Science Meeting – Scientific Report

Spring School

"Landscape genetics in transition to landscape genomics: challenges and opportunities to explore NGS data in a spatially explicit context"

Application Reference N°: 5028

1) <u>SUMMARY</u>

Spring School
"Landscape genetics in transition to landscape genomics: challenges and opportunities to explore NGS data in a spatially explicit context"

VENUE: The University Residential Centre of Bertinoro (Ce.U.B.), ITALY
DATE: 23 March - 29 March 2014
ORGANIZING COMMITTEE: *Prof Ettore Randi* (National Institute for Environmental Protection and Research, Italy) & *Dr. Aritz Ruiz-Gonzalez* (National Institute for Environmental Protection and Research, Italy &University of the Basque Country, Spain)

Landscape genomics is an exciting and rapidly growing discipline that combines genome-wide patterns of genetic variation, large environmental data sets and spatial statistical methods, to improve our understanding of both species ecology and ecological adaptation. The spring school *"Landscape genetics in transition to landscape genomics: challenges and opportunities to explore NGS data in a spatially explicit context"* aimed to provide an updated discussion of landscape genetics analysis in the new genomic era, guided by experts in genomics, spatial statistical analyses, and population genetics. The school included an assortment of conceptual, methodological and applied contributions, followed by hands-on training in order to provide an overview of novel approaches for analysing the environmental context of genomic variation, wit special emphasize in a conservation context.

The Landscape Genomics School took place in March 2014 in the "University Residential Centre of Bertinoro (Ce.U.B.), Italy. The event , organized by Prof. Ettore Randi (National Institute for Environmental Protection and Research , ISPRA) and Dr. Aritz Ruiz González (University of the Basque Country, UPV/EHU & National Institute for Environmental Protection and Research , ISPRA), consisted in five full-day sessions with an adequate balance between theory and computer practice. Thirty students from 14 EU countries attended the school and were taught by 4 experienced researchers with complementary skills in the multidisciplinary field of landscape genetics and genomics (Dr. Samuel Cushman-USDA Forest Service, Rocky Mountain Research Station. USA; Dr. Stephane Joost -Laboratory of Geographic Information Systems (LASIG), School of Architecture Civil and Environmental Engineering (ENAC). Switzerland; Dr. Robert Ekblom - Department of Evolutionary Biology. Evolutionary Biology Centre, EBC . Uppsala University. Sweden; Dr. Gernot Segelbacher - Wildlife Ecology and Management. University of Freiburg. Germany)

2) DESCRIPTION OF THE SCIENTIFIC CONTENT OF AND DISCUSSIONS AT THE EVENT

The spring school "*Landscape genetics in transition to landscape genomics: challenges and opportunities to explore NGS data in a spatially explicit context*" aimed to provide an updated discussion of landscape genetics analyses in the new genomic era, guided by leading researchers in genomics, spatial statistical analyses, and population genetics.

The specific objectives of this school were:

1) Promote better understanding links between the novel genomic information and spatially explicit analysis, in order to facilitate interdisciplinary communication and education in the new emerging field of landscape genomics

2) Provide an update of the current state of the landscape genetics field and the major challenges and opportunities by the incorporation NGS data.

3) Explore recent analytical advances in NGS of non-model species and gain experience about data collection, production and analysis strategies in population genomics.

4) Provide hands-on training for analysing the environmental context of genetic (neutral and adaptive) variation through spatial statistic and simulation modelling using the most recent methods on landscape genetics/genomics.

5) Address current research challenges and explore new opportunities to improve future landscape genomics applications, and positively contribute to the future growth of this promising field.

