards to enhance the transfer of taxonomic expertise, modeled after the highly successful PEET program at NSF. The primary purpose is to pass on taxonomic expertise in general, therefore, unlike the NSF PEET program, awards will not be limited to taxonomically understudied taxa.

The awards are designed to allow SSB members (students, post-docs, and faculty) to spend a summer or semester apprenticed to an expert in a particular taxonomic group. This could include either a trip to the taxonomists' laboratory, or pay for the taxonomist to visit the applicants' laboratory for a period of time. Applicants should NOT be members of a laboratory group currently supported by an NSF PEET award. Requests for support may be in any amount up to \$4,000.

A complete application includes:

- 1) a brief description of the project
- 2) justification of the importance of the taxon, and the appropriateness of the collaborating taxonomist
- 3) an itemized budget
- 4) a CV

The entire application should be no more than two pages long, not including the curriculum vitae. Application deadline is March 31 of each year.

Requests should be sent by e-mail to Dr. Kelly R. Zamudio, SSB Award Committee Chair, Cornell University, at krz2@cornell.edu. Applicants are encouraged to use pdf format for all documents.

For details on this and other SSB Student and Researcher Awards please visit the SSB website: <http://systbiol.org/> krz2@cornell.edu krz2@cornell.edu

SSCP analysis

Dear colleagues:

I am thinking about buying some equipment from

ElChrom, in order to make some SSCPs and microsatellites analysis. The equipment is the Sea2000 Electrophoresis apparatus (which basically allows to keep the temperature of the running gel constant) which is combination with the ready-to-use- gels from the same company will make it possible to analyse either RFLPs, microsatellites and SSCPs. I would like to ask first if anyone of you has this kind of equipment. If yes, do you recommend it? Are you happy with your results?

Even if you do not have this equipment, but are working with SSCPs, could you explain me what kind of methods you are using. I would like to find a more efficient (not so time consuming and more economic) way of doing it (without the need of using the polyacrylamide gels!!!).

Thanks for your help, Andreia
andreiamirald@yahoo.com

Sequence navigator OS10

Bonjour,

We just had the chance to receive a new Apple computer G5 ... that take advantage of Mac OS 10.3.8 ! They are also supposed to have a folder using the older OS9, that we also tried to use. Unfortunately Sequence Navigator, an important software for us, is not working well anymore. The software looks like normal when it is "open" but the modification done on the sequences became ... "surprising" ... you are never sure on which base you interfere for exemple. The software allows to compare multiple sequences, to compare them to a homebuild database (convenient for identification), seeing simultaneously the electrophoregrams (ie result of the sequencing machine), and even to edit and modify the sequences. Perkin Elmer sold Sequence Navigator with the sequencing machine, but doesn't develop it any more as far as we know. Does anybody have a trick to use Sequence Navigator on our new fancy Mac's OS10? Does anyone know an other software doing the same things so conveniently?

Thanks

vvincen@pasteur.fr

Sequence navigator OS10 answers

here are the answers of kind Evoldir members who helped to identify valuable alternatives to Sequence Navigator

Hi,

I'm using the same G5 as you, and I solved such problem by installing the MacOS-9 Classic from the MacOS 10.3.8 installing package. Thus, when I start SeqNav up I get into a virtual OS9 and everything works Ok!

Good luck, and have a nice day,

Eric, eric.rivera-milla@uni-konstanz.de

Hi there, we used to use sequence navigator when analysing data for MLST. As you have found, it has been rather left by the wayside. Nowadays we use the STARS program, which is a free staden interface developed for analysing polymorphisms within the same stretch of DNA (available from <http://www.molbiol.ox.ac.uk/~paediat/stars/>). It includes the ability to interrogate a database of alleles online and assign them to strains. I'm not sure if this would be useful for what you are doing (presumably with mycobacteria, yes?). You would need to work with it through an Xwindow on your new mac. Also install STADEN etc.

Alternatively, the new version of MEGA (MEGA3 megasoftware.net) has the ability to analyse electropherograms, align sequences etc. It's not ideal for these purposes but it might be better than worrying about 'surprising' sequence modifications. You would have to use a windows emulator on your mac, I'm afraid.

Unfortunately, these are both either UNIX (STARS) or PC based (MEGA). But they are both free.

I hope this helps. If anyone does write in with a way to extend the use of sequence navigator, please let me know!

Best

Bill

Dr. W. P. Hanage, Imperial College Faculty of Medicine, Department of Infectious Disease Epidemiology, St Mary's Hospital,

saw your post on EvolDir re. Sequence Navigator and OSX. I suggest to check out FinchTV by Geospiza

(www.geospiza.com/finchtv) which is great for viewing traces, and has the advantage to also view the raw data and do BLAST searches directly out of the program. 4Peaks (<http://www.mekentosj.com/4peaks/>) is also great for viewing and editing (more similar to Sequence Navigator I think).

best of all: both are free!

if you need a good OSX program for sequence editing and contig assembly, I suggest to check out Codon Code Aligner (www.codoncode.com), which is a great program (we are using it happily since more than a year) and has a very good licensing scheme, much more flexible than Sequencher, less than half the price (and no dongles), and very responsive support if you run into any trouble! Would be great if you could post all replies back on EvolDir.

Good luck

best wishes

Gert

Gert Wörheide Junior Professor for Geobiology Geoscience Centre Göttingen Dept. of Geobiology Goldschmidtstr.3 37077 Göttingen Germany

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– Veronique Vincent Centre National de Reference des Mycobacteries

Laboratoire de Reference des Mycobacteries Institut Pasteur 25 rue du Docteur Roux 75015 Paris Tel: 33 (0)1 45 68 83 60 FAX: 33 (0)1 40 61 31 18 vvincent@pasteur.fr

vvincent@pasteur.fr

Software COLONISE

Dear evoldir members,

We wish to introduce COLONISE, a user-friendly Microsoft Windows software for the study of colonization events in natural populations. It determines the composition of the newly colonized population and makes inferences about the factors that influenced individuals to establish a new population. COLONISE uses a hierarchical Bayesian model to combine multilocus genotype

data with demographic and environmental data, and a reversible jump MCMC algorithm to perform posterior density estimations. The software is written in C and C++ for the graphical user interface and is available at:

<http://www2.ujf-grenoble.fr/leca/-presentation.html#logiciels> The software integrates a tool to draw posterior density functions (histogram, running mean, traces, etc.) and to estimate parameters from them (mean, mode, variance, HPDI etc.)

The program can be cited as follows: Foll, M and OE Gaggiotti. COLONISE: a computer program to study colonisation processes in metapopulations. *Molecular Ecology Notes* (in press).

The method description can be found in: Gaggiotti, OE, SP Brooks, W. Amos and J. Harwood. 2004. Combining demographic, environmental and genetic data to test hypothesis about colonization events in metapopulations. *Molecular Ecology* 13: 811-825.

Best regards,

Oscar Gaggiotti –

Equipe Genomique des Populations et Biodiversite
Laboratoire d'Ecologie Alpine (LECA) UMR CNRS
5553 Université J. Fourier BP 53 38041 Grenoble France

Tel: 33 (0)4 76 51 41 15 Fax: 33 (0)4 76 51 42 79

Web: <http://www2.ujf-grenoble.fr/leca/membres/-WebPageOscar/Webpage.html> <http://www2.ujf-grenoble.fr/leca/projets/IMPBio/IMPBioFr.html>

Software **TreeViewX**

TreeView X is an open source program to display phylogenetic trees on Linux and Unix platforms. It can read and display NEXUS and Newick format tree files (such as those output by PAUP*, ClustalX, TREE-PUZZLE, and other programs). It has a subset of the functionality of the version of TreeView available for the Mac Classic and Windows.

Version 0.5 is the first version to use the same source code for all three major platforms (Mac OS X, Windows, and Linux). There is not much more in the way of new features compared to the previous version, apart from a few minor tweaks concerning the file open dialog, and support for saving pictures (SVG on Mac OS X, metafile on Windows).

Realistically this is likely to be the last release for a while, but I thought it worthwhile to get the program into a state where it was reasonably stable and there was a single code base. In the past I wrote the GUI for the Mac OS X version myself from scratch, but version 0.5 uses the same `wxWidgets` cross-platform library for the GUI.

Regards

Rod

–

Professor Roderic D. M. Page Editor Elect, Systematic Biology DEEB, IBLS Graham Kerr Building University of Glasgow Glasgow G12 8QP United Kingdom

Phone: +44 141 330 4778 Fax: +44 141 330 2792 email: r.page@bio.gla.ac.uk web: <http://taxonomy.zoology.gla.ac.uk/rod/rod.html> reprints: <http://taxonomy.zoology.gla.ac.uk/rod/pubs.html>

Join Systematic Biology through the Society of Systematic Biologists Website: <http://systematicbiology.org>
r.page@bio.gla.ac.uk

StanfordU HumanPopGenet Database

Other: Announcing the Human Population Genetics Database (Stanford University)

The Diversity in Human DNA Sequences Program Project Group at Stanford University is pleased to announce the public availability of the Human Population Genetics Database (HPGD). The HPGD may be accessed online at:

<http://hpgd.stanford.edu/> The HPGD is designed to provide broad views of genotype information for world populations by allowing the user to view the intersection between arbitrarily chosen populations and samples and arbitrarily chosen polymorphisms. These intersections may be viewed in a microscopic (actual allele types for particular samples) or macroscopic (allele frequencies, etc.) manner. This basic functionality is augmented by more sophisticated tools.

During the month of March 2005, we will be beta testing the public use of the HPGD, and welcome any feedback.

In addition, the classical marker frequency data from

The History And Geography Of Human Genes (Cavalli-Sforza, Menozzi & Piazza 1996) is available in curated form for direct download.

Please direct any questions or comments to Christopher Edmonds cedmonds@stanford.edu.

Thank you,

Christopher A Edmonds - cedmonds@stanford.edu Senior Application Software Developer/Research Department of Genetics, Stanford University Stanford, CA

SystBiol appendices

As part of efforts to upgrade the Society of Systematic Biologists' web site (<http://systbiol.org>) electronic appendices (such as data sets, sequence alignments, additional tables, technical appendices, etc.) for volume 53 (2004) onwards are now available from that web site. Appendices for earlier volumes are available at <http://hydrodictyon.eeb.uconn.edu/systbiol/-info/issues.html>. Eventually these too will be moved to the new site.

