

SECTION OF GENETICS AND ECOLOGY
DEPARTMENT OF BIOLOGICAL SCIENCES
UNIVERSITY OF AARHUS



Final Report of the ESF funded Summer School

“ECOLOGICAL GENOMICS”

October 19 - 24, 2009

Centro Residenziale Universitario di Bertinoro, Bertinoro (FC), Italy

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

Supported by ESF ConGen and ThermAdapt

The Congen and Thermadapt programs funded by the European Science Foundation have financed the summer school entitled “**ECOLOGICAL GENOMICS**”

This summer school was held in the Centro Residenziale Universitario di Bertinoro, Bertinoro (FC), Italy (<http://www.centrocongressibertinoro.it/>) from the October 19 - 24, 2009.

Theoretical background

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 microarrays 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, population genetics, and bioinformatics. Genomic methods have been developed and applied mainly to the study of human populations or in model organisms, so far. However, genomic approaches are very well suited to

the study of natural populations and to study the effects of selective pressures on populations, like for example those imposed by climatic changes. Classical population genetics in the last two decades made extensive use of electrophoretic methods to genotype individuals and characterize population through the use of very limited numbers of “neutral” markers (mainly microsatellites and mtDNA sequences). It has however been problematic (and often unsuccessful) to correlate such kind of population genetic data with the main domains of functional population genetics. Genome sequencing and the very first population genomic data clearly indicate that a significant proportion of the population DNA diversity could have been selected and functionally diverged in response to evolutionary adaptive pressures. Genomic methods can overcome the limitations of classical genetic marker approaches. Parallel sequencing and genome scan technologies allow genotyping thousands of genes, from a few randomly selected “neutral” markers to functional genetic systems, from mutational diversity at the DNA level to regulatory mechanisms and patterns of qualitative or quantitative gene expression. In this way it is now feasible to understand the functional role of genetic systems, the dynamics of selection processes, and the adaptive potential of natural populations to changing climate and environments.

An exciting forthcoming development is the extension of ecological genomics from populations to the natural communities and ecosystem levels. Recent experimental and field studies show that the genomic structure of key species can drive composition of the entire community and the evolution of ecosystems. These approaches can revolutionize studies of community ecology, and can also have deep applied consequences, such as the role of population genetics/genomics in restoration ecology and thermal adaptation related studies.

Variation of gene expression at functional genes has been studied in the past few years mainly using microarray methods. However, now massive parallel sequencing allows direct and rapid description of the entire transcriptomes also in non-model species. In this way it is now possible to survey the extent and patterns of sequence variation at expressed genes, with particular focus on adaptive mutations and regulatory changes. Thus ecologically differentiated populations that are adapted to different thermal regimes and/or other kinds of ecological pressures can be compared. Ecological and conservation genetics of natural populations will enormously benefit from such approaches.

Organization of the summer school

The summer school, which has been organized by Ettore Randi (ISPRA) and Cino Pertoldi (Department of Biological Sciences, Ecology and Genetics, Aarhus University, Denmark), consisted of four full-day sessions with an adequate balance between theory and computer practice oriented to handle genomic data bases, solve problems and test hypotheses. The Ecological Genomics Summer School took place in October 2009 in Bertinoro (Italy). It was located in the Centro Residenziale Universitario di Bertinoro. 33 students from 14 countries attended the school and were taught by 13 teachers. The selection of participants was done according to applicants' interest, CV, statement of interest quality, recommendation letters, and applicants' project significance in conservation genetics. Priority was given to applicants who come from countries that financially support the ConGen and ThermAdapt programmes. However, a balanced geographical representation, sex ratio among the participants, and broad project organism taxonomy coverage was ensured. Participants brought their own laptop computer and had software applications installed (information regarding the software were provided by the organizers in advance).

