
E v o l D i r

February 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.



Forward	1
Conferences	2
GradStudentPositions	10
Jobs	21
Other	33
PostDocs	50
WorkshopsCourses	66
Instructions	69
Afterward	70

Conferences

Auckland SMBE Jun19-23	2	Rothamsted MathMolBiol Mar21-22	6
Auckland SMBE05 Jun19-23 2	2	RoyalSocietyLondon SexualConflict May9-10	7
Fairbanks Evol05 Jun10-14	3	SouthernIllinoisU MEEC Mar11-13	7
Fairbanks Evol05 Jun10-14 StudentTravel	3	UGeorgia SEEC Mar11-13 2	7
Galapagos Evolution Jun9-12	4	UOregon Zebrafish Sept9-10	8
KristinebergSE AncestralSequeunceReconstruction Mar29-31	5	UOxford HapMap Mar15-18 Travel	9
Oslo phylogenetics call for symposia Jul25-29	5	UOxford HapMap Mar15-18 2	9
PennStateU NEEC Mar18-20	5	UWisconsinMadison PlantEvol Jun18-19	9

Auckland SMBE Jun19-23

The annual meetings of the Society for Molecular Biology and Evolution (www.smbe.org) will be held in Auckland, New Zealand, from June 19-23, 2005. It will highlight the latest research at the interface of molecular biology and evolution, especially highlighting the work of Allan Wilson. It is the joint annual meeting of SMBE and the Australasian Genetic Association.

Online conference and talk/poster registration are now available at www.mbe05.com. Deadline for ORAL/POSTER titles: March 1, 2005. Last date for early registration discount: March 15, 2005.

Sudhir Kumar <s.kumar@asu.edu>

Auckland SMBE05 Jun19-23 2

The annual meeting of the Society for Molecular Biology and Evolution (MBE05), to be hosted jointly with the Genetics Society of Australia, will be held at the Aotea Centre in Auckland, New Zealand from 19-23 June 2005.

Online conference and talk/poster registration is now available.

The conference web site can be accessed at: <http://www.mbe05.com> PLEASE BE AWARE OF THE FOLLOWING DEADLINES:

*The last day for talk/poster registration is 15 March 2005. Registration must be completed online before talk/poster submission. You will be advised by 27 March whether your talk has been accepted.

*The last day for discounted early registration is 1 May 2005. Conference fees will increase after this date with registrations closing on 31 May 2005.

OTHER HIGHLIGHTS:

*Information about accommodation in Auckland and a Partners Programme can be found on the website. There is an option to receive information for travel in both the North and South Islands of New Zealand.

*The request form for vendor and exhibitor registration can be found on the website.

*Sign up to receive conference updates by sending a message to mbe05-updates-subscribe@jevon.org.

A Lions Rugby Tour of New Zealand will commence soon after MBE05, we suggest you make your travel and accommodation arrangements as soon as possible.

—
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<http://AWCMEE.massey.ac.nz> Susan Wright
<s.m.wright@massey.ac.nz>

Fairbanks Evol05 Jun10-14

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/> 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.

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> *We anticipate that post-conference tour packages will be available the day after the conference, 15 June 2005. Information about these packages will soon be available on the web site, but space will be limited.

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**Fairbanks Evol05 Jun10-14
StudentTravel****STUDENT TRAVEL FUNDING FOR EVOLUTION
2005 - ARCTIC RESEARCH**

The Institute of Arctic Biology (<http://www.iab.uaf.edu/>) and University of Alaska Fairbanks (<http://www.uaf.edu/>) central administration have generously committed funding to assist graduate and undergraduate students presenting talks and posters at the Evolution 2005 Meeting, which will be held 10-14 June 2005 at the University of Alaska Fairbanks.

The conference website can be accessed at: <http://www.evolution05.uaf.edu/> Limited funding to cover the cost of the conference registration (and possibly more depending on the number of requests) currently is available for graduate and undergraduate students who *register and present talks or posters* that focus on themes of Arctic adaptation, physiology, genetics, or other areas of research conducted within the Arctic or sub-Arctic. These funds are intended to promote interdisciplinary interaction and joint participation of students and faculty in two Arctic-theme symposia that will take place at this conference:

Saturday, 11 June, 8 a.m.-Noon Sponsor: UAF-University of Alaska Museum Organizer: Link Olson Ecotypic Variation in the Context of Global Climate Change: Revisiting the "Rules"

Saturday, 11 June, 1:30-5 p.m. Sponsor: UAF-Institute of Arctic Biology Organizer: Matt Olson Population Genetics of Adaptation to Arctic and Alpine Environments

The symposia schedule is available online at: <http://www.evolution05.uaf.edu/symposia.cfm>

Students requesting funding should register their talks/posters online at the conference website (<http://www.evolution05.uaf.edu/registration.cfm>) no later than 31 March 2005 and then submit an email stating the nature of the financial need and an abstract (250 words maximum) describing the research to be presented.

Travel awards will be distributed after the 31 March talk/poster registration deadline.

Students from Fairbanks and Anchorage are not eligible for these awards.

Please include the words “student travel” in the subject line of your email, and send applications by email to:

Kevin G. McCracken email: fkgm@uaf.edu

Kevin G. McCracken Institute of Arctic Biology & Department of Biology and Wildlife University of Alaska Fairbanks Fairbanks, Alaska 99775 office (907) 474-6419

fkgm@uaf.edu

Galapagos Evolution Jun9-12

World Summit on Evolution Galapagos, June 9 to 12 2005

*Day 1: Evolution from the origins of life to humans Opening 8:45-9:00 Dr. Carlos Montufar (Universidad San Francisco de Quito, Ecuador)

Session I Chair: Dr. Sun Weiguo (Nanjing Institute of Geology and Palaeontology, China) 9:00-9:45 Dr. Antonio Lazcano (Universidad Autónoma de México, Mexico): Origins of life 9:45-10:30 Dr. Mikhail Fedonkin (Paleontological Institute RAS, Russia): Evolution in the Archean and Proterozoic Eons 10:30-11:15 Dr. Richard Fortey (British Museum of Natural History, England): Recent evolution in the Phanerozoic Eon 11:15-12:00 Discussion Commentators: Dr. William Schopf (University of California-Los Angeles, USA), Stefan Bengtson (Swedish Museum of Natural History, Sweden)

12:00-13:30 Lunch

Session II Chair: Dr. Gabriel Trueba (Universidad San Francisco de Quito, Ecuador) 13:30-14:15 Dr. Peter Gogarten (University of Connecticut, USA): Bacteria and the genetic basis of evolution 14:15-15:00 Dr. Geoff McFadden (University of Melbourne, Australia): Protists and cellular phenomena in evolution 15:00-15:30 Discussion Commentators: Dr. Margaret Riley (University of Massachusetts-Amherst, USA), Dr. Laura Katz (Smith College, USA)

15:30-16:00 Break

Session III Chair: Dr. Diego Quiroga (Universidad San Francisco de Quito, Ecuador) 16:00-16:45 Dr. Timothy White (University of California-Berkeley, USA): Human paleontology record 16:45-17:30 Dr. L. Luca Cavalli-Sforza (Stanford University, USA): Molecular evolution of the human animal 17:30-18:00 Discussion

Commentators: Dr. Eudaldo Carbonell (Universitat Rovira i Virgil, Spain),

Day 2: Evidence for evolution Session I Chair: Dr. Carlos Valle (Universidad San Francisco de Quito, Ecuador) 9:00-9:45 Dr. Leticia Avilés (University of British Columbia, Canada): Levels of selection 9:45-10:30 Dr. Joan Roughgarden (Stanford University, USA): Sexual selection in animals 10:30-11:15 Drs. Peter and Rosemary Grant (Princeton University, USA): Evolution and ecology in the Galapagos 11:15-12:00 Discussion Commentators: Dr. Trevor Price (University of Chicago, USA), Dr. Sean Rice (Yale University, USA), Dr. Patricia Gowaty (University of Georgia, USA)

12:00-13:30 Lunch

Session II Chair: Dr. Lourdes Torres (Universidad San Francisco de Quito) 13:30-14:15 Dr. Douglas Schemske (Michigan State University, USA): Microevolution in plant populations 14:15-15:00 Dr. Peter Stevens (Missouri Botanical Garden, USA): Systematics and diversity in plants 15:00-15:30 Discussion Commentators: Dr. John Avise (University of Georgia, USA), Dr. Kevin de Queiroz (Smithsonian Institution, USA)

15:30-16:00 Break

Session III Chair: Dr. Mary Jane West-Eberhard (Universidad de Costa Rica, Costa Rica) 16:00-16:45 Dr. Gunter Wagner (Yale University, USA): Development as an evolutionary phenomenon in animals 16:45-17:30 Dr. Kenneth Wolfe (University of Dublin, Ireland): Fungi genomics and bioinformatics 17:30-18:00 Discussion Commentators: Dr. Billie Swalla (University of Washington, USA), Dr. Masatoshi Nei (Pennsylvania State University, USA)

20:00-22:00 Student poster session

Day 3: Field Trip Dr. Frank Sulloway (University of California-Berkeley, USA): Tour leader

Day 4: What is evolution? Session I Chair: Dr. David Wake (University of California-Berkeley, USA) 9:00-9:45 Dr. William Provine (Cornell University, USA): The history of evolutionary thought 9:45-10:30 Dr. Elisabeth Vrba (Yale University, USA): What can evolution and evolutionist do 10:30-11:15 Dr. Niles Eldredge (American Museum of Natural History) USA), Unsolved problems in evolution 11:15-12:00 Discussion Commentators: Dr. Mary Winsor (University of Toronto, Canada), Dr. Bruce S. Lieberman (University of Kansas, USA), Dr. Douglas Futuyma (University of Michigan, USA)

12:00-13:30 Lunch

Session II Chair: Dr. Jan Sapp (York University,

Canada) 13:30-14:15 Dr. Lynn Margulis (University of Massachusetts-Amherst, USA): Evolution by symbiosis 14:15-15:00 Dr. Richard Michod (University of Arizona, USA): Evolution by genes 15:00-15:30 Discussion Commentators: Dr. Colleen M. Cavanaugh (Harvard University, USA), Dr. Pierre-Henri Gouyon (Université Paris-Sud, France)*

Gabriel Trueba <gabriel@usfq.edu.ec>

KristinebergSE
AncestralSequenceReconstruction
Mar29-31

USING ANCESTRAL SEQUENCE RECONSTRUCTION TO UNDERSTAND PROTEIN FUNCTION

Conference Information:

March 29-31, 2005

Kristineberg, Sweden

Registration Deadline: February 15, 2005

Website: <http://www.cbu.uib.no/asr> Contact Information: liberles@cbu.uib.no

Sponsored by ESF (the European Science Foundation) and Vetenskapsradet, the Swedish Research Council

David Liberles <David.Liberles@bccs.uib.no>

Oslo phylogenetics call for symposia
Jul25-29

24th meeting of the Willi Hennig Society, 25-29 July 2005 in Oslo, Norway.

FINAL CALL FOR SYMPOSIA PROPOSALS

Respond by 28 FEBRUARY for full consideration

Please email Victor A. Albert (victor.albert@nhm.uio.no) with concrete plans for symposia, including a 1-2 paragraph description, and a list of proposed speakers and their topics. These symposia proposals will be assessed in light of other proposals registered.

SYMPOSIA PROPOSALS SHOULD FOCUS ON

TOPICS OF PHYLOGENETIC OR PHYLOGENOMIC INTEREST, THEORETICAL AND/OR EMPIRICAL.

Symposia may be tightly or loosely circumscribed, but must center on an overarching theme. Student/postdoc/principal-investigator presentations may be mixed. All abstracts (each ISI listed) will be published in the journal CLADISTICS, and symposium proceedings proposals will be entertained.

This conference on PHYLOGENETIC BIOLOGY (both theoretical and empirical) will be held at the Quality Fagernes Hotell (<http://www.choicehotels.no/html/en-gb72665.jsp>) in the beautiful mountains just north of Oslo, Norway.

Single or double rooms with a full pension package will be available, as will cheaper options for youth hostel bookings with or without full pension at the nearby Quality Fagernes Hotell. Package rates have been negotiated to rather reasonable costs, and all sessions will be held on-site at the hotel.

Presentations are invited within pre-planned symposia (above), or as selected from contributions (e.g., from poster submissions) as time permits. 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.

Please check back on the Evoldir web site for full registration information, or for preliminary details, email the address above.

victor.albert@nhm.uio.no

PennStateU NEEC Mar18-20

Northeast Ecology and Evolution Conference 2005 March 18th-20th The Pennsylvania State University University Park, PA <http://www.ecology.psu.edu/nec> FINAL CALL FOR ABSTRACTS AND EARLY REGISTRATION Deadline: February 4, 2005

The Third Annual Northeast Ecology and Evolution Conference (NEEC) will be held March 18 - 20, 2005 at The Pennsylvania State University (University Park, PA)

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Abstract submission and early registration will be accepted via our secure server until February 4, 2005. We will accept late registrants until March 4, 2005.

To register now visit the conference website: www.ecology.psu.edu/nec NEEC is a professional meeting organized by graduate students and post-docs to provide a forum for advanced undergraduates, graduate students, and post-docs to present their research in the form of a poster or talk. NEEC fosters a low stress environment for students and postdocs in the environmental and life sciences to present their findings to their peers and develop friendships within their fields. It will

include 2 days of talks, open to undergraduates, graduate students, and post-docs, a poster session, and evening receptions and lectures.

The weekend will also include a reception and panel discussion on "Setting Up a Research Program" on Friday night and a keynote banquet on Saturday night. The keynote speaker will be Dr. Peter Kareiva. Dr. Kareiva has a very distinguished career in ecological research and presently serves as Lead Scientist for the Nature Conservancy. The title of his talk is Conservation Struggles to Mature from "Reactive Teenager" to "Judicious Adult": Salmon, Return on Investment, and Strategic Priorities

For further information visit the conference website at www.ecology.psu.edu/nec or contact us at nec2005@yahoo.com.

NEEC 2005 Organizing Committee

meisel@psu.edu meisel@psu.edu

Rothamsted MathMolBiol Mar21-22

LAST CHANCE TO REGISTER FOR MEETING/SUBMIT TALKS

MASAMB-2005 (Mathematical and Statistical Aspects of Molecular Biology)

The 15th Annual meeting of 'Mathematical and Statistical Aspects of Molecular Biology' will take place at Rothamsted Research, Harpenden on 21 and 22 March 2005.

The conference web site can be found at <http://www.rothamsted.bbsrc.ac.uk/bab/masamb> TALKS on research relevant to the workshop are invited. Abstracts must be submitted using the on-line system at

the MASAMB-2005 web site (see above). Submitted abstracts will be reviewed by the organising committee and selected speakers will be informed by the end of January. Speakers will be asked to make their presentation available in electronic form for inclusion on this website after the meeting (pdf or Powerpoint format). The meeting will contain approximately 12 half-hour talks selected from participants' submissions.

POSTERS (portrait format, maximum depth 120 cm) on research relevant to the workshop are also invited for the poster sessions to be held on both days. To submit a poster, send an abstract using the MASAMB-2005 web based abstract submission. Accepted abstracts will be displayed on the web site. Following the meeting, posters may be published on this web site (pdf format required)

REGISTRATION costs £90 which includes lunch on both days and the conference dinner. The cost for full-time students is £60. Registration must be made using through the MASAMB-2005 web system (see address above). The evening meal will take place at Rothamsted.

ACCOMMODATION may be requested through the workshop website at the designated conference hotel (Hertfordshire Moat House, Markyate, offering swimming pool and gymnasium) at a preferential conference rate of £80. Hertfordshire Moat House bookings not made through the conference website (which generates the booking form when you register) will have to pay standard hotel rates. Hotels in the Harpenden area tend to get fully booked. Please ensure that you arrange accommodation at an early date.

BACKGROUND Bioinformatics and statistical genetics, twin themes of the long-running series of annual MASAMB meetings (see the archive at <http://www.ebi.ac.uk/goldman-srv/masamb>), have gained huge impetus from large-scale genome sequencing projects and development of high-throughput biological assay systems, including gene-expression microarrays. These immense data resources, and the underlying complexities of molecular and cell biology, provide exciting research opportunities for numerate scientists.

With typically around 60-80 participants from mathematics, statistics, computer science, bioinformatics, biology and related fields, the MASAMB meetings provide an intimate setting for exchange of ideas in methodological and applied research. Research students and scientists newly entering the field of genomic and/or post-genomic research are particularly welcome.

Posted by Nick Goldman (goldman@ebi.ac.uk) on behalf of:

Paul J Verrier Biomathematics and Bioinformatics Division Rothamsted Research West Common, Harpenden, Hertfordshire. AL5 2JQ, UK tel: 01582 763133 ext 2415 fax: 01582 760981 email: paul.verrier@bbsrc.ac.uk

Royal Society London Sexual Conflict May 9-10

A Royal Society discussion meeting on 'Sexual conflict: a new paradigm?' is taking place in London on Monday 9 and Tuesday 10 May 2005. This meeting is organised by Dr Tracey Chapman, Dr Tom Tregenza and Dr Nina Wedell. A synopsis follows:

Sexual reproduction is fraught with conflict. The potential for mates to exploit one another leads to divergence in sex roles and two very different types of individual being built by the same genes. Knowledge of the conflicts between genes in males and females is shaping how we understand the evolution of mating systems, of sex ratios and of sex itself.

Speakers: Göran Arnqvist Adam Chippindale Andrew Clark Sergey Gavrilets David Haig Hanna Kokko Kate Lessells Geoff Parker Andrew Pomiankowski William Rice Locke Rowe Mike Siva-Jothy Willie Swanson

The meeting is FREE to attend and open to all, though pre-registration is essential. Full details, including an on-line registration form, can be accessed at www.royalsoc.ac.uk/events. Froniga Lambert Events Manager tel +44 (0) 20 7451 2574 fax +44 (0) 20 7451 2543 <http://www.royalsoc.ac.uk/events>

The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG

Registered Charity No 207043 The Royal Society - excellence in science

"Lambert, Froniga" <Froniga.Lambert@royalsoc.ac.uk>

Southern Illinois U MEEC Mar 11-13

Final call for papers

Early Registration and Abstract Deadline: February 1st, 2005

25th Annual Midwest Ecology and Evolution Conference

Southern Illinois University-Carbondale

March 11th-13th, 2005

The graduate students in the Departments of Plant Biology and Zoology at Southern Illinois University-Carbondale would like to invite graduate students and post-doctoral associates from the Midwestern United States to submit abstracts for oral and poster presentations at the 25th Annual Midwest Ecology and Evolution Conference (MEEC).

MEEC is a migratory conference hosted by universities in the Midwest eco-region that is organized by graduate students. This conference provides an informal venue for undergraduate, graduate, and post-doctoral students interested in ecology to present their research to an audience of their peers, fostering an environment of collaboration and communication between future scientists.

This year, MEEC will be hosted by Southern Illinois University in Carbondale, Illinois, and held at the Carbondale Civic Center from March 11-13, 2005. The conference will feature a keynote address by Dr. Robert E. Ricklefs, Curators' Professor of Biology at the Department of Biology, University of Missouri at St. Louis, and a plenary presentation by Dr. Jerry O. Wolff, Program Director for the National Science Foundation.

In addition to contributed sessions on topics in ecology and evolution, invited and contributed papers will be considered for two special

symposia: (1) Paleocology, and (2) Conservation and Climate Change. Manuscripts submitted from presentations will be considered for publication in a special issue of the American Midland Naturalist.

Deadline for submission of abstracts and early registration is February 1st, 2005. Early registration fee is \$40.

For more information, go to <http://mypage.siu.edu/-meec2005> or email meec2005@siu.edu.

Please forward this solicitation accordingly. Thank you.
bbensc01@siu.edu

UGeorgia SEEC Mar 11-13 2

LAST CALL FOR ABSTRACTS

SEEC 2005 SOUTHEASTERN ECOLOGY AND EVOLUTION CONFERENCE THE UNIVERSITY OF GEORGIA ATHENS, GEORGIA 11-13 MARCH 2005 www.uga.edu/seec REGISTRATION DEADLINE: 4 FEBRUARY 2005

We invite all graduate, undergraduate, and post-doctoral researchers studying in the environmental and life sciences to submit abstracts for either oral or poster presentations at the 2nd annual Southeastern Ecology and Evolution Conference (SEEC) to be held March 11-13, 2005, at the The University of Georgia in Athens, Georgia. Talks will be delivered by Drs. Whit Gibbons, John Avise and Gary Barrett.

SEEC is a professional meeting intended for students in the environmental and life sciences to present their research to their colleagues in a comfortable, fun, and low stress environment. Such events are designed to encourage new friendships within our field and to share newly developed research ideas for feedback. While we expect most SEEC participants to be from the Southeast, we encourage and welcome all interested individuals to submit abstracts and/or attend.

To encourage attendance, registration is only \$15 and covers meeting attendance, two continental breakfasts, snacks, coffee, a t-shirt, and \$100 cash awards for the best oral and poster presentations. The registration and abstract submission deadline is February 4, 2005, and may be completed at the following web site:

www.uga.edu/seec We look forward to seeing you at The University of Georgia in Athens for the 2nd Annual Southeastern Ecology and Evolution Conference this March!

For more information, go to www.uga.edu/seec or email Tom Luhring at tluhring@uga.edu

Thomas Luhring <tluhring@uga.edu>

UOregon Zebrafish Sept9-10

Dear Zebrafish Community,

This is an announcement for the Third Biennial West Coast Zebrafish Meeting, to be held September 9-10, 2005 at the University of Oregon in Eugene. Following the tradition of successful meetings held in Seattle in 2001 and Salt Lake City in 2003, we look forward to hosting another great conference. Please mark your calendar! These dates do not overlap with the

SDB meeting, the European Zebrafish Meeting, or the Woods Hole Zebrafish Course and early September is a beautiful time of year to visit Oregon.

The fish labs here in Eugene (Cresko, Darimont, Eisen, Guillemain, Kimmel, Postlethwait, Varga, Washbourne, and Westerfield) would be delighted to have you and your lab come and visit. While we anticipate that most attendees will be from the West Coast, everyone is welcome, and we hope that many U of O alumni will use this meeting as an opportunity to visit their old stomping grounds and reunite with friends.

Our intent is to have a fun, informal, and interactive meeting. We hope to attract researchers in all areas of zebrafish biology, as well as those working in related systems such as stickleback and medaka. We are particularly interested in providing a forum for graduate students and postdocs to present their work and to promote more discussion than is sometimes possible in the packed schedule of larger meetings. We also intend to keep this meeting affordable. There are direct flights from many West Coast cities to Eugene. Cheaper fares can sometimes be obtained by flying into Portland, which is an hour and 45 minute drive from Eugene. Rooms will be available at several motels in easy walking distance of the conference for ~\$80/double occupancy. We expect that registration fees will be in the range of ~\$150, which will include all meals during the conference (two breakfasts, two lunches, and two dinners) as well as coffee breaks and refreshments at the opening reception. We encourage people to stay over the weekend and will have planned outdoor activities for Sunday.

We hope that you will join us for the Third Biennial West Coast Zebrafish Meeting and we ask that you spread the word to other colleagues who might be interested. By the first of May we will post information about registration and abstract submission on our meeting website (<http://www.uoneuro.uoregon.edu/-wczm/wczm.html>). In the meantime, please feel free to email with comments, questions, or suggestions to: wczm@uoneuro.uoregon.edu.

See you in Eugene,

Karen Guillemain and Phil Washbourne

William Cresko <wresko@uoneuro.uoregon.edu>

UOxford HapMap Mar15-18 Travel

Two important things to note about the forthcoming conference on the HapMap and its applications.

- 1) NHGRI is making travel awards for young investigators, and
- 2) The deadline for submitting abstracts is January 28, 2005

The conference announcement and details regarding travel awards follow below for ease of reference.

Conference: Genomic Studies and the HapMap University of Oxford, UK March 15-18, 2005

The deadline for submitting an abstract is January 28, 2005. The deadline for registration/lodging reservations is February 25, 2005.

By March 2005, Phase I of the HapMap (600,000 common SNPs typed in 270 individuals) will be complete and Phase II (an additional 3-4M SNPs in the same samples) will be well underway. But there remain many unresolved questions about how best to utilize this information in genetic research. This conference will be hosted by the Department of Statistics at the University of Oxford, and supported in part by the Wellcome Trust, and its primary focus will be the use of the HapMap resource in genomic studies: human disease studies, and other population genetic and evolutionary analyses.

“Genomic Studies and the HapMap” will provide an important opportunity for a diverse community of investigators—those involved directly in the International HapMap Project, those in the broader analysis community, and those whose focus is disease studies—to come together to define and discuss a range of issues related to the use of the HapMap resource. It will also provide up-to-date assessments of the progress and results from the project. Invited speakers from outside the HapMap project include Andy Clarke, David Clayton, David Cox, Mark McCarthy, Rasmus Nielsen, Jonathan Pritchard, Matthew Stephens, and Simon Tavaré. This conference follows a successful meeting held in the spring of 2004, which brought together well over 100 participants interested in methods and analysis related to the International Haplotype Map Project.

The National Human Genome Research Institute is providing travel awards of \$750 to up to 13 young investigators from U.S. institutions (defined as completion of doctoral training within the last 6 years). U.S. citizenship is not a requirement. Qualified persons requesting consideration for a travel award must submit the following items to melindaagray@comcast.net, no later than January 28:

- 1) current CV

- 2) formatted abstract (please refer to the abstract submission guidelines on the conference Web site)

- 3) conference registration and lodging form (please refer to the registration page on the conference Web site, and note that your credit card will not be billed until early March)

Awards will be made based on the research submitted in the abstract and the academic promise of the candidate with some priority given to applications from women, underrepresented minorities, and applicants with disabilities. Submitted material will be reviewed, and funding decisions made, by the conference programme committee.

Complete instructions for abstract submission and registration, and further details of the conference, can be found at the conference Web site, www.hapmap.org/oxford_conference/default.html .
donnely@stats.ox.ac.uk donnely@stats.ox.ac.uk

UOxford HapMap Mar15-18 2

This is a final reminder that the deadline for abstracts, and for applications from US-based young researchers for travel support, is Friday January 28, 2005.

The conference, “Genomic Studies and the HapMap”, will be held at the University of Oxford, UK, from March 15-18, 2005.

Complete instructions for abstract submission and registration, and further details of the conference, can be found at the conference Web site, www.hapmap.org/oxford_conference/default.html .

UWisconsinMadison PlantEvol Jun18-19

AGA Annual Meeting and Symposium Plant Evolution: Genes and Phenotypes to be held jointly with the International Conference on Arabidopsis Research

Topics will include: Evolution & Development, Population Genetics and Quantitative Genetics

The Wilhelmine E. Key Lecture will be given by Professor June Nasrallah (Cornell). “Mating system evolution

in crucifers”

Plenary Session: Population Genetics

1. Professor Michael Purugganan (NCSU) - Adaptation and variation in Arabidopsis flowering 2. Professor Magnus Nordborg (USC) - Linkage disequilibrium mapping in Arabidopsis 3. Professor Tom Mitchell-Olds (MPI) - Evolution of ecologically important traits in relatives of Arabidopsis 4. Speaker chosen from the meeting abstracts

Parallel Session 1: Evolution and Development

1. Professor Vivian Irish (Yale) - Evolution of MADS box gene function in the angiosperms 2. Professor David Baum (UW-Madison) - The evolution of inflorescence architecture in Brassicaceae 3. Professor Neelima Sinha (UC-Davis) - Transcription factors, gene expression and leaf evolution 4. Speaker chosen from the

meeting abstracts

Parallel Session 2: Quantitative Genetics

1. Professor Susan McCouch (Cornell) - Discovery and characterization of alleles associated with domestication-related traits in rice 2. Professor Jeff Conner (Michigan State) - The roles of genetic integration and constraint in adaptive evolution: a floral case study 3. Professor John Willis (Duke) - Genetic Control of Adaptation and Reproductive Isolation in Mimulus 4. Professor Mark Rausher (Duke) - Identification of a gene causing reproductive isolation in Phlox

The meeting will be held at the Memorial Union of University of Wisconsin, Madison June 18-19, 2005 Registration, abstract submission and accommodation information will be available <http://www.union.wisc.edu/-conferenceservices/arabidopsis/> - jdoebley@wisc.edu

GradStudentPositions

AmericanU EvolBiol	10	UHelsinki SystematicsEvolutionMyrmicaAnts	17
Biodiversity Conservation	11	ULausanne 2 EvolSymbiosis	17
MarieCurieResearchNetwork 2 SEXASEX	11	ULouisianaMonroe FishSystematics	18
Mexico MarineNematodeEvol	12	UMassachusetts Modelling	19
MichiganStateU HunterSelection	13	UNEuchatel EvolEcol	19
MichiganStateU SelectiveHarvesting	14	UNewOrleans EvolBiol	19
Trondheim EvolAnimalBehaviour	14	USheffield EvolAgeing	20
UAlaskaFairbanks PopGenet	15	USouthDakota StalkEyedFlies	64
UCalgary EvolEcol	16	UVigo ComputationalEvolBiol	21
UDurham PopGenetics	16		
UEdinburgh LanguageEvol	16		

AmericanU EvolBiol

The Department of Biology at American University announces several graduate assistantships available for students interested in pursuing a M.A. or M.S. in Biology. The current stipend for a M.S./M.A. student is up to \$10,000, along with tuition remission and

an additional \$6750 in part time wages for teaching. Good students can be compensated up to \$20,000. Areas of faculty interest and current research in our department include: Population genetics and molecular systematics of coleoid cephalopods. Mapping of subterranean biodiversity for the U.S. and Europe. For more information about AU, the Biology Department, and to contact faculty directly, please visit our website: http://www.american.edu/cas/bio/-welcome_bio.html jm7224a@american.edu

Biodiversity Conservation

International PhD opportunities in Biodiversity and Conservation

The European Centre for Biodiversity and Conservation Research is pleased to announce topics for a cohort of international PhD studentships, to start in Autumn 2005. These EU-funded studentships are designed in part to foster mobility, and so are open to applicants from anywhere in the world except the UK (for specific eligibility rules see http://www.leeds.ac.uk/european/-information/marie_curie/marie_est.html). Marie Curie students will be treated as University employees, and so each of the projects listed below has both a project description and a job description associated with it.

