

Third GLOBALDIV Summer School

6-9 September 2010

By

EAAP, Mr Andrea Rosati and UCSC, Prof. Paolo Ajmone Marsan

The third edition of the GLOBALDIV Summer School was hosted at the Università Cattolica del Sacro Cuore in Piacenza, Italy, on September 6-9, 2010.

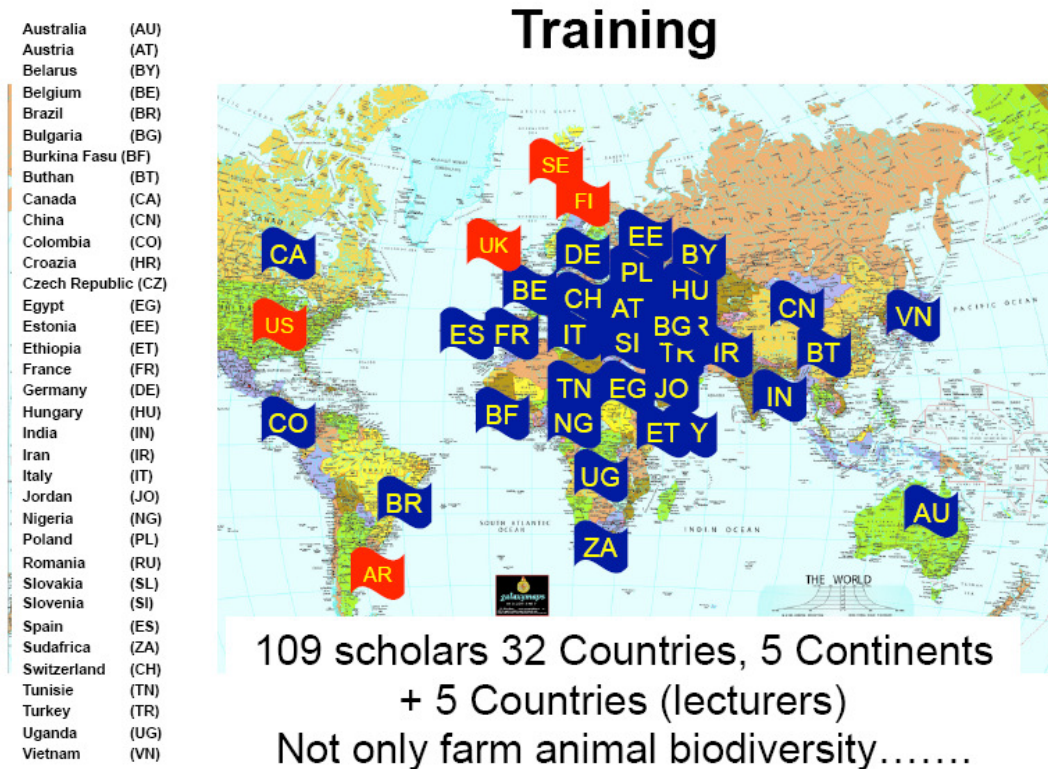
The 2010 School focused on the use of genomics for the characterization of genetic resources and on methods and software for large molecular data-set management and analysis. In addition, an update has been given on conservation strategy applied to wildlife that may be of interest for livestock management.

To stimulate interaction, students presented their own case studies.



http://www.globaldiv.eu/Summer_School_2010/Pictures_Participants.html

A total of 30 well qualified and motivated graduate students, post-docs and young researchers from 18 different Countries were admitted to the School. In the three editions of the Summer School, Globaldiv trained and fostered contacts between 109 young researchers from 32 Countries, spanning all continents (see figure 1)



As in 2008 and in 2009, also this year the atmosphere of the course was extremely friendly and collaborative, with active participation of the trainees and complete availability from the lecturers.