Aim of the Summer School was to introduce the new genomic approaches into the field of ecological genetics, conservation genetics and other related disciplines dealing with the consequences of climate related changes. We invited leading researchers in physiology, conservation genetics, evolutionary biology, ecology and genomics, working on various levels of biological organization from molecules to populations and species (list of participants and lecturers, and program are available at the web page: www.congen.biz and www.esf.org/congen and www.esf.org/thermadapt).

Many new next generation techniques were briefly introduced, and the potential of using whole genome data and the need of transition from neutral loci to functional loci analyses was emphasized. This was done by bringing together teachers who presented theoretical lectures and led practical computer work. Students were encouraged to discuss their own projects. The Summer School was structured with morning lectures and afternoon computer exercises in which the students were given datasets to analyse. An important part of the afternoon sessions formed presentations of students' scientific projects followed by discussions and suggestions for future progress. The course provided both an introductory overview of the most essential and commonly used Genomics technologies and methods of analyses plus their theoretical background. Rather than providing comprehensive coverage of any single technique, the course aimed to teach students how to identify the most appropriate technique(s) for specific types of data sets or questions.

Meeting programme

The invited speakers use a wide variety of methodological approaches in their research, which provided an inspiring setting for discussions on cutting edge approaches for studying adaptation in free living as well as laboratory organisms, particularly from a cross-disciplinary perspective. It was also clearly emphasized that insight are needed from several biological levels in order to understand the mechanisms behind adaptation. To understand what limits the ability of species to adapt to evolutionary pressures, including climate induced changes, there is a need to integrate (local) short-term and long-term changes, and to increase our knowledge on the importance of genetic and environmental components on the variability of ecological relevant traits.

Program

		Tuesday 20	Wednesday 21	Thursday 22	Friday 23	Saturday 24
Morning						
9:00 - 10:15	lecture	Wayne	Radwan	Wheat	Taberlet	H. Andersen
10:15 - 10:30	discussion					(computer)
10:30 - 11:00	coffee					
11:00 - 12:15	lecture	Ouborg	Rogers	Kofler	Vendramin	H. Andersen
12:15 - 12:30	discussion					(computer)
12:30 - 14:30	lunch					
Afternoon				excursion		Departure
14:30 - 15:45	lecture	Kondrashov	Rogers (computer)	excursion	Kofler (computer)	
15:45 - 16:00	discussion			excursion		
16:00 - 19:00	computer	Janssen	Bruggman	excursion	Coissac	
19:00 - 19:30	tea			excursion		
19:30 - 20:30	students			excursion		
Evening						
20:30 -	dinner					

Lectures

- R. K. Wayne Evolutionary and conservation genomics of *Canis*
- J. Ouborg Plant genomics and transcriptomics
- F. Kondrashov Ecology of gene duplications
- J. Radwan Transcriptomics of the response to selection on metabolic rate in the bank vole
- S. Rogers Integrating ecological genomics with field studies of natural selection in threespine stickleback
- P. Taberlet DNA barcoding for ecologists
- G. G. Vendramin Population genomics of trees
- R. Kofler Detecting positive selection in genomic data sets
- C. W. Wheat From molecules to metapopulations: finding the variation affecting butterfly dispersal in a fragmented and dynamic landscape

Computer sessions

- T. Janssen An introduction to expression microarray data analysis in R/Bioconductor. Some hands-on experience by means of case-studies in non-model organisms
- S. Rogers Genetic linkage and QTL mapping in natural populations using R
- R. Bruggman Analysis of next generation sequence data (e.g. SNP analysis, assembly, ChipSeq)
- D. Holm-Andersen Analysis of SNPchip data (GenomeStudio; HaploView)
- E. Coissac Biodiversity assessment and the next-generation sequencer
- R. Kofler PanGEA: identification of allele specific gene expression using the 454 technology

Students' presentations

Students' presentations covered a broad range of organisms including plants, invertebrates, birds or mammals. Students discussed their study species, preliminary results of their work and future directions. The presentations were followed by discussions and suggestions for future progress. Below, the students who presented their projects with the title of their talks are listed.