The closing date for applications is March 4th 2005. Interviews will be held in March/April 2005.

Marie Curie Studentship topics:

The causes and consequences of population size for genetic diversity and population viability: an experimental study. Supervisors: Tim Benton, School of Biology (t.benton@abdn.ac.uk) Steve Sait, School of Biology

Biodiversity impacts of invasive species at multiple spatial scales Supervisors: Bill Kunin, School of Biology (w.e.kunin@leeds.ac.uk) Oliver Phillips, School of Geography Andy Nelson, School of Geography

How does biodiversity affect critical ecosystem functions in tropical forests? Supervisors: Simon L. Lewis, School of Geography (s.l.lewis@leeds.ac.uk) Jon Lloyd, School of Geography Oliver L. Phillips, School of Geography Bonaventure Sonke, University of Yaounde

Understanding species responses to environmental change: Insect-plant interactions at range margins Supervisors: Steven Sait, School of Biology (s.m.sait@leeds.ac.uk) Bill Kunin, School of Biology

Modelling disease threats to island biodiversity Supervisors: Simon Goodman, School of Biology (s.j.goodman@leeds.ac.uk) Alison Dunn, School of Biology Andrew Cunningham, Institute of Zoology, Zoological Society of London

Biological invasions - does enemy release affect invasion success? Supervisors: Alison M. Dunn, School of Biology (a.dunn@leeds.ac.uk) Judith E. Smith, School of Biology

Biodiversity response to climate change during the Late Cretaceous (~70Ma) in Antarctica: investigating extinctions and radiations of Antarctic palynomorph floras Supervisors: Jane Francis, School of Earth & Environment (j.francis@earth.leeds.ac.uk) Jim Riding, British Geological Survey, Alistair Crame, British Antarctic Survey Chronis Tzedakis, School of Geography

Project descriptions and details can be found on the EBI studentship website:

<http://www.ebi.org.uk/studentships-proposals-mc.htm> Applicants for Marie Curie doctoral studentships in Biodiversity and Conservation research should apply through the Graduate School of the Faculty of Biological Sciences:

http://www.fbs.leeds.ac.uk/gradschool/-how_to_apply.htm Make sure to note on your application form that you are applying for a studentship through the Marie Curie EST in Biodiversity and Conservation Research, and name the project and supervisor(s) of interest. Marie Curie studentships are administered as contracts of employment, and consequently a separate job application will be required by successful studentship applicants at a later date.

If you have additional queries concerning a particular project, please contact the proposed supervisor(s). Queries about the Biodiversity and Conservation Research EST programme as a whole can be addressed to its co-ordinator, Dr. William Kunin (Tel: +44 113 343 2857; e-mail: w.e.kunin@leeds.ac.uk).

S.J.Goodman@leeds.ac.uk S.J.Goodman@leeds.ac.uk

MarieCurieResearchNetwork 2 SEXASEX

Marie Curie Research training network (MRTN) SEXASEX 2 positions available

Students and researchers interested in the paradox of sex in evolutionary biology are strongly encouraged to apply for a research position in the European Union Marie Curie Research Training Network SEXASEX, which is co-ordinated by Prof. Dr. Koen Martens, RBINSc, Brussels. Criteria of eligibility include: EU citizenship, less than 4 years of research experience for Young Researchers (YR), less than 10 years for Experienced Researchers (ER), and a willingness to work in a European country other than the country of origin. We

seek candidates who are enthusiastic about evolutionary biology, travelling and living abroad, learning in a multidisciplinary research environment and working in teams. All appointments will be for 3 years, YR are offered PhD positions, ER post-doc positions. YR will be expected to obtain a PhD at the end of the project. The application of female candidates is especially encouraged; detailed information on child care facilities at the different institutions will be provided upon request. Aid can be sought if accompanying spouses also require employment abroad.

Project overview: Sex is the queen of evolutionary problems. It will be tackled by SEXASEX in a multidisciplinary approach, providing training and transfer of knowledge for a total of 360 person-months. 10 network researchers (6 young researchers (YR) and 4 experienced researchers (ER)) will receive training in 9 institutions across as many countries. A wide array of research tools will provide excellent training opportunities, for example through individual career development plans, individual tutoring and secondments, which will be supplemented by participation in courses and external workshops. Network-wide training will exploit the extensive experience of the partner institutions through five courses and summer schools for all network researchers. Complementary skills such as management and communication (verbal, written) will be developed, and gender awareness will be raised, in two network-wide meetings. The networks theoretical and empirical research will apply 13 major approaches, including novel genomic and karyological approaches, intraspecific phylogeography, ecology, behavioural studies, GIS analyses and theoretical modelling. With this multidisciplinary toolkit, SEXASEX will investigate why sex exists at all, given its evolutionary costs, using the model organism *Eucypris virens*, a non-marine ostracod species with both sexual and asexual reproduction. What determines its gender, what are the genomic consequences of long-term asexuality, what is the cohesiveness of a species with mixed reproduction, how do asexuals and sexuals compete and what is their historical zoogeography? The pluralistic approach of SEXASEX is unique and timely, using highly novel methodologies and dealing with cutting edge science based on European excellence and tradition. Please refer to <http://www.naturalsciences.be/EVIRENS/> for more information.

Send full applications, comprising letter of interest, CV and coordinates of at least two potential referees before the 7th of February 2005 to

Dr Isa Schön, Royal Belgian Institute of Natural Sciences, Freshwater biology, Vautierstraat 29, B-1000 Brussels, Belgium E-mail

(Isa.schoen@naturalsciences.be) Fax : +32 2 62 74 113.

Correspondence by email is preferred.

Applications for the following two PhD positions starting beginning of November 2005 are now sought.

IMPORTANT REMARK: due to the fact that one of the promoters of positions PHD POSITION 6 has moved from Finland to Switzerland, the earlier announcements of these positions are herewith corrected: 1. the position will be shared by the labs in Zürich (Switzerland) and Montpellier (France), NOT by the labs in Oulu (Finland) and Montpellier (France). 2. Finnish candidates are now allowed to apply, but people with Swiss nationalities are no longer eligible.

PHD POSITION 2: GENETIC DIVERGENCE AND ISOLATION AMONGST SEXUAL AND BETWEEN SEXUAL AND ASEQUAL LINEAGES OF NON-MARINE OSTRACODS. Starting date: 1st November 2005 Duration: 36 months (2x 18 months) Salary: country-specific plus tax-free mobility allowance Persons in charge: Prof. Dr Roger Butlin, UK Prof. Dr Jan Zima, Czech Republic Locations: Sheffield, UK & Brno, Czech Republic Place of work: University of Sheffield, Department of Animal and Plant Sciences; Academy of Science, Institute of Vertebrate Biology & Charles University, Department of Zoology Job description: The student will measure the genetic variation within and differentiation between sexual populations of *Eucypris virens*. Similarly, the clonal diversity of asexual populations will be assessed. Together with sequence data from other members of the Network, the data will be used to

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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>

Mexico MarineNematodeEvol

PhD and MSc studentship positions are available to work on the coastal Nematofauna of the Gulf of California, Mexico at the "Centro de Investigacion Cientifica y de Educacion Superior de Ensenada" (CICESE).

I am seeking highly motivated students interested in developing graduate research on free living marine nematodes in a project aimed to characterize regional levels

of biodiversity. Specific research topics are open and may range from taxonomical, morphological, molecular, and ecological and/or evolutionary in nature. Candidates with a background in marine nematodes are highly encouraged to apply. The research will be carried out in the context of Biotic Surveys (National Science Foundation, USA) and Consejo Nacional de Ciencia y Tecnologia (CONACYT, Mexico) funded projects involving a network of collaborators at CICESE (Axayacatl Rocha-Olivares), Universidad Autonoma de Baja California (Dora Waumann), University of California Riverside (James Balwin, Paul de Ley, Manuel Mundo), University of New Hampshire (Kelley Thomas), and The Museum of Natural History in London (John Lambshead).

CICESE (www.cicese.mx) is one of the top Mexican federal research institutions with an internationally recognized division and graduate programs in marine sciences. Ensenada is located on the Pacific coast of Baja California ca. 100 km from the international border with the US.

Studentships are funded by CONACYT for a period of 3(PhD) or 2 (MSc) years and are contingent on admission to CICESE's graduate program in Marine Ecology (<http://ecologia.cicese.mx/posgrado/-index.htm>). There are no nationality requirements but because teaching is in Spanish, a working-level fluency is highly desirable. PhD applications will be reviewed as they are received and starting date is negotiable whereas MSc will be admitted for the Fall Quarter (starting in September 2005) and full applications must be received by May 2005.

Apologies for cross postings.

Prospective students please contact:

Axayacatl Rocha-Olivares, Ph.D. CICESE Biological Oceanography Department P. O. Box 434844 San Diego, CA, 92143-4844

DOMESTIC: Apartado Postal 2732 Ensenada, Baja California, CP 22830 Mexico

COURIER: Km 107 Carretera Tijuana-Ensenada Ensenada, Baja California, CP 22860 Mexico

Office: +52(646)175-0500 (ext. 24240) Lab: +52(646)175-0500 (ext. 24318) Fax: +52(646)175-0545

Email: arocha@cicese.mx <http://dob.cicese.mx/pag/-arocha.htm>

Axayacatl Rocha <arocha@cicese.mx>

MichiganStateU HunterSelection

M.S. Research Assistantship ? Michigan State University

A funded Graduate Research Assistantship is available for a student interested in investigating the evolutionary consequences of selective harvesting of Michigan white-tailed deer. This M.S. project will quantify hunter-induced selection and will include morphological measurement of harvested deer at deer-check stations (e.g. beam diameter, hind foot length, age, weight), hunter surveys to quantify effort and analysis of historical data to examine spatial and temporal patterns of deer harvesting in Michigan. This funded position includes stipend, tuition and benefits and will start in August 2005.

Candidates should have experience and interests in applied field biology, evolution and natural resource management and strong quantitative and interpersonal skills. Interested applicants should send a cover letter outlining their research interests and experience, CV and a copy of GRE scores and transcripts to:

Dr. Andrew McAdam Department of Fisheries and Wildlife Michigan State University East Lansing, MI 48823 Electronic materials are preferred (mcadama@msu.edu).

The deadline for receipt of materials is February 1, 2005.

The Department of Fisheries and Wildlife at Michigan State University (www.fw.msu.edu) promotes innovative and interdisciplinary approaches to natural resource management. In addition, the interdepartmental graduate program in Ecology Evolutionary Biology and Behavior (EEBB; www.msu.edu/~eebb) provides abundant opportunity for interaction and collaboration with faculty and students in several departments. The successful candidate will be expected to enroll and actively participate in the EEBB program.

----- Andrew G. McAdam Department of Fisheries and Wildlife, Department of Zoology Michigan State University East Lansing, MI 48824 tel: 517-432-0396 / fax: 517-432-1699 www.fw.msu.edu/people/McAdam/-Index.htm Andrew McAdam <mcadama@msu.edu>

MichiganStateU SelectiveHarvesting

M.S. Research Assistantship ? Michigan State University

A funded Graduate Research Assistantship is available for a student interested in investigating the evolutionary consequences of selective harvesting of Michigan white-tailed deer. This M.S. project will quantify hunter-induced selection and will include morphological measurement of harvested deer at deer-check stations (e.g. beam diameter, hind foot length, age, weight), hunter surveys to quantify effort and analysis of historical data to examine spatial and temporal patterns of deer harvesting in Michigan. This funded position includes stipend, tuition and benefits and will start in August 2005.

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---- Andrew G. McAdam Department of Fisheries and Wildlife, Department of Zoology Michigan State University East Lansing, MI 48824 tel: 517-432-0396 / fax: 517-432-1699 www.fw.msu.edu/people/McAdam/-Index.htm Andrew McAdam <mcadama@msu.edu>

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Rodrigo J. Goncalves

Igualdad - Equality

www.intermonoxfam.org

www.maketradeffair.org

www.oxfamamerica.org Libertad - Freedom

Rodrigo Goncalves <romadryn@yahoo.com>

Trondheim EvolAnimalBehaviour

PhD position in Animal Behaviour: "Sex role dynamics of gobies: proximate and ultimate causes" Norwegian University of Science and Technology, Trondheim

A PhD position in Animal Behaviour is currently being offered at the Dept. of Biology, Norwegian University of Science and Technology (NTNU), Trondheim. The position relates to the research project "Sex role dynamics in gobies: proximate and ultimate causes". The project is a collaboration between Elisabet Forsgren (PI), Trond Amundsen (co-PI), both at the NTNU, and Iain Barber (Univ. of Wales), Hanna Kokko (Univ. of Helsinki) and Ian Mayer (Univ. of Bergen), and is funded by the Research Council of Norway.

The Dept. of Biology at the NTNU (<http://www.bio.ntnu.no/eng/>) includes about 35 professors and associate professors and their research groups; about 20 of the professors work within the disciplines of animal behaviour, evolution, ecology and animal physiology. The department is situated in a new and well-equipped building at the main university campus.

The research project to which the position is linked aims to explore the strength of sexual selection and the understanding of animal sex roles, using the two-spotted goby, a small marine fish, as a model species. Studies within the project will include a combination of field and lab work, addressing both ultimate functions and proximate mechanisms, as well as theoretical modelling. The PhD plan of the appointed candidate will be affected by the candidate's interests and competence within these fields.

Field and lab work are planned at Kristineberg Marine Research Station at the west coast of Sweden, but the PhD position will be based at the NTNU, Trondheim.

Qualifications of importance in assessing candidates include: - educational background - ability to work both independently and in a group - writing skills - experience in presenting scientific material - written and

oral - ability to solve practical problems - organisational ability - motivation The decision on whom to appoint will essentially consider the applicants' potential for conducting a successful PhD project of a high quality. Short-listed candidates will likely be interviewed.

The position is for three years within which the candidate appointed is expected to complete her/his PhD. The monthly starting salary is NOK 23.958. There is a 2% reduction for superannuation.

For more information contact: Elisabet Forsgren, elisabet.forsgren@bio.ntnu.no, tel. +47 73 595365 (office) or +47 48062858 (mobile) or Trond Amundsen, trond.amundsen@bio.ntnu.no, tel. +47 73 596293 (office) or +47 91897293 (mobile)

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Dr Elisabet Forsgren Department of Biology Norwegian University of Science and Technology (NTNU) NO-7491 Trondheim NORWAY Tel: +47 73 595365 (direct), 596297 (secre.) Fax: +47 73 591309 e-mail: elisabet.forsgren@bio.ntnu.no Home: Tyrihansveien 9, NO-7056 Ranheim, tel. +47 73 571911 mobile phone: +47 48062858

Elisabet Forsgren <elisabet.forsgren@bio.ntnu.no>

UAlaskaFairbanks PopGenet

PH.D. RESEARCH ASSISTANTSHIP - UNIVERSITY OF ALASKA FAIRBANKS

A Ph.D. graduate research/teaching assistantship is available to participate in a NSF-funded study of the Population Genetics and Adaptive Properties of Hemoglobin Respiratory Proteins of Waterfowl Inhabiting the Andean Cordillera of South America. The study will include multiple collecting expeditions to South America and laboratory and data analysis at the University of Alaska Fairbanks.

Research/teaching assistantships of \$18,000/year are available for three years starting as soon as June 2005.

The successful applicant should speak Spanish (and English), and prospective graduate students from Argentina, Chile, Boliva, Peru, Ecuador, and Colombia are strongly encouraged to apply. Experience in collections-based research and genetic data collection/analysis are desirable.

The University of Alaska Fairbanks (<http://www.uaf.edu/>)

provides a dynamic setting in which to pursue your Ph.D. The biology program (<http://mercury.bio.uaf.edu/>) is highly collaborative (50+ faculty and >100 graduate students) and offers a diverse array of graduate student course offerings in evolutionary biology and genetics. Facilities include a modern core lab facility with high-throughput DNA sequencing, SNP detection, and microarray/proteomics capabilities, an ancient DNA extraction facility, and extensive natural history and genetic resources collections at the University of Alaska Museum (<http://www.uaf.edu/museum/>). The location of the university also offers unparalleled opportunities for research and recreation in understudied natural communities (the 365 million acre classroom), and the climate offers a great opportunity to enjoy winter sports and long summer days. The campus is situated on a sunny hill, overlooking the town of Fairbanks, with a view of the Alaska Range. Fairbanks is an extremely welcoming community, with many opportunities for outdoor sports. Groomed cross country ski trails start just outside the building, downhill skiing is less than fifteen minutes from campus, and there are many places for hiking, bird watching, fishing, rafting, and winter snow machining. Your graduate-student career will be an unforgettable life experience.

Applicants should submit: (1) Cover letter (2) CV (3) Statement of interest and experience (4) GRE & TOEFL scores (5) Unofficial copies of transcripts (6) Names and addresses of three references

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Becas de trabajo/investigación para doctorado UNIVERSIDAD DE ALASKA FAIRBANKS

Una beca de asistencia de investigación/ enseñanza para graduados está disponible para participar en la investigación del fondo de NSF sobre Genética de poblaciones y propiedades adaptativas de proteínas respiratorias de hemoglobina de aves acuáticas de la Cordillera de los Andes de Sur América. El estudio incluirá varias expediciones a Sur América, así como trabajo de laboratorio y análisis de datos en la Universidad de Alaska Fairbanks.

Becas de asistencia de investigación/ enseñanza de \$18,000/año estarán disponibles para comenzar tan pronto como en junio del 2005.

El postulante escogido deberá saber hablar Castellano (e Inglés), y se dará cierta prioridad a postulantes de Argentina, Chile, Bolivia, Perú, Ecuador, y Colombia. Se espera cierta experiencia en investigación basada en colecta, así como en colecta y análisis de datos genéticos.

Los postulantes deben mandar: (1) Carátula de pre-

sentación (2) CV (3) Manifestación de su interés y descripción de su experiencia. (4) Puntajes en GRE & TOEFL (5) Copias simples de sus certificados de grados y cursos universitarios (6) Nombres y direcciones de 3 referentes.

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

UCalgary EvolEcol

GRADUATE STUDIES IN EVOLUTIONARY ECOLOGY AT CALGARY

I am seeking to recruit graduate students interested in community and evolutionary ecology into my research group for September 2005. Calgary is a thriving, young city located a little over an hour away from the beautiful Canadian Rockies. Research in the lab focuses on the evolutionary consequences of interactions between natural enemies (e.g., predators, parasitoids, herbivores) and their prey, although I am also interested in the factors that affect oviposition decisions in phytophagous insects and understanding correlations between ecology and breeding system in flowering plants.

I am especially interested in students with experience with/genuine passion for insects to conduct research in one of two areas: (1) examining how the presence of parasitoid wasps affects competition and coexistence between sympatric strains and species of bruchid seed beetles, and (2) examining how predaceous dragonfly larvae affect community structure of dytiscid diving beetles. Project 1 will take place in the lab, and Project 2 will involve fieldwork and extensive sorting and identification of samples in the lab.

Research support will typically be provided by teaching assistantships during fall and winter terms and a stipend during the summer. Ample opportunities exist for candidates with strong academic backgrounds to supplement base income/research support through external scholarships and research funding <e.g., <http://www.biology.ualberta.ca/biodiversity/index.htm>> . Interested students should contact me <smvamosi@ucalgary.ca> with a CV, project of interest, and contact information for three

academic references by February 15th. Additional information can be found at <<http://homepages.ucalgary.ca/~smvamosi/>> and <<http://www.bio.ucalgary.ca/divisions/ecology/index.html>> . Steven M. Vamosi Assistant Professor and Ingenuity New Faculty Department of Biological Sciences University of Calgary Calgary AB T2N 1N4 CANADA <http://homepages.ucalgary.ca/~smvamosi/>

UDurham PopGenetics

We are advertising two PhD positions in the Molecular Ecology Group, School of Biological and Biomedical Sciences, University of Durham, Durham, UK. Note that full funding for these studentships is likely to be available to UK residents only:

Genetic structure of lamprey populations in relation to dispersal and homing

&

Extra-pair paternities and genomic correlates to lifetime reproductive success in the tawny owl

Details available at: <http://www.dur.ac.uk/a.r.hoelzel/megwebpageStud.htm> Application deadline: 1 March 2005

-Rus Hoelzel

a.r.hoelzel@durham.ac.uk

UEdinburgh LanguageEvol

MSc/PhD in the EVOLUTION OF LANGUAGE & COGNITION One year taught Masters & PhD programme

University of Edinburgh, UK

What is it that makes us human? How did our brains evolve? What are the origins of human language? Why do we think the way we do? What are the mechanisms of biological, cultural and linguistic evolution?

The University of Edinburgh is now in the second year of a successful Postgraduate Programme in the Evolution of Language and Cognition. Students tackle the key questions that are at the heart of the recent renaiss-

sance in the scientific study of the origins and evolution of human language and cognition.

The programme consists of two components: an interdisciplinary 1 year taught Masters degree, and a supervised PhD. Students will apply for one or the other degree, depending on background and experience. The MSc year can be used as preparation for the PhD.

Human evolution is a topic for cognitive scientists, psychologists, linguists, archaeologists, anthropologists, biologists, and computer scientists. Because of this, the postgraduate programme will suit students from a wide range of backgrounds. If you are interested in learning more about the evolution of human cognition and language, and about the many disciplines that contribute to its study, we'd like to hear from you.

We are now accepting applications for entry to the MSc in September 2005, and for entry to the PhD at any time.

To find out more about the course, and what it will be like to live and work in Edinburgh, go to our website. Here you will also find full details about how to apply.

<http://www.ling.ed.ac.uk/lec/elc> [Please feel free to pass on this email to anyone who might be interested.]

Simon Kirby Language Evolution & Computation Research Unit School of Philosophy, Psychology & Language Sciences University of Edinburgh
<http://www.ling.ed.ac.uk/~simon> Simon Kirby
 <simon@ling.ed.ac.uk>

UHelsinki SystematicsEvolutionMyrmicaAnts

Two four-year PhD student positions in systematics and evolution of *Myrmica* ants

We are inviting applications from students with a MSc degree to study the systematics and evolution of *Myrmica* ants for four years, starting in spring 2005, as a fulfilment of a PhD degree at the Department of Biological and Environmental Sciences, University of Helsinki, Finland. The project is funded by the Academy of Finland, and the supervisors are Drs Riitta Savolainen and Kari Vepsäläinen.

The PhD projects will be expanded around the following topics: (1) Molecular systematics and social parasite-host relationships of *Myrmica*, and (2) Phylogeography and speciation of *Myrmica rubra* and its

social parasite *M. microrubra*; for background information, please see PNAS 100:7169-74, 2003. The first project will include, among others, supervised collecting of *Myrmica* in the Holarctic region and sequencing of mitochondrial and nuclear genes. The second project involves supervised collecting of phylogeographic samples of *Myrmica rubra* and its social parasite *M. microrubra* in Europe, DNA sequencing, microsatellite analyses, and behavioural mating experiments.

We seek candidates with a background in ecology and evolutionary biology. Experience in generating DNA sequence and microsatellite data and analyzing them is of great advantage but not necessary to qualify for the positions. We expect strong commitment to the work by the selected candidates.

The monthly salary will be ca. 1700 euros, equivalent to the present Finnish graduate school salary.

Please send your curriculum vitae, details of research interests and current position, and names and email addresses of two referees to Riitta Savolainen by email (riitta.savolainen@helsinki.fi) by 15th of February 2005.

Riitta Savolainen Dept of Biological and Environmental Sciences P.O. Box 65 00014 University of Helsinki Finland

Riitta Savolainen <riitta.savolainen@helsinki.fi>

ULausanne 2 EvoSymbiosis

2 PhD studentship positions: in Symbiosis, Evolution, Evolutionary and Population Genomics- University of Lausanne, Switzerland

We are seeking 2 highly motivated students who are interested in Evolutionary Biology and Symbiosis to join our group working on mechanisms of evolution in symbiotic mycorrhizal fungi. These important fungi form mutualistic symbioses with plant roots and form large underground hyphal networks, where one individual connects plants of many different species. The fungi help plants to grow by providing essential nutrients. Although the fungi grow clonally, they have a highly unusual genome organization, harbouring genetically different nuclei that are passed from one generation to the next (see Hijri & Sanders, Nature 2005; Kuhn, Hijri & Sanders, Nature 2001). The goals of our research are to understand how this unusual organization of the genome affects their evolution and their adaptation to the different environments offered by the roots of differ-

ent plant species. Other than their unusual genome organization, the fungi have formed symbioses with plants ever since they colonized land over 400 million years ago and are thought to be the oldest putative ancient asexuals.

We hope to recruit one PhD student with an evolutionary or population biology background and the other should be familiar with molecular biology and have an interest in applying this knowledge to evolutionary questions. He/she should also be able to interact with the other group members who have lab-based projects on evolution and population biology of mycorrhizal fungi (see list of recent papers and our web site).

The successful candidates will be located in the Department of Ecology and Evolution at the University of Lausanne (Switzerland). The Dept. of Ecology and Evolution in Lausanne is situated on the shores of Lake Geneva and provides a pleasant & exciting research environment and a strong PhD program. It is also one of the largest institutions in Europe for research in ecology and evolutionary biology, comprising 17 different research groups. A genomics research centre has also been recently established at the same site.

The 2 PhD studentships are funded by the Swiss National Science Foundation for a period of 3 years. Starting date is negotiable. Applicants should contact Ian Sanders, Dept of Ecology and Evolution, University of Lausanne, Switzerland. Email: : Tel: +41 21 692 4261. More details can be found about our group at:

Recent group publications: Hijri H. & Sanders, IR. (2005). Low gene copy number shows that arbuscular mycorrhizal fungi inherit genetically different nuclei. *Nature* 433: 160-163. Koch AM, Kuhn G, Fontanillas P, Fumagalli L, Goudet I, Sanders IR. (2004). High genetic variability and low local diversity in a population of arbuscular mycorrhizal fungi. *PNAS* 101: 2369-2374. Hijri M, Sanders IR. (2004). The arbuscular mycorrhizal fungus *Glomus intraradices* is haploid and has a small genome size in the lower limit of eukaryotes. *Fungal Genetics and Biology* 41: 253-261. Sanders IR. (2002). Ecology and evolution of multigenomic arbuscular mycorrhizal fungi. *American Naturalist* 160: S128-S141. Kuhn G, Hijri M, Sanders IR. (2001). Evidence for the evolution of multiple genomes in arbuscular mycorrhizal fungi. *Nature* 414: 745-748.