The ESF GENOMIC RESOURCES project participated in the co-organization of 2010 edition by granting 350 Euros to 4 students from Spain, Italy, Slovenia (Austria) and Chezh Republic and by sponsoring the lecturers given by Dr. Carl Rubin, Dr.Miika Tapio, Dr.Timo Tiirikka, Prof.Niccolò Maciotta, Prof.Johan Soelkner and Prof.Ettore Randi

The programme was the following:

GLOBALDIV SUMMER SCHOOL 2010 PROGRAMME – 6-9 SEPT 2010					
	Monday 6th, Sept 2010	Tuesday, 7th Sept 2010	Wednesday 8th Sept 2010	Thursday 9th, Sept 2010	Friday 10th Sept 2010
8,30-10,30	Opening - Paolo Ajmone Marsan (8,30-9,00)	Introduction to genomics	8,30 - 10,00 - What can be done with whole genome sequence data	Conservation of biodiversity: lesson from wildlife	GLOBALDIV MEETING (only for partners and experts) NOT OPEN FOR STUDENTS
	A global view of wildlife biodiversity				
LECTURER	Mika Tapio (FI)	Paolo Ajmone Marsan (IT)	Timo Tiirikka (FI)	Godfrey Hewitt (UK)	
11,00-13,00	Livestock biodiversity	Large SNP datasets to estimate population structure and inbreeding	10,30-12,00 - What can be done with whole genome sequence data	Convergence between wildlife and livestock conservation	GLOBALDIV MEETING (only for partners and experts) NOT OPEN FOR STUDENTS
LECTURER	Jianlin Han (ILRI and CAAS)	Johan Solkner (AU)	Carl Rubin (SE)	Pierre Taberlet (FR)	
AFTERNOON					
	Monday 6th, Sept 2010	Tuesday, 7th Sept 2010	Wednesday 8th Sept 2010	Thursday 9th, Sept 2010	Friday 11th Sept 2010
14,00-16,00	Population genetics recall	SNP data analysis and opportunities	13,30-15,00 software session	students presentation	GLOBALDIV MEETING (only for partners and experts) NOT OPEN FOR STUDENTS
LECTURER	Ettore Randi (IT)	Ezequiel Luis Nicolazzi (IT)	Carl Rubin (SE)		
16,30-18,30	Quantitative genetics recall	interrogate genomes with bioinformatics	15,00-16,30 software session	students presentation	
LECTURER	Nicola Macciotta (IT)	Raffaele Mazza (IT)	17,00-18,30 - software session		
			Ezequiel Luis Nicolazzi (IT)	Conclusions and perspectives Paolo Ajmone Marsan (18,30-19,00)	

SYLLABUS AND LECTURERS PROFILE

Monday, 6th September

“A global view of wildlife biodiversity” - M. Tapio, MTT, Finland – COURSE SPONSORED BY ESF GENOMIC RESOURCES

Miika Tapio is a molecular population geneticist interested in why populations, individual organisms, or genes or genomes have their current (genetic) form, and how that form changes over time. In practice, this comes down to inferring population or gene history and searching evidence for selection at DNA level, and potentially combining DNA variation with phenotypic variation in real population (i.e. association or LD mapping). He is enthusiastic about improving maintenance of important genetic resources. Apart from population history or direct maintenance issues, two crucial questions there are what are we maintaining and for what use. My developing world experience has made it very clear that the main goal has to be sustainable increase in food production with minimized environmental and social costs.

Short syllabus of the course

The lecture will introduce the concept of biodiversity or biological diversity focusing on wildlife and the impact of agriculture on wildlife biodiversity. Biodiversity contains everything from diversity of ecosystems and ecological processes to diversity of genes. Especially during last decennia the trend has been the rapid erosion of biodiversity. The drivers of this trend stem from the needs of growing human population that is projected to increase, while availability of many non-renewable resources is not guaranteed. This might increase the pressure on other resources and lead to further erosion of diversity.

Second part of the lecture will focus on a general level why and how biodiversity is measured. There is no single approach to measure it, which complicates discussions especially between academia and users of biodiversity. With few simple modifications on how results are communicated researchers can improve the chance that the results are taken into account by policy makers. The last part of the lecture discusses more closely biodiversity that is either within the agricultural systems or is associated with those systems. This includes diversity of agricultural systems themselves.