Regards

Rod Page

Professor Roderic D. M. Page Editor, Systematic Biology DEEB, IBLS Graham Kerr Building University of Glasgow Glasgow G12 8QP United Kingdom

Phone: +44 141 330 4778 Fax: +44 141 330 2792 email: r.page@bio.gla.ac.uk web: <http://taxonomy.zoology.gla.ac.uk/rod/rod.html> reprints: <http://taxonomy.zoology.gla.ac.uk/rod/pubs.html>

Join Systematic Biology through the Society of Systematic Biologists Website: <http://systematicbiology.org>
r.page@bio.gla.ac.uk

Tissue storage

Dear All,

I am planning to establish a long-term tissue bank (hopefully lasting decades or longer) for molecular work and am wondering about the best way to store DNA. All our samples (mainly fin clippings of fish) so far are

stored in ethanol (90-95%), but we had previously some problems with tissues that have been stored for several years at room temperature. We now try to keep the tissues at 4°C, which seems to work fine, but requires spark-proof cooling space.

What is the experience out there with ethanol sample storage? Is it necessary to keep ethanol preserved samples at 4°C? Are there alternative methods for long term storage?

Many thanks

Lorenz Hauser

Dr Lorenz Hauser Assistant Professor School of Aquatic and Fishery Sciences University of Washington 1122 NE Boat Street, Box 355020 Seattle, Washington, 98195-5020 Tel: (206) 685 3270, Fax: (206) 685 6651 <http://www.fish.washington.edu/people/hauser/>

Tissue storage answers

Re: Long term tissue storage

Dear All,

Thank you for all your responses on the issue of long term tissue storage. Interestingly, there does not seem to be a good consensus on the best storage. By far most responses favor storage in ethanol in a cooled environment (-80°C - 4°C) though, on a larger scale, these methods require spark proof cooling units which are not cheap and not always feasible given local fire regulations. Preserving ethanol tissues at low temperature may have the advantage over frozen tissue that a freezer failure would not lead to the complete loss of the collection for that reason, expensive alarm systems would also not be required. Some scientists use DMSO, which is easier to ship, but a nasty chemical. Desiccating methods seem to be increasingly used, though there seems to be little experience on conservation problems under realistic conditions. For long-term storage, many people recommend storage in liquid nitrogen this may not always be feasible in the long term, given potential loss of collections because of failure to refill containers. However, a curating service such as that offered by the Ambrose Monell Cryo Collection at the American Museum of Natural History may be the best option for most of us. Below are responses, organized by the methods they propose. I also include some useful reviews at the end of this message.

Ethanol cooled * 4 deg is much preferred unless (a) samples are in small containers, e.g. 2ml, (which fin clips would be) with screw caps (including rubber o-ring), have a low tissue to Etoh volume, and are not watery tissue (fin clips ok I reckon; tissue lumps less so). Even so I would still seal any box that they are in with tape around the lid seam and avoid warm rooms. For big tissues (e.g. whole fish, etc.), I can't really see a viable way around 4 deg storage, unless you have a robot who likes topping up and perhaps completely replacing Etoh periodically. (David Weetman, Hull, UK)

* If possible, I'd invest in a -80C freezer and store your tissues (in ethanol) there. The ethanol won't freeze but it will be very cold and your tissue definitely won't degrade. I've worked in a few labs (mostly birds, but also marine mammals and other critters) and think the ethanol/-80C combination makes the most sense (especially if your tissues are in 2ml cyrovials - or something similar - b/c you can get an awful lot of tissue in a relatively small space). (Tammy Steeves, Canterbury, NZ)

* I too have found that freezing or refrigerating ethanol preserved samples increases the longevity of the samples for DNA extraction. In the past I have simply transferred the samples into small cryotubes and kept them in a -80 freezer. (Kevin Roe, Curator of Mollusks, Delaware Museum of Natural History, USA)

* There was a poster at the Conservation Genetics Meeting in 2001 comparing different storage methods. I can't recall whose it was though. The best way to store DNA for a long time was lyophilized DNA at -80°C. We keep samples in alcohol (changed after the first day) at -80°C. You might also try -20°C, but I strongly discourage you from trusting 4°C for long term DNA preservation. (Natalia Martinkova, York, UK)

* We are keeping our collection in -80 freezers, and that seems to work out fine (specimen are preserved in 95-100% ethanol). (Katharina Dittmar de la Cruz, BYU, USA)

* I've also been storing tissues, including lots of fish, at room temp, and also in the fridge and sometimes in a -20. I would like to hear what you find out. And, I'd also like to know more about the issue of spark-proof cooling. (Sarah Cohen, SFSU, USA)

* A few years ago, I extracted DNA from invertebrates stored in 75% EtOH since the early 1980s in room temperature and I was able to amplify mtDNA without any problems, but I personally keep my EtOH-preserved samples at -18C (freezer) and, if I can, -80C is better. (Sergios-Orestis Kolokotronis, American Museum of Natural History, USA)

Ethanol at room temperature * We had insect samples (mainly honeybees) stored for 5-7 years in 95% Ethanol at room temperature - no problems. (Ute Kryger, Pretoria, SA)

* Our lab has not noticed any prob-

lem with ambient storage of salmon tissues in ethanol (many 10s of 1000s of fin, muscle, and blood samples in our archive). 10- or 15-year-old samples typically amplify just fine; however, I can't say we've worked with alcohol-preserved fin clips much older than that. Our greatest concern for the alcohol-preserved samples, based on anecdotes from our museum curator colleagues, is that the laser-printed accession numbers on the labels (inside the tubes) might eventually fall off the paper. Fortunately, we've not yet seen this in any samples going back 15 years or more. Some years ago, we thought we saw problems with some types of denaturent use in commercial ethanol. Since

— / —

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>

Typha samples

All,

I am working on a hybridization study with cattails, genus Typha. So far, it looks as if our samples are all hybrids (T.glauca). If any of you can help me obtain, some pure strain samples of Typha lattifolia and Typha angustifolia, I would greatly appreciate it.

Reply To: kwessner@usgs.gov

Cheers, Kevin Wessner kwessner@usgs.gov Johnson Controls Inc. National Wetlands Research Center/USGS 337-266-8630

Kevin Wessner <kwessner@usgs.gov>

eJournal club

Hello everyone! this is a reminder for the Co-Evol (Italian Committee of Evolutionary Biologists - www.coevol.org) on-line article discussion initiative.

A new article is posted twice a month and a discussion forum takes place at:

http://it.groups.yahoo.com/group/-CoEvol_Journal_Club/ All italian evolutionary

biologists are encouraged to join, but you don't need to be Italian to participate: everyone is welcome!

Thanks!

Dr Stefano Mariani Marine Ecology & Evolution Biosciences - Zoology University College Dublin Belfield, Dublin 4 Ireland Tel: +353.1.716.2347

stefano.mariani@ucd.ie

evolnews

NEW WEBSITE FOR EVOLUTIONARY BIOLOGISTS

We're (a bunch of grad students in EEOB at ISU) are pleased to announce that the website www.evolnews.org is up and running. This web site contains summaries of current, peer-reviewed journal articles for evolutionary biologists, arranged by topic. You can just read the page, and catch up on what is new in the whole field, or you can join the mailing list and get a TOC- as well as modify the page to display what you want to see for topics. You can also contribute stories to 20 active topic areas, or start a new topic. If you have questions, email evolnews@evolnews.org

thanks, Ryan

Ryan Adam Rapp <rrapp@iastate.edu>

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CNRS URennes ChemicalEcol

Position: Postgraduate Researcher, chemical ECOLOGY IN Plant-insect interaction

A 1-year postdoctoral position will be available from June or September 2005 at the CNRS (French National Research Center) UMR6553-ECOBIO, Department of Evolutionary Ecology, in the research group "Interaction, Speciation and Adaptation" headed by Dr. Anne ATLAN at the University of Rennes, FRANCE. The position is funded by the CNRS. The salary will be between 1500 and 1700 per month. Applicants should

have recently obtained their PhD in the field of chemical ecology. They are expected to have a strong background in general chemical ecology techniques and a good knowledge of evolutionary biology. Familiarity with behavioral ecology would be appreciated. Study Context: Coevolution between gorse and its specific weevils. In Brittany, there are three species of gorse (*Ulex*, Fabaceae, Genisteae) which show a strong variation in flowering and fruiting phenologies: *U. minor* and *U. gallii* flower in autumn and *U. europaeus* flowers mainly in the spring, but also in autumn and winter. These gorse species can be found in sympatry. Specific weevils named Apions (Coleoptera, Curculionidae) parasitize the three *Ulex* species. The two main species are *Apion ulicis*, already described in the literature, and a new species discovered by our group. *Apion ulicis* spends winter at an adult state and lay its eggs in the spring. The new species lay eggs in autumn and spends winter at a larvae state. However, this new species never lay its eggs in autumnal pods of *U. europaeus* and is restricted to *U. minor* and *U. gallii*. The two *Apion* species present different life cycles as well as different host choices. In this context, the applicant will be working in collaboration with a PhD student who compares cold resistance of the two *Apion* species, and the differential attractiveness among three gorse species to apions. Preliminary works already showed that the two *Apion* species show differences in these two aspects.

Objectives: The person will be responsible of the identification and comparison of the chemicals involved in apions cold resistance and gorse chemical defense.

I- Chemical molecules involve in cold resistance of apions: The objective is to understand the adaptation of the weevils to the different types of gorse flowering and fruiting phenology. The post-doc will have to compare the compounds involved in cold resistance (glucose, glycerol, glycogen) synthesized under cold temperatures by the two *Apion* species.

II- Chemical defense of gorse: The objective is to understand the specificity of weevil choice for laying eggs. The post-doc will have to (1) compare the composition of chemical molecules of defense in the three gorse species and (2) determine what are the main chemical molecules that determine *Apion* choice. This will be achieved by searching for principal bioactive secondary metabolites generally involved in the gorses defense mechanisms: alkaloids and volatile compounds (terpenes...). To apply: Please send a curriculum vitae, including list of publications, research interests and names and email addresses of two referees to anne.atlan@univ-rennes1.fr before the 15th of May.

anne-gile.atlan@univ-rennes1.fr

CNRS Lyon PopulationGenetics

Postdoctoral position

A postdoctoral position from the CNRS is available in the UMR 5558: "Biométrie et Biologie Evolutive", in the team "Population genomics" of C. Biéumont and C. Vieira, Claude Bernard University Lyon1, Villeurbanne, France.

Title: Epidemiology of endogenous retroviruses: the transposable element *tirant* in *D. simulans*.