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

Tel (direct): +41 (0)21 692 4261 Tel (secretary): +41 (0)21 692 4260 Fax: +41 (0)21 692 4265 <http://www.unil.ch/dee>

www.unil.ch/dee New email!: ian.sanders@unil.ch

Ian.Sanders@unil.ch

ULouisianaMonroe FishSystematics

Masters Student/Collections Manager position in systematic ichthyology.

A graduate assistantship is available for a collections manager in the Museum of Natural History at the University of Louisiana at Monroe. The stipend is \$8,000 for nine months and can be renewed for a total of three academic years. The collection manager will oversee the extensive zoological collections including about 80,000 lots of fishes, 20,000 reptile and amphibian specimens and a small, but developing, collection of freshwater mussels. More information on the Museum is available at www.ulm.edu/~pezold/welcome.htm. Specific duties will include maintaining museum records, responding to loan and information requests, accessioning and cataloging acquisitions, overseeing student curatorial assistants, and some possible fieldwork in Africa. The position starts August 2005.

Qualifications: Student must be admitted to the Master of Science Degree Program in Biology for the Fall 2005 semester and have an interest in African freshwater fish diversity. Graduate program application materials are available at <http://www.ulm.edu/gradschool/admis.html>. Candidates with museum collection experience and African field experience will be given preference, but it is not required. RPCVs are especially invited to apply.

The successful candidate's thesis research will be a systematic study of West African fishes using morphological and molecular methods. Information about research in my lab is available at www.ulm.edu/~pezold/pezold.htm. Interested students should contact:

Frank Pezold Museum of Natural History University of Louisiana at Monroe Monroe, LA 71209-0504

ph: 318-342-1868 fax: 318-342-3312 email: pezold@ulm.edu

Russ Minton, Ph.D. Molecular Genetics Lab Coordinator & Curator of Invertebrates Museum of Natural History Assistant Professor, Department of Biology University of Louisiana at Monroe Monroe, LA 71209-0520 ph: 318-342-1795 fax: 318-342-3312 <http://homepage.mac.com/russminton/>

index2.htm Russ Minton <minton@ulm.edu>

UMassachusetts Modelling

Apologies for the short notice, but if you know anyone who might be interested:

This NSF-funded project focuses on using finite element modeling to address biological hypotheses about the relationship between skull shape and feeding behavior in the evolution of mammals. The student will learn methods of finite element modeling and analysis, bone strain analysis, and field methods for collecting behavioral and bite force data. The student will participate in this research but will also conduct independent M.Sc. or Ph.D. research. An interest in ecomorphology and evolution is essential. A strong background in mathematics and/or engineering and/or programming is a big plus. This research is funded for three years and will be supplemented with teaching assistantships through the Organismic and Evolutionary Biology Program at the University of Massachusetts at Amherst (<http://www.bio.umass.edu/oeb/>).

The application deadline is January 15th but they will be accepted until January 21st.

Contact: Dr. Betsy Dumont Office: 413 545-3565
Email: bdumont@bio.umass.edu

UNeuchatel EvolEcol

Sorry for doing this first wrong. Here is a graduate position available at the University of Neuchatel in Switzerland.:

PhD. Position in behavioural ecology

I'm offering a PhD position on the behavioural ecology of free living European mammals, to be based at the Institute of Zoology, Department of Biology at the University of Neuchâtel, Switzerland, starting April, 1st. 2005. Neuchâtel is a beautiful little city in the French speaking part of Switzerland, at the foot of the Jura mountains, with a big lake, and the Swiss Alps in the background. The major Swiss cities Zürich, Bern, Basel, Lausanne and Geneva are all within 90 min distance. The salary will be at 30,000 SFr per year for a

period of 4 years. The behavioural ecology group has been set up very recently in 2004, and we are currently developing our research profile. As a consequence, I do have two potential topics for the successful applicant to do his/her research (see below) but own suggestions by applicants will be considered as well. In any case, the successful candidate will have freedom in developing the project him/herself.

First I am interested in life history decisions and tactics of Alpine marmots, a cooperatively breeding animal. A research focus would be to test some of the claims about the importance of helpers experimentally. Further I am interested in the link between parasites (possibly in collaboration with the parasitology group) and costs of reproduction in this species. A second possible research topic is on feeding behaviour and sociality of Alpine ibex. In this study the main focus would be on the link between sociality and group decision making/group cohesion with respect to foraging behaviour/ruminating of different age and sex (body size) classes.

The successful applicant is expected to help tutoring behavioural practicals and excursions during terms. Knowledge of the French language would be an asset but not mandatory. Since both projects take place in the mountains the candidate should be fit and feel comfortable working in a harsh environment. Further it would be an advantage if the applicant had some experience in studying wildlife. Applications including CV, fields of interest and bibliography can be sent by e-mail, to Dr. Peter Neuhaus at peter.neuhaus@unine.ch or by 31st of January to:

Dr. Peter Neuhaus Adjunct Professor Department of Biological Sciences University of Calgary 2500 University Drive, N.W. Calgary, AB T2N 1N4 CANADA

peter_neuhaus@hotmail.com

UNewOrleans EvolBiol

Regents Fellowship in Conservation Biology at the University of New Orleans

The Department of Biological Sciences at the University of New Orleans announces a Doctoral Fellowship for fall 2005. The fellowship provides support for four years and includes a full tuition waiver, an annual stipend of \$22,000, and an allowance for research supplies and travel. The Department of Biological Sciences offers opportunities for graduate research in ecol-

ogy, genetics, systematics, evolution, reproductive biology, physiology and biochemistry. Applicants must be U.S. citizens. For more information, send e-mail to <mailto:biograds@uno.edu> biograds@uno.edu or see the website: <<http://biology.uno.edu/>> <http://biology.uno.edu/>> Application materials for the PhD program can be obtained online or by writing to: Director of Graduate Studies, Department of Biological Sciences, University of New Orleans, New Orleans, LA 70148. Review of applications will begin February 15, 2005.

Steve Johnson

Steven G Johnson <SGJohnso@uno.edu>

USheffield EvolAgeing

PhD Studentship in Human Behavioural Ecology

A funded PhD student position for 3 years is open at the Department of Animal and Plant Sciences, University of Sheffield, UK, on two alternative topics:

When to die? Evolutionary and ecological causes of ageing in humans
Ecological and hormonal causes of co-operation in humans

More information about these PhD topics is available at the APS website <http://www.sheffield.ac.uk/aps/graduate-information/graduate-opportunities.html>

The PhD project will be part of a long-term research project on life-history strategies in human populations. The student will join the large & lively Evolution & Behaviour research group in the Department of Animal and Plant Sciences in Sheffield. Students with a good first degree or Masters degree in areas such as Evolution, Behaviour, or Biological Sciences are encouraged to apply. The position is open to UK and EU nationals. Informal enquiries about this studentship should be addressed to V.Lummaa@sheffield.ac.uk. More information about the application system and the research group is also available at <http://www.sheffield.ac.uk/aps/> The deadline for applications is 25 February 2005. Applications should be addressed to:

Dr Virpi Lummaa Dept of Animal and Plant Sciences
Western Bank University of Sheffield Sheffield S10 2TN
United Kingdom

Fax: +44(0)114 2220002 Tel: +44(0)114 222 0122 e-mail: V.Lummaa@sheffield.ac.uk

Virpi Lummaa <V.Lummaa@sheffield.ac.uk>

USouthDakota StalkEyedFlies

Graduate Research in Evolutionary Physiology of Stalk-Eyed Flies

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

John G. Swallow

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

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

jswallow@usd.edu

UVigo ComputationalEvolBiol

PhD position in Spain: Computational Evolutionary Biology

A four-year doctoral position is available to work in the computational characterization and modeling of recombination in HIV-1, with David Posada at the University of Vigo, in Vigo (Spain).

This position is funded by the Spanish Ministry of Education and Science (MEC) under its “Research Personnel Training” program (FPI), to sponsor a PhD linked to a specific research grant. To compete for this position the candidate needs to apply directly at the FPI site (<http://www.mec.es/ciencia/becasfpi>). Application deadline is February 15, 2005. Unfortunately, all the information and application process is in Spanish.

Exact details are explained at the FPI web site, but Spanish or EU citizenship is not required. The fellowship lasts four years. The salary is 1100 euros per month, including benefits. Starting date should be around mid-2005.

We seek individuals who are independent and motivated. Ideal candidates will have programming skills and a background in mathematical statistics. Some knowledge about evolutionary biology and HIV is highly desirable. Spanish skills are not required but will be very convenient, especially to get through the application process. Information about the research in our lab is described in our web page.

Several related links are available from <http://darwin.uvigo.es> For any questions about this PhD position, email dposada@uvigo.es.

– David Posada Facultad de Biología Campus Universitario 36310 Vigo

Phone: +34 986 812038 Fax: +34 986 812556 Email: dposada@uvigo.es Web: darwin.uvigo.es

dposada@uvigo.es

Jobs

AustralianGov EnvironmentalAdaptation	22	UAlaskaFairbanks Microbiology	28
Boston AntimicrobialUse	22	UDurham MathBiol	29
FrenchPolynesia Entomology	23	UNottingham GenomeDynamics	29
INRA France MathEpidemiology	23	URegina EnvironmentalBiol	29
INRA France PopGenet Insects	24	URegina EvolEnvironmentalBiol	30
INRA U Bordeaux EvolEpidemiology	25	UVirginia DirectorBioStation	30
KewGardens Mycology	25	UVirginia SummerStudent	31
OxfordU 2 FieldAssist	25	UWesternOntario Genetics	31
PennStateU EvolBiol	26	UZurich PopGenetics	32
QueensU AmericanRedstart	26	UZurich SystematicBotany	32
RoyalHollowayU PopEvolGenet	27		
Spain FieldAssistants BehavEcol	27		

**AustralianGov
EnvironmentalAdaptation**

Australian Government Department of the Environment and Heritage Australian Antarctic Division

Program Leader, Adaptation to Environmental Change

APS Executive Level 2 - Senior Principal Research Scientist

\$115884 - \$126630 pa

Ongoing

The Program Leader, Adaptation to Environmental Change will be expected to develop a strong and coherent program based on the application of modern genetic and genomics research to questions in evolutionary biology and the consequences of environmental change. The successful applicant will work with biologists in the program with current projects on plant ecology, marine ecosystem structure and function, marine mammal and higher predator biology.

Please note: The successful applicant will have a PhD in genetics, molecular biology, or a closely allied field from an Australian university, or equivalent qualification from an overseas university, or other qualifications appropriate to the duties of the position. Other mandatory and job-specific criteria apply. Persons engaged as APS employees will normally have Australian Citizenship. Further information and selection documentation is available from the AAD website www.aad.gov.au <<http://www.aad.gov.au>> Applications addressing selection criteria should be forwarded to the Corporate Services Officer, Australian Antarctic Division, 203 Channel Highway, Kingston, Tasmania 7050 or via email to recruitment@aad.gov.au <<mailto:recruitment@aad.gov.au>> by 11 February 2005.

Applications will not be acknowledged. Engagement may be subject to conditions including probation, qualifications, health and security/character clearance requirements. A relocation allowance will be payable where the successful candidate is recruited from within Australia and is required to relocate to Southern Tasmania.

Contact Officer: Michael Stoddart - (03) 6232 3205 or email michael.stoddart@aad.gov.au <<mailto:michael.stoddart@aad.gov.au>>

Deb Jordan Corporate Services Officer Australian Antarctic Division E-mail debra.jordan@aad.gov.au Ph - (03) 62 323 579 Fax - (03) 62 323 256

Debra Jordan <Debra.Jordan@aad.gov.au>

Boston AntimicrobialUse

Applied Research Director for International Public Health

Opportunity for trained investigator to conduct studies concerning antimicrobial use and resistance.

Qualifications Ph.D. or M.D. with at least three years of post-doctoral experience in microbiology, epidemiology, population biology or related discipline; team management experience; a track record in peer reviewed publications and grant development. Mathematical modeling/risk analysis and infectious disease experience helpful.

Responsibilities Leads the organization's research activities. Serves as principal investigator on NIH projects and manager of scientific consortia and staff engaged in applied research and grant writing concerning infectious diseases.

§Oversees research coordination and consultant team
 §Designs scientific/clinical research objectives
 §Engages APUA's scientific advisory board
 §Analyses laboratory data on incidence and prevalence of infectious diseases
 §Develops and applies statistical methodologies for analyzing data
 §Takes the lead in large scientific meetings
 §Prepares and presents reports and articles for peer review
 §Prepares and oversees grant proposals
 §Represents organization at various national and international meetings
 §Develops global and organizational partnerships

The Alliance for the Prudent Use of Antibiotics (APUA) is a global organization dedicated to improving antimicrobial use through research and education. Founded in 1981 and located on the Tufts Medical School campus in Boston, APUA conducts its public health programs in coordination with affiliated chapters in over 50 countries and the leading national and international public health organizations.

Please forward resume and CV to: APUA Human Resources 75 Kneeland Street Boston, MA 02111-1901 apua-eaa@tufts.edu

Visit www.apua.org for more information about the Alliance for the Prudent Use of Antibiotics.

Revised: 12/29/04

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Jennifer Deerinwater Operations Department AL-
LIANCE FOR THE PRUDENT USE OF ANTIBI-
OTICS 75 Kneeland St Boston, MA 02145 Tel:
(617)636-0966 Fax: (617)636-3999 www.apua.org
med024 <med024@granite.tufts.edu>

FrenchPolynesia Entomology

JOB Entomology

Applicants are invited for a technician position in Entomology at the Plant Protection Department of French Polynesia, in the Agricultural Entomology Laboratory.

The successful applicant will be hired as a volunteer for development (CVD: contrat de volontaire au développement de la Polynésie Française). Due to the restrictions of the contract, the post is open to people who originate from French Polynesian or live in French Polynesia for at least 5 years. For more information about eligibility, please visit: <http://www.service-public.pf> The applicant will be involved in the classical biological control program conducted against the glassy-winged sharpshooter (GWSS) *Homalodisca coagulata* (Hemiptera: Cicadellidae), a major exotic pest in French Polynesia. This program is conducted by the University of California, Berkeley in association with the Plant Protection Department of French Polynesia. This program aims to introduce the exotic mymarid egg parasitoids *Gonatocerus ashmeadi* and *G. triguttatus* (Hymenoptera: Mymaridae) to control *H. coagulata* populations.

The successful candidate will be primarily responsible for parasitoids mass rearing and will participate to experimental and field work.

The position is 24 months and could be renewable. The successful candidate should have a MS in entomology or ecology with experience in laboratory work. The candidate must be highly motivated, independent, reliable, and a good communicator. Computer skills such as the use of word processing, spreadsheet, and e-mail programs are essential.

For more information or to apply please contact Dr Julie Grandgirard : juliegrandgirard@yahoo.fr. Please send a cover letter, a CV and names and contact information for three references. Applications will be reviewed as received, until the position is filled.

juliegrandgirard@yahoo.fr

INRA France MathEpidemiology

POSITION ANNOUNCEMENT (French version followed by the English version)

Modélisation des événements rares en épidémiologie animale

Modelling of rare events in veterinary epidemiology

Poste et localisation

Chargé de recherche CR2

Dans l'Unité d'Epidémiologie Animale à l'INRA (Institut National de la Recherche Agronomique)

Basée à Clermont-Ferrand - FRANCE

L'Unité d'Epidémiologie Animale est constituée de 12 personnes comprenant des vétérinaires, épidémiologistes et biostatisticiens.

Différents programmes sont en cours sur les Encéphalopathies Spongiformes Transmissibles, les maladies transmises par les tiques et les maladies émergentes.

Des collaborations scientifiques sont à développer avec la faculté de mathématiques de Clermont-Ferrand.

Qualification

Thèse d'université. Formation en mathématiques.

Fort intérêt pour les mathématiques appliquées, la biologie, l'épidémiologie.

Les candidats doivent avoir moins de 31 ans au 31 décembre 2005 (voir les dérogations d'âge dans le guide du candidat).

Candidature

AVANT LE 25 FEVRIER 2005 !!

Contact : Christian DUCROT (33) 4 73 62 42 63 - ducrot@clermont.inra.fr

Détails sur le poste : <http://www.inra.fr/drh/cr05/-bdd/profil.php?codeprofil=CR2-2005-8-SA-4> Détails sur la candidature : <http://www.inra.fr/drh/cr05/-docs/guide-CR2-FR.pdf>

ENGLISH VERSION :

Position and location

Full-time permanent research position (called chargé de recherche CR2)

Located in the Unit of Veterinary Epidemiology at the INRA (National Institute for Agronomic Research)

in Clermont-Ferrand - FRANCE

The Unit of Veterinary Epidemiology is composed of 12 people with scientific background in veterinary science, epidemiology, and biostatistics. Different programs are running on Transmissible Spongiform Encephalopathies, tick-borne diseases and emerging diseases.

Scientific collaboration is to be developed with the faculty of mathematics in Clermont-Ferrand.

Qualification

PhD required. Background in mathematics.

Strong interest in applied mathematics, biology, epidemiology.

Applicants have to be less than 31 years old on 31 December 2005 (see conditions to extend the age limit in the guide for CR applicants).

Application

BEFORE 25 FEBRUARY 2005 !!

Contact : Christian DUCROT (33) 4 73 62 42 63
ducrot@clermont.inra.fr

Details about position : <http://www.inra.fr/drh/cr05/bdd/profil.php?codeprofil=CR2-2005-8-SA-4>
<http://www.inra.fr/drh/cr05/bdd/profil.php?codeprofil=CR2-2005-8-SA-4> Details

about application : <http://www.inra.fr/drh/cr05/docs/guide-CR2-FR.pdf>
<http://www.inra.fr/drh/cr05/docs/guide-CR2-FR.pdf>

Christian DUCROT

Unité d'Epidémiologie Animale

INRA Theix

63122 Saint Genes Champanelle

France

tel (33) 4 73 62 42 63 - fax (33) 4 73 62 45 48

e-mail ducrot@clermont.inra.fr

Gwenael Vourc'h <gvourch@clermont.inra.fr>

insect species (I.N.R.A. France)

A permanent position in the field of population genetics is open for application at the Forest Zoology Unit in the French Institute for Agronomy Research (I.N.R.A.). This position is at the level "Chargé de Recherche 1ère classe" (young scientist with at least 4 year postdoctoral experience / no age limit). It is a full research position, without teaching load. The lab is located at Orléans (100 km South of Paris) and belongs to the Department of Forest, Grassland and Freshwater Ecology.

Lab research activities are directed towards a better understanding of forest insect population dynamics. The team is composed of both ecologists and population geneticists. The position is aimed at reinforcing and leading the population genetics research group composed by 2 young researchers (entomologists-geneticists) and 1 assistant engineer (molecular biologist). A fully-equipped molecular biology lab is available since 2001 (including a ABI 3100 sequencer). The candidates should have a good background in population genetics analyses and theoretical approaches. Previous knowledge of entomology helpful, but not required.

The deadline to return complete application files (dossiers de candidature) to INRA is the 28th February 2005 (files have to be downloaded before the 25th February). Applications must include a curriculum vitae, copies of PhD thesis and recent significant papers, a detailed report of previous research activities and a proposal of research project for the offered position.

Full details are available on the INRA web site : Position description : <http://www.inra.fr/drh/cr05/bdd/profil.php?codeprofil=CR1-2005-4-EFPA-1>
Application procedure : <http://www.inra.fr/drh/cr05/bdd/index.php> / <http://www.inra.fr/drh/cr05/docs/guide-CR1-FR.pdf> Salary : <http://www.inra.fr/drh/vieprof/indexsal.htm> Lab activities : <http://www.orleans.inra.fr/LeCentre/Unites/URZF/urzf.html> / <http://compact.jouy.inra.fr/compact/CONSULTE/INTER/externe/unites/ecrans/633>

Contact : Alain Roques (Directeur de recherche, Directeur d'Unité) ; Phone +33 2 38 41 78 58 ;
mailto:Alain.Roques@orleans.inra.fr

Marie-Anne.Auger@orleans.inra.fr
Marie-Anne.Auger@orleans.inra.fr

Marie-Anne.Auger@orleans.inra.fr

INRA France PopGenet Insects

INRA UBordeaux
EvolEpidemiology

Permanent position in population genetics of expanding

The research unit Biogeco (Biodiversity, Genes and Ecosystems) at INRA-University Bordeaux I offers a permanent position (CR2 INRA) in epidemiology.

Research theme Because of their relative simplicity (often involving an interaction between two species only), host-parasite systems are stimulating biological models for theoretical research in ecology. Yet their functioning may be crucial because of their possible negative impact on human, or human related, activities (forestry, agriculture.). As a consequence of high levels of human interference, these systems evolve in a rapidly changing environment at both local (changes in silvicultural practices, for example) and global (increase of exchanges and introductions of pathogens, climate change, etc) scales. In order to understand and forecast the evolution of forest pathosystems (interactions between trees and pathogens, mostly fungi) the objective of this new position is to strengthen theoretical work in evolutionary ecology and modelling and to complement ongoing research focused on the development of an experimental approach to understand the functioning of these biological systems. The candidate is expected to have an interest in theoretical (community ecology, evolutionary ecology of parasitism) as well as applied (risk analysis) fields of research.

Scientific environment The successful candidate will work in close collaboration with the researchers in the pathology group (3 epidemiologists, 1 population geneticist, 1 modeller in ecology/theoretical biology), have opportunities to interact closely with geneticists and ecologists in the research unit, Biogeco, and will become integrated into a local network for modelling in epidemiology, genetics and ecology (UMR Biogeco, UMR Santé Végétale (Plant Health), INRA-ENITAB, Laboratory of Applied Mathematics in University of Bordeaux I). <http://www.pierroton.inra.fr/-biogeco/index.html> (pathology)

How to apply? <http://www.inra.fr/drh/cr05/bdd/-index.php> DEADLINE = 28/02/2005

Contact ML Desprez-Loustau loustau@bordeaux.inra.fr

Dr Marie-Laure Desprez-Loustau

INRA Bordeaux - Domaine de la Grande Ferrade UMR 1202 BIOGECO Laboratoire de Pathologie forestière BP 81 33883 Villenave d'Ornon Cedex France

TEL : 05 57 12 26 47 (From abroad : 33 5 57 12 26 47)
FAX : 05 57 12 26 21 (From abroad : 33 5 57 12 26 21)

<http://www.pierroton.inra.fr/biogeco/index.html>
(équipe de pathologie)

Marie Laure Loustau <loustau@bordeaux.inra.fr>

KewGardens Mycology

Laboratory Manager - Mycology

REF: 244

HOURS OF WORK: Full-time

JOB STATUS: Permanent

SALARY PER ANNUM: From £17,505

DEPARTMENT: Royal Botanic Gardens, Kew

JOB DETAILS: Working within the Mycology Section you will manage, maintain and develop the culture collection of living fungi and undertake DNA isolation and PCR procedures for our research programmes. You will also be involved in the taxonomy of larger fungi, with the emphasis being on British and tropical species. You will co-ordinate the day-to-day management of facilities and maintain stocks.

ESSENTIALS: You will possess a sound knowledge of biological subjects (preferably educated to degree standard) and will have proven experience with DNA isolation techniques. You will also have proven experience with culturing techniques and a working knowledge of larger fungi.

Good written and oral communication skills are essential, as is the ability to organise your workload. You will be capable of making sound decisions based on interpretation of data, and of investigating and resolving problems.

Familiarity with laboratory practice and experience of handling specimens in a sensitive manner are essential.

CLOSING DATE: 4 February 2005

<http://lion.rbgkew.org.uk/aboutus/jobs/Ref244.html>
m.bidartondo@kew.org

OxfordU 2 FieldAssist

DEPARTMENT OF ZOOLOGY Wildlife Conservation Research Unit

Two Field Assistants

Ancillary Salary Scale: T01:01 £10,780 per annum

Applications are invited for two field assistant positions to investigate cooperative breeding and mate choice in the European badger *Meles meles*. The posts are available from February 2005 for six months. The first four months will combine fieldwork which entails daily maintenance of four infrared video surveillance units in Wytham Woods, Oxford, followed by daily preliminary analysis of videotapes. The last two months will involve behavioural analysis of these videotapes and report production. The successful applicants will have a strong academic interest in behavioural ecology. They will be self-motivated; organised; and able to carry out fieldwork outdoors, independently and in all weather conditions. Skills in planning and data management are required; an understanding of Microsoft Access is desirable and experience of behavioural analysis would be an advantage. The post-holders will work closely with each other and Oxfor's zoological team; excellent communication, liaison and teamwork skills are therefore essential. Applicants must hold a full UK driving license and be prepared to work variable hours.

Further particulars and application forms are available from General.Office@zoo.ox.ac.uk (Tel: 01865 271190). Applications including a covering letter, curriculum vitae and contact details of two referees should be sent to the Administrator, Department of Zoology, South Parks Road, Oxford, OX1 3PS, quoting reference AT05001/02. The closing date for applications is 28 January 2005. Interviews are likely to be held in Oxford on 3 February 2005.

PennStateU EvolBiol

Pennsylvania State University Assistant Professor (or above)

Evolutionary Biology / Astrobiology

The Eberly College of Science at Penn State invites applications for a tenure track faculty position in Astrobiology with the appointment to be made in one of the colleges departments including Biology, Biochemistry and Molecular Biology, and Chemistry (<http://www.science.psu.edu>). We seek a candidate interested in pursuing evolutionary research, with either prokaryotes or eukaryotes, on the early evolution of the Earth's environment and biota. Potential fields of study include, but are not limited to, molecular, cellular and developmental evolution, and paleontology. The ap-

pointee will have the opportunity to join our Astrobiology Research Center (<http://psarc.geosc.psu.edu>) and is expected to develop a strong, externally funded research program and participate in undergraduate and graduate teaching. Exceptional candidates at the rank of Associate or Full Professor may be considered. Applicants should send a PDF file containing their CV, statement of research and teaching interests, and contact information for three references to astro-bio@email.bio.psu.edu, or mail to:

Chair, Astrobiology Search Department of Biology 208 Mueller Laboratory The Pennsylvania State University University Park, PA 16802-5301

Review of applications begins January 3, 2005 and will continue until a suitable candidate is identified. Penn State is committed to affirmative action, equal opportunity, and the diversity of its workforce.

sbh1@psu.edu sbh1@psu.edu

QueensU AmericanRedstart

FIELD ASSISTANTS (1-2) needed for research on the demographics and breeding biology of a long-distance migratory bird, the American redstart. Field work will be conducted in mixed deciduous/coniferous forest at the Queen's University Biological Station (QUBS: <http://biology.queensu.ca/%7Equbs/>), Chaffey's Lock, southeastern Ontario. Strong applicants will have experience in some or all of the following areas: bird observation, territory mapping, nest searching, handling and bleeding birds, insect sampling. Applicants should also be meticulous in collecting and recording data and be willing to work long hours in the field, six or seven days a week. A competitive salary, plus room and board at QUBS will be provided. Positions will be for approximately three months, starting May 1st and ending in late July. Please send cover letter, CV, and the names and addresses of three references to MATTHEW REUDINK, Department of Biology, Queen's University, Kingston, Ontario K7L 3N6, or e-mail to reudinkm@biology.queensu.ca by 30 March 2003.

Matthew W. Reudink

Ph.D. Student Department of Biology Ratcliffe Lab Queen's University Kingston, ON, K7L 3N6 CANADA

reudinkm@biology.queensu.ca

[/biology.queensu.ca/](http://biology.queensu.ca/)

<http://reudinkm>

reudinkm@biology.queensu.ca

RoyalHollowayU PopEvolGenet

The School of Biological Sciences (SBS) at Royal Holloway-University of London seeks to make an appointment at

Lecturer or Senior Lecturer level

in the area of population or evolutionary genetics (as applied to plant, animal or related microbial ecosystems) or plant cell biology & molecular genetics.

The appointee is expected to contribute to teaching in genetics or related subjects and is expected to have a strong research record or showing considerable promise.

A more detailed description is given below. For further queries please contact me (vincent.jansen@rhul.ac.uk) or use the contact details given below.