“Livestock biodiversity” - J. Han – ILRI, China

Dr. Han Jianlin has strong interests and rich experience in livestock and poultry genetic diversity as well as functional genomics towards disease resistance. In 2001, he joined ILRI working on the genetic characterization of indigenous animal genetic resources in Asia and Africa.

Short syllabus of the course

There has been a significant explosion in our knowledge on the origin and distribution of biodiversity of livestock and poultry genetic resources through the intensive use of molecular tools in the past three decades. These studies revealed remarkably complex pictures of the origins of major livestock and poultry species and subsequently of their dispersal patterns to the world following the expansion of farmer societies, human migrations and trading. Mitochondrial DNA studies have not only revealed the ancestral wild species of most livestock and poultry species but also the multiple domestication and/or maternal introgression events. The large number of mitochondrial control region sequences provided new and unique opportunities to untangle the distribution of maternal diversity and to compare the patterns of domestication and migration among major livestock and poultry species. Y-specific markers similarly revealed multiple male lineages and questioned the extrapolation of history of livestock from single genes. Autosomal microsatellite markers applied at large geographical scales and on geo-referenced indigenous livestock populations allowed mapping of the continental distribution of livestock and poultry biodiversity. The legacy of these molecular studies has not only improved our archaeozoological views on the origin of livestock and poultry but also the design of conservation and utilization strategies of livestock and poultry genetic resources.

“Population genetics recall” - E. Randi - ISPRA, Italy - COURSE SPONSORED BY ESF GENOMIC RESOURCES

Ettore Randi, research director, is head of the Laboratory of genetics at the Italian Environmental Agency (ISPRA), Ozzano Emilia, Bologna. His research activity focus on phylogenetics, phylogeography and population genetics with specialization in conservation genetics of avian and mammals species. His research group is involved in long term monitoring programmes of endangered carnivores using non-invasive methods. They are working on the application of genomic concepts and tools to wildlife conservation.

Short syllabus of the course

Population genetics is undergoing a period of great changes, being definitely gone from a largely theoretical discipline in a science which sees wide applications in many fields of biodiversity conservation, agriculture and medicine. In my presentation, I will summarize some issues of classical population genetics, which was mainly theoretical, describing its transition to the empirical phase (marked by the application of electrophoretic methods), until the new procedures (coalescent and Bayesian modelling) implemented for data analysis,

and, finally, population genomics. Advances in population genetics are supported by the increasing potential of molecular genetics, which has developed and continues to develop new and powerful methods of analysis of genetic variability within and among population at decreasing costs. New statistical methods now enable to build more realistic models for the analysis of the main parameters of within-population variability and divergence between-populations.

“The evolution of diversity: lessons for conservation” –

G. Hewitt - University of East Anglia, UK

Godfrey Hewitt is now Professor Emeritus at the University of East Anglia preceded by periods in the University of Birmingham (1959-65), University of California (1965-66) and sabbatical at Australian National University (1973-74). He has studied the geographical patterns of genetic variation found in many organisms using classic and molecular methods, including hybrid zones and latterly Quaternary phylogeography to illuminate the genetic consequences of changing climates. He is a Highly Cited Author in Web of Science and Senior Editor for Molecular Ecology.

Short syllabus of the course

Natural biodiversity is generally high in the tropics and diminishes towards the poles, and there are several theories that attempt to explain this pattern. Combining such high species richness with threats from human activities to its existence allowed the definition of some 25 areas as “hotspots” (Meyers et al Nature 2000); the Mediterranean region is one of these. Using this region as an example this lecture will ask “How did this great biodiversity come to exist? What are the mechanisms involved in its generation and structure? What can these processes tell us about conservation in wild and domestic species?”

