

**MRG PRESENTS
Recruitment Road Show
INVITATION TO ATTEND AND HEAR MORE**

OPEN RESEARCH POSITIONS

IN

**COMPUTATIONAL GENETICS
QUANTITATIVE/ STATISTICAL GENETICS
POPULATION ECOLOGY AND
EVOLUTIONARY BIOLOGY
GENOMIC ANALYSIS AND EVOLUTION
BIOINFORMATICS RELATED TO
MOLECULAR IDENTIFICATION (BARCODING)
PATHOGEN EVOLUTION**

FOR

**UNDERGRADUATE STUDENTS
PHD STUDENTS**

POST DOCS

SUMMER ASSISTANTS

Wednesday 27th January, 16:00-
Finnish Museum of Natural History (Eiäinmuseo),
Pohjoinen Rautatiekatu 13, Helsinki
Short presentations about open positions and
discussions with MRG group leaders

**FREE ENTRANCE,
FREE BEER, CIDER, WINE AND
SNACKS**

AGENDA:
16:00-17:30 Introduction to research projects and open positions in MRG
Ilkka Hanski: Introduction to MRG and research projects on the Glanville
fritillary butterfly and tropical forest beetles in Madagascar
Rainer Lehtonen: Glanville fritillary ecology of wood-decaying fungi
Otso Ovaskainen: Metacommunity ecology of pathogen evolution
Anna-Liisa Laine (video greetings): Student's view
Jussi Nokso-Koivisto: Student's view
Questions and discussions with MRG group leaders

17:30- Snacks, drinks and free discussion with MRG group leaders
Please register to secure a seat and snacks by sending an email to
vira.forsblom@helsinki.fi

**The Metapopulation Research
Group
MRG**

is a highly international group of 47
researchers (11), post docs (7), post graduate
students (20) and supporting personnel (9)
representing 11 nationalities. The senior
researchers represent a wide range of
expertise including ecology and population biology,
conservation biology and population genetics,
computer science, bioinformatics, molecular biology
and genetics. MRG is the leading
research group worldwide in the biology of
metapopulations (spatially structured
populations) and one of the Centres-of-Excellence in
Finland (national research council) for 2000-2005
Research nominated by the Academy of
and 2006-11. For additional information:
www.helsinki.fi/science/metapop.

EXAMPLES OF OPEN RESEARCH POSITIONS IN MRG

PhD student position in genomic analysis of evolution in Malagasy dung beetles

We are looking for an applicant with background in genetics, bioinformatics or comparable studies to join a project on speciation and evolution of endemic dung beetles in Madagascar. We are using next-generation sequencing techniques to obtain comparative sequence data for related groups of species. The PhD project involves analyses of these data to construct refined molecular phylogenies and to analyse spatial genetic structure of species, hybridization between closely related species, and signatures of adaptive evolution in the genome.

Contact: ilkka.hanski@helsinki.fi

MSc thesis / PhD student / post doc position in bioinformatics related to molecular identification (barcoding)

We are looking for an applicant with background in bioinformatics or comparable studies to join a project working on metacommunity ecology of wood-decaying fungi. The data come from 454-sequencing of environmental samples (soil, saw-dust drilled from dead logs, spores sampled from air using cyclone sampler, etc.). The main task of the project is to develop methods for identifying the species in these samples and assessing the reliability of identifications. The identifications are based mainly by comparisons to an extensive reference database that we have acquired (and are further extending) in a Nordic collaborative project. The level of the project can be adjusted from MSc thesis to a post doc project depending on the skills and experience of the applicant.

Contact: otso.ovaskainen@helsinki.fi

PhD / post doc/ position in quantitative/statistical genetics

We seek for a PhD student or young post doc with background in genetics, bioinformatics or comparable studies to join a research project working on metapopulation ecology, evolution and functional genomics of the Glanville fritillary butterfly. The PhD project includes construction of a genetic recombination map, designing a genome-wide custom SNP-chip assay, and application of the SNP-chip for association and linkage analyses of flight metabolism. The Glanville fritillary is a well-known model system in population biology studied since 1991. The project is funded by the European Research Council and the Academy of Finland.

We have recently sequenced the transcriptome of the Glanville fritillary and are currently sequencing the entire genome using Roche 454 Titanium and SOLiD3.

The SNP-chip platform to be developed in this project will be used in many studies of Glanville fritillary population genetics, evolution and association and linkage analyses of life history and phenotypic traits. This PhD project is primarily focused on genetic variation in flight metabolism, which has high heritability and is under intensive study in the Metapopulation Research Group. In addition to general statistical methods, relevant software packages (Merlin, PLINK, FBAT etc.) will be implemented.