Research program: Transposable elements (TEs) represent a large portion of the genome of many organisms, and the invasion of the genome of an entire species can be a quick process. Although we have extensive evidence that TEs can horizontally transfer into new species, we do not know the extent to which recent new invasions are due to the emergence of new aggressive TE variants and, if so, how such new TE variants might arise. We propose to study this question by analyzing a particular retrotransposon, *tirant*, which is localized on the chromosome arms in only a few African populations of *D. simulans*, whereas *D. melanogaster* has many copies scattered over the chromosomes in all populations. The question arises on to why *tirant* has such an unusual distribution. Is such a distribution reflective of a recent invasion of *tirant* in the African populations, or is it a remnant in these populations of an ancient more global invasion of the element into the *D. simulans* / *D. melanogaster* ancestral species? Within a large programme aimed at analyzing the copies of *tirant* in the natural populations of *Drosophila*, we are looking for an experienced molecular biologist to investigate viral particles and the gag, pol, and env proteins of *tirant*. The objective is to test for a potential infectious characteristics of this TE.

Applicant qualifications: The position is opened to all nationalities. The candidate must have a strong background in molecular biology associated with retrovirology and virus proteomics (western blot, tissues in situ hybridization), with a high interest in population genomics. Knowledge on *Drosophila* would be appreciated. The fellowship is for one year starting September 2005. Monthly stipend: 2150 (1756.26 without taxes)

Interested candidates should send application and CV before April 15th 2005, at Biéumont Christian Tél: (33) 4 72 44 81 9! Fax: (33) 4 72 43 13 88

biemont@biomserv.univ-lyon1.fr

Vieira Cristina Tél: (33) 4 72 43 29 18 Fax: (33) 4 72 43 13 88 vieira@biomserv.univ-lyon1.fr

crisrina vieira-heddi <vieira@biomserv.univ-lyon1.fr>

CNRS MNHN early domestic mammals

Post-doc position : palaeogenetics

The French CNRS calls for a post-doc position untitled "Early domestic mammals, human migrations and transmission of knowledge through Neolithic Europe: archaeozoology and ancient DNA" (<http://www.sg.cnrs.fr/drhchercheurs/Post_doc.2005/-index.html>http://www.sg.cnrs.fr/drhchercheurs/Post_doc.2005/index.html>http://www.sg.cnrs.fr/drhchercheurs/Post_doc.2005/index.html>html)

Duration : 2 years (without any possibility to prolong) Start: 1st september 2005 Application form : http://www.sg.cnrs.fr/drhchercheurs/Post_doc.2005/-dossier_post-doc.2005.pdf Salary : 1800 Euros free of charge (2150 Euros including charges) contact : vigne@mnhn.fr

Description: Over the past three years, a multidisciplinary European research network has grown around the archaeozoology lab of the Natural History Museum in Paris. It aims to analyse the early husbandry of ungulates in the Old World. A better knowledge of these phenomena will contribute to understand the historical, socio-economic and cognitive mechanisms of the process of neolithisation on one hand, and to explain the present day structure of the genetic diversity of domestic animals on the other. The post-doc will contribute to the paleogenetic research of this European network, which aims to explore the diversity of wild ancestors and to determine the geographic origin of domestic Neolithic mammals. The work will be composed of two parts: - sampling, extraction and amplification of ancient DNA from archaeological bone, following the required protocols for reducing the risks of contamination and for authenticating the amplified ancient sequences; this part of the research will take place in one of the genetic labs of the network (Lyon, Paris-Jussieu, Grenoble, Dublin, Mayence); - acquiring sufficient knowledge of archaeozoological and archaeological techniques, practices and concepts, to be able to interpret the palaeogenetic results in terms of history and anthropology, and to contribute to their publication in

peer-reviewed journals; this will take place in the Museums archaeozoological lab in Paris. This post-doc aims to help a young scientist, preferably with experience in molecular biology but with or without experience in the field of ancient DNA, to increase her/his knowledge in historical anthropology in order to be able to act as an interface between the disciplines interested in paleogenetic techniques.

The applicant must hold a PhD in the field of the molecular biology, molecular phylogeny, molecular phylogeography, population genetics (animals or plants) or ancient DNA. He/she should have experience with ancient DNA or with similar substrates in small quantities. The candidate must take an interest in interdisciplinary approaches, in the application of phylogenetics to the history of human beings and their societies. Basic knowledge of Holocene prehistory would be an asset. He/she will have contact with other scientists involved in the research, and must be able to work in a team. The ability to read and speak English is required.

Jean-Denis Vigne <vigne@mnhn.fr>

CornellU VertebratePopGenetics

TITLE: Post Dr Associate - 03553

DESCRIPTION: Postdoctoral Position in Population Genetics. The Evolutionary Biology unit of the Cornell Laboratory of Ornithology seeks to fill the position of Postdoctoral Associate within the framework of an NSF-funded project "Unifying Models of Gene Flow at Multiple Scales in a Well-Studied Vertebrate." This project will generate a comprehensive understanding of dispersal in the threatened Florida Scrub-Jay by comparing robust field, model-based, and genetic patterns of gene flow. A large fraction of the world population of these jays is currently being screened with large panels of microsatellite and SNP markers; extensive field data regarding the distribution and dispersal of this species are available. The postdoctoral associate will work in collaboration with Cornell faculty Irby Lovette, Rasmus Nielsen, and John Fitzpatrick to develop and carry out population genetic analyses appropriate to this large dataset, including deriving estimators of gene flow from spatial genetic models appropriate for the Florida Scrub-Jay system and applying these methods to test hypotheses regarding dispersal patterns. Although the primary responsibilities of this two-year position are analytical and computational, it also offers

opportunities to become involved with field or laboratory work and/or to develop new avenues of inquiry using the Florida Scrub-Jay as a model system. This position involves the development of sophisticated population genetics methods and their application in a system where the results will have direct and ecosystem-wide impacts on conservation action. The position is based at the Cornell Laboratory of Ornithology (a research center comprising >200 staff and graduate students) and within Cornell's robust Genomics and Computational Biology community.

REQUIREMENTS: We seek candidates with a Ph.D. in genetics, mathematics/statistics, evolutionary biology, or related fields with research experience in theoretical, statistical, or data-analytical aspects of molecular ecology or population genetics. Evidence of research productivity as indicated by scholarly publications is required. No prior experience with birds or other wild organisms is required.

Send letter of interest, C.V., and three references by March 31, 2005 to Sue Taggart, Cornell Lab of Ornithology, 159 Sapsucker Woods Rd., Ithaca, NY 14850. Inquiries related to this position can be directed to Dr. Irby Lovette, Cornell University, Lab of Ornithology, 159 Sapsucker Woods Rd, Ithaca, NY 14853. Phone: 607-254-2140; Email IJL2@cornell.edu. Review of applications will begin immediately, and continue until the position is filled.

ijl2@cornell.edu ijl2@cornell.edu

INRA Orleans CropGenomeOrganization

Post doctoral position available at INRA-France

An INRA postdoctoral fellowship position is available at UAGPF INRA Orléans and UMRGV [1]www.evry.inra.fr. This position is available for one year from May 2005.

The project consists in cloning a major factor controlling partial resistance to *Melampsora larici populina* (Mlp) leaf rust in *Populus trichocarpa*. The foliar rust caused by *Melampsora larici-populina* Kleb. is the main disease affecting poplar stands in the northern part of France - more generally in Northern Europe. A major factor controlling partial resistance was fully characterized by genetic studies conducted on several *P. trichocarpa* x *P. trichocarpa* and *P. deltoides* x *P. tri-*

chocarpa families with seven strains of Mlp (Dowkiw and Bastien, 2004; Jorge et al. 2005). A BAC library of the *P. trichocarpa* parent is underway. A 14 equivalent genome is expected at the end of March 2005. High resolution mapping of the region of interest is applied on one segregant family of 1200 progenies. Physical map will be established by using markers tightly linked to the target locus. The project will be enhanced by comparison with the overall genome sequence of *Nisqually* already available.

Major duties will include high-density and high-resolution mapping of targeted region, BAC characterization and fingerprinting, sequence analysis, marker development, genetic and physical mapping, contig assembly. Plant material of more than 500 individuals in *P. trichocarpa*, *P. nigra* and *P. deltoides* species are already phenotyped for rust resistance as a first step of association studies.

Applicants should have a PhD in agricultural sciences or biology with proven expertise in molecular genetics. Experience on informatic tools for sequence analysis would be advantageous. Knowledge of French language is not required.

The candidate is supposed to have never worked in France up to now. Candidates should provide a cover letter describing the background and experience, a succinct curriculum vitae and two letters of recommendation.

For enquiries and applications, please contact Dr Patricia Faivre Rampant at [2]faivre@evry.inra.fr and Dr. Catherine Bastien at [3]Catherine.bastien@orleans.inra.fr before March 31, 2005.

Dowkiw A., Bastien C. (2004) Characterization of two major genetic factors controlling partial resistance to *Melampsora larici-populina* leaf rust in hybrid poplars : strain-specificity, field expression, combined effects and relationship with a defeated complete resistance gene. *Phytopathology*, 94, 1358-1367.

Jorge V., Dowkiw A., Faivre Rampant P., and Bastien C. (2005). Genetic architecture of qualitative and quantitative *Melampsora larici-populina* leaf rust resistance in hybrid poplar: genetic mapping and QTL detection. *New Phytologist* in press

P. Faivre Rampant

Patricia Faivre Rampant <Patricia.Faivre-Rampant@evry.inra.fr>

IndianaU EvolGenomics

POSTDOC IN POPULATION AND COMPARATIVE GENOMICS

A postdoctoral position in evolutionary genomics is available in the lab of Matthew Hahn in the Department of Biology at Indiana University. There is a wide variety of research going on in the lab, including studies of nucleotide, gene family, and gene expression variation within and between species. Specific research projects will be determined based on the joint interests of the successful candidate and supervisor; the candidate will also be encouraged to carry out independent computational or empirical work. For a summary of research, please see <http://www.bio.indiana.edu/facultyresearch/faculty/Hahn.html>. The candidate must have a Ph.D., preferably in population genetics, statistical genetics, computational biology, or phylogenetics. Programming skills are not required, but the candidate must be willing to learn. Salary is \$40-\$45K (plus benefits) commensurate with experience. The anticipated start date for this position is August 1, 2005.

Indiana University has a large and active group in evolutionary genetics, and considerable resources are offered by IU's Center for Genomics and Bioinformatics. Bloomington is situated in scenic, hilly southern Indiana, near several parks and wilderness areas. The cultural environment provided by the University is exceptionally rich in art, music, and theater.

To apply, please send a CV and contact information for at least two referees to Margi Lockhart at malockha@bio.indiana.edu. Review of applications will start April 15th and will continue until the position is filled.