name	e-mail	affiliations	title of the talk
Malgorzata Tokarska	tokarska@zbs.bialowieza.pl	Mammal research Institute PAS	European bison genetics. Illegitimate gene expression.
Robert Ekblom	r.ekblom@sheffield.ac.uk	Univ. of Sheffield	Ecological genomics in birds
Barbara Fussi	baba104@gmx.net	Federal Research Centre for Forestry	Chasing grey poplar
Jonathan Ellis	J.Ellis@exeter.ac.uk	Univ. of Exeter	A lightning research overview
Bastiaan Star	bastiaan.star@bio.uio.no	Univ. of Oslo	The Atlantic cod genome project Ground beetle genetic diversity in relation to pesticide presence and agricultural intensiveness
Chiara Marchi	chiarapuspa@gmail.com	Aarhus university	Ecogenomics of inbreeding depression in scabiosa columbaria
Francesco Angeloni	f.angeloni@science.ru.nl	Radboud university Nijmegen	Next generation sequencing in bank vole, a non model organism
Michal Stuglik	stuglik@gmail.com	Jagiellonian University	FishPopTrace
Sarah Helyar	s.helyar@bangor.ac.uk	Bangor university	FishPopTrace
Alessia Cariani	alessia.cariani@unibo.it	University of Bologna	FishPopTrace
Morten Limborg	mol@aquadtu.dk		FishPopTrace
Alain Frantz	alainfrantz@yahoo.co.uk	University of Sheffield	Genetics & Wildlife Management
Jake Gratten	j.gratten@sheffield.ac.uk	University of Sheffield	Ecological genomics in a classical avian study system
Aines Castro	castro@izw-belin.de	Leibniz Institute for Zoo and Wildlife Research	Immune gene diversity in free-ranging Namibian cheetahs
Faith Walker	faith.walker@nau.edu	Northern Arizona University Department of Molecular Biology, Max Planck Institute for Developmental Biology, Tübingen, D72076, Germany	Does beaver herbivory drive genetic structure in cottonwoods?
Eva-Maria Willing	eva.willing@tuebingen.mpg.de		Adaptation in wild guppies - Molecular Analyses
Tatiana Teixeira	tteixeira@igc.gulbenkian.pt	Instituto Gulbenkian de Ciência	Demographic and Genetic Responses to Habitat Fragmentation and Habitat Loss in Large Forest Mammals
Romolo Caniglia	romolo.caniglia@gmail.com	ISPRA Bologna Italy	Non-invasive genetic monitoring of wolves in the northern Apennines
Elena Fabbri	elena.fabbri@infs.it	ISPRA Bologna Italy	SNPs vs STR in non invasive genetic monitoring project
Marco Galaverni	marcogalaverni@iol.it	ISPRA Bologna Italy	Wolf Olfactory Receptor (OR) genes
Jelena Aleksić	aleksic_jelena@yahoo.com.au	Institute for Molecular Genetics and Genetic Engineering IMGGE	Secrets of Serbian spruce
Laura Corrigan	l.j.corrigan@durham.ac.uk	Durham University	Phenotypic and genetic divergence in Arctic charr
Dagmar Cizkova	dejsha@seznam.cz	Institute of vertebrate biology, Czech Academy of Sciences	OMICs in the house mouse hybrid zone
Zuzana Starostova	z.starostova@post.cz	Department of Zoology, Charles University in Prague, Czech Republic	Temperature-induced phenotypic plasticity in the gecko <i>Paroedura picta</i>
Sylwia Czarnomska	s_czarnomska@zbs.bialowieza.pl	Mammal Research Institute PAS, Bialowieza, Poland	Genetic population structure of the wolf <i>Canis lupus</i> in Poland
shaohua Fan	shaohua.fan@uni-konstanz.de	department of biology, university of konstanz	natural selection and divergence time estimation for young divergent cichlid fish
Licia Colli	licia.colli@unicatt.it	Institute of Zootechnics, University of Piacenza	The study of biodiversity in livestock and wildlife species
Carolina Corrales	carolina.corrales@ebc.uu.se	Uppsala University	Landscape Genetics and Phylogeography of black grouse