The Spring school was aimed at early-career researchers (PhD students, postdoctoral researchers, but also faculty who wish to gain training in this area) who have some background knowledge in population genetics and landscape genetics but who have an interest in improving their skills with regards to the analysis of the environmental context of genome-wide genetic variation obtained from novel NGS data. Among the 120 received applications. 30 participants from 14 EU countries were selected based on CV, motivation letter, applicants' project significance in the field of landscape genetics / genomics and date of registration. Priority was given to applicants who come from contributing members organizations of the ESF ConGenomics programme. Overall a balanced geographical representation, research experience, sex ratio among the participants, and broad project organism taxonomy coverage was ensured (see annexes 4b and 4c for further details).

During this spring school, novel approaches for analysing the ecological and spatial context of genome-wide genetic variation were discussed in different sessions. Each session was lead by different experts in the specific topic covered, which presented an assortment of conceptual, methodological and applied contributions, followed by hands-on training (all the hands-on training exercises were developed on a full equipped computer room -30 PCs- with all the software applications pre-installed by the organizers in advance)

Session 1: FROM LANDSCAPE GENETICS TO LANDSCAPE GENOMICS (Monday 24 March)

A field that combines molecular markers, genetics and landscape structure was first described by Manel et al. (2003). In the following ten years the field has rapidly evolved (Storfer et al. 2010; Andrew et al. 2013; Manel et al. 2014) and has been the subject of many review articles (e.g. Storfer et al. 2007, 2010; Holderegger & Wagner 2008; Balkenhol et al. 2009a; 2010; Segelbacher et al. 2010; Sork & Waits 2010) and methods papers (Balkenhol et al. 2009b, 2011; Cushman & Landguth 2010a,b; Shirk & Cushman 2011; Spear et al. 2010; Cushman et al. 2013).

Landscape genetics has traditionally used a few selectively neutral genetic markers and focused on the impact of landscape features in spatial patterns of genetic variation (Storfer et a. 2010; Andrew et al. 2013). However, the recent availability of genome-wide sequences, even for non-model species, due to emerging next-generation sequencing (NGS) tools, has facilitated the transition from landscape genetics to landscape genomics (Joost et al. 2007; 2013; Schwartz et al. 2010; Schoville et al. 2012; Andrew et al. 2013).

*During the introductory session **Dr. Stephane Joost** provided a comprehensive overview about the state of the art and the challenges for a proper transition from landscape genetics to landscape genomics ("Ten years of landscape genetics: where are we now? and "Landscape genomics: a brief perspective")*

While landscape genomics is, in one sense, simply landscape genetics with lots of data (> precision and < variance), its qualitatively different nature (adaptive, potentially non-independent), and analytical approaches associated with these data are different enough to produce a profoundly different field (Joost et al. 2007, 2013; Schwartz et al. 2010; Schoville et al. 2012; Andrew et al. 2013). Thus, landscape genomics has been proposed as a framework for studying adaptive and neutral genomic variation at the population/indivual level in a spatially explicit context (Joost et al. 2007; Schoville et al. 2012). This framework merges large environmental data sets, spatial statistical methods, and high-resolution sampling of genomic variation to improve our understanding of both species ecology and ecological adaptation (Manel et al. 2010; Schoville et al. 2012; Andrew et al. 2013).

*During the first day hands-on training session **Dr. Joost** focused on landscape genomic analysis of large datasets by presenting a detailed computer exercisebased on a real case-study. The practical session used the open access GIS software (Quantum GIS and OpenGeoDa) and a specific landscape genomic software implementing a correlative approach to detect signatures of natural selection and spatial statistics named Samβada.*

Session 2: SPATIALLY EXPLICIT MODELS FOR LANDSCAPE GENETICS AND GENOMICS (Tuesday 25 March & Wednesday 26 March)

A major scientific contribution of landscape genetics/genomics is the provision of a valuable analytical framework for testing the influence of landscape structure and composition on dispersal and gene flow (Manel et al. 2003; Balkenhol et al. 2009; Holderegger & Gugerli 2012; Manel et al. 2014). Thus, landscape genetic approaches have valuable applications in conservation biology and landscape planning (Segelbacher et al. 2010; Luque et al. 2012), by empirically testing and optimizing resistance maps (Epps et al. 2007; Shirk et al. 2010; Wasserman et al. 2010; Short Bull et al. 2011) in order to evaluate whether landscape and environmental changes have interfered with gene movement (Cushman et al. 2013) or the presence of corridors facilitated it (Epps et al. 2007). In addition, the main questions in this field require the development and application of sophisticated simulation tools to explore gene flow, genetic drift, mutation and natural selection in landscapes with a broad range of spatial and temporal complexities.