Indiana University is an Equal Opportunity / Affirmative Action Employer.

Matthew W. Hahn Assistant Professor Department of Biology and School of Informatics Indiana University Bloomington, IN 47405 Email: mwh@indiana.edu <http://www.bio.indiana.edu/facultyresearch/faculty/Hahn.html> <http://www.bio.indiana.edu/~hahnlab>

McMasterU StatGenetics

We seek a postdoctoral researcher for up to two years to work on statistical methods and modeling in population genetics and molecular evolution as part of a group at McMaster University, Hamilton Canada. The applicant must have completed their Ph.D. preferably in population genetics, statistical genetics, computational biology, or phylogenetics and must have training in statistical methods and modeling in population genetics, molecular evolution and/or phylogenetics. Projects will center around the 'Barcode of Life' (BoL) initiative and Genome Canada funded work. Specific research projects will be determined based on the joint interests of the successful candidate and supervisor; the candidate will also be encouraged to carry out independent computational or empirical work.

Salary is approximately \$40-45K, pending qualification level. Applicants should contact Brian Golding (Golding@McMaster.CA) with special reference to this particular position. Submissions should include letters of reference, a complete CV and contact information. Review of applications will start May 1st and will continue until the position is filled.

Golding@McMaster.CA

Montpellier Phylogenetics

One year postdoc position at Montpellier, France, starting September 2005

"Probabilistic and mixture models in phylogenetics"

Project

The exponential increase in the number of sequences (DNA, RNA, and proteins) available makes now possible to build and infer complex and realistic models of sequence evolution. The standard models are Markovian and describe the substitution probabilities from one character (nucleotide, amino acid, or codon) to another. However, it was recently proposed [1] to build more powerful models via the use of mixtures of Markovian models. The mixture approach has shown to be

effective in numerous domains (e.g. pattern recognition and classification) and its application to evolutionary studies and phylogenetics is quite promising. The postdoc subject is to explore this new approach at the statistical and/or algorithmic level, within the maximum likelihood framework and the PHYML software [2].

LIRMM (Montpellier) Bioinformatics Group

Our group has been involved in phylogenetics for more than 10 years, with strong interests on the mathematical, statistical and computational tools and concepts [3]. We authored several well known software, e.g. BIONJ and PHYML, and our publications can be seen from our URL: <http://www.lirmm.fr/w3ifa/-MAAS/>. Research on realistic evolutionary models (and thus understanding how sequences did evolve) is an hot topic in our group.

Candidate

The candidate will have a solid background in statistical modeling and computer science, and strong interests in bioinformatics, evolutionary biology and phylogenetics.

Contact

Olivier Gascuel LIRMM-CNRS, 161 rue Ada, 34392 - Montpellier - France gascuel@lirmm.fr, <http://www.lirmm.fr/~gascuel/> References

[1] Pagel, M., and Meade, A., 2004. A phylogenetic mixture model for detecting pattern-heterogeneity in gene sequence or character-state data. *Systematic Biology* 53(4):571-81.

[2] Guindon, S., and Gascuel, O., 2003. A simple, fast and accurate method to estimate large phylogenies by maximum-likelihood. *Systematic Biology* 52(5):696-704. "Fast breaking paper" award (February 2005) by ISI Essential Science Indicators.

[3] Gascuel O., ed., 2005. *Mathematics of Evolution and Phylogeny*, Oxford University Press.

gascuel@lirmm.fr

NetherlandsInstEcol AvianDemography

The Netherlands Institute of Ecology (NIOO-KNAW) focuses on fundamental, strategic research into individual organisms, populations, ecological communities and ecosystems. More than 240 staff are employed at

three centres as well as the head office. The Centre for Limnology (CL) in Nieuwersluis focuses its research on freshwater ecology. The Centre for Estuarine and Marine Ecology (CEME) in Yerseke deals with ecosystems in brackish and salt water and the emphasis at the Centre for Terrestrial Ecology (CTE) in Heteren is put on land-based ecology. The Netherlands Institute of Ecology is a research institute of the Royal Netherlands Academy of Arts and Sciences (KNAW)

The Department of Animal Population Biology is looking for a:

Post-doc Ecologist (m/f) (reference number CTE-PVD-05091)

for a project on spatial aspects of avian demographic processes. This project is a joint project of the departments Spatial Ecology (CEME), Plant Animal Interactions (CL) and Animal Population Biology (CTE) and within the project a twinned position at Plant Animal Interactions has been filled.

Function description The Post-doc will apply and develop approaches for spatially explicit analyses of avian demographic processes. The aim of the analyses is to improve insight in dispersal and its consequences for demography, using large sets of data on ringing, resighting, reproduction, survival, feeding and other characteristics of birds. Two large datasets are already available at the institute. One of these datasets covers distribution patterns of Bewick's Swans, which move from the North to the South of the Netherlands in the course of the winter, using resightings of individually marked birds. Actual movement patterns will be compared to predictions from optimality models. Furthermore, the post-doc will analyse dispersal patterns using a large 12-year dataset on reproduction and survival of Swallows at seven sites in the Netherlands. The aim is to determine how dispersal affects the spatial structure of populations, especially how differences in dispersal are related to habitat properties. The Swallow data set offers good possibilities to study variation in dispersal among habitats and any interactions with sex and date of birth. The Swallow data have been collected by volunteers linked to the Dutch Ringing Centre, which is part of Animal Population Biology. Finally, the post-doc is encouraged to collaborate with other members of Animal Population Biology on spatial aspects of the Animal Population Biology research.

Function requirements The candidate should possess a PhD in Ecology, a strong background in quantitative approaches and statistics. Knowledge of GIS and/or of multi-strata survival analysis is desired. The candidate should have good verbal and writing skills.

Conditions of employment The appointment will be for 1.5 years starting on the 1st June 2005 at CTE Heteren and will be in accordance to the CAO-NU of the KNAW. The gross monthly salary will be maximum 3.453, – depending on experience.

Information and application For additional information please contact Dr Marcel Visser (m.visser@nioo.knaw.nl <mailto:m.visser@nioo.knaw.nl>) tel. 031-264791253. Information on the Netherlands Institute of Ecology (NIOO), the Centre for Terrestrial Ecology and the Department of Animal Population Biology can be found at <http://www.nioo.knaw.nl> <<http://www.nioo.knaw.nl/>> . Applications, quoting the reference number and including a detailed Curriculum Vitae and the names of three scientific referees, should be sent to Prof. Dr J.A. van Veen, Centre Director, Centre for Terrestrial Ecology, NIOO-KNAW, P.O. Box 40, 6666 ZG Heteren, The Netherlands or by e-mail to h.vanveen@nioo.knaw.nl <mailto:h.vanveen@nioo.knaw.nl> . Closing date 15th April 2005.

Dr. Marcel E. Visser Head of Department Animal Population Biology Netherlands Institute of Ecology P.O. Box 40 6666 ZG Heteren The Netherlands

Phone: +31-26-4791253 Fax: +31-26-4723227 E-mail: m.visser@nioo.knaw.nl Website: www.nioo.knaw.nl Personal page: www.nioo.knaw.nl/ppages/mvisser

ESF Network e-bird: e-bird.cefe.cnrs.fr <<http://e-bird.cefe.cnrs.fr/>> Netherlands Society for Behavioural Biology: www.gedragbiologie.org M.Visser@nioo.knaw.nl

NorthCarolinaStateU PlantEvolGenetics

Two postdoctoral fellowship positions in plant evolutionary and ecological genomics are available beginning Fall 2005. We are looking for creative, innovative individuals who are interested in bridging the fields of evolution, ecology, development and molecular genetics. Postdoctoral scientists will work in an interdisciplinary setting, with research focusing on the evolutionary and ecological genomics of adaptation in Arabidopsis and rice. The postdoctoral scientists are also encouraged to initiate and develop independent research projects. For more information on our laboratory, go to <http://purugganan.gnets.ncsu.edu> . Review of applications

begin immediately and will continue until the positions are filled. To apply, please submit curriculum vitae and 3 professional references either via email or postal mail to:

Michael D. Purugganan Department of Genetics Box 7614/3513 Gardner Hall North Carolina State University Raleigh, NC 27695 USA

email:michaelp@unity.ncsu.edu

NC State is an Equal Opportunity/Affirmative Action Employer. Men and women of diverse racial/ethnic backgrounds and cultures are encouraged to apply.

michaelp@ncsu.edu michaelp@ncsu.edu

PennStateU EvolGenomics

A postdoctoral position is available in the group of Kateryna Makova at the Department of Biology at Penn State University. The focus of the group is in the evolutionary genomics of mammals. Currently we are particularly interested in the variation of mutation rates in the genome (e.g., male mutation bias). For a background, please see several recent publications:

- Makova, K. D., and W.-H. Li. 2002. Strong male-driven evolution of DNA sequences in humans and apes. *Nature*, 416, 624-6. - Li, W.-H., S. Yi, and K. D. Makova. 2002. Male-driven evolution. *Current Opinions in Genetics and Development*, 12, 650-656. - Makova, K.D., S. Yang, and F. Chiaromonte. 2004. Indels are male-biased too: a whole genome analysis in rodents. *Genome Research*14: 567-573.

I am seeking highly motivated applicants with strong interest in molecular evolution and bioinformatics. Prior experience in programming and/or managing large amounts of biological data is required. International applicants are encouraged to apply. The successful applicant will be guaranteed support for one year with a possibility of extension to additional 1-2 years depending on the applicant's performance and lab's funding.

You have an opportunity to join a dynamic group that enjoys vivid interactions with the Center for Comparative Genomics and Bioinformatics (www.bx.psu.edu) and the Institute of Molecular Evolutionary Genetics (<http://www.bio.psu.edu/IMEG/>) at Penn State. The collaborative environment at Penn State is outstanding and computational facilities are clearly suitable for the state-of-the-art large-scale evolutionary analysis. The

Makova Lab has been participating in the analysis of the rat and chicken genome and is currently a member of the Chimpanzee Sequencing and Analysis Consortium.

Penn State is situated in State College. It is a college town located in beautiful hilly central Pennsylvania. The town is famous for its affordable living, excellent public schools, and the lowest crime rates in the country.

Inquiries should be addressed to Kateryna Makova (kdm16@psu.edu). Applications should be sent electronically to kdm16@psu.edu and should include a CV, statement of research interests, and names and e-mail addresses of three recommenders (I will contact them directly asking for recommendations). For more information on the group, see the website: http://www.bx.psu.edu/makova_lab/. The review of applications will continue until the position is filled. All applications received before May 1 will be given consideration. The starting date for the position is negotiable.