Vincent Jansen

— The School of Biological Sciences (SBS) at Royal Holloway-University of London (RHUL) (<http://www.rhul.ac.uk/Biological-Sciences>) constitutes four highly-integrated and dynamic research centres: Biomedical Sciences; Plant Molecular Sciences; Ecology, Evolution & Behaviour; Chemical & Bioanalytical Sciences. Housed in the Bourne-Wolfson Laboratory complex, the School is engaged in leading-edge research across the spectrum of molecular and organismal bioscience. The School holds grade 5 research assessment (RAE) status, which denotes generalised international excellence, and a maximum grade 24 teaching quality assessment (QAA) rating. Research and teaching activities are underpinned by technologies spanning functional genomics, metabolomics, molecular genetics, microbiology, gene therapeutics, advanced cell biology, model organism analyses, population studies, ecology, evolutionary biology, mathematical biology, and advanced microscopy facilities (eg CLSM, FRET). As part of a major expansion in research strength across the College, applications for appointments in the School at Senior Lecturer or Lecturer levels are invited from exceptional internationally-recognised researchers with proven track records of scholarship, research productivity and attracting research funds. Appointees will be required also to teach, supervise and examine undergraduate and graduate students, and to contribute to administration of the School.

Post: Senior Lecturer/ Lecturer in Plant Molecular Science or Ecology (Quote Ref: KB/000743): SBS is seeking an appointment to complement activities in the SBS Centre for Plant Molecular Sciences and/or Centre for Ecology, Evolution & Behaviour. Individuals with research interests in one of the following areas are particularly encouraged to apply: population or evolutionary genetics (as applied to plant, animal or related microbial ecosystems), plant cell biology & molecular genetics. Salary will be in the range 29,250 - 44,707 per annum (inclusive).

Informal inquiries may be directed to Head of School, Professor George Dickson (Tel: 44+(0)1784 443545; Email g.dickson@rhul.ac.uk), the School's Director of Research, Professor Peter M Bramley (Tel: 44+(0)1784 443555; E-mail: p.bramley@rhul.ac.uk).

Further details and an application form are available from the Personnel Department, Royal Holloway, University of London, Egham, Surrey, TW20 0EX; fax: 01784 473527; tel: 01784 414241; web-site: <http://www.rhul.ac.uk/Personnel/JobVacancies.htm> Please quote the appropriate reference. Closing date for the receipt of applications is Noon, Friday 28 January 2005.

We positively welcome applications from all sections of the community.

Vincent Jansen Professor of Mathematical Biology Head of the Centre for Ecology, Evolution and Behaviour School of Biological Sciences Royal Holloway - University of London Egham, Surrey TW20 0EX, U.K.

Tel : (..) 44 1784 443179 Fax : (..) 44 1784 470756 Email: vincent.jansen@rhul.ac.uk Web : <http://web.rhul.ac.uk/Biological-Sciences/jansen>

Spain FieldAssistants BehavEcol

Field Assistants Wanted - Behavior & Physiological Ecology in Spain

Field assistants are needed for a study examining the relationship between testosterone and fitness in male vertebrates. This project investigates behavior, steroid levels and lifetime reproductive success of individuals in small insular populations of lizards, in order to test predictions of handicap signaling and conditional strategy theories. Correlational and experimental methods will be combined to examine both the fitness costs and benefits of elevated testosterone levels, and to examine whether testosterone levels are optimized for indi-

viduals. The subjects are Iberian rock lizards, *Podarcis hispanica*, living on small islands in the Ría de Arousa (Galicia, Spain). Research assistants will focus on gathering behavioral, physiological and morphological data on the lizards.

Field assistants will be provided with housing and a stipend to cover living costs. Travel costs to the field site must be paid by the assistant. Time Frame: Spring and Summer, 2005 (preferably 1 April - 31 June).

If interested, please email your resume/curriculum vitae and an explanation of your research interests and experience. Please also indicate 2 or 3 professors or scientists (with their emails and phone numbers) who can serve as references for you. Email to:

Kevin M. Pilz, Ph.D. kevin.pilz@cornell.edu NSF-IRFP Post-doctoral Fellow Dept. of Evolutionary Ecology Museo Nacional de Ciencias Naturales Madrid, Spain

Kevin M. Pilz, Ph.D. Department of Evolutionary Ecology Museo Nacional de Ciencias Naturales José Gutiérrez Abascal, 2 28006 Madrid Spain

Email: kevin.pilz@cornell.edu Office phone: (34) 91 411 1328 ext. 1111 (when calling the museum you will get a recording; dial 1, then dial the extension: 1111) Mobile phone: (34) 655 77 1016 Fax: (34) 91 564 5078

kevin.pilz@cornell.edu

UAlaskaFairbanks Microbiology

As seen in the 14 January issue of Science: The University of Alaska Fairbanks

TWO TENURE-TRACK FACULTY POSITIONS IN MICROBIOLOGY

The Department of Biology and Wildlife and the Institute of Arctic Biology at the University of Alaska Fairbanks seek applications for TWO joint tenure-track faculty positions in microbiology at the assistant professor level. Applicants must have earned a Ph.D. and post-doctoral and teaching experiences are preferred. Successful applicants for both positions will be expected to establish independent and externally funded research programs. Teaching duties will be two courses per year. We seek microbiologists with a background in either of the following two areas:

1. Applicants working on microorganisms, preferably prokaryotes, with research interests in molecular bi-

ology, ecology, biogeochemistry, or digestive physiology. We expect this hire to develop a research program relevant to high-latitude biology. Teaching duties could include an undergraduate general microbiology course and opportunities at the advanced undergraduate/graduate level. Please reference PCN # 204206/REQ # FF204206-01.

2. Applicants working on infectious agents, particularly those causing zoonotic diseases. Preference will be for applicants with research interests relevant to biomedical research. Teaching duties could include an undergraduate microbiology or an infectious disease course and opportunities at the advanced undergraduate/graduate level. Please reference PCN # 247945/REQ # FF247945-01.

Field and laboratory facilities include the DNA and Proteomic Core Facility, the Alaska Stable Isotope Facility, a new animal research facility, the R.G. White Large Animal Research Station, Toolik Field Station, Bonanza Creek LTER site, and instrument facilities that house transmission and scanning electron microscopes, a confocal microscope, and a FACS Aria flow cytometer. Our Bioinformatics Program provides access to the Arctic Region Supercomputing Center. A State of Alaska Public Health Diagnostic Laboratory is adjacent to the Institute of Arctic Biology. The Biology and Wildlife Department and the Institute of Arctic Biology have approximately 50 faculty, 20 postdoctoral fellows, and 300 undergraduate and 120 graduate students, including 40 Ph.D. students.

Applicants are encouraged to consult the Institute/Departmental websites and faculty profiles at <http://mercury.bio.uaf.edu>. Applications will be reviewed starting 15 February 2005. Please provide a signed application form (http://www.alaska.edu/hr/forms/PDF_ent/-applicant_form_ent.pdf), cover letter, curriculum vitae, statements of teaching and research interests, letters from three references and submit to: Terry Chapin, C/O UAF Human Resources, P.O. Box 757860, Fairbanks, Alaska 99775-7860, Phone (907) 474-7700, Fax (907) 474-5859. If you have specific questions about this announcement, please contact Terry Chapin at (907) 474-7922, terry.chapin@uaf.edu.

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

Matt Olson <matt.olson@uaf.edu>

UDurham MathBiol

Post available:

Lecturership in Mathematical Biology

Department of Biological & Biomedical Sciences University of Durham, Durham, UK

Candidates should have a doctorate in a biological, mathematical or related field and relevant post-doctoral experience. With interests in spatial analysis, environmental process modelling, population ecology and/or evolutionary processes (including inference based on DNA sequence or phylogenetic reconstructions), or ecological genetics. Applicants with experience in the application of MCMC, Bayesian and/or likelihood methods to modelling and data analysis are particularly encouraged to apply.

Go to: <https://jobs.dur.ac.uk/home.asp> Click on 'vacancies', and search for 'vacancy reference' 0606

Advertised in Nature on 6 January, Deadline for applications: 4 March 2005.

-Rus Hoelzel

a.r.hoelzel@durham.ac.uk

whose research builds links between them, particularly in the area of genome stability.

Salary will be within the Professorial range, minimum £44,874 per annum.

Informal enquiries may be addressed to Professor J D Brook, tel: 0115 839 3217 or Email: David.Brook@Nottingham.ac.uk. Further information about Genetics at Nottingham is available at: <http://www.nottingham.ac.uk/genetics>. Further details and application forms are available on the WWW at: <http://www.nottingham.ac.uk/hr/-vacancies/senior.html> or from the Human Resources Department, Highfield House, The University of Nottingham, University Park, Nottingham, NG7 2RD. Please quote ref. RAL/073. Closing date: 31 January 2005.

This post is open until filled - review of applications from 31 January 2005.

- Dr. Angus Davison

Institute of Genetics The University of Nottingham Queen's Medical Centre Nottingham NG7 2UH

email angus.davison@nott.ac.uk tel 0115 849 3239 (int. 35239) fax 0115 970 9906

www.nottingham.ac.uk/genetics

homepages.ed.ac.uk/adavison

dia.cap.ed.ac.uk/mollusca.html

zel-

URegina EnvironmentalBiol

UNottingham GenomeDynamics

Institute of Genetics School of Biology

Professor of Genome Dynamics

Applications are invited for the post of Professor of Genome Dynamics in the School of Biology and Institute of Genetics. The successful candidate will be expected to establish an international quality programme of research. The Professor will also become an academic member of the School of Biology and will be expected to contribute to teaching.

Genetics at Nottingham was rated Grade 5 in the 2001 Research Assessment Exercise. Research in the Institute falls into the broad categories of microbial genetics, human genetics, developmental genetics, and population and evolutionary genetics. Applications are invited from candidates who strengthen any of these areas, or

Could you kindly distribute this ad to members of our organization? Many thanks. Bill Chapco.

Faculty Position - Environmental Biology NSERC University Faculty Award Program Department of Biology, University of Regina

The Department of Biology at the University of Regina intends to sponsor an application for an NSERC University Faculty Award (UFA; see www.NSERC.ca for eligibility criteria). We invite applications from women for an Assistant Professor level tenure-track position, effective when the award is granted. We are seeking an individual who has expertise in the area of Environmental Biology with a preference for individuals with expertise in Environmental Ecotoxicology or Environmental Microbiology. Candidates must have a PhD, a productive research record, and postdoctoral experi-

ence is an asset. We expect the successful candidate to establish an externally funded research program (as per the program guidelines), and teach a limited number of undergraduate and graduate courses (maximum of one per year). Start-up research funds will be provided. The Faculty of Science has superior computational facilities (Laboratory of Computational Discovery, see <http://www.icd.uregina.ca/>), a new stable isotope laboratory (EQAL, see <http://uregina.ca/equal/>), first-rate optical microscopy and molecular biology capabilities and a field research station. To apply for the position, submit a letter of application outlining research and teaching goals, a curriculum vitae, samples of research publications, and arrange for three letters of reference to be sent to: Dr. W. Chapco, Head, Department of Biology, University of Regina, Regina, SK, S4S 0A2 Canada. (fax 306-585-4894; phone 306-585-4231; e-mail William.Chapco@uregina.ca). The closing date for applications is February 28, 2005. Further information about the department is available at: <http://www.uregina.ca/science/biology>. All qualified female candidates are encouraged to apply; however, only Canadian citizens or permanent residents are eligible for the award.

Dr. W. Chapco, Head Department of Biology University of Regina Regina, Canada SK S4S 0A2 Phone: 306-585-4478 Fax: 306-337-2410 e-mail: chapco@uregina.ca

to establish an externally funded research program (as per the program guidelines), and teach a limited number of undergraduate and graduate courses (maximum of one per year). Start-up research funds will be provided. The Faculty of Science has superior computational facilities (Laboratory of Computational Discovery, see <http://www.icd.uregina.ca/>), a new stable isotope laboratory (EQAL, see <http://uregina.ca/equal/>), first-rate optical microscopy and molecular biology capabilities and a field research station. To apply for the position, submit a letter of application outlining research and teaching goals, a curriculum vitae, samples of research publications, and arrange for three letters of reference to be sent to: Dr. W. Chapco, Head, Department of Biology, University of Regina, Regina, SK, S4S 0A2 Canada. (fax 306-585-4894; phone 306-585-4231; e-mail William.Chapco@uregina.ca). The closing date for applications is February 28, 2005. Further information about the department is available at: <http://www.uregina.ca/science/biology>. In accordance with Canadian immigration requirements, this advertisement is directed to Canadian citizens and permanent residents.

Dr. W. Chapco, Head Department of Biology University of Regina Regina, Canada SK S4S 0A2 Phone: 306-585-4478 Fax: 306-337-2410 e-mail: chapco@uregina.ca William.Chapco@uregina.ca

URegina EvolEnvironmentalBiol

Faculty Position - Environmental Biology NSERC University Faculty Award Program Department of Biology, University of Regina

The Department of Biology at the University of Regina intends to sponsor an application for an NSERC University Faculty Award. The University Faculty Awards program aims to increase the representation of women and Aboriginal peoples in faculty positions in the natural sciences and engineering. We invite applications from eligible candidates (eligibility criteria at www.nserc.ca) for an Assistant Professor level tenure-track position, effective when the award is granted. We are seeking an individual who has expertise in the area of Environmental Biology with a preference for individuals with expertise in Environmental Ecotoxicology or Environmental Microbiology. Candidates must have a PhD, a productive research record and postdoctoral experience is an asset. We expect the successful candidate

UVirginia DirectorBioStation

Evolution - Ecology - Behavior - Conservation - Systematics Director, Mountain Lake Biological Station The University of Virginia

The University of Virginia is seeking an outstanding biologist as Director of Mountain Lake Biological Station. He or she will have a record of accomplishment and the expectation of continued excellence in research and teaching. The Director will be a resident tenured member of the Department of Biology in Charlottesville during the academic year. Mountain Lake Biological Station is located 3 hours southwest of Charlottesville in the Allegheny Mountains surrounded by the Mountain Lake Wilderness Area and the Jefferson National Forest. The station is a center for research in population biology and community ecology and is now in its 75th year of offering summer courses in field biology. Applicants should submit a curriculum vitae, research and teaching statements, a letter explaining

their anticipated contribution to the field station, and names and addresses of four references to: Dr. Janis Antonovics, MLBS Search Committee Chair, Department of Biology, PO Box 400328, Charlottesville, VA 22904-0328. Applications are encouraged by February 15th 2005, but the search will remain open until the position is filled. Additional information can be found at www.mlbs.virginia.edu or by e-mail to antonovics@virginia.edu.

The University of Virginia is an equal opportunity/affirmative action employer.

UVirginia SummerStudent

PLEASE FORWARD TO YOUR STUDENTS.

Greetings,

The Mountain Lake Biological Station (<http://www.virginia.edu/~mtlake>mlbs.org>, University of Virginia) announces paid research opportunities for undergraduates and university-level credit courses in field biology. We offer students hands-on experience and training in a wide variety of biological field studies. Students are invited to join us for an exciting and unforgettable summer in a beautiful and stimulating teaching and research environment. Scholarships and financial aid for courses are available.

NSF-Funded Research Experience for Undergraduates (REU) Program <http://www.mlbs.org/-REU.html> [mlbs.org/REU.html](http://www.mlbs.org/-REU.html) We match undergraduate students with visiting scientists for 10 weeks of advanced, independent research on a project of the student's own design. REU positions come with a stipend of \$3,500 and pay all room and board expenses. Minority students are especially encouraged to apply. Deadline for receipt of applications is March 1.

Field Courses

<http://www.mlbs.org/-courses.html> [mlbs<http://www.mlbs.org/-courses.html>.org/courses.html](http://www.mlbs.org/-courses.html)

1) Field Entomology May 15 - 29. Upper-level undergraduate and graduate course on the ecology and diversity of insects. 2) Field Geology May 31 - June 24. Introduction to field techniques used by geologists. 3) Ecology Of Wildlife Diseases May 31 - June 24. Introduction to the ecology and evolution of parasites in wild animal populations. 4) Plant Biodiversity And Conser-

vation June 27 - July 22. The extraordinary diversity of the Southern Appalachians will serve as a backdrop to explore the world of plants. 5) Evolutionary Ecology June 27 - July 22. Will examine how individuals, populations, and communities respond to their environments and how those responses are influenced by their evolutionary history. 6) Biodiversity In The Southern Appalachians July 25 - Will teach students how historical processes and current land-use patterns shape the compositions of ecological communities. 7) Ecology And Conservation Of Freshwater Fishes July 25 - August 5. An investigation of the ecology and conservation of freshwater fishes through a series of discussions, lectures, lab and field exercises.

Our field station is located on a mountaintop in southwestern Virginia and is home to a lively research, teaching and social community. For details on these programs, full course descriptions, application material, and a list of research areas see our web page:

<http://www.virginia.edu/~mtlake>mlbs.org> Thank you very much for your help.

Contact our office at : Mountain Lake Biological Station , University of Virginia, 238 Gilmer Hall, PO Box 400327, Charlottesville VA 22904-4327, U.S.A. <mailto:mlbs@virginia.edu> mlbs@virginia.edu 434-982-5486 .

Eric S. Nagy, Ph.D. Associate Director, Mountain Lake Biological Station Assistant Professor, Department of Biology University of Virginia, 238 Gilmer Hall, P.O. Box 400327 Charlottesville, VA 22904-4327 USA Street Address: 485 McCormick Road 434-982-5486 office (540-626-5227 summer office) 434-982-5626 fax (540-626-5229 summer fax) 434-906-3122 cell Email: <mailto:enagy@virginia.edu> enagy@virginia.edu Personal page: <http://faculty.virginia.edu/-nagy>faculty.virginia.edu/nagy> Mountain Lake Biological Station: <http://www.mlbs.org/>mlbs.org> enagy@virginia.edu

UWesternOntario Genetics

THE UNIVERSITY OF WESTERN ONTARIO DEPARTMENT OF BIOLOGY

The Department of Biology at The University of Western Ontario invites applications for the following position effective July 1, 2005:

Geneticist:

Applications are invited for a probationary (tenure track) ASSISTANT or ASSOCIATE PROFESSOR position in genetics. The candidate's research interest should encompass the areas of molecular biology, genetics, evolutionary genetics, and/or genomics. The applicant should have a broad background and training in modern genetic and molecular techniques in order to contribute to the broad range of undergraduate courses offered by this department. Applicants must have a Ph.D. and appropriate postdoctoral training or equivalent expertise and a proven research record, including publications of high quality. The successful applicant will be expected to develop an innovative program of independent, externally funded research and to teach at both the undergraduate and graduate levels. The successful candidate will be a member of the Molecular Genetics Unit within the Department of Biology and have access to a joint core facility and a dynamic research community in London. In particular, we are looking for an enthusiastic individual who is well versed in genetic and molecular principles, able to work well with others and contribute to the undergraduate Honours Program in Genetics and related fields.

Applications, including a curriculum vitae, names and addresses of three referees whom we may contact, copies of recent significant papers and a one page summary of proposed research should be forwarded to:

Dr. Brock Fenton, Chair Department of Biology The University of Western Ontario London, Ontario N6A 5B7 Canada

Deadline for applications is February 15, 2005.

Position is subject to budget approval. Applicants should have fluent written and oral communication skills in English. All qualified candidates are encouraged to apply; however Canadian Citizens and permanent residents will be given priority. The University of Western Ontario is committed to employment equity and welcomes applications from all qualified women and men, including visible minorities, aboriginal people and persons with disabilities.

Dr. Shiva M. Singh, Professor (Molecular Genetics) Distinguished Research Professor Senior Research Fellow, OMHF Department of Biology and Division of Medical Genetics University of Western Ontario London, Ontario, Canada N6A 5B7

Office; 307 Molecular Genetics, Western Science centre tel. 519.661.3135 Lab; 313 Molecular Genetics, Western Science Centre tel. 519.679.2111 ext 6928

FAX: 519.661.3935

ssingh@uwo.ca

UZurich PopGenetics

The Faculty of Science at the University of Zurich invites applications for an Assistant Professorship in Population Genetics at the Institute of Zoology.

We seek applicants with a record of excellent postdoctoral research in population and evolutionary genetics, especially its theoretical foundations, statistical treatment including analysis of molecular data, and its application to natural populations. The successful candidate is expected to develop a strong, independent research program, partly supported by external funding, and to interact with existing groups (e.g. Animal Behaviour, Ecology and Evolutionary Biology, and Molecular and Developmental Biology). Candidates will also be expected to teach at the undergraduate and graduate levels. Detailed information on existing research areas in Zoology, teaching programs in Biology and other Institutes in the Faculty of Science can be found at <http://www.zool.unizh.ch/>, <http://www.zool.unizh.ch/>, and <http://www.biologie.unizh.ch/>. The position is a non-tenure track assistant professorship for six years. Some resources, such as additional positions, lab and office space, are included in the offer. Applications including a curriculum vitae, a publication list and a short summary of past and future research interests (less than two pages each), copies of three key publications and names and addresses of three potential referees should be sent by March 15, 2005 to Prof. Dr. P. Truöl, Dean of the Faculty of Science (MNF), University of Zurich, Winterthurerstrasse 190, CH-8057 Zurich, Switzerland. The application material should also be submitted in a single PDF-file to jobs@mnf.unizh.ch. For inquiries please contact Prof. Dr. H.-U. Reyer, Institute of Zoology, E-mail: ulireyer@zool.unizh.ch

Lukas Keller <Lukas.Keller@zoolmus.unizh.ch>

UZurich SystematicBotany

The Faculty of Science (Mathematisch-naturwissenschaftliche Fakultät) of the University of Zurich invites applications for a

Professorship (Ordinarius, Extraordinarius, or Assistant Professor with Tenure Track) in Systematic Botany

at the Institute for Systematic Botany, to commence on October 1, 2007. The new professor is expected to establish and lead a successful research group, contribute to the graduate teaching in Systematic Botany, and the undergraduate teaching in Biology. She or he will find an excellent library, herbarium, laboratory infrastructure, and botanical garden, as well as a stimulating environment. The institute is associated with the Zoological Museum, the Palaeontological Institute and other related research institutes in a School of Biology, and with other botanical Institutes of the University, the ETH and the University of Basel in the Zurich-Basel Plant Science Center. Current research interests at the institute include molecular and morphological phylogenetic systematics, comparative evolutionary biology, and biogeography.

We are looking for excellent researchers in systematic botany with an interest in micro-evolution, palaeobotany, reproductive biology, morphology, or other fields that will complement existing research strengths in the institute.

Applicants are invited to submit by April 31, 2005 a curriculum vitae, a publication list, and a summary of their research interests to Prof. Dr. P. Truöl, Dean of the Faculty of Science (MNF), University of Zurich, Winterthurerstrasse 190, CH-8057 Zurich, Switzerland. The application material should also be submitted in a single Word or PDF file to jobsmnf@zuv.unizh.ch.

For further information, contact Prof. H.P. Linder, Institute for Systematic Botany, phone +41 1 6358410, email: plinder@systbot.unizh.ch, or visit the institute homepage at www.systbot.unizh.ch ContiElena@access.unizh.ch

Other

ChicagoBotanicGarden UndergradInternship	34	MapMarker1000 answers	42
Discussion lists	34	Maynard Smith Prize	43
Drosophila Stocks	34	Microsat cloning answers	44
Edinburgh AdaptiveSystems	36	PCR amplification answers	45
Effective vs census pop size	36	PCR amplification problems	46
Evol Meeting Proposals	36	PCR plates	46
Evolution games	37	Phylogenetics web site	47
Evolution wars	37	SYNTHEsys SystematistTravelFunds	47
Genemapper AFLP data	38	Sankoff wins WeldonMedal	48
Genome Evolution	38	Software BAPS 3 1	48
Georgia Evolution ruling	39	Software Prottest	48
Hampton L Carson 1914-2004	40	Software TreeFinder 2	49
Haplodiploid relatedness	40	Spectrophotometer	49
Human mitochondrial database mtDB	40	Tetraploid SSRdata	50
IIASA Austria SummerStipends	41	WeldonMedal Winners	50
Isolation by distance	41	old polymer	50
LongnoseDace samples	42		
MapMarker 1000	42		

Chicago Botanic Garden Undergrad Internship

Below is an advertisement for a NSF funded summer research internship in Plant Biology and Conservation. The program is aimed at undergraduates in the latter stages of their degree. If you could pass it onto any interested parties and advertise it within your respective departments, it would be much appreciated. For applications and any additional inquiries please contact Dr David Lentz, (dlentz@chicagobotanic.org).

Cheers

SUMMER INTERNSHIPS AT CHICAGO BOTANIC GARDEN

NATIONAL SCIENCE FOUNDATION RESEARCH EXPERIENCES FOR UNDERGRADUATES 2005 Summer Undergraduate Research Fellowships

PLANT BIOLOGY AND CONSERVATION Application deadline: March 15, 2005

The Chicago Botanic Garden and Northwestern University are accepting applications for a Summer Research Program in Plant Biology and Conservation Science (June 15 - August 30, 2005) supported by a National Science Foundation-REU site grant. This year we will offer up to 8 awards to qualified undergraduates interested in conducting plant research. Stipends of \$3,000 plus accommodation costs will be awarded to successful applicants. Funds are also available to support research and travel. We offer students hands-on experience and training in a wide variety of field studies, including: plant demography, quantitative genetics, molecular ecology, plant breeding, invasive plant dynamics, paleoethnobotany, economic botany, soil ecology, and remote sensing. Responsibilities may include field sampling, laboratory studies, and data analysis. Core program activities include the design and execution of independent, mentored research projects, and participation in weekly seminars. Through these activities, students will learn the fundamentals of experimental design, the use of the scientific literature, data collection and analysis, and oral presentation. At the end of the summer, students will analyze their data, prepare an abstract, and present their findings at a student research symposium. Applications and further information can be obtained from Dr. David Lentz (dlentz@chicagobotanic.org). Completed applications (see form attached) for the summer of 2005 must be received by March 15 and notification of acceptance

into the program will be provided by April 20. Acceptance into the program will be based on academic performance, your professional goals and research interests.

Lab@cbgnt.chicagobotanic.org

Discussion lists

Dear friend,

Do you know about a good discussion list on evolutionary biology ? I interested in a list to discuss the evolutionary mechanisms, the history of evolutionary biology, creation versus evolution and also about teaching material !

Also, I am interested in real articles (not websites) discussing the creation X evolution debate! I need real published material to use with my students.

Could you help me please ?

Thanks !!

Voltolini

Prof. J. C. VOLTOLINI Grupo de Estudos em Ecologia de Mamíferos (ECOMAM) Universidade de Taubate - Departamento de Biologia Taubate, SP. 12030-010.

E-Mail: jcvoltol@uol.com.br Website: <http://jcvoltol.sites.uol.com.br/> Currículo Lattes: <http://lattes.cnpq.br/buscaoperacional/> Fotos: <http://jcvoltol.fotoblog.uol.com.br/> VOLTOLINI <jcvoltol@uol.com.br>

Drosophila Stocks

TUCSON DROSOPHILA SPECIES STOCK CENTER NEW STOCKS ISOFEMALE LINES AND ADDITIONS TO THE PERMANENT COLLECTION“

The Tucson Drosophila Species Stock Center has recently received new isofemale lines from the following species. These Isofemale lines are available until last day April 2005:

Drosophila affinis: 9 isofemale lines from Johnson Co. Park, Iowa City, Iowa (2003). Collected by Bryant McAllister.

Drosophila affinis: 6 isofemale lines from Cedar River, Muscatine, Iowa (2003). Collected by Bryant McAllister.

Drosophila affinis: 7 isofemale lines from Iowa River, Near Johnson Co., Iowa (2003). Collected by Bryant McAllister.

Drosophila americana: 4 isofemale lines from Iowa River, Iowa (2004). Collected by Bryant McAllister

Drosophila arizonae: 10 isofemale lines from La Pintada, Sonora, Mexico (2003). Collected by Sergio Castrezana.

Drosophila arizonae: 18 isofemale lines from Tucson, Arizona (07/2004). Collected by Mariana Mateos.

Drosophila arizonae: 2 isofemale lines from Tucson, Arizona (11/2004). Collected by Mariana Mateos.

Drosophila busckii: 3 isofemale lines from San Antonio de Guadalupe, Zumpahuacan, Edo. Mexico (2004). Collected by Mariana Mateos.

Drosophila immigrans: 5 isofemale lines from Rocky Point, New York (2004). Collected by Thomas Merritt

Drosophila mojavensis: 3 isofemale lines from La Pintada, Sonora, Mexico (2003). Collected by Sergio Castrezana.

Drosophila nigrospiracula: 5 isofemale lines from Tucson, Arizona (2004). Collected by Therese Markow.

Drosophila pseudoobscura: 20 isofemale lines from Santa Fe, New Mexico (2004). Collected by Therese Markow.

Drosophila pseudoobscura: 3 isofemale lines from Tucson, Arizona (2004). Collected by Mariana Mateos.