*The second and third day of the school was guided by **Dr. Samuel Cushman**, aiming to present the main and the most updated spatially explicit models for landscape genetics and genomic studies. The practical exercises focused on teaching methods to analyze and interpret empirical landscape genetic data and spatial heterogeneity of genetic diversity (sGD software). More advanced exercises were conducted during the third day by dealing with simulation modeling of landscape genetic processes (CDPOP software), and modeling population connectivity (UNICOR software).*

Session 3: PRODUCING AND ANALYSING NGS DATA OF NON-MODEL SPECIES (Thursday 27 March)

The ongoing NGS revolution is transforming genotyping strategies for landscape genomics studies by providing new opportunities for large-scale SNP discovery and genotyping (Ekblom & Galindo 2010, Seeb et al. 2011; Hohenlohe et al. 2012) and the simultaneous study of tens-to-hundreds of markers, ideally including markers in candidate adaptive genes (genes under selection) (Joost et al. 2007; Schoville et al. 2012; Hohenlohe et al. 2012).

*During the fourth day of the school **Dr. Robert Ekblom** provided a general overview about NGS genome analysis in non-model species (genome and transcriptome sequencing), with different hands-on training sessions dealing with important topics to properly handle NGS data for further landscape and population genetics studies (Microsatellite identification of assembled transcriptome data; Identifying differentially expressed genes in RNA-Seq data; Illumina read mapping; SNP calling on genome sequencing data; Population genomics analyses of SNP data sets).*

Session 4: LANDSCAPE GENETICS IN TRANSITION TO LANDSCAPE GENOMICS: CHALLENGES AND OPPORTUNITIES IN A CONSERVATION CONTEXT

With the increasing sophistication of computational and analytical tools in population genomics together with the emergence of large genomic resources and environmental data sets, it is now possible to identify ecological factors that influence genetic diversity patterns, including both natural and anthropogenic variables driving genetic adaptation (Lowry, 2010; Manel et al. 2010; Parisod and Holderegger 2012; Schoville et al. 2012) Consequently, landscape genomics can add another dimension to decision-making and prediction in conservation biology (Funk et al. 2012), particularly in modeling potential adaptive responses of conservation concern species to global change (Schoville et al. 2012).

*The last day of the school, guided by **Dr. Gernot Segelbacher**, was focused on presentations of students' scientific projects, followed by discussions and suggestions for future progress, with special emphasize on the role of landscape genetics in a conservation context. The introductory talk entitled "Landscape genetics in transition to landscape genomics: challenges and opportunities in a conservation context" provided the framework for the school closure "Round Table" where all the school participants and lecturers exchanges ideas and suggestions about the main research challenges and new opportunities to improve future landscape genomics applications.*

3) ASSESSMENT OF THE RESULTS AND IMPACT OF THE EVENT ON THE FUTURE DIRECTIONS OF THE FIELD

This spring school gave a comprehensive overview about the main challenges and opportunities in the rapidly growing discipline of landscape genomics. Undoubtedly, this event has provided an excellent opportunity to introduce young scientists to the complex field of landscape genomics and familiarize them with the application of novel analyses from different disciplines that merge within this novel field. Moreover, the school provided a unique opportunity to meet together talented students and leading scientist to promote better understanding links between the novel genomic information obtained by NGS techniques and spatially explicit analysis, in order to facilitate interdisciplinary communication and education in this emerging field, with positive outcomes for all groups.