We shall consider studies in three diverse fields – plate tectonics, Quaternary climate and phylogeography – which have advanced greatly in recent times and combined provide an increasingly clear picture of how the last few million years have moved and moulded the ranges and genomes of present day species. (Hewitt PTRoySoc 2004). With the collision of African and European plates the emergent land in the Mediterranean region varied and moved, so the peninsulas of Iberia, Italy, Greece and Balkans, and Turkey were dynamic and composite. The ranges of the Pyrenees, Alps, Carpathians and Atlas were formed. The climate cooled progressively from the Eocene optimum (50My) and the Quaternary (2My) has seen the periodic ice ages. The effects of these on the distribution and genetic structure of species will be discussed in some detail in the light of phylogeographic information. The role of southern Europe as glacial refugia for interglacial colonisation to produce hybridization in northern Europe, and that of Mediterranean peninsulas to produce and accumulate divergence will be emphasised.

We see that divergence within and between species has developed in certain locations through long time periods with geographic and climatic causes. This is applicable to other parts of the world. Such great biodiversity in these places would require a long time to regenerate, if lost, and we may gauge this time. Climatic oscillations have caused repeated range changes with range

fragmentation, population expansions and contractions. In many (all?) species, populations will have suffered great reductions in size (bottlenecks, pioneers) and hence loss of alleles (drift, inbreeding). Expansions in range cause hybridization between diverged genomes – hybrid zones – with enhanced allelic variation. However, the hybrids produced are usually less fit than parents, but such hybridization can sometimes produce novel genetic combinations – even new species.

A few examples of fragmentation, small population size, and hybridization in wild animals will be used to illustrate these genetic effects relevant to conservation (Glanville fritillary, cheetah, lions, Florida panther), and the Holocene phylogeography of domestic animals will illustrate its value in determining their origins. These latter may lead into later sessions and discussion. As may the consideration that domestic animals and plants were derived through selection by Man from wild species recently ~ 12000 years, and yet they comprise only a handful of species of the ~30 millions that exist presently. Spread of agriculture is a threat to natural biodiversity, so the increase in use of a few animal and plant crops is in conflict with conservation of biodiversity. Much natural biodiversity is under threat from Man's activities.

Tuesday, 7th September

“Quantitative genetics recall”- N. Macciotta - COURSE SPONSORED BY ESF GENOMIC RESOURCES

Nicolò Macciotta is associated professor of animal breeding at the faculty of agriculture of the University of Sassari. He gives courses in animal breeding for both ungraduated and graduated students, and in statistics for PhD students. He is chair of the PhD programme in Animal Science. His research activity has focused mainly on mathematical and statistical techniques applied in animal science, and in particular on quantitative genetics. Specific fields of interest are: analysis of repeated measurements, mathematical modelling of lactation curves in different species; development of genetic models for dairy cattle; optimisation of selection schemes for dairy traits; QTL detection, evaluation of gene expression, analysis of association between phenotypes and gene polymorphisms; genomic selection. He is author or co-author of more than 100 scientific papers and abstracts, referee of several international scientific journals.

Short syllabus of the course

Concept of quantitative trait. The infinitesimal model. Means, values and variances. The phenotypic model. Genetic parameters. The breeding value. Basic concepts of selection programmes. Approaches for estimating the genetic merit of selection candidates. The selection index. The additive relationship between individuals. Inbreeding and heterosis. The BLUP methodology. Examples of calculation of breeding values with selection index and BLUP. The concept of economic index. Sire and animal models. Test day models. Breeding programmes for livestock species. The finite locus model. Basic concepts of marker assisted selection.

“Introduction to genomics” - P. Ajmone Marsan, Università Cattolica del S. Cuore, Italy

GLOBALDIV Coordinator, associate professor in Animal Breeding and Animal Biotechnology and head of the Animal Biotechnology Laboratory at the Università Cattolica del S. Cuore in Piacenza, Italy. His research interest is focused on molecular genetics and diagnostics applied to plants and farm animals. Prof. Ajmone Marsan participated to a number of national and international research programmes (including ECONOGENE, RESGEN, TRACE, INTRABIODIV and BOVGEN), also as a Coordinator.