Nina Overgaard Therkildsen	nit@aqua.dtu.dk	DTU Aqua	Historical genetic analysis in Atlantic cod Implication of climate change on the susceptibility of the european lobster (<i>Homarus gammarus</i>)
Philipp Kraemer	philipp.kraemer@uni-oldenburg.de	Carl von Ossietzky University of Oldenburg	Assembly-free comparative analysis of rainforest tree genomes
Matt Helmus	mrhelmus@wisc.edu	Xishuangbanna Tropical Botanic Garden-China	Immunogenetics variability at different habitats: an intra-specific level approach
Joaquin Munoz	quini@ebd.csic.es	Donana Biological Station (CSIC), Seville, Spain	Conservation genetics of Tatra chamois
Petra Hajkova	hajkova@ivb.cz	Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Brno	

Assessment of the results and impact of the event on the future direction of the field

The Ecological Genomics Summer School provided a unique opportunity to bring together talented students and well-established capacities from conservation and ecological genetics, with positive outcomes for all. The students received important information about the present state of the art of genomic techniques and future directions of the research in the field. The selected students were very active and collaborative, and we believe that both the knowledge and personal contacts will be very useful for their future scientific careers. Lectures and discussions outlined specific areas that will surely be explored in the near future of conservation and ecological genetic. Based on positive feedback, both students and lecturers expressed the willingness to organize and/or participate in similar schools in the coming years.

The Summer School covered the role of next-generation sequencing and other genomic technologies as applied in the field of population and conservation genetics. Particular emphasis was given to the study of functional genes and adaptation in natural non-model organisms. It was extensively discussed how the new perspectives offered by genomics could be applied to solve theoretical and practical ecological and conservation genetics problems. The School has provided an updated overview on major genomic methods by introducing several case-studies in ecological genomics. In this way it has stimulated the audience to develop new perspectives in the application of genomic methods in studies of natural plant and animal populations. Participants were 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 function in evolution, ecology and conservation.

The questions addressed during the summer school have generated important scientific spin-offs for the whole field of ecology and evolution. This is an important achievement as there is a need for detailed studies on how variation at the level of genes and gene regulation translates, through developmental and physiological processes, into phenotypic variation for ecologically important traits. To obtain this information we need European groups with different expertises to work together, and this school should have contributed to that. The knowledge acquired from the School should also provide crucial information for many young researchers, which should lead to better insights into the possible consequences of climate induced changes such as habitat fragmentation, extinction risk, or the dynamics of adaptation of species to new environmental conditions.

The main challenges of Ecological Genomics in the near future discussed during the summer school were:

- 1) Taking advantage of modern genomic tools such as the variety of recently developed "-omics" approaches
- 2) Bridging the gap between the statistical and biological models
- 3) Transition from neutral markers to functional variation
- 4) New approaches for species delimitation and identification based on population genetic principles (as opposed to phylogenetic methods).
- 5) Find new “omics” ways to use a cross-disciplinary approach to increase our understanding of thermal adaptation in space and time in poikilotherms and small homeotherms.
- 6) The study of speciation mechanisms: genomics allow to search efficiently for the genetic systems responsible for reproductive isolation.
- 7) Bringing together people with different expertise within this field, and trying to improve our understanding of the genetic and physiological basis of thermal adaptation, from individual molecules and cells to whole ecological systems.

BUDGET

Categories

Details

Euro

Transport	Travel of invited speakers, transport of all participants from Bologna to Bertinoro,	8.268,07
Accommodation	Participants (double and single rooms), Invited speakers (single rooms)	14.669,40
Food	Lunches and dinners, coffe breaks, ceremonial evening	4.492,30
Cost of extra labour of Bertinoro staff and costs of Summer school organization	Printing of conference materials, insurance, administrative costs	1.230,00
TOTAL		28.659,77