Drosophila robusta: 7 isofemale lines from Iowa River, Near Johnson Co., Iowa (2003). Collected by Bryant McAllister.

Drosophila robusta: 5 isofemale lines from Iowa River-Iowa (2004). Collected by Bryant McAllister.

Drosophila simulans: 2 isofemale lines from Chiricahua AZ, Arizona (2004). Collected by Mariana Mateos.

The Tucson *Drosophila* Species Stock Center has added new strains of wild type flies to the permanent collection. Check website for collection information:

Isofemale lines:

D. affinis 14012-0141.06 (Iowa River, Iowa. 2003).
D. algonquin 14012-0161.01 (Rorher, IL. 2003). *D. algonquin* 14012-0161.02 (Rocky Point, N.Y. 2004).
D. azteca 14012-0171.07 (Jalisco, Mexico. 2004). *D. azteca* 14012-0171.08 (Oaxaca, Mexico. 2003). *D.*

melanogaster 14021-0231.29 (Santa Fe, New Mexico. 2004). *D. melanogaster* 14021-0231.30 (Oaxaca, Mexico. 2003). *D. melanogaster* 14021-0231.31 (Nayarit, Mexico. 2004). *D. melanogaster* 14021-0231.32 (Sinaloa, Mexico. 2004). *D. melanogaster* 14021-0231.33 (Jalisco, Mexico 2004). *D. mojavensis* 15081-1352.23 (Hermosillo, Mexico. 2003). *D. nigrospiracula* 15081-1503.08 (Tucson, Arizona. 2004). *D. nikananu* 14028-0601.01 (Lake Awing, Cameroon. 2003). *D. pseudoobscura* 14011-0121.98 (Estado de Mexico, Mexico. 2004). *D. pseudoobscura* 14011-0121.100 (Oaxaca, Mexico. 2003). *D. pseudoobscura* 14011-0121.102 (Sinaloa, Mexico. 2004). *D. robusta* 15020-1111.10 (Iowa River, Iowa. 2003) *D. simulans* 14021-0251.200 (CHAZ, Arizona. 2004). *D. simulans* 14021-0251.201 (Nayarit, Mexico. 2004). *D. simulans* 14021-0251.202 (Estado de Mexico, Mexico. 2004). *D. simulans* 14021-0251.203 (Jalisco, Mexico 2004). *D. simulans* 14021-0251.204 (Nayarit, Mexico 2004). *D. simulans* 14021-0251.205 (Oaxaca, Mexico 2003). *D. teissieri* 14021-0257.01 (Lake Awing, Cameroon. 2003). *D. tolteca* 14012-0201.01 (Jalisco, Mexico. 2004). *D. willistoni* 14030-0811.28 (Jalisco, Mexico. 2004). *Scaptomyza pallidosa* 34000-0010.00 (Eagle Heights, Wisconsin. 2004).

Multifemale strains: *D. affinis* 14012-0141.03 (Iowa City, Iowa. 2003). *D. affinis* 14012-0141.04 (Muscatine, Iowa. 2003). *D. affinis* 14012-0141.05 (Iowa River, Iowa. 2003). *D. aldrichi* 15081-1251.15 (Baja South, Mexico. 1985). *D. aldrichi* 15081-1251.16 (Tucson, Arizona. 2001). *D. arizonae* 15081-1271.21 (Tucson, Arizona. 2004). *D. arizonae* 15081-1271.22 (La Pintada, Son. Mexico. 2003). *D. busckii* 13000-0081.29 (Estado de Mexico, Mexico 2004). *D. hamatofila* 15081-1301.05 (Tucson, Arizona 2001). *D. hexastigma* 15081-1302.04 (Puebla, Mexico. 1997). *D. longicornis* 15081-1311.13 (Tucson, Arizona. 2001). *D. longicornis* 15081-1311.16 (Hidalgo, Mexico. 2000). *D. mainlandi* 15081-1315.01 (Baja South, Mexico. 1996). *D. mettleri* 15081-1502.12 (Catalina Island, CA. 1991). *D. mojavensis* 15081-1352.24 (La Pintada, Son. Mexico. 2003). *D. nigrospiracula* 15081-1503.07 (Tucson, Arizona. 2004). *D. pachea* 15090-1698.01 (Organ Pipe National Monument, Arizona. 1997). *D. pachea* 15090-1698.02 (Sonora, Mexico. 1996). *D. propachuca* 15081-1411.05 (Jalisco, Mexico. 2000). *D. pseudoobscura* 14011-0121.96 (Baja, Mexico. 2003). *D. pseudoobscura* 14011-0121.97 (Chisos Basin, Texas. 2004). *D. pseudoobscura* 14011-0121.99 (Oaxaca, Mexico. 2003). *D. pseudoobscura* 14011-0121.101 (Sonora, Mexico. 2003).

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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>

Edinburgh AdaptiveSystems

Dear Colleagues,

High-quality scientific papers are solicited for two special sessions at the IEEE Congress on Evolutionary Computation (2-5 Sept. 2005, Edinburgh Scotland). Follow the links for details:

“Artificial Life” <http://homepages.feis.herts.ac.uk/~comqcln/IEEE-CEC05-AL.html> “Complex Adaptive Systems: Towards Predictive Methodologies” <http://homepages.feis.herts.ac.uk/~comqcln/IEEE-CEC05-CAS.html> Hoping to see you there!

Best Regards,

Chrystopher Nehaniv University of Hertfordshire, UK
c.l.nehaniv@herts.ac.uk

Effective vs census pop size

Dear colleagues,

I vaguely recall seeing a paper some years ago, perhaps 10-15, which suggested that the ratio of Ne/N is smaller the larger is N. Can anybody give me this reference?

Thanks,

Bill Birky C. William Birky, Jr. Professor of Ecology and Evolutionary Biology Member, Graduate Interdisciplinary Programs in Genetics Biological Sciences West 1041 E. Lowell University of Arizona Tucson, AZ 85721 Office phone: 520-626-6513 Lab phone: 520-626-5108 Fax: 520-621-9190 Email: birky@u.arizona.edu

birky@u.arizona.edu

Evol Meeting Proposals

Dear Colleagues,

- Have you long dreamed of a grand enterprise that can only be addressed by large-scale collaboration? - Would the results from other fields be greatly more relevant to your work if they you could make a slight change to their research program? - Is there a group of scientists that you are dying to get in a room and pepper with questions? - Would you like to make the case to individuals in another field that your work can advance theirs?

The National Evolutionary Synthesis Center (NES-Cent) announces a call for meeting proposals, with a deadline of March 15, 2005 <http://www.nescent.org/-nescent/Meetings.html> Cross-Disciplinary Network Catalysis Meetings

These one-time meetings of ~30 scientists from diverse disciplines to focus on a major question or research area. These meetings are intended to identify avenues for synthesis, and classes of primary data that must be collected before grand-scale synthesis is possible. These meetings are intended to increase the scale and ambition of our scientific vision. By allowing interaction beyond the “usual suspects”, these meetings will facilitate the assembly of networks to collect the primary data needed for synthesis, and networks that will apply for funding such as NSF Research Coordination Networks or NESCent’s “working groups” (see below).

Working Group Meetings

Working Groups involve small groups of scientists (10-12 participants) collaborating intensively on the analysis or synthesis of data, models or both, to address a major question in evolutionary biology, or to solve a particular analytical problem.? The working groups will typically meet 3 times over two years (a 4th meeting can be requested later). Each meeting may last between 4-10 days.? NESCent will not fund collection of new data or field research, but encourages the mining of public and private databases. Products from working groups might include (but are not restricted to) - Synthetic papers and reviews - Databases allowing others to build on the foundation you lay - Software or mathematical tools that solve a major analytical problem

Cliff Cunningham Director National Evolutionary Synthesis Center Box 90338 Duke University Durham, NC 27708

919-660-7356

www.nescent.org Cliff Cunningham <cliff@duke.edu>

Evolution games

I'm a computer science PhD student working on an educational software project centered around natural selection/evolution. As a first step, we're trying to gather as much information about *existing* games in this vein as we can. We're aware of GenScope and MIT's Live Long and Prosper, but we were wondering if there are other examples out there that you're aware of. Mind you, we're just as interested in "bad" examples as "good examples" - we'd rather not reproduce the mistakes of others, if possible! If you're moved to make a commentary on the game(s) with respect to their accuracy/educational utility, that would be appreciated as well. Thanks in advance to anyone who can help us with this!

- Leilah

leilah@gmail.com

Evolution wars

<http://www.salon.com/news/feature/2005/01/10/-evolution/index.html> The new Monkey Trial

By persuading the Dover, Pa., school board to teach creationism, Christian zealots have provoked a showdown over the status of not just evolutionary theory, but science itself.

----- By Michelle Goldberg

Jan. 10, 2005 | DOVER, Pa. – It was an ordinary springtime school board meeting in the bedroom community of Dover, Pa. The high school needed new biology textbooks, and the science department had recommended Kenneth Miller and Joseph Levine's "Biology." "It was a fantastic text," said Carol "Casey" Brown, 57, a self-described Goldwater Republican and the board's senior member. "It just followed our curriculum so beautifully."

But Bill Buckingham, a new board member who'd recently become chair of the curriculum committee, had an objection. "Biology," he said, was "laced with Darwinism." He wanted a book that balanced theories of

evolution with Christian creationism, and he was willing to turn his town into a cultural battlefield to get it.

"This country wasn't founded on Muslim beliefs or evolution," Buckingham, a stocky, gray-haired man who wears a red, white and blue crucifix pin on his lapel, said at the meeting. "This country was founded on Christianity, and our students should be taught as such."

Casey Brown and her husband, fellow board member Jeff Brown, were stunned. "I was picturing the headlines," Jeff said months later.

"And we got them," Casey added.

Indeed, by the end of 2004, journalists from across the country and from overseas had come to Dover to report on the latest outbreak of America's perennial war over evolution. By then, Buckingham had succeeded in making Dover the first school district in the country to mandate the teaching of "intelligent design" – an updated version of creationism couched in modern biological terms. In doing so, he ushered in a legal challenge from outraged parents and the ACLU that could turn into a 21st century version of the infamous "Scopes Monkey Trial."

The Dover case is part of a renewed revolt against evolutionary science that's been gathering force in America for the past four years, a symptom of the same renascent fundamentalism that helped propel George Bush to victory. Since 2001, the National Center for Science Education, a group formed to defend the teaching of evolution, has tallied battles over evolution in 43 states, noting they're growing more frequent.

After 1987, when the Supreme Court declared the teaching of creationism in public school unconstitutional in *Edwards vs. Aguillard*, the doctrine seemed to be shut out of public schools once and for all. In the last few years, though, intelligent design has given evolution's opponents new hope. Now, emboldened by their growing political power, religious conservatives are once again storming the barricades of science education.

The same month Bush was reelected, the rural Grantsburg, Wis., school district revised its curriculum to allow the teaching of creationism and intelligent design. After a community outcry – including a letter of protest from 200 Wisconsin clergy – the district revised the policy but continued to mandate that students be taught "the scientific strengths and weaknesses of evolutionary theory," a common creationist tactic that fosters the illusion that evolution is a controversial theory among scientists.

Other anti-evolution initiatives have affected entire

states. In the November election, creationists took over the Kansas Board of Education. The last time the board had a majority, in 1999, it voted to erase any mention of evolution from the state curriculum. Kansas became a laughingstock and the anti-evolutionists were defeated in the next Republican primary, leading to the policy's reversal. Now, newly victorious, the anti-evolutionists plan to introduce the teaching of intelligent design next year.

Similarly, this past December, the New York Times reported that Missouri legislators plan to introduce a bill that would require state biology textbooks to include at least one chapter dealing with "alternative theories to evolution." Speaking to the Times, state Rep. Cynthia Davis seemed to compare opponents of intelligent design to al-Qaida. "It's like when the hijackers took over those four planes on Sept. 11 and took people to a place where they didn't want to go," she said. "I think a lot of people feel that liberals have taken our country somewhere we don't want to go. I think a lot more people realize this is our country and we're going to take it back."

Right-wingers in Congress, on talk radio and on cable TV, are stoking the anti-evolution rebellion, insisting that academic freedom means the freedom

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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>

Genemapper AFLP data

Dear all,

I was wondering if anyone knew a way to transfer AFLP data collected by Genemapper 3.05 from an ABI 3100 to Genographer 1.6 or an other program able to perform AFLP analysis.

I Thank you in advance.

Sincerely,

Jerome Vrancken

Jerome Vrancken, PhD student Unité d'Ecologie et de Biogéographie Université catholique de Louvain Croix du Sud, 4-5 B-1348 Louvain-la-Neuve Tel. +32 10 479228 Belgium e-mail vrancken@ecol.ucl.ac.be

Genome Evolution

Dear Colleagues,

I am nevertheless pleased to announce here that Elsevier/Academic Press has released "The Evolution of the Genome", a book edited by T.R. Gregory and containing chapters by numerous prominent genome researchers. I post the announcement here because I believe the subject matter of the book will be of considerable interest to many EvolDir members and their students.

In brief, the volume covers most of the major issues in genome evolution, reviews these topics in an integrative manner, provides important conceptual and historical context in addition to prospects for future research, and is written in such a way as to make the material accessible to young researchers, postdocs, advanced grad students, and researchers in related fields. I also did my best to ensure that, despite the length (740pp), the price would remain accessible to postdocs, students, and others who can't write it off as a grant expense!

For your interest, I include the chapter and author list below, and invite you to visit <http://www.genomesize.com/rgregory/book> for additional details.

The Evolution of the Genome

- 1) Genome size evolution in animals by T. Ryan Gregory
- 2) Genome size evolution in plants by Michael D. Bennett and Ilia J. Leitch
- 3) Transposable elements by Margaret G. Kidwell
- 4) B chromosomes by Juan Pedro M. Camacho
- 5) Small-scale gene duplications by John S. Taylor and Jeroen Raes
- 6) Large-scale gene and ancient genome duplications by Yves Van de Peer and Axel Meyer
- 7) Polyploidy in plants by Jennifer Tate, Douglas E. Soltis, and Pamela S. Soltis
- 8) Polyploidy in animals by T. Ryan Gregory and Barbara K. Mable
- 9) Comparative genomics in eukaryotes by Alan Filipksi and Sudhir Kumar

10) Comparative genomics in prokaryotes by T. Ryan Gregory and Rob DeSalle

11) Macroevolution and the genome by T. Ryan Gregory

I hope you find the book interesting and useful, and wish everyone the best for the upcoming year.

Cheers,

- Ryan

T. Ryan Gregory, Ph.D. Dept. of Zoology University of Guelph Guelph, Ontario N1G 2W1 Canada

<http://www.genomesize.com/rgregory/> rgregory@genomesize.com

Georgia Evolution ruling

I thought that given recent postings to EvoDir that members might want to hear a small bit of good news regarding the teaching of evolution in the U.S.

Rodney Mauricio University of Georgia

From CNN <http://www.cnn.com/2005/LAW/01/13/evolution.textbooks.ruling/index.html> Judge: Evolution stickers unconstitutional

Markers in science textbooks violated church-state separation

Thursday, January 13, 2005 Posted: 12:22 PM EST (1722 GMT)

ATLANTA, Georgia (CNN) – A federal judge in Atlanta, Georgia, has ruled that a suburban county school district's textbook stickers referring to evolution as "a theory not a fact" are unconstitutional.

In ruling that the stickers violate the constitutionally mandated separation between church and state, U.S. District Judge Clarence Cooper ruled that labeling evolution a "theory" played on the popular definition of the word as a "hunch" and could confuse students.

According to The Associated Press, the stickers read, "This textbook contains material on evolution. Evolution is a theory, not a fact, regarding the origin of living things. This material should be approached with an open mind, studied carefully and critically considered."

The disclaimers were put in the books by school officials in 2002.

"Due to the manner in which the sticker refers to evolution as a theory, the sticker also has the effect of undermining evolution education to the benefit of those Cobb County citizens who would prefer that students maintain their religious beliefs regarding the origin of life," Cooper wrote in his ruling.

Cooper said he was ruling on the "narrow issue" of the case, brought against the Cobb County School District and Board of Education by four parents of district students, was whether the district's stickers violated the Establishment Clause of the First Amendment.

His conclusion, he said, "is not that the school board should not have called evolution a theory or that the school board should have called evolution a fact."

"Rather, the distinction of evolution as a theory rather than a fact is the distinction that religiously motivated individuals have specifically asked school boards to make in the most recent anti-evolution movement, and that was exactly what parents in Cobb County did in this case," he wrote.

"By adopting this specific language, even if at the direction of counsel, the Cobb County School Board appears to have sided with these religiously motivated individuals."

The sticker, he said, sends "a message that the school board agrees with the beliefs of Christian fundamentalists and creationists."

"The school board has effectively improperly entangled itself with religion by appearing to take a position," Cooper wrote. "Therefore, the sticker must be removed from all of the textbooks into which it has been placed."

Five parents of students and the American Civil Liberties Union had challenged the stickers in court, arguing they violated the constitutional separation of church and state.

The case was heard in federal court last November. The school system defended the warning stickers as a show of tolerance, not religious activism as some parents claimed.

"The Cobb County school board is doing more than accommodating religion," Michael Manely, an attorney for the parents, argued during the trial, according to a report from The Associated Press. "They are promoting religious dogma to all students."

Lawyers for Cobb County, however, argued in court that the school board had made a good-faith effort to address questions that inevitably arise during the teaching of evolution.

"Science and religion are related and they're not mutu-

ally exclusive,” school district attorney Linwood Gunn said in an AP report. “This sticker was an effort to get past that conflict and to teach good science.”

According to the AP, the schools placed the stickers after more than 2,000 parents complained the textbooks presented evolution as fact, without mentioning rival ideas about the beginnings of life.

–

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Lab Web Page: <http://www.genetics.uga.edu/mauriciolab/mauriciohome.html> Evolution at UGA:
<http://www.genetics.uga.edu/evolution/evoluga.html>
Rodney Mauricio <mauricio@uga.edu>

Hampton L Carson 1914-2004

With great sadness I pass on the news that Professor Hampton L. Carson died December 13, 2004, about five weeks after his 90th birthday. He is perhaps best known for his work on chromosomal evolution and speciation, particularly the founder principle, which arose from his deep knowledge of the Hawaiian *Drosophila*. The range of his contributions to evolutionary genetics is found in his over 250 publications produced over a period of 70 years, the most recent appearing in 2003. Many of his ideas were the subject of a symposium held in honor of his retirement (1).

Many of Hamp’s papers (1921-1993) are in the collections of the American Philosophical Society, Philadelphia <www.amphilsoc.org/library/mole/-c/carson.htm> . 1) Giddings, L.V., K.Y. Kaneshiro, and W.W. Anderson. 1989. *Genetics, Speciation, and the Founder Principle*. Oxford University Press, ISBN 0195043154.

– Richard H. Thomas, PhD Voice: 618-453-7425 Department of Zoology Fax: 618-453-2806 Life Science II, Mail Code 6501 email: rthomas@zoology.siu.edu Southern Illinois University 1125 Lincoln Drive Carbondale, IL 62901 USA

Haplodiploid relatedness

Dear all,

I want to partition a cohort of ca 1000 haplodiploid individuals (hymenopteran parasitoids) into full sib groups, using seven microsatellite loci. I need to use data from both males and females and I have no information on the number or the genotypes of parents. Does anyone know a program allowing to construct reliable sibship partitions for haplodiploid species?

Thank you in advance. Cédric. e-mail: tentelie@antibes.inra.fr

Cédric Tentelier UMR 1112 Réponse de Organismes aux Stress Environnementaux INRA 400 routes des Chappes BP 167 06903 Sophia Antipolis Cedex

Tel : +33 (0)4 92 38 64 89 Fax : +33 (0)4 92 38 65 57

Cédric Tentelier <tentelie@antibes.inra.fr>

Human mitochondrial database mtDB

mtDB is a database for complete human mitochondrial genomes and is intended for use in both human population genetics and medical genetics. This site has been up for 4 years now but there seem to be plenty of researchers that don’t know about it.

<http://www.genpat.uu.se/mtDB> Of the more than 2000 complete, or near complete, mitochondrial genomes that have been published to date, less than half are available through GenBank. As far as I know, our website is the only place online where many can be obtained. Not only are all the sequences available here but also a compilation of all variable sites among these (currently 2056) sequences. It is also possible to identify which sequences vary at each site. We have recently added a search function where one can input up to 10 criteria of site/variant and output a list of sequences that match. This can be useful, for example, for identifying sequences that fall in to a particular haplogroup.

Max Ingman

Section of Medical Genetics Department of Genetics and Pathology University of Uppsala 751 85 Uppsala SWEDEN

max.ingman@genpat.uu.se

Max Ingman <max.ingman@genpat.uu.se>

IIASA Austria SummerStipends

SUMMER PROJECT STIPENDS FOR YOUNG SCIENTISTS AVAILABLE AT THE INTERNATIONAL INSTITUTE FOR APPLIED SYSTEMS ANALYSIS

Funding is available for young scientists interested in three months of collaborative research in one of the following fields

Population Ecology Evolutionary Ecology Spatial Ecology Fisheries Science

PhD students, as well as young postdoctoral researchers and relatively experienced master students, are invited to apply.

The Young Scientists Summer Program (YSSP) is hosted from June 1 to August 31, 2005, by the International Institute for Applied Systems Analysis (IIASA), Laxenburg, Austria. IIASA is located in the former summer palace of the Habsburgs, ca. 10 km south of Vienna. IIASA's summer program offers exceptional opportunities for acquiring experience in an international and interdisciplinary research environment. Research training is based on intensive personal interaction with advising senior scientists, and typically leads to a publication in an international journal (and often to a chapter in a candidate's PhD thesis).

Young scientists from all countries are eligible for stipends covering travel and accommodation. Students from Austria, China, Egypt, Estonia, Finland, Germany, Japan, the Netherlands, Norway, Poland, Russia, Sweden, and the USA are eligible for additional stipends covering extra living expenses.

Proposals are invited for research projects relating to any of the following areas

Adaptive Dynamics Simplifying Spatial Complexity Virulence Management Evolution of Cooperation Fisheries Management Hierarchical Selection Evolutionary Algorithms and Artificial Evolution Evolutionary Conservation Biology Adaptive Speciation

described in some detail under "Research Activities" on

www.iiasa.ac.at/Research/ADN. Candidates are welcome to discuss specific research interests and plans with the program leader of the Adaptive Dynamics Network, Ulf Dieckmann (dieckmann@iiasa.ac.at).

Review of applications will commence on January 10. To receive full consideration, online applications have to be completed before January 25, 2005 (earlier IIASA documents may mention a January 15 deadline, which has since been extended).

Some useful links: + www.iiasa.ac.at/yssp/register/-index.html Details about the summer program, and online application + www.iiasa.ac.at/Research/ADN

Information about the Adaptive Dynamics Network + www.iiasa.ac.at/Research/ADN/Students.html

Some examples of successful student projects + www.iiasa.ac.at/docs/IIASA_Info.html General information about IIASA

Ulf Dieckmann Phone +43 2236 807 386 Program Leader +43 2236 807 275 (secretary) Adaptive Dynamics Network +43 2236 807 231 (secretary) International Institute Fax +43 2236 71313 for Applied Systems Analysis Email dieckmann@iiasa.ac.at A-2361 Laxenburg Web www.iiasa.ac.at/Research/ADN Austria www.iiasa.ac.at/~dieckman dieckman@iiasa.ac.at

Isolation by distance

Dear all,

I wish to test for isolation-by-distance amongst populations of a stream-dwelling salmonid. In many published papers this is approached by testing for a positive correlation between F_{st} and distance. However, other authors perform this test using $1/(1-F_{st})$ instead of F_{st} , following Rousset (1997). Can someone advise me which is the correct test statistic, and why?

Thank you.

Victoria Pritchard.

Rousset, F. 1997. Genetic differentiation and estimation of gene flow from F -statistics under isolation by distance. *Genetics*,145:1219-1228.

Victoria L. Pritchard, School of Fishery & Wildlife Sciences, New Mexico State University, P.O. Box 30003, MSC 4901, Las Cruces, NM 88003-8003, U.S.A Tel: +(505) 646 3576 Email: vpitcha@nmsu.edu [gen-
vlp@hotmail.com](mailto:gen-
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vpritch@nmsu.edu

LongnoseDace samples

Hi.

I am a PhD student working on a phylogeography of the longnose dace (*Rhinichthys cataractae*), a common cyprinid of North American rivers. I have performed an extensive sampling of the Quebec rivers (Quebec, Canada) and in order to confirm the post-glacial origin of those populations, I need samples from Missouri/Mississippi or Great Lakes watersheds, from the northeastern part of Ontario as well as from the Atlantic region (Canada and/or USA).

I would be grateful if anyone would be able to provide me with DNA and/or conserved tissue/specimen (preferably in 95% ethanol) from those localities. If you are able to provide me with any of the above samples or know of anyone that might be able to help, I would appreciate your feedback.

Please contact me to the address given below.

Thank you very much for your help!

Philippe Girard M. Sc. Département des Sciences Biologiques Université de Montréal Courriel: philippe.girard@umontreal.ca Tél. (514) 343-6111 poste 1051

philippe.girard@UMontreal.CA

MapMarker 1000

Dear evoldir list,

We are considering using the MapMarker 1000 size standard made by Bioventures to score microsatellite loci with alleles larger than 500bp on the ABI 3130. Has anyone had experience using this product or another size standard that will score alleles up to 600bp?

Thank you, Caren Goldberg

gold0191@uidaho.edu gold0191@uidaho.edu

MapMarker1000 answers

Dear evoldir list,

Below are the responses to my inquiry about MapMarker1000 ladder. Thank you to everyone who responded, your comments were very helpful. I am now trying a free sample of MapMarker on our new 3130xl.

In summary, some researchers are pleased with the results of this size standard while others are unsatisfied. Specific advice was to increase the run time on the machine and to check every lane for correct size calling. There were also suggestions for other size standards for scoring >500bp fragments.

Thanks again, Caren

We use Mapmarker 1000 routinely on the MJ Basestation (a gel based sequencer) to size microsatellite alleles and it works great.

Hi Caren,

My lab uses a custom ladder from Bioventures to score large fragments for T-RFLP. We really like their product: nice consistent, even peak heights and no double peaks. We've run them on a 377 and a 3100.

Lee

I haven't used MapMarker 1000, but you the attached reprint details how to make your own size standard that will allow scoring of alleles up to 1000 bp...

Good luck,

Andrew DeWoody (DeWoody et al. 2004 was attached)

Caren,

I used MapMarker 1000 to score microsats sized between 500 and about 900 bp. However, it turned out to be a major pain because the analysis software consistently made incorrect calls for the size standard peaks. Therefore, for every LANE I had to check to see if the size standard had been scored correctly and then correct the samples that had not been correctly scored. If the analysis software has been updated and can now make the correct calls, then I would suggest you go for it. On the other hand, if the analysis software still cannot consistently call the peaks of the size standard then you want to find an alternate marker.

-Eric

Caren,

Bioventures markers are very good. I have used them in the past and they are reliable and consistent. The problem with marker sets that go up to 1000 basis is that you get poor resolution and sizing is no longer linear after 500 basis when using denaturing electrophoresis conditions. ABI software will not score the fragments well. If you run the samples on non-denaturing conditions, your migration becomes sequencing dependent instead of purely based on the size of the fragment. The 3130 (we have one) have not been design with denaturing run in mind. Either way, it might take you a lot of effort to fine tune things if you need good accuracy on allele discrimination, specially if they are very close in size. In the past I have tried working on the issue for couple of different projects but we did not find the results to be satisfactory. I confess we did not spend a lot of time on it, though. We opted to change marker sets or redesigning primers, if possible. We got acceptable results only when overall peak pattern was needed for AFLP projects and not accurate size calling.

I would appreciated if you would let me know if you hear from anybody who has consistently been successful genotyping larger than 500 bp frags on a ABI capillary machine.

Best wishes,

Helaman

Hi Caren, I've had some success using ABI's ROX double stranded 2500bp ladder. I usually label the left hand peak under denaturing conditions and you'll have to contact tech services for sizing as the fragments migrate differently using this application. I usually change the default module and run for a further 20 mins using our ABI3100 machine. I can reproducibly size fragments up to about 2kb. Obviously ABI won't support this application so I do this work when the array is at the end of its lifespan.