Short syllabus of the course

New low-cost high-throughput technologies have opened the genomic era to agricultural species. All major farm animals have been completely sequenced and HapMap projects are completed or in progress. Low, Medium and High Density SNPs are available or under construction. Information on many thousand markers and on complete genomes foster a number of applications in basic and applied research. In this lecture an overview of new technologies of the characteristics of SNP markers and on their potential applications in basic research and applied breeding will be provided.

“Large SNP datasets to estimate population structure and inbreeding” - J. Solkner, BOKU, Austria - COURSE SPONSORED BY ESF GENOMIC RESOURCES

Professor of animal breeding and population genetics at University of Natural Resources and Life Sciences (BOKU) Vienna. Expertise in statistical methodology (e.g., co-author of the Survival Kit). Currently involved in developing procedures of genomic selection for Fleckvieh, Brown Swiss, Pinzgauer, Tyrol Grey. Interested in using SNP chip genotypes for estimation of inbreeding and crossbreeding (admixture). Work in developing countries (e.g. Uganda, Ethiopia) characterising populations and developing village breeding schemes.

Short syllabus of the course

The large number of SNP chip genotypes (currently more than 50.000 for cattle, pig, sheep and horse) have found very quick use in genomic selection (estimation of breeding values from genomic data) of cattle and in mapping of genes via linkage population wide disequilibrium in all the species mentioned. We will explore use of that information for other purposes, estimation of levels of admixture in crossbred populations and estimation of levels of autozygosity (inbreeding) in purebred populations. Levels of admixture: we check the validity of methods developed in human genetics, hidden markov models, and compare them with estimation based on identity by descent in a crossbred Awassi x Merino sheep resource population in Australia, with four generations of fully genotyped sheep. We then apply the hidden Markov models to the Simmental x Red Friesian cattle population of Switzerland and find good correspondence with pedigree levels of crossbreeding. Levels of autozygosity: we compare different methods of estimating levels of inbreeding from SNP chip data. Finding and adding the homozygous segments of a particular length (4 megabases or longer)

in the genome seems to provide a much more accurate predictor of inbreeding levels than the procedures currently used when setting of molecular relationship matrices in genomic selection. Both, estimation of levels of admixture and levels of inbreeding provide potentially useful applications for livestock populations in developing countries.

“SNP data analysis and opportunities” - E. L. Nicolazzi, Università Cattolica del S. Cuore, Italy

Ezequiel L. Nicolazzi is currently a PhD student at Università Cattolica del Sacro Cuore (Piacenza, Italy). His PhD program is mainly focused on dairy cattle genetic evaluations, which involves research on both “traditional” and genomic selection. He is also involved in other aspects of SNP data analysis, from genome-wide association studies and genetic population structure to the search for selection signatures in Italian cattle breeds.

Short syllabus of the course

In the past few years, genome-wide SNP data have become available and reasonably cost-effective. A large number of possible analyses can be performed on these data. In this presentation we will focus on two interesting aspects: i) the search for signals of (recent and positive) selection and; ii) the search for phenotype-genotype associations genome-wide. Firstly we'll address the identification and characterization of selection signatures at the molecular (genomic) level, by searching patterns of genetic variation departing from the neutral model (governed by genetic drift). An overview of the available analytical approaches will be shown, together with some of the problems that have to be taken into account when performing such analyses. The second part of the presentation will focus on genome-wide association studies, giving a brief introduction on the history of association studies, and explaining why we expect more from genome-wide SNP data. Then, we will focus on some practical issues to consider, as population stratification and multiple testing. Some remarkable case-studies, both in human and livestock populations, will also be presented.

Wednesday, 8th September

“What can be done with whole genome sequence data” - T. Tiirikka – MTT, Finland - COURSE SPONSORED BY ESF GENOMIC RESOURCES

Timo Tiirikka works as a bioinformatician at the MTT Agrifood Research Finland and has a keen interest in Next Generation Sequencing methods, especially in terms of data analysis. He has experience in 454, Illumina and SOLiD platforms and has developed algorithms for SNP discovery. Currently he is working with RNA-Seq and bovine re-sequencing projects.