The students received the most updated information about the present state of the art of landscape genetics and genomic analyses opening new research opportunities field with the more routinely application of large scale datasets produced by NGS methods. 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 and promote future scientific collaborations between European groups with different capacities.

The school has provided an assortment of major conceptual, methodological and applied contributions, followed by hands-on training sessions introducing case-studies. The school was clearly devoted to the practical aspects of data analyses of landscape genetics and genomics data. Hands-on training sessions clearly stimulated the audience to understand real case-studies and facilitate future applications of novel approaches in the study of natural plant and animal populations in Europe. In order to further explore the content of the course and promote future utility by other researchers, a Dropbox folder with all the school material (most relevant bibliography in the field, computer hands-outs together with software and datasets and speaker's and participant's presentations).was created and shared at the end of the event

Based on positive feedback, both students and lecturers expressed the willingness to organize and/or participate on similar schools/courses that further explore the developments in the field in the next years. The outcome of the event was seen as very helpful in further development of specific skills that are going to be applied in the respective research projects of the participants.

The questions addressed during the school has generated important scientific spin-offs for further improvement and development of landscape genomics, which is an important achievement as

there is a need for detailed studies on how the environmental context interact with genomic variation, specially for conservation concern species. During the whole week, it has been extensively discussed how the new perspectives offered by landscape genomics could be applied to solve theoretical and practical ecological and conservation problems. Future landscape genomics analyses will allow the identification of ecological factors that influence genetic diversity patterns, including both natural and anthropogenic variables driving genetic adaptation. Consequently, landscape genomics add another dimension to decision-making and prediction in conservation biology, particularly in modeling potential adaptive responses of conservation concern species to global change

Overall, this school has facilitated addressing current research challenges and explores new opportunities to improve future landscape genomics applications, and consequently positively contribute to the future growth of this promising field. The rapid production of sufficient data with recent technologies—be it landscape or genetics—may no longer be a bottleneck in landscape genetics. However, the adequate merging of genomics with landscape genetics includes more than just the incorporation of a new genomic toolbox. Collabrative and interdisciplinary working-groups are essentials for sucessful and comprehensive landscape genomic studies, Thus, a comprehensive transfer of genomic knowledge into landscape genetics approaches is urgently needed, together with an increasing cross talk between the different disciplines merging in this interdisciplinary field (molecular ecology, geo-environmental sciences and bioinformatics), in order to develop a roadmap for the future of landscape genomics.

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4) ANNEXES

4A) PROGRAMME OF THE MEETING

4B) FULL LIST OF PARTICIPANTS

4c) FULL LIST OF PARTICIPANT PRESENTATIONS

4d) PHOTOGRAPH OF THE SCHOOL PARTICIPANTS AT CEUB

ANNEX 4A: PROGRAMME OF THE MEETING

- **Sunday 23 March**

ARRIVAL AND OPENING OF THE SCHOOL *

10:00- 20:00* Reception and registration of participants - Hotel Fontanelle (Via Loreta, 27, Fratta Terme) http://www.hotelfontanelle.it/hotel-1.html

20:00- 20:30 Introductory talk about the aims and scope of the spring school on "***Landscape genetics in transition to landscape genomics: challenges and opportunities to explore NGS data in a spatially explicit context***"   *Prof. Ettore Randi & Dr. Aritz Ruiz-Gonzalez*

20:30 Welcome Buffet

> ** On Sunday 23 March (Late Morning & Afternoon) it will be available a Shuttle bus from Bologna airport to the School venue. The Reception and registration will be open until 22:00, but we encourage arriving before 20:00.*

- **Monday 24 March**

FROM LANDSCAPE GENETICS TO LANDSCAPE GENOMICS

Dr. Stephane Joost

8:30-9:00 - Ten years of landscape genetics: where are we now?