Kateryna Makova Assistant Professor Department of Biology Center for Comparative Genomics and Bioinformatics 518A Mueller Lab Penn State University University Park, PA 16803 E-mail: kdm16@psu.edu Tel: (814)863-1619 Fax: (814)865-9131

Kateryna Makova <kmakova@bx.psu.edu>

RochesterU EvolGeneticsNasonia

Postdoctoral Position: Evolutionary Genetics in Nasonia

Description: A 2-3 year postdoctoral position is available to study evolutionary genetics in the parasitoid wasp genus *Nasonia*. *Nasonia* is an emerging model system for genetic research, which has recently been selected for full genome sequencing (<http://www.genome.gov/13014443>). Genome sequencing has been approved by NIH for 6-fold sequencing of *N. vitripennis* and 1-fold sequencing of the two sibling species, *N. giraulti* and *N. longicornis*. *Nasonia* is a complex of three closely related species that are interfertile, allowing movement of genes between them. The three species differ in many interesting aspects of morphology and behavior. An NIH-funded project investigates the genetic basis of a 2.5 fold difference in male wing-size between two species (*N. vitripennis* and *N. giraulti*). This represents a recent evolution of male- and organ-specific regulation of cell size and number, and our ge-

netic analyses indicates that the difference is due primarily to 3-4 genetic regions of large effect. Fine-scale mapping and introgression of wing size genes from one species into the other has been accomplished. The goal of this project is to use positional cloning methods to identify candidate genes involved, and to investigate their patterns of molecular evolution, and gene expression in wing imaginal discs. Depending upon interest, the postdoctoral researcher will also have opportunities to become involved in aspects of the *Nasonia* EST project (70,000 ESTs are currently being sequenced in the two species), *Nasonia* microarray, and molecular evolutionary studies emerging from the *Nasonia* genome project.

Additional information on *Nasonia* and related projects can be obtained through my website below

Requirements: PhD. Experience with some combination of the following: insect genetics, DNA sequencing and analysis, molecular evolution, QT-PCR, cDNA microarrays, BAC library hybridization

Salary: \$33,500 38,500 per year, depending upon experience level. Health Insurance is also included. Rochester has a moderate cost of living with readily available and affordable housing.

Deadline: The position is available immediately. Applications will be accepted until the position is filled.

Please send by email a statement of interest, CV and contact information for three references to: Dr. John (Jack) Werren, Department of Biology, University of Rochester, Rochester, NY 14637. email: werr@mail.rochester.edu website: <http://www.rochester.edu/College/BIO/labs/WerrenLab/> Professor of Biology Department of Biology University of Rochester Rochester, N.Y. 14627 email: werr@mail.rochester.edu fax: 585-275-2070 phone: 585-275-3694 website: <http://www.rochester.edu/College/BIO/labs/WerrenLab/index.html> "John (Jack) Werren" <werr@mail.rochester.edu>

SevillaSpain 2 PlantAnimalInteractions

JOB OFFERS (ONE GRADUATE STUDENT, AND ONE POSTDOC)

We are a young, interdisciplinary research group recently awarded with a European Young Investigator

Award, working on networks of plant-animal interactions. Our research is aimed at the characterization of how coevolutionary interactions are shaped in species-rich communities. We combine different approaches to characterize network structure, how such structure affects community persistence, and which mechanisms lead to the observed structure. To expand our highly motivated team we are seeking:

1. Postdoctoral position on phylogenetic analysis of plant-animal coevolutionary networks. We are looking for a postdoctoral fellow with experience in the comparative method and phylogenetic analysis of animal or plant groups. The project involves the analysis of the phylogenetic relationships between plants and animals in coevolutionary networks. The candidate should analyze Genbank data sets, and obtain new DNA sequences. The ultimate goal is to understand which component of the structure of plant-animal networks is explained by phylogeny as opposed to ecological correlates.

The candidate should have an excellent publication record on phylogenetic analysis, comparative methods, and related issues. He/She should be seeking to work in collaboration with other members of the team. The position is for two years.

Applications (CV, description of research interests, up to 3 letters of reference, 2 selected reprints, and a cover, motivation letter) should be sent by post mail to:

Jordi Bascompte *c/o* EURYI Search Committee (Postdoc)

Estación Biológica de Doñana, Pabellón del Perú

Avda. Maria Luisa s/n Sevilla 41013, Spain

Deadline for submission is 10 April, 2005.

2) Ph.D. Fellowship, plant-animal coevolutionary networks. We are looking for a highly motivated student with a degree in biology who seeks to obtain a Ph.D. The project involves the combination of data set analysis of networks of plant-animal interactions, and original field work. This could be complemented with lab analysis of phylogenetic relationships between plants and animals in close collaboration with a postdoctoral fellow.

The candidate should be familiar with statistical analysis. Familiarity with some computing language (Matlab, C, or similar) will be valued. He/She should be seeking to learn new techniques and work in collaboration with other members of the team. The position is for four years.

Applications (CV, up to 3 letters of reference, and a cover, motivation letter) should be sent by post mail

to:

Jordi Bascompte *c/o* EURYI Search Committee (Graduate student #1)

Estación Biológica de Doñana, Pabellón del Perú

Avda. Maria Luisa s/n Sevilla 41013, Spain

Deadline for submission is 10 April, 2005.

Candidates from other European and non-European countries are highly encouraged. The candidates will benefit from a unique combination of computing, lab, and field facilities, creative environment, and an international program of visitors. For information about the group see <http://ieg.ebd.csic.es>, <http://ieg.ebd.csic.es>. Questions can be addressed to euryi@ebd.csic.es

– Jordi Bascompte Estación Biológica de Doñana, CSIC Apdo. 1056, E-41080 Sevilla (Spain)

Phone: (+34) 954 232340 Fax: (+34) 954 621125 e-mail: bascompte@ebd.csic.es <http://bascompte.org>

Jordi Bascompte <bascompte@ebd.csic.es>

TrinityU 2 EvolBiol

POSTDOCTORAL TEACHING POSITIONS

Two teaching postdoctoral positions lasting 2 years each are available to assist in the development and implementation of an interdisciplinary introductory curriculum in biology, a project funded by the Howard Hughes Medical Institute. Postdoctoral fellows will work with faculty from biology, chemistry, mathematics and physics to infuse interdisciplinary perspectives across the introductory courses in these fields. They will also teach one or two laboratory sections of our current introductory courses. In addition, these fellows will be encouraged to initiate research collaborations with Trinity faculty, working toward establishing their own independent research program in anticipation of their first faculty appointment. The postdoctoral fellows will be invited to participate in the full range of faculty life, including department meetings, faculty meetings, and faculty development programs such as teaching seminars and colloquia, as well as travel to professional meetings. Ideally, we seek to hire one person whose expertise lies in cellular and molecular biology and another whose expertise lies in ecological and/or evolutionary biology. Applicants should send curriculum vitae, a statement of teaching interests, a state-

ment of research interests, and arrange for three letters of reference to be sent to: Dr. David Ribble, Chair, Department of Biology, Trinity University, One Trinity Place, San Antonio, TX 78212. Review of applications will begin 15 April 2005. For further information, please see our website at: www.trinity.edu/org/hhmi. Women and minority candidates are strongly encouraged to apply. Trinity University is an Equal Opportunity Employer.

Bobbye Hernandez

“Hernandez, Roberta” <Roberta.Hernandez@Trinity.edu>

<http://www.personnel.bham.ac.uk/vacancies/-printableFurtherParticulars.htm?refNo9243>

Application forms (returnable by 14th March 2005) and details from Personnel Services, The University of Birmingham, Edgbaston, Birmingham B15 2TT. Tel: 0121 415 9000, web: <<http://www.personnel.bham.ac.uk/vacancies>> www.personnel.bham.ac.uk/vacancies Please quote ref: H39243

Dmitry Filatov <D.Filatov@bham.ac.uk>

UBirmingham IslandSpecies

THE UNIVERSITY OF BIRMINGHAM SCHOOL OF BIOSCIENCES

Research Fellow

Adaptive and purifying selection in island and mainland plant species

Applications are invited to work on a BBSRC-funded project in the laboratory of Dr Dmitry Filatov. The project is to study the adaptive and purifying natural selection at the molecular level during recent adaptive radiation in the Hawaiian endemic genus *Schiedea* (Caryophyllaceae) and to compare it to the mainland genus *Silene* (Caryophyllaceae).

The successful candidate will be responsible for most of the laboratory molecular genetics work and data analysis, as well as preparation of the manuscripts for publication. Applicants should have proven experience in (preferably plant) experimental molecular population genetics and evolution (at least one published paper is required). Lab experience in molecular genetics methods is required and experience in computer programming would be advantageous. Applicants should have a PhD in population genetics / molecular evolution, strong interest in evolutionary genetics and desire to study evolutionary questions using a plant system. Experience with all aspects of DNA sequencing, including experience with software for sequence analyses and population genetic analyses is essential.

Starting salary on scale £19,460 - £21,640 a year depending on qualifications and experience. Informal enquires to Dr D Filatov email: <<mailto:d.filatov@bham.ac.uk>> d.filatov@bham.ac.uk

More details on the website:

UDelaware HostSpecificity

Postdoctoral Research Associate - The Beneficial Insect Introductions Research Unit seeks a post-doctoral research associate to participate in research on the evolution of host use in *Heliothis* species. The project is to identify candidate genes involved in use of novel host plant species by positional cloning and knockout of candidate genes through transformation to induce RNA interference. The research involves bioassays of larval feeding and adult oviposition in progeny of interspecies hybrids and selected populations, mapping quantitative trait loci using molecular markers, developing probes from markers associated with QTL, probing a BAC library, sequencing candidate clones, identification of candidate genes, transformation of insects (using transposon-based vectors) to knock out gene function by expression of hairpin RNA sequences designed from candidate gene sequences. Recent Ph.D. in Genetics, Molecular Biology, Entomology, or Ecology is required. Knowledge of quantitative genetics and QTL mapping and skill in molecular biology required; knowledge of genetic transformation desirable. Annual salary is \$48,748 plus benefits; position is for 2 years. The position is available 1 October 2003. Please send curriculum vitae and names, addresses (including e-mail), and phone numbers of three references to Dr. Keith R. Hopper, USDA-ARS, 501 South Chapel St., University of Delaware, Newark, Delaware 19713; email khopper@udel.edu, telephone 302-731-7330 ext 238, fax 302-737-6780. ARS is an equal opportunity employer.

khopper@udel.edu khopper@udel.edu

UEdinburgh 2 MolEvolPhyloGenomics

Two Jobs in Molecular Evolution, Phylogeny and Genomics

at The University of Edinburgh, School of Biological Sciences / Institute for Evolution

Position 1 is for Post-Doctoral Researcher (36 months)
Position 2 is for a Graduate Research Associate (34 months)

Title: Linking Genomes to Ecology: Evolution of Daphnia Immune System Genes

Supervisors: Tom Little (tom.little@ed.ac.uk) and Mark Blaxter (mark.blaxter@ed.ac.uk). This NERC-funded project is focused on disease resistance and immunity genes in Daphnia, the first crustacean to have its genome fully sequenced. Depending on your interest or skill, the work may emphasize aspects of comparative genomics, molecular evolution, or the ecology and evolution of disease resistance, but preferably the candidate will have an interest in all these things.