Hope this helps you. Jake

Caren,

We have not tried the MapMarker size std, but I have several pieces of relevant advice for you (size stds are a frequent topic of discussion in our lab).

I highly recommend The Gel Company's size standards. They make a 50-1000 bp std, available in Rox (MRK1000) or Tamra. We tested their MTK500 (Tamra) and found it to be high quality, very clean, with sharp peaks, comparable to ABI's T500XL but a fraction of the cost. It's the best size std we tested. The Gel Co. is very customer-service oriented, too, which is a bonus.

STAY AWAY from GenSize! We followed instructions,

tried multiple gels, and still it looked awful, absolutely unusable. I can't believe they sell that stuff!

If making your own size std is an option, see DeWoody et al. 2004, *BioTechniques* 37: 348-352 for primer seq and protocol. We tried this and it worked quite well, with clean peaks, though it is somewhat labor-intensive. Posts range from 79-1007 bp but we just used 79-560 because we didn't need the larger rungs.

Good luck! I would be interested to see other replies to your query.

Libby

dear Caren,

we successfully used MapMarker 1000 to size microsats in *Cepaea nemoralis*, that partly were > 600 bp on a ABI 310 machine. We had first tried the Genescan 1000 but that did not work. The marker is really good 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/evodir.html>

Maynard Smith Prize

= Extended deadline for the 2005 John Maynard Smith Prize.

We are still seeking candidates for the 2005 JMS prize. We are therefore extending the deadline for nominations until March 1, 2005. Details of how to nominate a candidate are detailed below.

= The European Society for Evolutionary Biology has established The John Maynard Smith Prize to be awarded to outstanding young researchers in the field of evolutionary biology. The fifth prize winner will be announced at the 2005 congress of the society in Krakow, Poland.

Nomination Candidates for the prize must be nominated by a senior colleague; the nomination must be accompanied by the candidate's CV, a list of publications, a short description of future research plans, the names and addresses of two referees, and a letter from the candidate approving the nomination. Candidates for the 2005 prize must have received a PhD (or equivalent) degree no earlier than January 2003.

The nominations (three copies if sent by mail) should

be sent to: Michel Raymond, Institute for Evolutionary Sciences, University of Montpellier II, F-34095 Montpellier, France e-mail: raymond@isem.univ-montp2.fr

and postmarked no later than March 1, 2005. The winner is expected to attend the 2005 congress, where he or she will deliver the John Maynard Smith Lecture. The society will pay registration, accommodation, and travel expenses (economy fare). =====

CC065, UMR 5554 Institut des Sciences de l'Evolution Université de Montpellier II 34095 Montpellier cedex 05, France

raymond@isem.univ-montp2.fr Fax: (33) [0]4 67 14 36 22

Michel Raymond <raymond@isem.univ-montp2.fr>

Microsat cloning answers

Dear all,

Thanks everyone who sent comments and suggestions regarding the microsat cloning problems. Please find the answers below.

John

Hi there,

One way to increase your chance of getting micros with good flanking sequence is to select for bigger genomic inserts. Have you tried using different restriction enzyme combinations? It may be that the particular combination you are using at present is giving you a lot of small inserts. I would suggest trying other enzyme combos and/or using a smaller number of restriction enzymes to increase the size of your genomic inserts.

There may well be another reason why you are getting this pattern but looking enzyme choice is a relatively easy thing to play with when trying to solve problems like this.

Good luck Andy Given

Hi John

I am not sure if that post was our lab or not, but we did have similar questions. I t has been awhile since I've done that procedure, and my responses are not much more then semi-educated guesses, but here goes. First are your inserts relatively short on average? We are working with copepods, and qualitatively the genomes are probably fairly different at times, but I noticed that

many of our msats were surrounded by other imperfect msats, or what might be called 'simple sequence'. It is highly repetitive DNA, but not perfectly repetitive. I did not test it directly but it was obviously fairly far from random at times. This could restrict the number of restriction sites to less (or more) then we might expect by chance, and since everything was fairly repetitive primer design was a nightmare. Also there are a great number of selective steps in that enrichment process; multiple PCR amplifications, and the cloning itself are going to be selective for products or inserts of a smaller size. Hence, small fragments will amplify more in the genome amplification and any amplification after enrichment. During cloning it seems smaller fragments will be taken up preferentially, as well as the possibility that clones with larger fragments, that tend to be repetitive, could grow slower.

Some or none of these situations may be occurring, and I am sure we could all keep on guessing about why, so here a few of the things we did.

The key for us was increasing average insert size that we sequenced and just doing a lot of enrichments. We tried different enzymes first judging just by the amount of digestion, and if that went well, then by the quality of the fragments we were getting back. Second, we noticed that we got more large fragments from freshly transformed cells. The frequency of large inserts went down each day they waited in the fridge before they were grown up and prepped. Third, and I think one of the most important was we began to screen our clones before we sequenced them. By screening I mean for size. When picking colonies we put one toothpick stab in LB to be grown up over night and another stab from the same colony was put into water agitated then boiled, spun down, chilled, and a few microliters added to a PCR rxn with M13 primers. We then only chose to prep the clones with fragments over 700 bp, about 200 bp were plasmid so 500 bp or more was our target. We did 650 or 600 if we were desperate. There are probably many things you could do within the protocol to address your situation, and someone will probably mention some of them who knows more then I. However our approach was to clone like mad, prep them early, and only prep and sequence the biggest ones. Once you have the enrichment dialed in for your organism, it seemed more time and cost efficient to just keep making libraries, using the ones that seemed to have a better return and using only the largest fragments. Our best looking msats were undoubtedly butted up to the restriction site or comprised only a short almost repetitive bit of sequence to work with for designing primers.

Dennis L. Peterson

Dear colleague

I am just leaving town for a couple of days , and I dont have time to look into your protocol, but it look similar to the ones I have used. I had that problem also. It was solved after using a probe in the enrichment step modified in the 5' so that it could not work as a primer in the PCR at th end of the enrichment step.

This is well described in the by Koblízková et al . (1998), see the reference in the primer note I am sending in attach. This solved the problem for many people out there. What you are getting is sequences that start in the mast region because in the PCR step the probe (the probe should not reach that step but it does!) is working as a primer annealing to the msat region of your sequences and thus starting the sequence rihgh there!

Best regards

Filipe Alberto

This is the paper:

Blackwell Publishing Ltd.

PRIMER NOTE

Isolation and characterization of microsatellite markers for the seagrass *Cymodocea nodosa*

— / —

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

PCR amplification answers

Hello,

Here are the first replies on my question considering pcr amplification using fluorescent labelled primers. Apparently a lot of people experience the same problem!

Thank you very much for all the response!

MY QUESTION:

I work with microsatellites and have managed to get amplification for three different primer pairs (based on agarose + EtBr visualisation). Now I wanted to switch to fluorescent labelled primers (the 5' of the forward primer is Hex labelled), and I don't seem to get any amplification using the same pcr conditions. I have

checked (and doublechecked) and there are no mistakes in the primer sequence. I also tried different primer concentrations, but still no amplification. I wonder what could be the cause of my problem, since I have already had good results with other fluorescent labelled primer pairs.

Thanks and best wishes

Anja

THE RESPLIES:

Hi Anja – I have just finished converting 12 loci from P33 labelling to flourescent labelling. I used a few PCR reaction mixes when testing each loci to start and found that tweaking the MgCl2 and TAQ concentrations was necessary for a few of them. In these cases less TAQ and a smaller amount of MgCl2 usually increased the PCR product. All of them that exhibited a nice product on agarose gels are working fine upon genotyping. These microsats range in size from about ~100bp to ~250bp.

Good luck. Cheers, Stephanie

—

Dear Anja,

Have you checked your PCR-product using fluorescent labelled primers on an agarose + EtBr visualisation? At least you can check whether you have a product or not. Sometimes primers are not synthesised correct or cleaned properly.

Best wish

Bo

—

Hi Anja, I never use HEX labelling. The dye gives a very week signal and I think the fluorescent moiety may affect the stereo-specificity of the PCR reaction. If you need a 'green' dye try VIC. It performs like 6-FAM and isn't problematic. You can run VIC labelled fragments with ABI's dye set G5 (LIZ 500-250 ladder) and also D (ROX 400HD, high density ladder). Hope this helps. Jake

—

Dear Anja, maybe the fluorescent tags on your primers are faulty. Can you see any fluorescent signal from them at all (like primer dimers or left over primer)? If not, then the tags probably don't work. Have you tried getting new ones? Good luck, Barbara

—

Dear Anja.

I am sorry that I can't solve the mystery in order to help you. I just want to tell you, that I experienced a

similar problem for one pair of my primers. In my case the unlabelled primer pair performs much better than do the labelled ones. So, if someone can give you an answer to that trouble, maybe you can send it to the EvoDir members as well, thanx very much in advance. And all the best for your work.

Sébastien

Dear Anja,

I cannot help you solve the problem, but I would like to inform you that this also happened to me. I asked the company which made the labelled primers to send me new ones (free of charge), but it didn't help. I just gave up with these primers.

All the best,

Sophie

Hi Anja,

in response to your EvoDir question, apparently fluorescently labelled primer is a different molecule (carrying label) so indeed it may happen that a fluorescently labelled primer may not work as it had as non-labelled. I don't really have solution better than re-design primer. However, sometime there are also manufacturing problems other than primer sequence itself, e.g. quality of the primer, so perhaps try to re-order primer. I've dealt with a similar problem: my fluorescent primers were not as efficient as non-labelled, but still produced a bit of products. I didn't have time to re-design and test new primers, hence, I run PCRs with non-labelled primers first and then these products used for a few additional PCR cycles with labelled primers to get it labelled. It worked. I'm uncertain whether it's of any use to you, but it may give you an idea perhaps... good luck

Monika

Hi Anja,,

I have had the exact same problem. I was also using primers tagged with HEX.....I had great PCR results with my non-fluorescent primers and then when I switched to using the fluorescent primer I saw nothing at all. I'm not sure if something was inhibiting the reaction or not. I tried everything....changed the annealing temp, used more taq, changed the concentration of magnesium etc. but nothing worked until I called the company and they sent me a new fluorescent primer!! Then it worked fine! I was surprised because

the sequence was not incorrect...so it must have had something to do with the fluorescent tag. I would definitely call them and tell them your problem and likely they'll replace it. I am happy to hear that I was not the only one with this problem. Perhaps HEX is extra sensitive? They told me to be sure that I resuspended my HEX primer in 1XTE pH of 8, but I

— / —

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

PCR amplification problems

Hello,

I work with microsatellites and have managed to get amplification for three different primer pairs (based on agarose + EtBr visualisation). Now I wanted to switch to fluorescent labelled primers (the 5' of the forward primer is Hex labelled), and I don't seem to get any amplification using the same PCR conditions. I have checked (and doublechecked) and there are no mistakes in the primer sequence. I also tried different primer concentrations, but still no amplification. I wonder what could be the cause of my problem, since I have already had good results with other fluorescent labelled primer pairs.

Thanks and best wishes

Anja

avgeert@vub.ac.be

PCR plates

Does anyone have a recommendation for a 96 well PCR plate that has wells that have 'etched' inside surfaces?

To clarify, we are using a protocol to 'clean up' sequencing reactions prior to running them through our CEQ 8000 (automated sequencer).

The protocol uses an ETOH precipitation and requires the plates to be spun, inverted to spin off the ETOH. In all of the PCR plates we have tried so far the inside

surface of the tubes is smooth and the DNA pellet does not remain stuck to the bottom of the tubes (i.e. its lost with the ETOH).

Ideally these plates would also fit into the sequencer (that means semi-skirted, chimney topped, notched out at the A1 corner of the plate).

The sequence manufacturer can provide a plate with these exact specs but they are incredibly expensive so I am looking for a cheaper alternative.

Please reply to me directly and I will forward the replies to anyone that expresses an interest.

Best,

Bonnie

Bonnie Woolfenden, PhD. Room 203G Lumbers Building Department of Biology, York University 4700 Keele Street, Toronto, ON M3J 1P3 (416) 736-2100 x 22331 (voice) (416) 736-5698 (fax)

Phylogenetics web site

There is a new site for the phylogenetic community. <http://www.yphy.org/phycom/> There is news (articles, programs, updates, etc.), a forum for questions and discussion, links to labs, programs, etc., eventually downloads of scripts and how-tos (and more). To view and download everything you can just go, to contribute, just register on the site, and then you are free to contribute to whatever sections you wish. Pass the word. Thanks Stephen Smith

Stephen A. Smith Department of Ecology and Evolutionary Biology Yale University web: <http://www.phylodiversity.net/ssmith> web2:<http://www.phylodiversity.net/donoghue/people/stephen.html> web3:<http://www.yphy.org> Stephen Smith <stephen.smith@yale.edu>

SYNTHESYS Systematist Travel Funds

Dear Scientist,

Next Deadline: 18 March 2005

The SYNTHESYS Office is pleased to announce the Second call for proposals under the European Commission's FPVI European-funded Integrated Infrastructure Initiative. SYNTHESYS Project funding is available to provide scientists (Users) based in European Member and Associated States to undertake short visits to utilize the infrastructure (namely the collections, staff expertise and analytical facilities) at one of the 20 partner institutions (see full list below) for the purposes of their research. The 20 partner institutions are organised into 11 national TAXonomic Facilities (TAFs). TAF Users will be hosted by a TAF staff member.

As part of SYNTHESYS Access proposals are being sought from researchers working in the molecular aspects of taxonomy and systematics (including DNA barcoding). Where available TAFs are able to offer access to molecular facilities in addition to the specimen collections. Local policies on DNA extraction from specimens will apply.

The 11 TAF institutions represent an unparalleled resource for taxonomic research offering: Collections amounting to over 337 million natural history specimens, including 3.3 million type specimens. Internationally renowned taxonomic and systematic skill base Chemical analysis, molecular and imaging facilities. Proposals will be welcomed from high calibre researchers seeking access for short-term visits.

SYNTHESYS is able to meet the Users' costs for:

Research costs* International travel Local accommodation whilst based at the TAF A per diem to contribute towards living costs * Research related costs including: bench fees and consumables (including molecular biology at some TAFs).

See www.synthesys.info for more information or contact <<<mailto:synthesys@nhm.ac.uk>> synthesys@nhm.ac.uk

TAF visits will be scheduled from December 2004 until January 2009. SYNTHESYS is a five-year project comprising two parts which together aim to create an integrated European infrastructure for researchers in the natural sciences. SYNTHESYS Partners: GB-TAF Natural History Museum, Royal Botanic Gardens, Kew, Royal Botanic Garden Edinburgh. ES-TAF Museo Nacional de Ciencias Naturales, Real Jardín Botánico Naturales. DK-TAF The Natural History Museum of Denmark. FR-TAF Museum National d'Histoire Naturelle. SE-TAF Naturhistoriska Riksmuseet. NL-TAF University van Amsterdam, Nationaal Herbarium Nederland, Centraalbureau voor Schimmelcultures, National Natural History Museum Naturalis. DE-TAF Museum fur Naturkunde, Botanis-

cher Garten und Botanisches Museum. AT-TAF Naturhistorisches Museum, Wien. HU-TAF Hungarian Natural History Museum. PL-TAF Museum and Institute of Zoology, Polish Academy of Sciences. BE-TAF Royal Belgian Institute of Natural Sciences, Koninklijk Museum voor Midden-Afrika, National Botanic Garden of Belgium.

1 The SYNTHESYS Partners are inviting applications from researchers based in the Member States of the EU: Austria, Belgium, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, Netherlands, Poland, Portugal, Slovakia, Slovenia, Spain, Sweden, United Kingdom plus the Associated Countries of the EU: Switzerland, Iceland, Israel, Liechtenstein, Norway and Candidate Countries of the EU Bulgaria, Romania and Turkey.

Gemma Robinson

SYNTHESYS Administrator

Natural History Museum Cromwell Road London SW7 5BD r.cowan@rbgkew.org.uk

Sankoff wins Weldon Medal

Congratulations to Prof. David Sankoff. He has been awarded the Weldon Memorial medal for 2004.

This prize was established through the efforts of Karl Pearson and others almost 100 years ago in memory of W.R.F. Weldon. It is presented by Oxford University every year (previously every three years) "without regard to nationality or membership of any university", to the person who in the judgment of the Electors has in recent years published the most noteworthy contribution to Biometric Science (the development of mathematical or statistical methods applied to problems in biology).

Among the previous 35 winners are statisticians and geneticists RA Fischer, ES Pearson, JBS Haldane, P Mahalanobis, Sewell Wright, Frank Yates, JD Finney, Motoo Kimura, MS Bartlett, DG Kendall, LL Cavalli-Sforza, Robert May, David Cox, John Maynard Smith, Joe Felsenstein and Warren Ewens. The board of electors is currently chaired by Robert May.

Brian Golding

Golding@McMaster.CA

Software BAPS 3 1

I'd like to inform evolutionary biologists about the release of BAPS 3.1 upgrade software for analysis of genetic population structure. Main improvements in the software compared with the earlier version 3.0 are:

1. Better usability, several estimation runs can now be processed simultaneously, by providing a vector input to field where the maximum number of clusters is specified.
2. Algorithm improvement, several new search steps have been added.
3. Possibility to use training data for specifying the prior for allele frequencies.
4. Program output has been enhanced.

Please, check the manual for details. The software is freely available at:

<http://www.rni.helsinki.fi/~jic/bapspage.html> Regards

Jukka Corander Department of Mathematics and statistics P.O.BOX 68 00014 University of Helsinki Finland

corander@mappi.helsinki.fi

Software Protttest

Dear colleagues,

We have implemented a new program called ProtTest for the selection of empirical models of amino acid substitution, which can be downloaded from

<http://darwin.uvigo.es> ProtTest reads protein alignments in Phylip and Nexus formats and calculates AIC, AICc and BIC values, obtaining a rank of model fits, model-averaged parameter estimates, or measures of parameter importance. It is available for Mac OSX, Linux and Windows, and it can be run in three ways: using a GUI, at the command-line, and through a web server.

Citation: Abascal F, Zardoya R, Posada, D. ProtTest: Selection of best-fit models of protein evolution. Bioinformatics: in press.

In addition, given that ProtTest uses intensively Phym1

and PAL, we encourage users to cite these programs as well when using ProtTest: [Phyml] Guindon S, Gascuel O. 2003. A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. *Syst Biol.* 52: 696-704. [PAL] Drummond, A., and K. Strimmer. 2001. PAL: An object-oriented programming library for molecular evolution and phylogenetics. *Bioinformatics* 17: 662-663.

Best,

– David Posada Facultad de Biología Campus Universitario 36310 Vigo

Phone: +34 986 812038 Fax: +34 986 812556 Email: dposada@uvigo.es Web: darwin.uvigo.es

Software TreeFinder 2

Sorry folks,

I just discovered an error in the November-TREEFINDER: There is a switch missing in the frontend, which is necessary to estimate the codon position rates. Those interested in this feature should get the December version, which is now online at www.treefinder.de.

By the way - I would like to do a little survey measuring the discontent among scientists. If you like, you can send me the following data:

- (1) Your name.
- (2) Your country.
- (3) The duration of your professional scientific career so far.
- (4) The amount of money that you feel that whatever organization is owing to you for your unpaid work, after taxes, and summing over your whole scientific career. If you feel overpaid, then you may send me a negative value. In order to make debts comparable in different economic environments, please relate your amount to the price of a house that you would buy in your country. For example, the Deutsche Forschungsgemeinschaft is owing me 0.86 houses for my unpaid work on TREEFINDER. Be as exact as possible. If you have worked in more than one country, please send me (3) and (4) for each country separately.

If there is enough response, I will publish the distribution of these 'felt debts to the average scientist' on my webpage. I will not publish your name, it is just to

ensure that everybody is counted only once. Please tell all your colleagues about the survey!

I wrote the world's fastest maximum likelihood phylogeny program. I did, what the established bioinformatics community was unable to achieve for years. And still, nobody feels responsible to support the further TREEFINDER development by offering me an adequate position in Munich. Look at them! They are sitting on well-paid and everlasting positions and prevent innovation by keeping young competitors outside.

Am I ridiculous? Or is it the established science? Is 'biologist' a serious profession or is it just a hobby for the rich? Is idealism a reliable basis for scientific progress? Or does it keep the intelligent people away from science? Is saying 'yes' all the time a good strategy in life? Or is it the cause of ridiculous payment and stupid funding regulations? Should students be warned against starting a scientific career? Can anybody tell me why I should continue this project?

Happy New Year 2005!

Gangolf

Spectrophotometer

Dear evoldir members, I am looking into the purchase of a UV spectrophotometer for routine quantification of RNA, DNA and cells. If any of you has positive or negative experiences to report with equipment purchased during the past five years I would highly appreciate your feedback. Combined feedback will be posted if deemed significant.

Many thanks in advance,

Markus Friedrich

– Markus Friedrich Associate Professor Department of Biological Sciences Department of Anatomy and Cell Biology Wayne State University 5047 Gullen Mall Detroit, MI 48202

office: 313 577 9612 lab: 313 577 5120 fax: 313 577 6891 web: <http://bio.wayne.edu/mf/Markuslab.html>

Tetraploid SSRdata

Dear evoldir,

I am working with microsatellite marker for autotetraploid plant species. I encountered 1-4 alleles per individual. Since the genotyping on the basis of allele dosage not working I scored each individual on the basis of allele presence e.g. one band (150), two band (150, 154), three band (150, 152, 154) and four band (150, 152, 154, 156). Last year I put this problem in this forum for calculating genetic diversity from such data and the suggestions i got were useful. But now, I want to perform gene flow study and paternity analysis from such type of allelic information. For that I have a population of about 100 trees and all of them were investigated. From that, 10 trees were sampled for harvesting seeds (30 seeds per tree). The seeds are half-sib family and each seed was scored like above example to perform paternity analysis. The genotypes (allelic information) of mother trees are known. I would highly appreciate if any one can suggest me whether there are some computer software to do gene flow and paternity analysis from such data sets. Thank you in advance for your help. Sincerely yours,

Madhav Pandey Email: mpandey@gwdg.de

Madhav PANDEY (Ph.D. Student) Institute of Forest Genetics and Forest Tree Breeding Faculty of Forest Science and Forest Ecology University of Goettingen Buesgenweg 2, D-37077, Goettingen, Germany Tel. +49-551-393539, Fax +49-551-398367 <http://www.uni-forst.gwdg.de/forst/fg/index.htm>

mpandey@gwdg.de

WeldonMedal Winners

It was pointed out to me that my previous listing of Weldon Memorial Medal winners was incomplete.

I have obtained the complete list and have appended it below. Congratulations to all, it is great to have the contributions of members of our community recognized.

WELDON MEMORIAL PRIZE Past Prize-winners

1911 David Heron 1914 Charles Goring 1914-17 Suspended 1920 James Arthur Harris Additional Prize: Ethel M Elderton 1923 Johannes Schmidt 1926 Major Greenwood 1929 Ronald Aylmer Fisher 1932 Geoffrey Mills Morant 1935 Egon Sharpe Pearson 1938 John Burdon Sanderson Haldane 1941 Julia Bell 1944 Prasantachandra Mahalanobis 1947 Sewall Wright 1950 Lionel Sharples Penrose 1953 Frank Yates 1956 David John Finney 1959 Edmund Brisco Ford 1962 K. Mather 1965 Motoo Kimura 1968 I. Michael Lerner 1971 M.S. Bartlett 1974 D.G. Kendall 1977 L.L. Cavalli-Sforza 1980 Robert McCredie May 1983 D.R. Cox 1986 Tomoko Ohta 1989 Roy Anderson 1992 George Oster 1994 Michael P. Hassell 1996 Martin A. Nowak 1998 John Maynard Smith 2000 Joe Felsenstein 2001 Elizabeth Thompson 2002 Warren J. Ewens 2003 Sir Richard Peto 2004 David Sankoff

old polymer

Hello,

We have a pretty large quantity of polymer for the ABI 3100 on our hands and it's about to expire. I'm wondering that if the concern over polymer quality is because of crystallization, has anyone tried filtering it, much like you would standard acrylamide?

I'll be happy to distribute any recommendations I receive.

Cheers, David

dhamm@gs.washington.edu

CNRS UParisSud MicrobialGenomics	51	59	
CornellU AmphibianMHC	52	StockholmU PhenotypicPolymorphisms	59
Drosophila songs	52	UArizona HumanGenomicDiversity	59
DukeU PostDocSabbaticals	52	UEdinburgh ButterflyColourPatterns	60
FerraraItaly PopConsGenetics	53	UHelsinki EvolEcol	60
France comparative genomics	53	UHouston SocialInsectEvol	61
ImperialCollege EvolVertEcology	54	ULausanne EvolFuncGenomics	61
ImperialCollege VectorBiology	54	UOxford PlantEvol	62
IndianaU EvolGenetics	55	UQueensland PopEcolGenetics	63
LancasterU StatGenetics	55	USheffield RiceResistance	63
MacquarieU MarineConservationGenetics	56	USouthDakota StalkEyedFlies	64
MarieCurieResearchNetwork SEXASEX	57	UWisconsinMadison SexualSelection	64
MichiganStateU GeneticalGenomics	58	UppsalaU ComparativeGenomics	65
NetherlandsInstEcology PlantEvolEcol	58	YaleU ReproductiveBehaviour	65
Princeton DNA Rearrangements,Small RNAs,Bioinformatics			

CNRS UParisSud MicrobialGenomics

A one year postdoctoral position is available in the group of Dr. Bernard Labedan "Molecular Evolution and Genomics", (see complete address below) on the following theme. Studying the fluidity of microbial genomes and reconstructing minimal genomes. The advent of the complete sequence of numerous microbial genomes has underlined an unexpected variability in the panoplys of genes between closely related species. We have compared exhaustively more than one hundred genomes of various bacteria, archaea and fungi and we have built a suite of informatic tools to identify all orthologues and paralogues. The project will be to analyse these data in order to identify the genes which are omnipresent at different phylogenetic and taxonomic levels and those which are specific to organisms or groups of organisms. This would allow to uncover the essential genes which were present in more and more distant ancestors and to reconstruct the corresponding minimal genomes. The expected results will be important to understand (i) the molecular processes crucial to gene and genome evolution, (ii) the mechanisms of adaptation to various environments and life styles, (iii) the process of speciation in microorganisms. The candidate (under 35) must have a good experience in Microbiology and a solid knowledge of the informatic tools used for sequence analysis. He (she) is supposed (i) to have never worked in France up to now, (ii) to defend his (her) Doctoral Thesis (PhD level) before the end of summer 2005. Position is for 12 (minimum) - 18 (maximum) months. The targeted starting date is

September 1, 2005, but is flexible. It is part of a special program provided by the French Ministry of Research and accordingly any visa procedure will be accelerated. The salary will be 1830 per month. A Social Security cover will be provided by the University of Paris-Sud. There will be no funding for travel expenses. Knowledge of the French language is not required. Any people interested must contact me ASAP and before the 24th of Feb. 2005. I need a detailed CV and a short introduction letter.

Contact : Bernard Labedan,
<mailto:bernard.labedan@igmors.u-psud.fr>bernard.labedan@igmors.u-psud.fr, 33 1 69 15 35 60 Institut de Génétique et Microbiologie, Université de Paris-Sud, Bâtiment 400, 91405 Orsay Cedex, France <<http://www.igmors.u-psud.fr/LABEDAN/-LABEDAN-eng.htm>><http://www.igmors.u-psud.fr/-LABEDAN/LABEDAN-eng.htm> — Bernard Labedan, Directeur de Recherche au CNRS <mailto:>bernard.labedan@igmors.u-psud.fr

Please note my NEW address

Evolution Moleculaire et Bioinformatique des Genomes
Institut de Genetique et Microbiologie, CNRS UMR
8621 Universite Paris Sud, Batiment 400, pièce 101
91405 Orsay Cedex, France Tel : +33 1 69 15 35 60
Fax : +33 1 69 15 72 96 <http://www.igmors.u-psud.fr/-LABEDAN/LABEDAN.htm>

bernard.labedan@igmors.u-psud.fr

CornellU AmphibianMHC

Postdoctoral Researcher in Evolution of Amphibian Immunity

A postdoctoral position is available in the laboratory of Kelly Zamudio, Department of Ecology and Evolutionary Biology, Cornell University, to study the evolution of MHC genes in amphibian populations recently exposed to an emergent infectious disease. The position is part of the Biogeochemistry and Biocomplexity Initiative, fostering interactions among faculty in different fields. The primary responsibilities of this position include 1) conducting laboratory research to clone and characterize MHC class II genes in non-model amphibian taxa and measure selection in populations that have suffered disease-related declines, 2) analyzing data and writing manuscripts, 3) contributing to preparation of grant proposals for future work, and 4) coordinating projects of undergraduate students involved in the research. For additional information about research in our laboratory please visit our web site (<http://www.eeb.cornell.edu/zamudio/KZhome.html>).