9:00-9:30 – Landscape genomics: a brief perspective

9:30:-9:45 - Coffee break

DETECTION OF GENOMIC REGIONS UNDER SELECTION IN LANDSCAPE GENOMICS

Dr. Stephane Joost

9:45- 10:45 - Designing a landscape genomic approach

10:45-12:15 - Landscape genomics for detection of candidate loci under selection: promises and pitfalls

12:15-13:30 - SamBada integrated software for landscape genomic analysis of large datasets (*Hands-on training*)

13:30- 14:30 - Lunch

14:30-16:30 - SamBada integrated software for landscape genomic analysis of large datasets (*Hands-on training*)

16:30-16:45 - Coffee break

16:45-18:30 - SamBada integrated software for landscape genomic analysis of large datasets (*Hands-on training*)

20:00-20:30 - Dinner

- **Tuesday 25 March**

SPATIALLY EXPLICIT MODELS FOR LANDSCAPE GENETICS AND GENOMICS (1)

Dr. Samuel Cushman

9:00-10:30 - Analysis of empirical landscape genetic data (Introductory Lecture)

10:30-11:00 - *Coffee break*

11:00-13:30 - Analysis of empirical landscape genetic data and landscape genetic modeling with R (*Hands-on training)*

13:30- 15:30 - *Lunch*

15:30-17:30 - Analysis of spatial heterogeneity of genetic diversity with sGD (*Hands-on training)*

17:30-18:00 - *Coffee break*

18:00-20:00 - Analysis of spatial heterogeneity of genetic diversity with sGD (*Hands-on training)*

20:30-21:30 - *Dinner*

- **Wednesday 26 March**

SPATIALLY EXPLICIT MODELS FOR LANDSCAPE GENETICS AND GENOMICS (2)

Dr. Samuel Cushman

9:00-10:30 - Simulation of gene flow with CDPOP software (*Hands-on training)*

10:30-11:00 - *Coffee break*

11:00-13:30 - Simulation of gene flow with CDPOP software (*Hands-on training)*

13:30- 15:30 -*Lunch*

15:30-17:30 - Modelling population connectivity with UNICOR (Hands-on training)

17:30-18:00 - *Coffee break*

18:00-20:00 - Modelling population connectivity with UNICOR (Hands-on training)

20:30-21:30 - *Dinner*

- **Thursday 27 March**

PRODUCING AND ANALYSING NGS DATA OF NON-MODEL SPECIES

Dr. Robert Ekblom

9:00-10:00 – NGS genome analysis in non-model species: a general overview -Genome sequencing-

10:00-10:15 - Coffee break

10:15-11:15 – NGS trascriptome analysis in non-model species: a general overview –Trascriptome sequencing-

11:15 -13:00 - Microsatellite identification of assembled transcriptome data *(Hands-on training)*

13:00- 14:30 - Lunch

14:30-16:00 Identifying differentially expressed genes in RNA-Seq data *(Hands-on training)*

16:00-16:15 Coffee break

16:15- 18:30 - Illumina read mapping and SNP calling on genome sequencing data *(Hands-on training)*

18:30-20:30 Population genetic analyses of SNP data *(Hands-on training)*

20:30-21:30 - Dinner

- **Friday 28 March**

LANDSCAPE GENETICS IN TRANSITION TO LANDSCAPE GENOMICS: CHALLENGES AND OPPORTUNITIES IN A CONSERVATION CONTEXT

Dr. Gernot Segelbacher

9:00-10:30 - Landscape genetics in transition to landscape genomics: challenges and opportunities n a conservation context (*Introductory talk*)

10:30-11:00 - Coffee break

11:00-13:30 - Brief presentations (<5min) of school participant's research projects. *Open discussion*.

13:30- 15:30 *Lunch*

15:30- 17:30 - Brief presentations (<5min) of school participant's research projects. *Open discussion*.

17:30 -19:00 - Round table: Exchange of ideas and suggestions about research challenges and new opportunities to improve future landscape genomics applications. This session will be guided by Dr. Gernot Segelbacher and with the participation of Dr. Samuel Cushman, Dr. Robert Ekblom and Dr. Ettore Randi and all the school students.