Details: 1) Postdoctoral Research Fellow (quote ref: 3004165)

BRIEF BACKGROUND AND GOALS OF THE PROJECT: Parasitism may dramatically modulate the genetic structure of populations. Natural populations vary tremendously in their levels of parasitism and pathogen virulence, and although host genetic polymorphism often mediates these patterns, rarely is it known which genes are involved. Addressing this issue requires studying parasitism in a organism that is both a genetic model and a model for studies of natural variation. This Project will exploit emerging genomic knowledge of Daphnia pulex. Daphnia, unlike traditional models for genetic study, are extremely well-characterised in terms of their ecology and natural patterns of variation, which includes intriguing variation in levels of recombination. The project will first involve searching the Daphnia genome for immunity genes (based on homology with the range of other sequenced arthropods) to gain a broad perspective on the immune-related genome of the first sequenced crustacean (sensu Christophides et al. Science 298:159-165 (2002)). Second, the project will study natural levels of variation at candidate immunity genes. In particular, we aim to determine which immune system genes are the foci of coevolutionary in-

teractions by examining DNA polymorphism between and within species to test for the footprint of pathogen-mediated selection in natural populations (e.g. Ford, M. J. Molecular Ecology 11, 1245-1262 (2002); Little et al. Journal of Molecular Evolution 59:498-506 (2004)). Thus, this Project will combine bioinformatics, population genetics and evolutionary ecology, possibly including field work. The candidate will have a strong interest in some or all of these areas. The Job is based in Edinburgh, but travel to North American study sites is likely. The candidate will join a working environment that is extremely strong in evolutionary ecology, population genetics, genomics and coevolutionary interactions (see: <http://www.icapb.ed.ac.uk/>)

Post title: Post Doctoral Researcher Funding body: NERC Start date: June 1, 2005 (negotiable) Grade: ARIA Post Doctoral Research Assistant Salary scale: £19460-£29128 Hours: 40/week Duration: 36 months Supervisor: Tom Little Enquiries: tom.little@ed.ac.uk Location: School of Biological Sciences, ICAPB, Ashworth Laboratories, Kings Buildings, West Mains Road, Edinburgh EH 9 3JT

Please quote ref: 3004165 Closing date: 19 April 05

Formal Application MUST be made through the website: www.jobs.ed.ac.uk Or by phoning 0131 650 2511

2) Graduate Research Associate (quote ref: 3004163)

This three year project involves the study of parasitism in a model organism, the crustacean Daphnia. The project involves analysis of the immune system of Daphnia, which is the first crustacean to have its genome fully sequenced. This post will assist with the collection of DNA polymorphism data from natural populations. The candidate requires a BSc. and experience in molecular biology (DNA extraction, PCR and sequencing). An interest in evolutionary ecology and field work (collecting Daphnia from freshwater ponds) will be helpful. Job is based in Edinburgh, but travel to North American study sites likely. The candidate will join a working environment that is extremely strong in evolutionary ecology, population genetics, genomics and coevolutionary interactions (see: <http://www.icapb.ed.ac.uk/>)

Post title: Graduate Research Associate Funding body: NERC Start date: June 1, 2005 (negotiable) Grade: AR1B Research Assistant Salary scale: £19460-£21640 Hours: 40/week Duration: 34 months Supervisor: Tom Little Enquiries: tom.little@ed.ac.uk Location: School of Biological Sciences, ICAPB, Ashworth Laboratories, Kings Buildings, West Mains Road, Edinburgh EH 9 3JT

Please quote ref: 3004163 Closing date: 19 April 05

To apply online or view more job opportunities, visit our website

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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>

U**Edinburgh DrosophilaImmunity**

Postdoctoral Researcher

Institute of Evolutionary Biology University of Edinburgh

Genetic variation in *Drosophila* immune responses

Individuals and populations of *Drosophila melanogaster* vary considerably in their susceptibility to infection and parasitism. This project will begin by examining the genetic architecture of this variation; the numbers of loci, the size of their effects, epistatic interactions and whether genes are specific to certain parasite genotypes. We will then attempt to identify the genes themselves. This will not only allow population genetic analyses of the processes maintaining so much genetic variation, but it also provides a novel approach for identifying 'immunity genes' in *Drosophila*.

The project will take a stepwise approach. Initially, we will use recombinant lines to identify regions of the genome containing quantitative trait loci (QTLs) affecting immune competence. Then, we will refine the location of these QTLs by deficiency mapping. Finally, we will identify genes by complementation tests and association mapping.

The lab is working on both specific parasites of *Drosophila* (parasitoids and the sigma virus) and general insect pathogens (bacteria and fungi). You will work in the lab of Dr Frank Jiggins, and collaborate with Dr Sara Knott on the quantitative genetic aspects of the project. There are two graduate students and a technician working on closely related projects.

Candidates: Will have a PhD in an appropriate discipline and must have experience relevant to the project, preferably in host-parasite coevolution, insect immunity, *Drosophila* biology or quantitative genetics.

Further details, and the application form will appear shortly on <https://www.jobs.ed.ac.uk/> Frank Jiggins

Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh West Mains Rd Edinburgh EH9 3JT Tel: +44 (0)131 650 5476

francis.jiggins@ed.ac.uk

U**Helsinki 18positions**

Hanna Kokko, Department of Biological and Environmental Science PO Box 65 (Viikinkaari 1), 00014 University of Helsinki, Finland Tel. +358-9-1915 7702, fax +358-9-1915 7694 www.helsinki.fi/~hmkokko/ Ad: title: 18 postdoctoral positions in Helsinki

18 postdoctoral positions (across all fields of science) are available at Helsinki University, Finland. The duration is 2 years, and research funding of 3000 EUR/year is included. For more information, see <http://www.helsinki.fi/university/openpositions.htm> Hanna Kokko <hanna.kokko@helsinki.fi>

U**Idaho Biofilms**

Postdoctoral Position at the University of Idaho: Monitoring and Modeling the Spatial Dynamics of Plasmid Transfer

A postdoctoral position is immediately available for a period of two years or more. The postdoctoral scientist will study the dynamics of antibiotic resistance plasmid spread and persistence in biofilms. The project is in collaboration with the group of mathematician Dr. Steve Krone, who develops cellular automata models that allow prediction of spatially explicit patterns of plasmid spread. The position offers the opportunity to carry out research in a dynamic and interdisciplinary research environment with excellent resources (<http://www.sci.uidaho.edu/biosci/-CRePE/index.html> and <http://styx.ibest.uidaho.edu/-ibest/index.html>). The project is funded by a 5-year NIH grant. The candidate should have a Ph.D. in microbiology, molecular biology, bioengineering, or related discipline, a background in prokaryotic molecular biology or genetics, and the ability to work well in an interdisciplinary team. The candidate should have at least one year of experience working with bacterial cultures.

Experience working with chemostats or flow cells, and experience with confocal laser microscopy are a plus. A fundamental understanding of the biology and ecology of plasmids and antibiotic resistance is desired.

For more information, candidates can write to Dr. Eva M. Top, University of Idaho (evatop@uidaho.edu). Please apply via the website (<http://www.hr.uidaho.edu/default.aspx?pid5496>), send your curriculum vitae to Eva Top, and include the names and contact information of three references.

The University of Idaho is an equal opportunity/affirmative action employer

Dr. Eva Top Associate Professor Department of Biological Sciences University of Idaho 347 Life Sciences South Moscow ID 83844-3051 Phone: 1-208-885-5015 Fax: 1-208-885-7905 <http://www.sci.uidaho.edu/biosci/labs/-top/>

UManchester Imprinting

We are looking to appoint a Postdoctoral Research Associate as part of a project funded by a Biotechnology and Biological Sciences Research Council (BBSRC) project grant for three years. You will investigate the contribution of genomic imprinting and maternal effects to the genetic architecture of size and growth related traits in mice. The project will utilise a very large set of genotypic and phenotypic data available from multiple generations of an experimental population of mice, providing a very powerful means to address a number of questions related to non-Mendelian effects in genetic architecture. The project also provides significant flexibility to examine a number of other related questions about the structure and evolution of genetic architecture and its consequences for multivariate evolution. Research will be done in collaboration with Professor James Cheverud (Washington University in St Louis).

You should have a strong interest in genetics and quantitative analysis and will possess a PhD degree in a relevant biological discipline. Quantitative and computing skills are essential as is the ability to work both independently and collaboratively as part of a research team. Some skills or an interest in obtaining skills in theoretical population or quantitative genetics is preferred but not required. You will have good interpersonal and communication skills and preferably experience in quantitative genetics, population genetics, ge-

nomics, or multivariate statistics.

The appointment is for a period of one year in the first instance and, upon successful completion of this probationary period, is available for a further two years. (i.e., this is a THREE YEAR position, but the first year is necessarily considered probationary as per University policy). The start date for this position is flexible and subject to negotiation, but ideally the position would start on or before September 1st 2005.

Informal enquiries can be addressed to Dr Jason Wolf, Tel: +44 (0) 161 275 3861, E-mail: wolf@manchester.ac.uk. For more information about the Evolutionary Biology research group at the University of Manchester please see:

<http://www.ls.manchester.ac.uk/research/themes/-evolution/> . The closing date for applications is the 28th March 2005.

Application forms and further particulars are also available from: The Directorate of Human Resources Faculty of Life Sciences G.100 Stopford Building, The University of Manchester Oxford Road Manchester, M13 9PT Tel: ++44 (0) 161 275 8836 Email: Lifesciences-hr@manchester.ac.uk Please quote reference: LS/030/05

Applications should be returned by the closing date to:

Dr Jason Wolf Faculty of Life Sciences The Michael Smith Building The University of Manchester Oxford Road Manchester, M13 9PT UK

jason@evolutionarygenetics.org

UMaryland StalkEyedFlies

POSITION ANNOUNCEMENT

Description: This is a two-year (minimum) postdoctoral position to participate in an NSF-funded project on genomic analysis of sexual dimorphism in stalk-eyed flies.