To qualify, applicants should have a Ph.D. in evolution, molecular biology, or related field, demonstration of strong laboratory and writing skills, and the ability to work independently. Starting salary is \$ 35,000, plus Cornell University Contract College benefits; funds are available for two years, pending satisfactory progress. The position is available starting April 15, 2005; starting date is negotiable. Review of applications will begin February 15 and continue until a suitable candidate is found.

To apply, please send cover letter, CV, and names and contact information for three references that are familiar with your work. Please include in your letter a description of your past and current research experiences and goals. Applications (e-mail preferred) can be sent to Kelly Zamudio (krz2@cornell.edu), Department of Ecology and Evolutionary Biology, Cornell University, E209 Corson Hall, Ithaca, NY-14853-2701, USA. For questions about the position call Kelly Zamudio at (607) 254 4212.

Cornell University is an equal opportunity, affirmative action educator and employer. Applications from women and minorities are encouraged.

krz2@cornell.edu krz2@cornell.edu

Drosophila songs

Postdoctoral Research Associate

Department of Animal and Plant Sciences, University of Sheffield, UK

Ref: PR2109 Closing Date: 11/02/05 Salary: Salary from Ukpound 19,400 pa Grade: RIA

The post holder will work with Professor Roger Butlin to investigate the evolution and genetics of sexual signals and responses in *Drosophila virilis* group flies, especially *D. montana*. This is a component project of a Marie Curie Research Training Network (see <http://people.cc.jyu.fi/mirror/anhoikka/EU/>). Applicants must have a PhD and a good grounding in evolutionary biology. The successful applicant will have experience of using a range of laboratory and analytical methods for molecular ecology, and an enthusiasm for interdisciplinary research. This post is available for a fixed-term of one year.

Due to the restrictions of the grant, the post is open to citizens of the European Union who are not UK nationals or permanent residents (see http://europa.eu.int/comm/research/fp6/mariecurie-actions/pdf/rtn_hand.pdf for details of eligibility criteria).

For information on how to apply, go to <http://www.shef.ac.uk/jobs/research.html> For informal enquiries about the post, please contact me:

Roger Butlin Professor of Evolutionary Biology

Department of Animal and Plant Sciences The University of Sheffield Western Bank Sheffield S10 2TN

r.k.butlin@sheffield.ac.uk

Tel. +44 (0)114 2220097 FAX +44 (0)114 2220002

DukeU PostDocSabbaticals

I am pleased to announce the National Evolutionary Synthesis Center (NESCENT) is pleased to announce calls for proposals for up to 10 PostDoctoral and 5 Sabbatical fellowships.

Please see www.nescent.org for details about applications

PostDoctoral and Sabbatical Fellowships to support ambitious, synthetic research on any aspect of evolutionary biology and relevant disciplines: -Open to fellows of ALL nationalities -Research projects should be carried out primarily on-site -We will begin reviewing

applications on February 1, 2005 -We will stop accepting applications on March 1, 2005 -Starting dates will be before September 2005

Proposals can include any type of synthetic project, but cannot include time at the bench or in the field. Projects can be entirely theoretical and may involve developing analytical methods and software. Projects can also be purely empirical, synthesizing data from:

- the literature - existing databases - new databases built with NESCENT help - visits to museums or other data centers - cooperating laboratories anywhere in the world

Cliff Cunningham Director National Evolutionary Synthesis Center Box 90338 Duke University Durham, NC 27708

www.nescent.org Cliff Cunningham <cliff@duke.edu>

FerraraItaly PopConsGenetics

Postdoc in Population and Conservation Genetics University of Ferrara, Italy

Applications are invited for a postdoctoral research position in the population genetics group (<http://web.unife.it/progetti/genetica/>), Department of Biology, University of Ferrara, Italy.

Applicants must have a Ph.D. (or at least three years of research experience after graduation) in a relevant area of research, such as conservation genetics, population genetics, molecular ecology, phylogeography, or statistical genetics.

Part of the postdoc project is supported by the Dolomiti Bellunesi National Park (www.dolomitipark.it), and it will consist in a genetic study (using STR markers and one MHC locus) of the alpine chamois. Genetic analyses will be used to elucidate the population structure of neutral and adaptive variation, and to understand the possible relationship between MHC variation and resistance to the sarcoptic mange.

In a more flexibly planned part of his/her work, the appointee will also have the opportunity to take part to other projects regarding genetic typing and data analysis in different vertebrate species with conservation/management implications.

Experience with molecular typing and data analysis is

desirable. Enthusiasm and independence are essential.

The position is for a one-year period, possibly extended to a second year.

Review of applications will begin IMMEDIATELY and continue until a suitable candidate is identified. The appointee is expected to start between March and June 2005.

Salary is 15.200 Euros p.a. Health insurance is provided. To be compared with current life costs, the average cost of a room in a shared apartment in Ferrara is between 180 and 300 Euros per person per month.

If you wish to apply, please send a curriculum vitae and the names of at least two referees (via e-mail) to: Giorgio Bertorelle, ggb@unife.it

Giorgio Bertorelle Sezione di Biologia Evolutiva Dipartimento di Biologia Università di Ferrara Via Borsari, 46 44100 Ferrara Italy Phone: +39 0532 291743 Fax: +39 0532 249761 WEB PAGE: <http://www.unife.it/genetica> ggb@dns.unife.it

France comparative genomics

Our group plan to apply for a post doc position available at the french ministry research <http://www.recherche.gouv.fr/appele/2005/acpostdoc.htm> the dead line is the first of March

To apply to such project we need a candidate with bioinformatics /comparative genomics back ground This is a quick overview of the lab project, note that the post doc will focus in the genome reconstruction part. For more information see our web site .

<http://www.up.univ-mrs.fr/evol> The project proposed here is included in the general goal of our laboratory To trace back the life story, taking into account the Earth History. We are focusing on bilaterian metazoan evolution as well as their genome reconstruction. This project will allow evidencing the plesiomorphy, the apomorphy and the convergence of characters between actual species. Furthermore, this work will allow better knowledge neo biology (biology of species living today). The comparison as well as the evidence of ancestral organisation will be investigated at several levels: genomic and post genomic, proteome, interactome, transcriptome and at long term at anatomical and physiological level. In a first place we are redrawing the bilaterians story by data base and bibliography mining.

It will be followed by new analyses, using novel phylogenetic tools. We will complete data by cloning of new markers from phylogenetic new informative species not well represented in data bases (Rotifer, Gastrotrich&.). We will also, as far as we can, determine the Urbilateria proteome and genome organisation by deciphering the orthologues clusters in the different sequenced (even partially) species (including out group species : Cnidarians..) and by comparing their genomic organisation. The duplication events in the different available bilaterian lineages will be identified. Biochemical functional shift of non duplicate orthologues or duplicate orthologues will be deciphered by phylogenetic analysis. One of the aspects of the biochemical function being the protein interaction; the biochemical shift could be evidence at the interactome level. Deduction of the ancestral interactome and its evolution in the different lineage in regards to duplication will be realized from known interactome. The deciphering of ancestral transcriptomes as well as their evolution will be performed by expression analysis of the different cluster of urbiorthologues. We will perform data mining of tissues and cell Expressed Sequence Tags data bases, as well as micro arrays experiments data bases. Finally, we will reinvestigate comparisons between Bilaterians at anatomic and morphologic level. Informations coming out from this project will help to decide new informative species that kept as much as possible ancestral character of ancestral state bilaterians model. In turn these new species will allow us to pursue our quest.

– Pierre Pontarotti EA 3781 EGEE (Evolution Génome Environnement) Université d'Aix Marseille I Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 <http://www.up.univ-mrs.fr/evol>
We organize the 8th Evolutionary Biology Meeting at Marseille <http://www.up.univ-mrs.fr/evol/congres/pierre.pontarotti@up.univ-mrs.fr>

ImperialCollege EvolVertEcology

Postdoctoral Researcher

NERC CENTRE FOR POPULATION BIOLOGY Imperial College London, Silwood Park Campus

Large-scale vertebrate ecology

We seek an ecologist or evolutionary biologist to work on applying demographic models to understand macroecological phenomena in vertebrates, with respect to temporal, spatial or phylogenetic variation.

The successful applicant will be given considerable latitude to develop their own projects within this broad field.

The three-year appointment will be on the Imperial College scale R&E B (£19068- £28042) depending on qualifications and experience.

For further details and application forms (required) contact:

Sarah Snellin, CPB, Imperial College London, Silwood Park Campus, Ascot, Berks, SL5 7PY. Tel: 020 7594 2346; e-mail: s.snellin@imperial.ac.uk (<http://www.cpb.bio.imperial.ac.uk/>)

Applications to be received by 11th Feb 2005.

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

<http://www.bio.ic.ac.uk/research/iowens/welcome.htm> Ian Owens <i.owens@imperial.ac.uk>

ImperialCollege VectorBiology

Postdoctoral Researcher

NERC CENTRE FOR POPULATION BIOLOGY Imperial College London, Silwood Park Campus

Population biology of insect vectors

We seek a scientist with a background in biology or the mathematical sciences to work on modelling the population biology and population genetics of insect vectors of human and animal diseases.

The successful applicant will be given considerable latitude to develop their own projects within this broad field.

The three-year appointment will be on the Imperial College scale R&E B (£19068- £28042) depending on qualifications and experience.

For further details and application forms (required) contact:

Sarah Snellin, CPB, Imperial College London, Silwood Park Campus, Ascot, Berks, SL5 7PY. Tel: 020 7594 2346; e-mail: s.snellin@imperial.ac.uk (<http://www.cpb.bio.imperial.ac.uk/>)

Applications to be received by 11th Feb 2005.

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

<http://www.bio.ic.ac.uk/research/iowens/welcome.htm> Ian Owens <i.owens@imperial.ac.uk>

IndianaU EvolGenetics

POSTDOCTORAL POSITIONS IN EVOLUTIONARY GENETICS / GENOMICS Three postdoctoral positions are available in the laboratory of Michael Lynch, Department of Biology, Indiana University, Bloomington, Indiana: Molecular evolutionary consequences of recombination and asexuality in *Daphnia*. This project takes advantage of the burgeoning set of genomic tools available for *Daphnia pulex* (including a complete-genome sequence, high density genetic map, microarrays, etc.), as well as the widespread distribution of asexual and sexual lineages in the study species, and a 'living-fossil' record that can be extracted from lake sediments. Numerous subprojects related to this system are available, as part of a larger NSF FIBR grant on the role of recombination in evolution. Among other things, this work is intended to establish *Daphnia* as a major model organism for ecological / evolutionary genomics. Candidates must have strong molecular skills, and background and/or interest in population genetics. Characterization of spontaneous-mutation properties in eukaryotes. Taking advantage of several sets of long-term mutation accumulation lines of several species (including *C. elegans*, *Daphnia pulex*, and *S. cerevisiae*), we are attempting to quantify the entire mutational spectrum at the molecular level, with a long-term goal of establishing generalities across eukaryotes. Other species lineages may be developed for these purposes, and we are concerned with extending this work to quantify the transcriptional error rate (i.e. the proliferation of errors at the mRNA level). Candidates must have strong molecular skills. Evolution of spliceosomal introns and eukaryotic gene processing mechanisms. The goals here are to shed light on a number of unanswered questions regarding eukaryotic genes, including those concerned with the origin and proliferation of introns, the evolution of untranslated regions (UTRs) of genes, and nonsense-mediated

decay and other aspects of mRNA processing. Candidates must have strong skills in the area of bioinformatics / computational biology and a good working knowledge of molecular and/or population genetics. All three openings are immediately available and will remain open until suitable candidates are located. For immediate consideration, please send email applications (including a cover letter outlining your interests, complete CV, and contact information for three individuals willing to supply evaluations) by 1 March 2005 to: Margi Lockhart, malockha@bio.indiana.edu. Indiana University is an Equal Opportunity / Affirmative Action Employer

Michael Lynch mlynch@bio.indiana.edu Dept. of Biology Phone: 812-855-7384 Indiana University FAX: 812-855-6705 Bloomington, IN 47405 Lab Research: <http://www.bio.indiana.edu/facultyresearch/faculty/Lynch.html> IU Biology: <http://www.bio.indiana.edu/> NSF Training Grant in Evolution, Development, and Genomics: <http://evodevo.uoregon.edu/> *Daphnia* Genomics Consortium: <http://daphnia.cgb.indiana.edu/> Michael Lynch <mlynch@bio.indiana.edu>

LancasterU StatGenetics

LANCASTER UNIVERSITY

DEPARTMENT OF MATHEMATICS AND STATISTICS

RESEARCH ASSOCIATE POSITIONS IN STATISTICAL GENETICS

Reference: A407

Salary: 19,460-29,128 UKP

A research associate position is available within a programme of collaborative research between the Lancaster Statistics Group and the Veterinary School at Liverpool University. Within the Statistics Group, the research will be led by Prof. Peter Diggle, Prof. Gareth Roberts and Dr. Paul Fearnhead.

The Department: The Lancaster Statistics Group is one of the strongest in the UK (RAE Grade 6*) with an emphasis on the development and application of methodology motivated by substantive applications, and particular strengths in spatial and longitudinal statistics, statistical genetics and computationally intensive statistical methods. The Group currently includes 16 academic staff positions and around 30 re-

search students and research associates.

The research programme: The overall aim of the research is to further our understanding of the transmission and evolution of food-borne zoonotic pathogens. A specific aim is to model the spatio-temporal distribution and genetic evolution of human *Campylobacter* infections, using data derived from all recorded cases of human *campylobacter* gastroenteritis in the Preston district since 1993.

The Position. The primary focus of the post-holder will be to develop suitable stochastic models and inference methods for population genetic data from pathogens such as *Campylobacter*, and apply such methods to learn about the biological factors which effect the evolution of *Campylobacter*. The methods for analysing the population genetic data will involve the use of modern computationally-intensive statistical methods. The post-holder will also be expected to interact with other members of the Statistic group at Lancaster working in the area of statistical genetics.

This position is for a two-year period, available from 1 May 2005.

The applicant: Applicants should have a higher degree in statistics or statistical/population genetics, a commitment to collaborative research and either a track-record or clear potential for research in statistical genetics. Experience of computationally-intensive statistical methods and good computing skills are desirable. Background in population genetics would be useful but is not essential.

Informal enquiries can be made to Dr Paul Fearnhead (p.fearnhead@lancaster.ac.uk).

The closing date for applications is January 31st 2005 Further details, including an on-line application form can be obtained at

<http://www.personnel.lancs.ac.uk/-vacancydets.aspx?jobid=A407>

Alternatively please contact Personnel Services, quoting reference A407, answerphone (01524) 846549.

MacquarieU
MarineConservationGenetics

“POSTDOC IN MARINE CONSERVATION GENETICS, MACQUARIE UNIVERSITY, SYDNEY”

A two-year Postdoctoral position is available to work on dispersal of marine organisms. The successful candidate will join a recently created multi-disciplinary team (Molecular Ecology Group for Marine Research) that will study dispersal in four codistributed groups of marine organisms: sea-urchins, abalones, oysters and sharks. Results from the four individual projects will be combined to address key topics in marine biodiversity, such as design of marine protected areas and conservation and management of marine resources.

Applicants must have a Ph.D. in a relevant area of research, such as conservation genetics or phylogeography. Preference will be given to candidates with strong experience in analyses of gene flow based on microsatellite markers and with a background in marine ecology and/or oceanography. Familiarity with isolation and characterization of microsatellites is desirable but not essential.

The appointee will be responsible for collecting and analyzing data for three of the four projects and supervising activities of a research assistant. In addition, he/she is expected to dynamically communicate and collaborate with other members of our thriving research group (marine biologists, population geneticists and PhD students).

Salary will be established according to Macquarie University guidelines (around \$53,500 + 26% on costs per annum). Please e-mail a letter summarizing research interests and experience along with a CV including the names, addresses and e-mails of three referees to Luciano Beheregaray: <mailto:luciano.beheregaray@bio.mq.edu.au> luciano.beheregaray@bio.mq.edu.au

Review of applications will begin immediately and continue until a suitable candidate is identified. The appointee is expected to start in March 2005.

For further information about the lab and related publications please visit our “under construction” web site at <<http://www.bio.mq.edu.au/-molecularecology>>www.bio.mq.edu.au/-molecularecology or send an e-mail to the address above.

Dr Luciano B. Beheregaray Department of Biological Sciences Macquarie University Sydney, NSW 2109 Australia Phone: 61(2)9850 8204 Fax: 61(2)9850 8245 E-mail: Luciano.Beheregaray@bio.mq.edu.au

“Luciano B. Beheregaray”
<Luciano.Beheregaray@bio.mq.edu.au>

MarieCurieResearchNetwork
SEXASEX

Marie Curie Research training network (MRTN) SEXASEX 1 position available

Students and researchers interested in the paradox of sex in evolutionary biology are strongly encouraged to apply for a research position in the European Union Marie Curie Research Training Network SEXASEX, which is co-ordinated by Prof. Dr. Koen Martens, RBINSc, Brussels. Criteria of eligibility include: EU citizenship, less than 4 years of research experience for Young Researchers (YR), less than 10 years for Experienced Researchers (ER), and a willingness to work in a European country other than the country of origin. We seek candidates who are enthusiastic about evolutionary biology, travelling and living abroad, learning in a multidisciplinary research environment and working in teams. All appointments will be for 3 years, YR are offered PhD positions, ER post-doc positions. YR will be expected to obtain a PhD at the end of the project. The application of female candidates is especially encouraged; detailed information on child care facilities at the different institutions will be provided upon request. Aid can be sought if accompanying spouses also require employment abroad.

Project overview: Sex is the queen of evolutionary problems. It will be tackled by SEXASEX in a multidisciplinary approach, providing training and transfer of knowledge for a total of 360 person-months. 10 network researchers (6 young researchers (YR) and 4 experienced researchers (ER)) will receive training in 9 institutions across as many countries. A wide array of research tools will provide excellent training opportunities, for example through individual career development plans, individual tutoring and secondments, which will be supplemented by participation in courses and external workshops. Network-wide training will exploit the extensive experience of the partner institutions through five courses and summer schools for all network researchers. Complementary skills such as management and communication (verbal, written) will be developed, and gender awareness will be raised, in two network-wide meetings. The networks theoretical and empirical research will apply 13 major approaches, including novel genomic and karyological approaches, intraspecific phylogeography, ecology, behavioural studies, GIS

analyses and theoretical modelling. With this multidisciplinary toolkit, SEXASEX will investigate why sex exists at all, given its evolutionary costs, using the model organism *Eucypris virens*, a non-marine ostracod species with both sexual and asexual reproduction. What determines its gender, what are the genomic consequences of long-term asexuality, what is the cohesiveness of a species with mixed reproduction, how do asexuals and sexuals compete and what is their historical zoogeography? The pluralistic approach of SEXASEX is unique and timely, using highly novel methodologies and dealing with cutting edge science based on European excellence and tradition. Please refer to <http://www.naturalsciences.be/EVIRENS/> for more information.

Send full applications, comprising letter of interest, CV and coordinates of at least two potential referees before the 7th of February 2005 to

Dr Isa Schön, Royal Belgian Institute of Natural Sciences, Freshwater biology, Vautierstraat 29, B-1000 Brussels, Belgium E-mail (Isa.schoen@naturalsciences.be) Fax : +32 2 62 74 113.

Correspondence by email is preferred.

The deadline for applications for Postdoc 3 is extended till February 7th.

IMPORTANT REMARK: due to the fact that one of the promoters of position POSTDOC 3 6 has moved from Finland to Switzerland, first announcements of these position are herewith finally corrected: 1. the position will be shared by the labs in Zürich (Switzerland) and Montpellier (France), NOT by the labs in Oulu (Finland) and Montpellier (France). 2. Finnish candidates are now allowed to apply, but people with Swiss nationalities are no longer eligible.

POSTDOC POSITION 3: PLURALISTIC MODELS ON THE PARADOX OF SEX. Starting date: 1st May 2005 Duration: 36 months (2x 18 months) Salary: country-specific plus tax-free mobility allowance Scientists in charge: Dr Jukka Jokela, Switzerland Dr Yannis Michalakis, France Locations: Zürich, Switzerland & Montpellier, France Place of work: EAWAG, Department of Limnology/Aquatic ecology; Génétique et Evolution des Maladies Infectieuses GEMI, JRU 2724 CNRS IRD Job description: More than 25 hypotheses attempt to explain the prevalence of sexual reproduction in plant- and animal species, indicating that none of these by themselves are deemed to be sufficient to solve the paradox of sex. In the present project, you will take a synthetic approach by constructing models that combine sets of these extant hypotheses, for ex-

ample ecological (parasite or otherwise fitness related) and genetic (good- and bad-allele

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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>

MichiganStateU GeneticalGenomics

Genetical Genomics postdoctoral position in the Department of Animal Science, Michigan State University

Applications are invited for a two-year postdoctoral position in genetical genomics under the joint supervision of Guilherme Rosa and Robert Tempelman in the Department of Animal Science at Michigan State University. The successful applicant will participate in a USDA funded research project involving 960 F2 pigs generated from a Duroc Pietrain resource population established at Michigan State University. The research project has a rich and comprehensive database containing growth, carcass merit, meat quality and sensory phenotypes as well as genetic marker data on F0, F1 and F2 pigs. In addition, gene expression microarray data comparing within-litter phenotypic extremes for loin muscle area and backfat based on a selective phenotyping experimental design will be available. Excellent training in statistical genetics is required, particularly with respect to quantitative trait loci (QTL) analysis. Experience with multiple trait QTL analysis and linkage disequilibrium mapping is highly desired. The ultimate objectives of the project will be to estimate QTL effects for gene expression jointly with observed phenotypes in an effort to discover new candidate genes for growth, carcass merit and meat quality, as well as to infer upon potential regulatory pathways. The successful candidate is then expected to assist in the development of statistical methodologies that integrate genetical genomics information into schemes used for improving livestock populations as well as publish their findings in a timely fashion. Applications will be accepted until the position is filled. Intended starting date is July 1, 2005. Interested candidates are encouraged to email their curriculum vitae and names of two references jointly to rosag@msu.edu and tempelma@msu.edu.

Dr. Guilherme J. M. Rosa Department of Animal Science Department of Fisheries and Wildlife Michigan

State University 1205-I Anthony Hall East Lansing, MI 48824-1225 USA Phone: + 1 (517) 353-5102 Fax: + 1 (517) 353-1699 E-mail: rosag@msu.edu <http://www.msu.edu/~rosag/> Dr. Robert J. Tempelman Dept. of Animal Science Michigan State University 1205-J Anthony Hall East Lansing, MI 48824-1225 USA Phone: + 1 (517) 355-8445 Fax: + 1 (517) 353-1699 E-mail: tempelma@msu.edu <http://www.msu.edu/~tempelma/> -

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

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

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

NetherlandsInstEcology PlantEvolEcol

Dear colleague,

At the department of Plant-Animal Interactions, Centre for Limnology, Netherlands Institute of Ecology (NIOO-KNAW) we have a POST-DOC vacancy for a plant ECoLOGIST.

Detailed information on this vacancy can be obtained at <http://www.nioo.knaw.nl/JOBS/CONTENT/-vacCL.htm>

Please forward this message to any colleagues that may consider this vacancy of interest.

I apologize for the inconvenience in case you receive this message via multiple sources.

Sincerely,

Marcel Klaassen

Head of Department Plant Animal Interactions

Centre for Limnology

Netherlands Institute of Ecology (NIOO-KNAW)

PO Box 1299, 3600 BG Maarssen

tel. +31-294-239317

fax +31-294-232224

<http://www.nioo.knaw.nl/PPAGES/mklaassen/-index.htm> <<http://www.nioo.knaw.nl/PPAGES/-mklaassen/index.htm>>

M.Klaassen@nioo.knaw.nl

Princeton DNA Rearrangements, Small RNAs, Bioinformatics

PRINCETON UNIVERSITY Postdoctoral/research staff positions in the Department of Ecology and Evolutionary Biology available immediately to study

(1) the evolution and mechanism of scrambled gene/genome rearrangements in ciliates, particularly the role of either small RNAs or molecular intermediates in this process using experimental tools.

(2) A second position is available that uses primarily computational tools to collaborate with several experimentalists in the lab, as well as to complement the *Oxytricha* genome project, currently underway at the Wash U Genome Sequencing Center.

Relevant experience, a Ph.D., ability to work independently, and strong research and written/oral communication skills are necessary for either position.

The initial appointment is for one year; and can be extended, upon mutual agreement. Send CV and names of three references to

Laura Landweber Dept. of Ecology & Evolutionary Biology, Princeton University, Princeton, NJ 08544. ll@Princeton.edu

Princeton University is an equal opportunity/affirmative action employer.

StockholmU Phenotypic Polymorphisms

Postdoctoral Position in Theoretical Evolutionary Biology

Department of Zoology, Stockholm University, Sweden

Research topics for the project include theory of the evolution of phenotypic polymorphism and the evolution of individual variability.

The position is a one year stipend of 230000 SEK (appr.

25000 EUR), with possible extension to another year. It is funded via grants from the Swedish Research Council. The starting date is flexible.

Phenotypic polymorphism is a widespread phenomenon, with examples like males and females in sexual species, and winged and wingless individuals in certain insects. Variation in so-called personality between individuals of social species could also be regarded as phenotypic polymorphism. The project deals with the evolution of the alternative phenotypes and, in particular, with the evolution of systems of phenotype determination. Examples of such systems are genetically controlled polymorphisms, phenotypic plasticity, and stochastic (randomizing) polymorphisms. The focus of the project is on the basic, conceptual issues of the evolution of systems of phenotype determination.

Applicants should have a PhD in a field like evolution, ecology, population genetics, or possibly applied mathematics.

Candidates with good conceptual, analytical and computer skills are preferred. To apply, send CV, list of publications, relevant reprints, statement of research interests and skills, and contact information for three references to:

Olof Leimar Department of Zoology Stockholm University SE-10691 Stockholm, Sweden email: olof.leimar@zoologi.su.se tel: +46-8-164056 fax: +46-8-167715 <http://www.zoologi.su.se/research/leimar/>

Application by email is acceptable and informal inquiries are welcome.

UArizona Human Genomic Diversity

Postdoc in Human Genomic Diversity

A postdoctoral fellow position is open to work on a five-year NSF project (HOMINID) titled "A Novel Genetic Database to Test Models of Human Origins". This project is a collaborative effort between the laboratories of Michael Hammer at the University of Arizona and Jeff Wall at USC to gather new data and design novel analytical methods to answer long-standing questions in human evolution. As part of the project we will be examining patterns of nucleotide variation in over 90 regions of the human genome. Statistical and computational methods will be developed for rigorously testing the predictions of alternative hypotheses. Further description of the

project can be seen at: http://lifescience.arizona.edu/faculty.php?faculty_id=2891&string=hammer

The selected postdoc will participate in experiment design, oversee data collection at the University of Arizona, and analyze data in conjunction with collaborators at USC. Previous experience in large-scale DNA sequencing projects is preferred.

Application Instructions for Job No. 32142: All applicants must apply on-line using Internet Explorer or Netscape Navigator (see browser settings on the following web site). To apply, please visit <https://www.uacareertrack.com/applicants/jsp/-shared/frameset/Frameset.jsp?time=1086366632125>.

Select "Search Postings" and enter job #32142. Select "view" located below the Position Title. Select "Apply to this Posting" and follow instructions. For consideration, complete requested documentation must be received by midnight of the closing date.

Minimum Qualifications: * PhD in relevant field * Graduation date no later than 31 December 2004 * DNA sequencing experience (preferably high volume) * Training in evolutionary biology or population genetics

* Benefits: Yes * Salary: DOE (NIH scale) * Hours: Full Time (40 hrs/week) * Opening: 12/31/05 * Closing: until filled

– Michael Hammer Dept. EEB Biosciences West University of Arizona Tucson AZ 85721 mfh@u.arizona.edu (520) 621-9828

Michael Hammer <mfh@u.arizona.edu>

UEdinburgh ButterflyColourPatterns

I am looking for someone to fill a BBSRC-funded postdoc, to study the genetic basis of colour patterns in mimetic *Heliconius* butterflies. This is a re-advertisement of a post that has become vacant, and will be for up to 27 months, starting as soon as possible.