20:00 Workshop Closing dinner

- **Saturday 29 March**

DEPARTURE*

* On Saturday 29 (Morning) it will be available a Shuttle bus from the School venue to Bologna airport.

ANNEX 4B) FULL LIST OF PARTICIPANTS

Surname	Name	Current position	Country	Affiliation	e-mail
Selected Participants					
Gonzalez	**Javier**	Lecturer	Germany	Heidelberg University	j.gonzalez@uni-heidelberg.de
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Fior	Simone	Postdoc	Switzerland	ETH Zurich - Plant Ecological Genetics, Institute of Integrative Biology (IBZ)	simone.fior@env.ethz.ch
Cox	Karen	Researcher	Belgium	Instituut voor Natuur- en Bosonderzoek (INBO) - Research Institute for Nature and Forest -	Karen.cox@inbo.be
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Lecturers & Organizing Committee					
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ANNEX 4c) FULL LIST OF PARTICIPANT PRESENTATIONS

- **Anna Maria Addamo**, Museo Nacional de Ciencias Naturales, MNCN-CSIC, Spain (PhD student)
Ttitle: **Systematics, phylogeography and seascape genetics of deep-sea coral *Desmophyllum dianthus* (Anthozoa, Hexacorallia).**

- **Javier Gonzalez**, Heidelberg University, Germany (Lecturer)
Title: **Phylogeography and landscape genetics of Austral temperate rainforest bird species.**

- Paloma Torroba, Forest Research Centre, INIA, Spain (PhD Student)
Title: **Adaptive processes, environmental gradients and demography in the *Symphonia* genus.**

- **Katherine Hayden**, INRA / Université de Lorraine, France (Postdoc)
Title: **Adaptation of poplar rust to the poplar varietal landscape.**

- **Joost de Jong**, Resource Ecology Group, Wageningen University, The Netherlands (PhD student)
Ttitle: **Landscape genomics of wild board (*Sus scrofa*) in Europe using the porcine SNP60 beadchip.**

- **Rachael Dudaniec**, Lund University, Sweden (Postdoc)
Title 1: **Landscape genomics of blue tailed dasemflies (*Ischnura elegans*)** using a GBS approach.
Title 2: **Making resistance surfaces for landscape genetic studies.**

- **Valentina Rovelli**, Roma Tre University & ISPRA, Italy (PhD student)
Title: **Applying genetic and genomic methodologies for the conservation of *Euproctus platycephalus*, *Salamandrina perspicillata* and *Rana italica.***

- **Marcos Peso**, Museo Nacional de Ciencias Naturales – MNCN – CSIC , Spain (PhD student)
Title: **Spatial genetic diversity and gene flow of *Rana pyrenaica* :evolution under global change scenarios.**

- **Luca Cornetti**, Fondazione Edmund Mach, Department of Biodiversity and Molecular Ecology, Conservation Genetics,Italy (PhD student)
Title: **Application of Rad-tag sequencing to investigate the evolutionary transition from oviparity to viviparity in squamate reptile (*Zootoca vivipara*).**

- **Pietro Milanesi**, Laboratorio di Genetica, ISPRA & Università di Bologna, Italy (PhD student)
Title: **Landscape ecology and genetics of the wolf in Italy.**

- **Urtzi Laconcha**, AZTI Tecnalia Tecnology Centre, Marine Research Division, Spain (PhD student)
Title: **World-wide population structure of Albacore and its temporal genetic structure in the Bay of Biscay using novel SNPs markers.**

- **Mafalda Costa**, Centro de Biologia Ambiental, Faculdade de Ciências da Universidade de Lisboa, Portugal. OnE & Organisms and Environment Division, School of Biosciences, Cardiff University, United Kingdom. (PhD student).
Title: **Phylogeography and hybridisation in the European polecat (*Mustela putorius*).**

- **Aapo Kahilainen**, University of Jyväskylä, Finland(PhD student)
Title: **Interactions and patterns between species and genetic diversity.**