The goal of the research is to identify variation in gene expression and DNA sequence that is associated with morphological innovation and rapid diversification in head shape of stalk-eyed flies. These flies have undergone, to varying degrees, elongation of the head into stalks as a consequence of sexual selection. The primary strategy of the project will be to identify candidate loci involved in sexually dimorphic development

of eye-stalks and then quantify molecular variation at these genes. Candidate loci will be chosen based on an analysis of differential gene expression in the eye-antennal imaginal discs of these flies. Differential gene expression will be identified using an EST database of over 2500 unique cDNA clones and microarray analysis to reveal quantitative differences in gene expression between two species *Cyrtodiopsis dalmanni* and *Cyrtodiopsis quinqueguttata* that differ in the degree of sexual dimorphism. Both male and female gene expression in eye-antennal imaginal discs will be examined in the microarray experiments. The person in this position will have primary responsibility for conducting the microarray experiments using a well-staffed microarray facility (<http://www.umbi.umd.edu/~cbr/macore/-macorestart.htm>).

In collaboration with colleagues at the Joint Genome Institute, genomic libraries constructed for both species will then be screened to obtain both protein coding and flanking sequence data for several candidate loci. Comparison of sequence variation within one of these species, *C. dalmanni*, will be used to provide SNPs that can be included as molecular markers to determine if putative candidate genes map to previously identified QTL sites. Analyses of molecular variation will be used to test whether candidate genes or gene regions exhibit 1) association with phenotypic variation in eye-stalk size, 2) signatures of directional or stabilizing selection and 3) altered levels of genetic diversity.

The successful applicant will join an active lab with six graduate students, research technician, and several undergraduates involved in research and will be able to participate in campus initiatives involving genomics.

Requirements: PhD in the biological sciences. Experience with spotted cDNA microarrays, DNA sequencing, SNP genotyping, and QTL analysis is desirable.

Salary: \$35,000 per year

Health Insurance: Up to \$4000 supplement available.

Deadline: The position is available now. Applications will be accepted until the position is filled.

Send statement of interest, CV and contact information for three references to:

Dr. Jerry Wilkinson Department of Biology University of Maryland College Park, MD 20742

Web: <http://www.life.umd.edu/faculty/wilkinson>
Phone: 301-405-6942 fax: 301-314-9358 email: wilkinso@umd.edu

Jerry Wilkinson <wilkinso@umd.edu>

UNewCastle EvolCellBiol

Closing date: April 11th 2005 Position Title: Postdoctoral position in Evolutionary Cell biology

Position Location: University of Newcastle Upon Tyne, England, UK

Position Description: Postdoctoral Associate position in Evolutionary Cell Biology. Research areas include the application of molecular biology to understanding the structure and function of the microsporidian mitochondrion (see Nature 2002. 418: 865-869). Requires solid molecular biology experience and an interest in evolutionary biology. Doctoral degree in Biology or Molecular Biology or related field required.

For more information regarding the position contact Prof. T. Martin Embley. Please supply a statement of interest and curriculum vitae including the names of three referees. Employment through a grant from the Leverhulme Trust.

Dr. T. M. Embley Professor of Evolutionary Molecular Biology School of Biology The Devonshire Building University of Newcastle upon Tyne NE1 7RU UK email: martin.embley@ncl.ac.uk

UNewcastle FieldOrnithologist

Dear Colleagues,

please distribute the information below as widely as possible to all interested parties. If you know of any appropriate mailing lists, feel free to forward the ad.

A post-doctoral position in avian neuroecology is available for an experienced field ornithologist in a project that aims to describe the exact pattern of neurogenesis and apoptosis across the seasonal cycle in two closely related songbird species: the willow tit (*Parus montanus*) and the great tit (*Parus major*). Willow tits hoard food, whereas great tits do not, but both species sing seasonally. Seasonal patterns in neuronal turnover will be related to the seasonal patterns in behaviour in the field in Oulu (Northern Finland). You should have extensive experience studying tit behaviour, and be in-

terested in expanding your skills into more mechanistic approaches.

The project is based in the 5* rated Psychology, Brain <<http://www.ncl.ac.uk/biol/research/psychology/-index.htm>> and Behaviour Group at the University of Newcastle upon Tyne, and is run in collaboration with the research group of Prof. Markku Orell at the University of Oulu in Finland, where the field work will take place. The candidate should be willing to spend part of the year in Finland and part in England.

For informal enquiries, please contact Dr. Tom Smulders (tom.smulders@ncl.ac.uk). Further details of the research going on in the laboratory can be found at <http://www.staff.ncl.ac.uk/tom.smulders>. The post is available from 1 July 2005, but is open to negotiation. Closing Date:13.04.05.

More details about the job can be found at <http://www.ncl.ac.uk/vacancies/vacancy.phtml?ref=D325R>

Thank you very much

Sincerely,

Tom Smulders

Tom Smulders, Ph.D., Lecturer School of Biology (Psychology, Brain and Behaviour) The Henry Wellcome Building for Neuroecology, University of Newcastle Newcastle upon Tyne, NE1 7RU; Tel: ..44-(0)191-222-5790; Fax: ..44-(0)191-222-5622 <http://www.staff.ncl.ac.uk/tom.smulders> isab972@yahoo.co.uk

UNewcastle MolPhylogenetics

Closing date: April 11th 2005 Position Title: Postdoctoral position in genome-wide molecular phylogenetics

Position Location: University of Newcastle Upon Tyne, England, UK

Position Description: Postdoctoral Research Associate position in phylogenetics and computational biology. To investigate the origins of the eukaryotic proteome and the minimal function of mitochondrial homologues. Requires solid computing/phylogenetics experience and an interest in evolutionary biology. Doctoral degree in Computing, Biology or related field required.

For more information regarding the position contact Prof. T. Martin Embley. Please supply a statement of interest and curriculum vitae including the names of

three referees. Employment through a grant from the BBSRC.

Dr. T. M. Embley Professor of Evolutionary Molecular Biology School of Biology The Devonshire Building University of Newcastle upon Tyne NE1 7RU UK email: martin.embley@ncl.ac.uk

UOslo ChloroplastEvol

Take a look at the Bioportal site: <http://www.bioportal.uio.no> Phylogenomic site: <http://www.bioportal.uio.no/applications/phylogenomic/> POSITION AS RESEARCH FELLOW (post doc) in biology (molecular evolution) available at The Centre of Ecological and Evolutionary Synthesis (CEES), Dept. of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo

The position is on the project 'Evolution of chloroplast replacements?' (Norwegian Research Council). Attempts will be made to prolong the period. The aim of the project is to unravel the biological processes leading to the diversity of plastids in photosynthetic protists. Central issues are serial endosymbioses, evolutionary origin of genes with a symbiosis-derived genome, and transport of proteins into the plastid. In addition, the evolutionary history of chromoalveolates will be addresses. Dinoflagellates, haptophytes and related species (within the chromists and alveolata) are among the groups to be investigated. The methods employed include screening/sequencing of genomic libraries (BAC- and plastid) and EST/cDNA libraries, ultrastructural studies, bioinformatic techniques and phylogenetic/phylogenomic analyses.

The applicant should have a background in either genomics, molecular biology/genetics, molecular evolution or algal/protist biology. Hands on experience in genomics and gene analysis (or RNA experience) will be required. Knowledge of bioinformatics, phylogenetic methods, experience with algal or protist systems and culturing of algae will be useful, but it is not a prerequisite for the position.

The succesful candidate will work in an active group of researchers, post docs, PhD candidates, engineers and master students. The position is associated with the Centre for Ecology and Evolutionary Synthesis (CEES). CEES represents a leading research environment in evolutionary biology in Norway and has re-

cently built new molecular biology facilities.

The successful applicant will also collaborate with participants in a newly initiated "Triple alliance" project (UiO, The Veterinary School and the University of Environment and Biosciences) on haptophytes and dinoflagellates. Resources such as culture facilities, gene libraries and knowledge of biological systems will be parts of mutual collaborations.

The letter of application should include a curriculum vitae, with a list of published and unpublished works, a statement summarizing the applicant's scientific work and interests, one set of certified copies of certificates, and four copies of publications.

The requirement for a postdoctoral position is an obtained doctoral degree (PhD or similar). Candidates who have submitted their thesis, but not yet defended it, may apply but can eventually be employed only after the PhD is acquired.

For more information about post doc positions at the University of Oslo see: <http://www.uio.no/-admhb/reglhb/personal/tilsettingvitenskapelig/guidelinespostdoctor.html>

The University would like to see more women in scientific positions - women are therefore particularly encouraged to apply.

For further information please contact: professor Kjetill Jakobsen, tlf. 22 85 46 02, e-mail: kjetill.jakobsen@bio.uio.no post doctor Kamran Schalchian-Tabrizi, e-mail: kamran.shalchian-tabrizi@bio.uio.no

Information about the centre and the project can be found at: <http://www.bio.uio.no/cees> Pay grade: 51 ? 53 (depending on qualifications)

Deadline for application: April, 15.

REF. NR.: 05/7345

Applicants should submit a letter of application, CV, a list of published and unpublished works and four copies of published papers. One set of certified copies of certificates should also be submitted.

Applications (marked with the REF. NR.) should be sent to the Faculty of Mathematics and Natural Sciences, att. Senior Executive Officer Bente Schjoldager, P. O. Box 1032, 0315 OSLO The position is available for a period of two years.

kamran Schalchian-Tabrizi <kamran@bio.uio.no>

VirginiaCommonwealthU Bioinformatics

Postdoctoral Fellow in Bioinformatics Virginia Institute of Psychiatric and Behavioral Genetics, Virginia Commonwealth University

A postdoctoral position is available immediately, but can be flexible, at Virginia Institute of Psychiatric and Behavioral Genetics, Virginia Commonwealth University. Our research focuses on (1) evolutionary analysis of single nucleotide polymorphisms (SNPs) in the mammalian genomes and (2) the bioinformatics for the projects in psychiatric genetics. The successful candidate may participate in one or both of the projects above and join the research program in the Center for the Study of Biological Complexity. The candidate will work in a dry lab environment. The university is located in Richmond, the state capital of Virginia, within 90 minutes from the mountains, the beach, and Washington, D.C. More information can be found at the website <http://bioinfo.vipbg.vcu.edu/>. Virginia Commonwealth University is an equal opportunity/affirmative action institution

The qualified candidates should be highly motivated in research and have a Ph.D. in molecular biology or a related field at the time of appointment. Experience in programming or data analysis is preferred, but not required. Applicants should send a CV, brief statement of research interests, and reference to: Zhongming Zhao (zzhao@vcu.edu).

