

Ecological Genomics

Sponsored by ESF ConGen and co-sponsored by ThermAdapt Summer School 2009

October 19 – 24, 2009

Centro Residenziale Universitario di Bertinoro

Bertinoro (FC), Italy

<http://www.centrocongressibertinoro.it/>

DNA sequencing technology is undergoing exceptional improvements. Next-generation parallel sequencers can generate millions of DNA sequences overnight at reduced costs. SNP detection technology is evolving fast from massive microarray to a variety of lower scale and less expensive technologies. These methods are changing the way of planning research and experimental protocols in theoretical and applied evolutionary and population genetics, and bioinformatics. Aim of the Summer School is to introduce the new genomic approaches into the field of ecological and conservation genetics. Genomic methods have been developed and applied mainly to the study of human populations or model organisms. However, genomic approaches are very well suited to the study of natural populations, as well. Classical population genetics in the last two decades made extensive use of very limited numbers of “neutral” markers (mainly microsatellites and mtDNA sequences), while the study of functional genetic systems has been substantially limited. Consequently, it has been problematic (or even impossible) to correlate such kind of population genetic data with the main domains of functional population genetics, that is the dynamics of whole genome heterozygosity and the genetic control of phenotypic variation. Genome sequencing and the very first population genomic data clearly indicate that a significant proportion of the population DNA diversity have been selected and functionally diverged in response to evolutionary adaptive pressures. Genomic methods might straight overcome the limitations of classical genetic marker approaches. Parallel sequencing and genome scanning technologies allow genotyping thousands of genes, covering both mutational diversity at the DNA level, regulatory mechanisms and patterns of qualitative or quantitative gene expression. In this way it is now feasible to understanding the functional role of genetic systems, the dynamics of selection processes and the adaptive potential of natural populations to changing climate and environments.

The Summer School is dedicated to design the role of next-generation sequencing and other genomic technologies as applied in the field of population and conservation genetics. Particular emphasis will be given to the study of functional genes and adaptation in natural non-model organisms. Aim of the School will be to show how the new perspectives offered by genomics could be applied to solve theoretical and practical ecological and conservation genetics problems. The School will provide updated overview on major genomic methods, introduce case-studies in

ecological genomics, and in this way it will stimulate the audience to develop new perspectives in the application of genomic methods in the study of natural plant and animal populations. Participants will be asked to share information and discuss genomic research approaches in wildlife species to gain a more profound understanding of the variation of genes and their functions in evolution, ecology and conservation. The School will emphasize the use of bioinformatic tools and software, and will further stimulate collaboration among international research groups within the field of ecological genomics.

The School, organized by Ettore Randi (Bologna) and Cino Pertoldi (Aarhus), consists in four full-day sessions with an adequate balance between theory and computer practice, oriented to handle genomic data bases, solve problems and hypothesis testing. There will be morning and afternoon sessions featuring invited speakers, practical computer sessions, and evening poster session dedicated to the students' own research projects. The School is primarily intended for young researchers at the doctoral and post-doctoral stages. Participants must have their own laptop computer and have software applications installed (information regarding the software a will be provided by the organizers in advance). Candidates should preferably have some background in genomics and conservation genetics, as well as some experience in bioinformatics, and molecular evolutionary biology.

Invited speakers:

Robert K. Wayne (UCLA, Los Angeles, California)

Fyodor Kondrashov (Barcelona, Spain)

Joop Ouborg (Nijmegen, The Netherlands)

Thierry K.S. Janssens (Amsterdam, The Netherlands)

Jacek Radwan (Kracow, Poland)

Remy Bruggmann (Zurich, Switzerland)

Pierre Taberlet (Grenoble, France)

Eric Coissac (Grenoble, France)

Michael M. Hansen (Silkeborg, Denmark)

Ditte Demontis (Aarhus, Denmark)

Christian Schlötterer (Wien, Austria)

Christopher W. Wheat (Helsinki, Finland)

Giovanni Giuseppe Vendramin (Firenze, Italy)

The School will be held in Bertinoro, a nice small hill town close to **Bologna (Italy)**, in collaboration with the University of Bologna Conference Centre (CeUB). A maximum of **25 students** will be selected on the base on their CV, which should be sent only by e-mail **before August 17, 2009**, to:

Ettore Randi

ettore.randi@ifs.it

(indicating in Subject **ECOLOGICAL GENOMICS 2009**)

Acceptance will be communicated by email by **August 21, 2009**.

ESF will provide founding covering permanence and living costs to all the students attending the School. Participant should pay their own travelling costs to Bologna. Transport from Bologna Airport or Railway station will be provided by the organization.

Bologna Airport

<http://www.bologna-airport.it/>

Bologna by train

<http://trenitalia.it/>

Bologna by car

<http://www.comune.bologna.it/>

Centro Residenziale Universitario

<http://www.centrocongressibertinoro.it/>

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