Contact: rainer.lehtonen@helsinki.fi

Post Doctoral Research Associate in life-history ecology and evolution of the Glanville fritillary butterfly

We are seeking an outstanding young post doc with background in population or evolutionary biology or population genetics to join a large research group working on metapopulation ecology, evolution and functional genomics of the Glanville fritillary butterfly. The successful candidate has strong quantitative skills. We are currently sequencing the genome of the Glanville fritillary and plan extensive association and linkage analyses of phenotypic and life history traits. The project is funded by the European Research Council and the Academy of Finland.

Description of the position: The post doc will conduct common garden experiments in large out-door population cages using butterfly material originating from different types of populations and landscapes. In addition to conventional life-history studies, the project involves analyses of variation in the coding region and gene expression in relation to individual performance and the structure of the population of origin.

Contact: ilkka.hanski@helsinki.fi

Etsimme genetiikan opiskelijaa gradutyöntekijäksi

Gradutyö on osa laajaa tutkimusprojektia, jossa tutkitaan täpläverkkoperhosen metapopulaatiobiologiaa, ekologiaa ja evolutiikkaa molekyyligeneettisten työkalujen rooli tutkimuksessamme on kasvanut merkittävästi viime aikoina. Olemme sekvensoineet täpläverkkoperhosen transkriptomin ja olemme parhaillaan sekvensoimassa koko genomia käyttäen uusimpia massasekvensointimenetelmiä. Sekvenssiedon perusteella olemme suunnitelleet useita kandidaattigenejä kattavan genotyypauspaneelin (30 SNP markkeria, Sequenom), jolla on tarkoitus kartoittaa aluksi 360 täpläverkkoperhosen geneettinen variaatio. Näistä perhosista on olemassa kattavaa tietoa fenotyypeistä ja kelpoisuuskomponenteista aiempien tutkimusten perusteella.

Tässä gradutyössä analysoidaan tuotettu variaatiotiedon tarkastellaan variaation kytkeytyvyyttä ja assosiaatiota yksilöiden fenotyypisiin ominaisuuksiin ja populaatioiden keskeisiin parametreihin. Työ sisältää aineiston laadun arviointia sekä kytkentä- ja assosiaatioanalyysijä olemassa olevilla ohjelmilla (esim. Merlin, PLINK, PBAT, FBAT). Kyseinen datapaneeli toimii myös tärkeänä pilottihankkeena laajempien genotyypausprojektien suunnittelussa. Menestyksekkäälle gradun tekijälle voidaan tarjota mahdollisuutta väitöskirjaprojektiin.

Yhteydenotot: rainer.lehtonen@helsinki.fi

PhD Student Position in Pathogen Evolution

Are you interested in coevolution? Have you ever wondered how pathogens evolve to overcome the resistance strategies of their hosts?

Applications are invited for a 4-year PhD fellowship to study pathogen evolution by combining ecological, evolutionary and molecular approaches. Motivated students with a MSc degree in ecology, evolutionary biology or molecular biology (or other related fields) are encouraged to apply. Prior expertise in experimental design, statistical analysis or laboratory work using genetic markers are a bonus but your most important assets are enthusiasm for research, motivation to learn new things, and ability to work independently while being an active member of a research team.

The project is centered on the interaction between host plant *Plantago lanceolata* and its fungal pathogen *Podosphaera plantaginis* in the Åland Islands. Prior research on this interaction has shown that the pathogen persists as a metapopulation. Despite rapid turnover of local populations there is evidence of rapid ongoing evolution between these species. In your project you will ask how processes at different spatial scales – molecular, within host, within population and metapopulation – affect the diversity and evolution of pathogens. In practice, you will carry out field surveys in the Åland Islands, conduct experimental work in the laboratory and genotype pathogen isolates.

Contact: Anna-Liisa.Laine@helsinki.fi

SUMMER RESEARCH ASSISTANT POSITION in HOST-PARASITE COEVOLUTION at the UNIVERSITY of LIVERPOOL in JUNE-JULY 2010

You should have completed some studies in ecology, evolutionary biology or microbiology (or other related fields). Prior experience in experimental or laboratory work is a bonus but your main assets are enthusiasm and interest to learn new things. You will be working in close collaboration with another research assistant, but we also expect you to be able to work independently. You should be fluent in English.

Contact: Anna-Liisa.Laine@helsinki.fi

APPLICATION DEADLINE 19TH FEBRUARY 2010

www.helsinki.fi/science/metapop