- **Paolo Franchini**, University of Konstanz, Germany(Postdoc)
Title: **Genomic bases of phenotypic diversification in cichlid fish.**

- **Miguel Camacho**, Doñana Biological Station-CSIC, Spain (PhD student)
Title: **Adaptatation and Diversification of Small Mammals in Sundaland.**

- **Simone Fior**, ETH Zurich, Plant Ecological Genetics, Institute of Integrative Biology (IBZ), Switzerland (Postdoc)
Title: **Altitudinal adaptation in carnation (*Dianthus*) using a genome wide-approach.**

- **Karen Cox**, Instituut voor Natuur- en Bosonderzoek (INBO) - Research Institute for Nature and Forest-, Belgium (Researcher)
Title: **Landscape genomics of the stone marten (*Martes foina*).**

- **Astrid Vik Stronen**, Department of Biotechnology, Chemistry and Environmental Engineering - Aalborg University, Denmark (Postdoc)
Title: **Population structure and environmental adaptation of European wolf using 67K SNPs.**

- **Jelena Pantel**, Laboratory of Aquatic Ecology, Evolution, and Conservation, KU Leuven, Belgium (Postdoc)
Title: **Population genetic and community ecological responses to environmental variability in freshwater ponds.**

- **Cecile Vanpè**, UMR CNRS 5558 - LBBE, "Biométrie et Biologie évolutive", France (Postdoc)
Title: **Roe deer behavioural Plasticity and Adaptation To landscape Changes.**

- **Soraia Barbosa**, CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos /InBIO Laboratório Associado, Universidade do Porto, Portugal (PhD student)
Title: **Using landscape genetics and genomics to assess the distribution and connectivity of two endangered voles in Iberia.**

 -**Vaclav Gvozik**, Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Czech Republic (Researcher)
Title: **Phylogeography of European tree frogs (Hyla sp.) in Europe.**

- **Mariona Ferrandiz-Rovira**, Biométrie et Biologie Évolutive - Univ. de Lyon, France (PhD student)
Title: **Mate choice for major histocompatibility complex: an integrative approach**.

- **Janne Swaegers**, Laboratory of Aquatic Ecology, Evolution and Conservation. Univ. Leuven, Belgium (PhD student)
Title: **Genetic consequences of rapid range expansion in a damselfly using a GBS approach.**

- **Adriana Villamor**, Laboratorio di Ecologia Sperimentale, Centro Interdipartimentale di Ricerca per le Scienze Ambientali in Ravenna - Università degli Studi di Bologna, Italy (Postdoc)
Title: A m**ultispecies Rad-seq approach: General connectivity patterns and marker development.**

- **Anita Norman**, Department of Fish, Wildlife and Environmental Studies, Swedish University of Agricultural Sciences, Sweden (PhD student)
Title: **Brown bear (*Ursus arctos*) genomics.**

 -**Martina Temunovic**, Department of Forest Genetics, Dendrology and Botany, Faculty of Forestry, University of Zagreb, Croatia (Postdoc)
Title: **Genetics, ecology, distribution, evolution and hybridization of tree genus *Fraxinus* (Oleaceae) in Europe.**

- **Alexandra Jansen van Rensburg**, University of Zurich, Switzerland (PhD student)
Title: **Gene flow and selection in *Rana temporaria.***

- **Lies Ghysels**, Terrestrial Ecology Lab, Ghent Universit, Belgium (PhD student)
Title: **Pathogen-driven variation in MHC genes in natural populations under stress: house sparrows as a model**

ANNEX 4c) PHOTOGRAPH OF THE SCHOOL PARTICIPANTS AT CEUB

Spring School

Landscape genetics in transition to landscape genomics:
Challenges and opportunities to explore NGS data in a spatially explicit context

The University Residential Centre of Bertinoro (Ce.U.B.), ITALY
23-29 March, 2014

EUROPEAN SCIENCE FOUNDATION
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