Zhongming Zhao, Ph.D. 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

WageningenU EvolGenet

Postdoc position in the Laboratory of genetics of Wageningen University, the Netherlands.

The Laboratory of genetics consists of two sections: evolutionary genetics and botanical genetics. Research

in evolutionary genetics includes the understanding of the evolutionary role of sex, recombination and mutation rates, the evolution of senescence, and the origin and maintenance of biodiversity. Bacteria and fungi are used in experimental projects to address these issues.

A post-doc position is available in the evolutionary genetics group to work on the role of mitochondria in mechanisms of ageing, using microbial genetic and molecular methods. The project is part of the EU financed Integrated project MIMAGE and involves close collaboration with groups in Frankfurt and Paris.

Profile: PhD in Genetics, Evolutionary Biology or Microbiology. Preferably experience with genetic and molecular research on fungi; experience with molecular techniques on DNA / RNA. Affinity with evolutionary biology and statistical data analysis highly desirable.

The position is available for two years with possible extension. Max. salary ??? 3453 per month before tax.

Applications: Submit enquiries or applications (including CV, letter of motivation and names and contact info of two references) before April 2 to Rolf Hoekstra, rolf.hoekstra@wur.nl or to Fons Debets, fons.debets@wur.nl. Wageningen University is a small modern and well-equipped university in the center of

the Netherlands, whose research output was top-ranked in a recent survey of Dutch universities. The Department of Genetics was ranked 4.5 (scale 0-5) in another recent international evaluation.

Arjan de Visser

“Visser, Arjan de” <Arjan.deVisser@wur.nl>

YaleU PlacozoanDiversity

Postdoctoral position available immediately to work with Leo Buss (Yale-EEB) and Stephen Dellaporta (Yale-MCDB) on development of genomic tools for the study of placozoan diversity. The Trichoplax genome is slated for completion later this year and this position offers the opportunity to join a small group participating in this effort. Prior experience in molecular biology essential and in genomics or bioinformatics preferred. Contact leo.buss@yale.edu with CV and list of three referees.

leo.buss@yale.edu

WorkshopsCourses

London Parthenogenesis Sep22-24	72	UAlgarve MolEvol May6-12	74
MBL MolEvol Jul24-Aug5	73		
TrinityCollege ComparativeGenomics Sep18-20	74		

London Parthenogenesis Sep22-24

FIRST ANNOUNCEMENT for the ESF-Linnean Society workshop on “The Paradox of Asex: an evaluation” 22-24 September 2005 London.

Organizers: Hugh Loxdale (Rothamsted), Claudia

Ricci (Milano) and Peter van Dijk (Heteren)

Sponsors: European Science Foundation <http://www.esf.org/> and the Linnean Society of London <http://www.linnean.org/> TOPIC The workshop will be centered round six main themes:

* Developmental constraints on the evolution of asex * Maintenance of genetic variation in asexuals * Mutations and the maintenance of sex vs. asex * Asexuality and disease * Lineage sorting and group selection * Ap-

plied aspects of sex vs. asex

Our workshop is the last out of four within the Parthenogenesis Network (PARTNER), an initiative funded by the European Science Foundation (ESF). PARTNER is aimed to bring together empiricists and theorists who work in the field of parthenogenesis in botany and zoology (for more information, see <http://www.nioo.knaw.nl/networks/partner>).

LOCATION The workshop will be held at the rooms of the Linnean Society of London, Burlington House Piccadilly London W1J 0BF, United Kingdom.

CONFIRMED SPEAKERS Irina Arkhipova (Cambridge, MA), Laura S. Corley (Pullman & London), Brian Fenton (Dundee), Steve P. Foster (Harpending), Ueli Grossniklaus (Zürich), Rosalind John (Cardif), Peter D. Keightley (Edinburgh), Alexey S. Kondrashov (Bethesda), Ryszard Korona (Krakow), Curtis M. Lively (Bloomington), Thierry de Meeûs (Montpellier), Leonard Nunney (Riverside), Sarah Otto (Vancouver), Dave Parker (Aarhus), Joel R. Peck (Sussex), Charley Spillane (Cork) and Christoph Vorbuenger (Zürich).

APPLICATIONS We are happy to invite ca. 20 additional participants. Each invited attendant is expected to contribute a short oral presentation during the workshop (ca. 15 min). Applications should include a short CV and a brief description of the research interests (together max. two pages). Selection among the applicants will be based on research record and topic. The workshop organization will cover the accommodation costs in the facilities provided by the organization for invited attendants, but cannot cover their travel expenses. Applications, by email, should be submitted before April 23, 2005 to: p.vandijk@nioo.knaw.nl

“Dijk, Peter van” <P.vanDijk@nioo.knaw.nl>

MBL MolEvol Jul24-Aug5

Workshop on Molecular Evolution

<http://workshop.molecularevolution.org/> Michael P. Cummings, Director

24 July - 5 August 2005 plus extended special topics session 6 August - 12 August 2005

Application Deadline 1 March 2005

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; biogeography; 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

Preliminary List of Faculty -

Peter Beerli Joseph Bielawski Michael Cummings
Scott Edwards Joseph Felsenstein Claire Fraser Mark Holder Mary Kuhner Paul Lewis Axel Meyer Michael Miyamoto William Pearson David Rand Margaret Riley David Swofford Steven Thompson Paul Turner Daniel Voytas Anne Yoder Shozo Yokoyama

Preliminary list of Teaching Assistants -

Carlos Daniel Cadena Kelly Dyer Johanna Fehling Amy

Lawton-Rauh Naiara Rodriquez-Ezpeleta

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/>

TrinityCollege ComparativeGenomics Sep18-20

CALL FOR PAPERS Deadline: May 15, 2005

Third Annual RECOMB Satellite meeting on Comparative Genomics

September 18-20, 2005, Trinity College Dublin, Ireland

MEETING WEBSITE: http://www.gen.tcd.ie/-recomb_cg/ PROGRAM CO-CHAIRS: Daniel Huson, Center for Bioinformatics, Tuebingen University Aoife McLysaght, Trinity College, Dublin

ORGANIZERS: Daniel Huson, Center for Bioinformatics, Tuebingen University Jens Lagergren, Stockholm Bioinformatics Center & KTH Aoife McLysaght, Trinity College, Dublin David Sankoff, University of Ottawa, Canada

THEME AND SCOPE: Large-scale genome sequencing projects are generating vast amounts of data for a multitude of organisms including mammals and other vertebrates, invertebrates, fungi, plants, bacteria, and viruses. As the data increase so do the opportunities and the challenges for scientists to interpret them. By endeavouring to make sense of the process and pattern of genome evolution, comparative genomics lies at the forefront of this challenge.

The core of comparative genome analysis is the establishment of the correspondence between genes (orthology analysis) or other genomic features in different organisms. It is these intergenomic maps that make it possible to trace the evolutionary processes responsible for the divergence of two genomes. A multitude of evolutionary events acting at various organizational levels shape genome evolution. At the lowest level, point mutations affect individual nucleotides. At a higher level, large chromosomal segments undergo duplication, lat-

eral transfer, inversion, transposition, deletion and insertion. Ultimately, whole genomes are involved in processes of hybridization, polyploidization and endosymbiosis, often leading to rapid speciation. The complexity of genome evolution poses many exciting challenges to developers of mathematical models and algorithms, who have recourse to a spectrum of algorithmic, statistical and mathematical techniques, ranging from exact, heuristic, fixed parameter and approximation algorithms for problems based on parsimony models to Monte Carlo Markov Chain algorithms for Bayesian analysis of problems based on probabilistic models.

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

SUBMISSION GUIDELINES: Papers submitted for review should represent original, previously unpublished work. At the time the paper is submitted to the conference, and for the entire review period, the paper should not be under review by any other conference or scientific journal.

Successful submissions will be invited for a 25-minute presentation, and the paper will be printed in the conference proceedings, which will be published by Springer in the "Lecture Notes in Bioinformatics" series.

Papers should not exceed 10 pages (all inclusive) and must be submitted via the conference website http://www.gen.tcd.ie/recomb_cg/. KEY DATES: May 15, 2005 Paper submission deadline June 12, 2005 Notification of paper acceptance June 19, 2005 Poster submission deadline June 26, 2005 Final manuscript due

REGISTRATION: Please register via the conference website http://www.gen.tcd.ie/recomb_cg/ mclysaga@tcd.ie

UAlgarve MolEvol May6-12

Workshop on Molecular Evolution

The Biodiversity and Conservation Group (BioCon) of the Center for Marine Sciences of the University of Algarve is pleased to announce the Workshop on Molecular Evolution to be held from 6-12 May 2005. Lecturers: David Swofford, Gavin Naylor and Mark Holder from

Florida State University, USA Place: Quarteira, Algarve, Portugal Application deadline: 31 March 2005 Notification of acceptance: 11 April 2005 Payment deadline: 25 April 2005 Fee: 1200 all inclusive Course Fee, room (in twin bedroom) & board (breakfast, lunch and dinner) as well as all documentation provided at no additional charge. The course fees do not include travel or other subsistence costs. The organizing committee is trying to organize transport from the airport to the meeting place. Alternatively students may arrange their own accommodation, meals and transport from the airport to the meeting place, and the course fee will be 600. The course will consist of lectures, demonstrations of software implementing the concepts, and labs in which students will use software on their own computers to analyze both example data and their own data. Topics covered: Estimating phylogenies - distance and character-based (parsimony, likelihood and Bayesian) approaches - assessing confidence - supertree and split-based methods. Models - how do we choose

the an appropriate model - dealing with data from heterogeneous or non-stationary processes - inconsistency Uses of inferred trees - ancestral characters state reconstruction - inferring aspects of the evolutionary process - biogeography - estimating divergence times

How to apply Eligible participants:

This workshop is intended for last year PhD students or post-docs, with a basic knowledge of phylogenetics. Students must have their own datasets to analyze. Students must bring a laptop (Mac or PC) to work on during the workshop.

The organization will try to maximize the participation of different laboratories and the greatest number of European countries.

To apply send an email to rcastil@ualg.pt, subject Workshop.

Rita Castilho <rcastil@ualg.pt>

Instructions

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

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

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L^AT_EX 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 formatted) the message will be sent 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 preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.