Project description: This is an exciting opportunity to investigate the molecular genetic basis of a classic evolutionary system. *Heliconius erato* and *H. melpomene* have evolved over 20 distinct geographic races that are convergent between the species due to mimicry. This project aims to identify genes controlling the radiation

of *H. melpomene* and conduct a comparative analysis with the co-mimic *H. erato*. We will develop ESTs from wing tissue sampled at different stages in development, and identify regions of the genome involved in pattern formation using linkage mapping. Population genetic analyses and studies of gene expression will then be used to investigate candidate loci. There is the opportunity for genomics, population genetics or evo-devo approaches to this problem that could depend on the interests of the candidate.

The project will involve collaboration with Mark Blaxter and the bioinformatics group at the University of Edinburgh; Owen McMillan in the University of Puerto Rico and Richard French-Constant at the University of Bath.

Contact me (chris.jiggins@ed.ac.uk) or follow this link for application details: <https://www.jobs.ed.ac.uk/-jobs/index.cfm?action=jobdet&jobid=3003608> and see my web site for more details of our research; www.heliconius.org Chris Jiggins Institute of Evolutionary Biology School of Biology University of Edinburgh Edinburgh EH9 3JT Scotland UK Tel: (+44)(0)131 650 8624 Fax: (+44)(0)131 650 6564 <http://neruda.cap.ed.ac.uk/> Chris Jiggins <chris.jiggins@ed.ac.uk>

UHelsinki EvolEcol

Postdoctoral Position in Evolutionary Ecology

Department of Biological and Environmental Science, University of Helsinki, Finland

A one-year postdoctoral position is available to study the evolutionary ecology of territoriality in birds, using both data analysis and modelling. The starting date is flexible, as is the ratio of either type of work. The task is to examine how strategies of breeding site choice create and modify density dependence and other population-level phenomena. The position is in the lab of prof. Hanna Kokko (see www.helsinki.fi/~hmkokko/-LEED.html), where several postgraduate & postdoctoral researchers work on combining theoretical developments and empirical datasets to gain insight on both evolutionary and ecological processes. This provides a very good environment for developing theoretical skills for an interested empiricist, or alternatively, a chance for a theoretician to learn to apply modelling results to large datasets.

The main dataset available is a long-term (> 20 years) collection of breeding records for hundreds of individually marked guillemots *Uria aalge*, and this part of the work will be done in collaboration with researchers in Scotland (prof. M. Harris and Dr. S. Wanless; see Kokko et al. 2004 *J. Anim. Ecol.* 367-376). There are also possibilities to develop models of migration and breeding strategies of black-tailed godwits *Limosa limosa* that migrate between England and Iceland, based on a collaboration between prof. Kokko and Drs. Jenny Gill and Tomas Gunnarsson and Prof. Bill Sutherland (University of East Anglia, UK), as well as to analyze breeding site choice of blue-footed boobies *Sula nebouxii* (collaborative partner: Dr. Roxana Torres, UNAM, Mexico).

Successful applicants should have a Ph.D. in evolution, ecology or a related field. We expect someone with strong analytical skills, with an emphasis on either modelling or data analysis. Review of applications will begin immediately and continue until a candidate is selected. The annual salary is 31320 EUR.

To apply please send a cover letter expressing research interests, CV, and names and e-mail addresses of three references to: Prof. Hanna Kokko (hanna.kokko@helsinki.fi), Laboratory of Ecological and Evolutionary Dynamics, Dept of Biological and Environmental Sciences, PO Box 65, 00014 University of Helsinki, Finland.

– Hanna Kokko Laboratory of Ecological and Evolutionary Dynamics, Dept of Biological and Environmental Sciences, PO Box 65, 00014 University of Helsinki, Finland tel +358 9 1915 7702, fax - 7694, hanna.kokko@helsinki.fi <http://www.helsinki.fi/~hmkokko> Hanna Kokko <hanna.kokko@helsinki.fi>

UHouston SocialInsectEvol

Postdoctoral Researcher in Social Insect Evolution and Behavior at the University of Houston

A postdoctoral position is available to study the behavior and ecology of the western harvester ant, *Pogonomyrmex occidentalis*. The position is in the lab of Blaine Cole and Diane Wiernasz in the Department of Biology and Biochemistry and is part of an NSF-funded project to examine the relation of genetic diversity in colonies and colony performance in the lab and in the field. The project involves linking physiology, behavior and colony genetic variability. The research for this po-

sition requires making behavioral observations of ants in laboratory colonies and combining observations of behavioral tempo and variation with controlled temperature changes. Familiarity with ant behavior is an advantage, but not a requirement. The research will be a part of the long-term population study of this ant in western Colorado, USA and there will be opportunities to develop independent projects. We envision that the applicant will be involved in all phases of the project including data collection, analysis and writing of manuscripts. More information about the project can be obtained at: www.bchs.uh.edu/~bcole/pogo/

Successful applicants should have a Ph.D. in evolution, ecology or a related field. We expect someone with strong analytical skills. The position is available for two years pending satisfactory progress. The position can begin as early as May 1, 2005. Review of applications will begin immediately and continue until a candidate is selected.

To apply please send a cover letter, CV, and names and e-mail addresses of three references to: Blaine J. Cole (bcole@uh.edu), Department of Biology and Biochemistry, University of Houston, Houston TX, 77204-5001, USA. The University of Houston is an Equal Opportunity Employer.

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Blaine J. Cole Department of Biology and Biochemistry University of Houston Houston, TX 77204-5001 <http://www.bchs.uh.edu/~bcole/pogo/> Phone:713-743-2679 Fax: 713-743-2636

Blaine Cole <bcole@uh.edu>

ULausanne EvolFuncGenomics

TWO POSTDOC POSITIONS: EVOLUTIONARY FUNCTIONAL GENOMICS OF HUMANS

Two EU-funded positions will be available starting May 1 (2005) in the group of Henrik Kaessmann at the recently founded Center for Integrative Genomics, University of Lausanne, Switzerland.

We focus on the origin and evolution of primate genes and gene structures. We are particularly interested in characterizing the (adaptive) evolution of young genes in the human genome that originated recently on the primate lineage and therefore may be relevant with respect to human/hominoid-specific phenotypes. To this end, we explore available data from genomic

databases and generate complementary data by experimental analysis.

For more information on the group and our institute more generally, see the website: <http://www.unil.ch/cig/page7858.en.html> For one of the positions, we are seeking highly qualified and motivated applicants with a background in molecular evolution, who have strong experimental lab skills in molecular biology, because we want to functionally characterize newly emerged genes. However, dedicated biochemists or molecular biologists with an evolutionary interest are encouraged to apply as well.

The other position focuses on bioinformatics (data mining) and evolutionary analyses of available genomic data, which may be complemented by data generated in our lab. Thus, we seek highly motivated applicants for this position with a background in molecular evolution and with strong skills in computational biology (bioinformatics, preferably with experience in data mining and comparative genome analysis). Statisticians and/or population geneticists with strong programming skills and an interest in human evolutionary genomics are also encouraged to apply.

The positions are available for three years. The salary is approximately 45,000 Euros per year.

The language of the institute is English, and its members form an international group that is rapidly expanding. The institute is in Lausanne, a beautiful city at Lake Geneva amidst an impressive alpine scenery.

Informal inquiries may be addressed to: Henrik.Kaessmann@unil.ch

Applications including a CV, statement of research interest, copies of relevant publications, and two letters of recommendation should be emailed or mailed to me at the address below. Review of applications will begin immediately.

Henrik Kaessmann, Ph.D. Assistant Professor Center for Integrative Genomics BEP University of Lausanne CH-1015 Lausanne Switzerland Phone : 41-(0)21-692-3907 (administrative assistant: -3900) Fax : 41-(0)21-692-3905 E-mail : Henrik.Kaessmann@unil.ch Internet : <http://www.unil.ch/cig/page7858.en.html>

UOxford PlantEvol

Postdoctoral Research Assistant in Plant Evolution

Department of Plant Sciences, University of Oxford, UK

“The quantitative genetic architecture of sex allocation and the selection of combined versus separate sexes in an annual plant”

Research grant holders: John Pannell (Plant Sciences) and Robert Freckleton (Zoology)

This is a 3-year research project funded by NERC with ideally a start date of 1st April 2005, although there is some flexibility. The successful candidate will join a small research team in John Pannell’s lab that is directing its efforts at understanding the evolution and maintenance of plant sexual diversity, largely using as a model the plant species *Mercurialis annua*. *M. annua* displays outstanding variation in its sexual system, including monoecy, dioecy, and the rare androdioecy. Much of the recent and ongoing research in the lab is focused on addressing the importance of population subdivision and metapopulation dynamics for sexual-system diversity in the species complex, combining phylogenetic and phylogeographic analyses, glasshouse and field experiments, the analysis of population demographic data at a range of spatial scales in Spain and north Africa, and population genetic, ecological and evolutionary modelling. A central aim of the research is the integration of demographic and ecological research with population and quantitative genetics, from both a theoretical and empirical perspective.

The successful applicant for the postdoc position will work on the quantitative genetic basis of natural variation in sex allocation in *Mercurialis annua*, using traditional approaches (the species is not yet amenable to marker-based QTL analysis), as well as of variation in experimental populations under directional selection. There will be scope for collaboration on other related projects underway in the lab.

Informal enquiries should be directed to John.Pannell@plants.ox.ac.uk. For particulars about the research lab and the current focus of work being conducted in it, see John Pannell’s website under ‘People’ at <http://dps.plants.ox.ac.uk/external/> Candidates should have completed, or be about to complete, a PhD or equivalent in plant population genetics, ecology and/or evolution. Candidates will ideally have experience in empirical and/or theoretical research on mating systems and sex allocation, preferably with respect to plants, and be familiar with the design, execution and analysis of field and/or glasshouse experiments with plant populations. Experience of experimental quantitative genetics would be an advantage.

Further particulars and additional selection criteria can be obtained from John Pannell.

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

john.pannell@plants.ox.ac.uk

<http://dps.plants.ox.ac.uk/external/> tel. +44-(0)1865-275145 fax. +44-(0)1865-275074 tel. +44-(0)1865-275145 fax. +44-(0)1865-275074

UQueensland PopEcolGenetics

Postdoc in Population Ecology with an interest in metapopulation modeling (statistical and process-based), population genetics and field work.

We are very likely to have funds available for a three year postdoc to work in the Ecology Centre at The University of Queensland www.ecology.uq.edu.au. The position is tied to a 3-year Australian Research Council (ARC) Linkage grant part funded by industry (WMC Pty Ltd). The grant written by Dr Chris Wilcox, Dr Jessica Worthington Wilmer (Queensland Museum), Prof Hugh Possingham and Mr Darren Niejalke (WMC Pty Ltd) was for Dr Wilcox however he now has a job with CSIRO. The short summary of the grant is:

A Bayesian framework for metapopulation dynamics of species in endangered communities: integrating demographic, environmental and genetic data.

Biodiversity conservation is a spatial and temporal problem. Populations change in time, constrained by the structure and spatial division of their habitat. This study will develop a tool that can be used to assess the influence of environmental fluctuations and landscape heterogeneity on the persistence of endemic species in the mound springs of the Great Artesian Basin. Using a Bayesian framework to integrate data from diverse sources, we will develop models for the biodiversity impacts of groundwater withdrawal and climate change in central Australia. These tools are essential for management of this ecosystem, which has been listed as an "endangered community" under the Environmental Protection and Biodiversity Conservation Act of 1999.

We need to identify an outstanding person so we can transfer the grant to this person. Dr Wilcox will remain involved in the coordination of the grant. We would prefer someone who:

1. can lead two to four weeks of fairly intense field work

on Mound Springs snails in the Australian desert 2. can build, run and test metapopulation models 3. has an interest and familiarity with the generation and application of population genetic data to ecological problems (specifically using microsatellite data)

Interested applicants should send the following, by email, to Prof Hugh Possingham (hpossingham@zen.uq.edu.au) and Dr Chris Wilcox (c.wilcox@uq.edu.au): 1.Full CV 2.One paragraph on why you would like a postdoc like this.

Conditional on the ARC accepting our proposed staffing change, we would like someone to start between March and July 2005. Review of applications will start at the end of Jan 2005 and will continue until a suitable applicant is found.

Dr Jessica Worthington Wilmer Queensland Museum PO Box 3300 South Brisbane, QLD 4101 AUSTRALIA

Office Ph: (61-7) 3840 7707 Lab Ph: (61-7) 3840 7708 Fax: (61-7) 3846 1226 Email: jessicaww@qm.qld.gov.au

USheffield RiceResistance

THE UNIVERSITY OF SHEFFIELD Department of Animal and Plant Sciences

Post-doctoral Research Assistant Salary: £19,460 to £21,640 p.a. Grade: RA1A Closing date: 3rd February 2005

A vacancy exists for a post-doctoral research assistant to work with Professors Julie Scholes, Malcolm Press and Dr Jon Slate on a project to determine the molecular genetic basis of resistance in rice (*Oryza sativa*) to the parasite *Striga hermonthica*.

Applicants should have a background in molecular biology or quantitative genetics and have a PhD in a relevant discipline.

The post is for 2 years initially with possibility of extension for a further year. Start date: 1st April 2005 or as soon as possible thereafter.

Additional Information: This is an ideal opportunity for a PDRA to join an active research group in a large, high profile RAE 5* research-led department. The successful applicant will be based in refurbished laboratories with access to all facilities required for modern plant molecular biology. The aims of this project are to take an integrated approach to identify the molecular genetic basis of resistance in rice to *Striga hermonthica*.

ica by : - Fine mapping existing QTL for resistance to *Striga* in order to begin the identification of molecular markers for use in marker assisted breeding programmes. - Analysing differences in gene expression of key rice cultivars (following inoculation with *Striga hermonthica*) using oligonucleotide microarrays and RT-PCR. - Carrying out bioinformatic analyses of microarray data and, in conjunction with the QTL analysis, identifying sets of candidate resistance genes.

Job description

- Modify existing chromosome substitution lines by crossing and subsequent genotyping of progeny. - Screening chromosome substitution lines for resistance to *S. hermonthica*. - Performing a QTL analysis to fine map resistance QTL. - Bioinformatic analysis of microarray data. - Analyse gene expression patterns using microarrays and RT-PCR - Write 3 monthly reports for funding agency and attend meetings with sponsors as required. - Write manuscripts, give oral and poster presentations. - Undertake other duties as requested by the grant holder or his nominees.

Person Specification

- Careful and precise working. - Good knowledge of laboratory practice, materials and etiquette. - Display initiative in the absence of supervisor. - Ability to prioritise and meet deadlines. - Ability to work with others.

Informal enquiries may be made to: Prof. Julie Scholes
Tel: (0114) 2224780 email: j.scholes@sheffield.ac.uk
Dr Jon Slate - Tel: (0114) 2220048 email: j.slate@sheffield.ac.uk
j.slate@sheffield.ac.uk

USouthDakota StalkEyedFlies

University of South Dakota: Post-Doctoral Research in Evolutionary Physiology of Stalk-Eyed Flies

A postdoctoral position is available to study performance and fitness consequences of insect ornaments in stalk-eyed flies. The position is part of an NSF-funded CAREER project in the laboratory of John Swallow (<http://www.usd.edu/~jswallow/index.html>), Biology Department, University of South Dakota. The position calls for quantitative analyses of eye span and flight performance to test for trade-offs between secondary sexual traits and aerodynamic and physiological adaptations

for flight via direct measurements of flight performance, load lifting capacity, and flight energetics. Primary responsibilities for this position include: 1) conducting laboratory research on flight biomechanics and performance, 2) analyzing data and writing manuscripts, and 3) helping to coordinate projects of undergraduate and graduate students involved in the project.

Successful applicants should have a Ph.D. in comparative physiology, evolution, or a related field. Preference given to candidates with experience in measuring flight biomechanics or performance. Salary is \$30,000 plus benefits, and funds are available for 4 years pending satisfactory progress. The position can begin as early as May 1 2005. Review of applications will begin immediately and continue until a candidate is selected.

To apply, please send a cover letter, a statement of research interests, CV, and names and e-mail addresses of three references to John Swallow (jswallow@usd.edu), Biology Department, University of South Dakota, Vermillion, SD 57069, USA.

USD is an equal opportunity/affirmative action employer.

John G. Swallow

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

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

jswallow@usd.edu jswallow@usd.edu

UWisconsinMadison SexualSelection

Postdoc: Sexual selection & speciation

I am looking for a postdoc to join my lab to study sexual selection and speciation in threespine sticklebacks. This NSF-funded project investigates how ecology can cause divergent sexual selection between stickleback species pairs. The project includes both field and lab work. Position initially for 1 year with possibility of renewal. Ideal start time is Spring 2005. Experience in quantitative or ecological genetics, mating behavior, or working with sticklebacks is desired.

The University of Wisconsin at Madison provides a vibrant intellectual environment with strong groups in Evolution <http://www.evolution.wisc.edu/dev/index.asp> and in Behavior spanning the depart-

ments of zoology, psychology, entomology, and anthropology. Madison is a small, safe city with more than it's share of culture and outdoor opportunities, and is a great place to live.

Interested? Please send a letter of interest, a CV, a list of publications, and the contact information of three references to: Jenny Boughman Department of Zoology University of Wisconsin-Madison Madison, WI 53706

jboughman@wisc.edu (608) 262-2636 <http://www.wisc.edu/zoology/faculty/fac/Bou/Bou.html>

Informal inquiries by email also welcome.

UppsalaU ComparativeGenomics

TWO POSTDOCTORAL POSITIONS IN COMPUTATIONAL BIOLOGY/COMPARATIVE GENOMICS

The Linnaeus Centre for Bioinformatics Uppsala University, Uppsala, Sweden

Two postdoctoral positions are available: one funded privately by Carl Tryggers Stiftelse and the other as an employee of Uppsala University with benefits. The positions are guaranteed for one year with possible extensions of an additional year. They have flexible starting dates.

The projects will involve the use of bioinformatics (Hidden Markov and other probabilistic sequence models, expression analysis, statistical model selection) and molecular evolution (comparative genomics, phylogenetic inference, statistical hypothesis testing) to study robustness and plasticity in the translation, transcription and splicing mechanisms that act on prokaryotic and eukaryotic genomes. Key interests in the lab include evolution of operons and genes for tRNAs and other components of the translational apparatus, prediction and evolution of prokaryotic promoters and regulatory elements, coadaptation between genomes and the transcriptional and translational machinery, and evolution of tRNA identity determinants in the three domains of life.

These projects provide opportunities to collaborate with experimental groups at the Biomedical Center in Uppsala. Applicants should have a Ph.D. in biology, genetics, statistics, computer science, or a related field. Programming skills in UNIX and Perl and experience in molecular evolution are highly desirable, but can be developed on-site. Programmers and statisticians look-

ing to deepen their training in biology are encouraged to apply.

Until February 7th, applications should be sent by mail to arrive by that date to: Registrator, UFV-PA 2004/4801, Uppsala Universitet, Box 256, 751 05 Uppsala, Sweden; by email to registrator@uadm.uu.se; or by fax to +46 18 471 2000. Applications sent by email or fax should be followed by originals in the mail as soon as possible. Salary for the university position is set after experience. Please include a salary request in your application.

After February 7th, applications for the CTS position should be sent by email to tRNA@lcb.uu.se or by mail to: David Ardell, Linnaeus Centre for Bioinformatics Box 598, Biomedical Center, SE- 751 24 Uppsala, Sweden.

Please include CV, cover letter with research interests, relevant reprints or doctoral thesis, and contact information for at least two, preferably three, references in all applications.

For more information please see <http://www.lcb.uu.se/~dave> and contact me by email at tRNA@lcb.uu.se or by telephone at +46 (0)18 471 6694.

YaleU ReproductiveBehaviour

A postdoctoral position is currently available in the lab of Suzanne Alonzo (PI) at the department of Ecology and Evolutionary Biology at Yale University to study the evolution of alternative reproductive tactics. The successful candidate will use mathematical models to develop novel theory on the evolution and ecology of alternative reproductive behaviors in both males and females.

For this position, a Ph.D. in evolution, ecology, mathematical theory or related field is required. Prior experience developing mathematical models is necessary as well as knowledge of behavioral and evolutionary ecology. Prior experience with some of the following theoretical approaches is desirable: game theory, genetic algorithms, individual-based simulations, quantitative genetics, population genetics or adaptive dynamics. The postdoctoral researcher will work independently and in collaboration with the PI to develop new theory. Field or laboratory work is possible but not required.

Review of applications begins immediately and will continue until the position is filled. Start date is flexible but the position is available immediately. The position is for two years and is renewable contingent on the availability of funding. Please submit curriculum vitae, brief statement of research interests, up to 3 relevant manuscripts and 3 professional references to Suzanne H. Alonzo by email (Suzanne.Alonzo@Yale.edu) or mail (Department of Ecology and Evolution, Yale University, P.O. Box 208106, New Haven, CT 06520-8106).

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

Suzanne H. Alonzo Department of Ecology and Evolutionary Biology Yale University P.O. Box 208106 New Haven CT 06520-8106 phone (203) 432 0690 fax: (203) 432 3854 www.eeb.yale.edu Suzanne.Alonzo@Yale.edu

WorkshopsCourses

BodegaMarineLab AppliedPhylogenetics May7-14 .	66	UHawaiiManoa GeneticProgramming	68
MBL MolEvol Jul24-Aug5	67	UVirginia EcolWildlifeDiseases	69
NorthCarolinaStateU StatGenetics May23-Jun10 ..	68		

BodegaMarineLab AppliedPhylogenetics May7-14

UC Davis WORKSHOP IN APPLIED PHYLOGENETICS at Bodega Marine Laboratory, Bodega Bay, California May 7-14, 2005

Sponsored by the Center for Biosystematics, Bodega Marine Laboratory, and Center for Population Biology, University of California, Davis

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

is an area of special excitement, innovation, and controversy, and perspectives vary widely.

In May, 2005, for the sixth year, we will teach a workshop for graduate students interested in applying phylogenetic methods to diverse topics in biology. The one-week course will be an intensive exploration of problems to which modern phylogenetic tools are being applied, including topics in biogeography, ecology, conservation biology, phylogenomics, functional morphology, macroevolution, speciation, and character evolution. The course leads off with recent advances in phylogenetic methodology, and then turns to methods and tools that can be brought to bear to address these "applied" issues in the context of a given phylogeny.

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

Specific topics to be covered in the course include:

- * Finding, evaluating and interpreting phylogenetic trees; phylogenetic databases
- * Recent advances in tree reconstruction: Bayesian inference; stochastic op-

timization strategies; divide-and-conquer methods * Analysis of character evolution—theory: parsimony, likelihood and Bayesian approaches; null models and statistical testing * Analysis of character evolution—form and function of complex character systems * Phylogenetic biogeography and phylogeography; coalescent methods for inferring migration rates and patterns * Phylogenetic comparative methods * Phylogenetic perspectives on biodiversity and conservation biology * Data mining of sequence databases for phylogenetic analysis * Estimation of divergence times from sequence data

Instructors for the workshop.

* Dr. H. Bradley Shaffer * Dr. Michael Sanderson * Dr. Peter Wainwright * Dr. Tom Near * Dr. Amy Driskell * Dr. Rich Glor * Dr. Campbell Webb * Dr. Gordon Burleigh * Dr. Shelley McMahon * Dr. Justen Whittall

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

Admission and Fees. Students will be admitted based on academic qualifications and appropriateness of research interests. The course fee is \$375. This includes room and board at BML for the duration of the course. UC Davis students may take the course for credit and can apply for a partial waiver of this fee.

Application Deadline. Applications are available at the course website: <http://ginger.ucdavis.edu/sandlab/ap2005.htm> and are due by February 28, 2005. Please send a completed application form, and one letter of recommendation from your major advisor. We encourage applications to be sent via email as PDFs to pqspinks@ucdavis.edu. Sorry, but due to the limited size of the class, postdocs and faculty are discouraged from applying. Students will be notified via e-mail by March 18 of acceptance.

If sending application via surface mail, send all materials to:

Dr. Phillip Q. Spinks Section of Evolution and Ecology
2320 Storer Hall University of California Davis Davis,
CA 95616 email: pqspinks@ucdavis.edu

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 Rile-
 y 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 Naira Rodriguez-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/> - Michael P.
 Cummings Center for Bioinformatics and Computa-
 tional Biology University of Maryland Agri/LFSc Surge
 Building #296 College Park, MD 20742-3360 USA
 mike@umiacs.umd.edu 301.405.9903 voice 301.314.1341
 facsimile <http://serine.umiacs.umd.edu/>

NorthCarolinaStateU StatGenetics May23-Jun10

Applications for registration and scholarships are now
 being accepted for the 10th Summer Institute in Statis-
 tical Genetics at North Carolina State University (May
 23-June 10, 2005) and also the Asian Institute in Statis-
 tical Genetics at Yonsei University, Seoul (July 25-29,
 2005).

Online registration is available at <http://-statgen.ncsu.edu> Bruce Weir weir@stat.ncsu.edu

UHawaiiManoa GeneticProgramming

A 3-credit hour graduate course on Genetic Program-
 ming is being offered online through the University of
 Hawaii Outreach College for Spring 2005:

ICS 691: Genetic Programming (Topics in Software)
 Faculty: Lee Altenberg <altenber@hawaii.edu> De-
 partment of Information and Computer Sciences, Uni-
 versity of Hawaii at Manoa.

Genetic Programming (GP) is a developing field at the
 nexus between computer science and evolutionary biol-
 ogy. The elements of Darwinian evolution are applied
 to populations of computer programs as a method of
 automatic programming. Fitness is defined by a high-
 level specification of the program's purpose, and varia-
 tion is produced by program mutation and recombina-
 tion operators. Genetic programming exhibits higher-
 order evolutionary phenomena such as robustness and
 the evolution of evolvability, and thus may serve not
 only as an engineering technique, but as a model evo-
 lutionary system for theoretical work.

The course is designed to prepare and engage the stu-
 dent as quickly as possible in original research in the
 field of genetic programming. The subject is presented
 at a depth necessary for the student to become familiar
 with and evaluate controversies within the field, appre-
 hend open areas for new research, and engage in origi-
 nal research with the goal of publication. The course
 is entirely on line and asynchronous.

Texts: Genetic Programming: An Introduction: On
 the Automatic Evolution of Computer Programs and
 Its Applications by Wolfgang Banzhaf et al.. Morgan
 Kaufmann (December 1, 1997). ISBN: 155860510X .

Genetic Programming IV: Routine Human-
 Competitive Machine Intelligence (Genetic Pro-
 gramming Series) by John R. Koza et al. Kluwer
 Academic Publishers, Bk & DVD edition (July 2003).
 ISBN: 1402074468

Dates: The course begins January 10. The last day to
 register is January 19.

To Register: The course listing: <http://-myuh.hawaii.edu/pls/uhdad/avail.class?i=MAN&t=-200533&c=3569> The guide to registration: http://-www.outreach.hawaii.edu/myuh/quick_guide.asp
 Detail on the course content: <http://dynamics.org/-Altenberg/UH.ICS/691.GP/> Questions about
 the course can be e-mailed to Lee Altenberg
 <altenber@hawaii.edu>

-
 Lee Altenberg, Ph.D. Associate Professor, Information
 and Computer Sciences University of Hawai'i at Manoa
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UVirginia EcolWildlifeDiseases

Dear colleagues:

We would like to announce a summer field course on the Ecology of Wildlife Diseases at the Mountain Lake Biology Station (May 31-June 24, 2005). This course will focus on the ecology and evolution of parasites in wild animal populations. We will emphasize hands-on experience with field and laboratory techniques, including capture and examination of insects, birds, amphibians, small mammals and other wildlife near MLBS. The Mountain Lake Biological Station is a dynamic research and teaching environment formally affiliated

with the University of Virginia, and located in the Appalachian Mountains.

Please see the attached PDF flyer for more information on this course, and post or forward to both graduate and advanced undergraduate student who might be interested in this experience.

Tuition scholarships and service awards that cover room and board are available. For more information on tuition, fees and an online application see: www.mlbs.org

Thank you for helping us advertise this opportunity!

Amy Pedersen and Sonia Altizer

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Instructions

Instructions: To be added to the EvoDir 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 EvoDir 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 EvoDir direct them to the email evodir@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.