Short syllabus of the course

In the lecture "What can be done with whole genome sequence" we will start by identifying the central concepts regarding Next Generation Sequencing (NGS) methods. The most common methods will be covered from wet lab procedures to data analysis. Next we will go through set of published examples how whole genome information has been previously used. We will also present a "pipeline" of a re-sequencing study using own bovine data. The focus will be on analysis

methods and future implementations. The software session consists of exercises and worked examples of the most common assemblers, aligners and SNP callers mentioned in the lecture.

“A case study on chicken genome resequencing” - C. Rubin, Uppsala University Sweden - COURSE SPONSORED BY ESF GENOMIC RESOURCES

Carl Rubin got my PhD in Molecular Medicine in 2008 at the Dept. of Medical Sciences, Uppsala University Sweden. During his time as a PhD-student I studied functional genomics of bone metabolism using a chicken model. He joined Prof. Leif Andersson's lab at the Dept. of Medical Biochemistry and Microbiology in 2009 where he started working with next-generation sequencing data from various chicken populations. Most of the projects he is involved in involve resequencing of domestic animal genomes to gain understanding of the alterations introduced by artificial selection for phenotypic traits.

Short syllabus of the course

Domestic animals are excellent models for genetic studies of phenotypic evolution. They have evolved genetic adaptations to a new environment, the farm, and have been subjected to strong human-driven selection leading to remarkable phenotypic changes in morphology, physiology and behaviour. Identifying the genetic changes underlying these developments provides new insight into general mechanisms by which genetic variation shapes phenotypic diversity. Here we describe the use of massively parallel sequencing to identify selective sweeps of favourable alleles and candidate mutations that have had a prominent role in the domestication of chickens (*Gallus gallus domesticus*) and their subsequent specialization into broiler (meat-producing) and layer (egg-producing) chickens. We have generated 44.5-fold coverage of the chicken genome using pools of genomic DNA representing eight different populations of domestic chickens as well as red jungle fowl (*Gallus gallus*), the major wild ancestor. We report more than 7,000,000 single nucleotide polymorphisms, almost 1,300 deletions and a number of putative selective sweeps. One of the most striking selective sweeps found in all domestic chickens occurred at the locus for thyroid stimulating hormone receptor (TSHR), which has a pivotal role in metabolic regulation and photoperiod control of reproduction in vertebrates. Several of the selective sweeps detected in broilers overlapped genes associated with growth, appetite and metabolic regulation. We found little evidence that selection for loss-of-function mutations had a prominent role in chicken domestication, but we detected two deletions in coding sequences that we suggest are functionally important. This study has direct application to animal breeding and enhances the importance of the domestic chicken as a model organism for biomedical research.

In the lecture he will go through the study outline and results gained. He will also in more detail describe the data analysis steps that we performed in the paper above. Finally he will talk about possibilities of novel technology and analysis methods other than those used in the paper that may be useful to analyze animal

genomes. **Reference: Whole-genome resequencing reveals loci under selection during chicken domestication.** Rubin CJ, Zody MC, Eriksson J, Meadows JR, Sherwood E, Webster MT, Jiang L, Ingman M, Sharpe T, Ka S, Hallböök F, Besnier F, Carlborg O, Bed'hom B, Tixier-Boichard M, Jensen P, Siegel P, Lindblad-Toh K, Andersson L. *Nature*. 2010 Mar 25;464(7288):587-91. Epub 2010 Mar 10.

Thursday, 9th September

“Bioinformatics to mine the genome” - R. Mazza, Università Cattolica del S. Cuore, Italy

Raffaele Mazza is a PostDoc at the Animal Genetics Laboratory of the Zootechnic Institute of the Università Cattolica in Piacenza. His research activity focuses on Bioinformatics applied to animal genomes. His specific tasks range from biological database mining and genome annotation to software programming oriented to the handling and analysis of molecular dataset. He participated in international projects the Bovine HapMap and Bovine Genome Annotation.

Short syllabus of the course

The advances in sequencing technologies over the last decade have transformed biology into an information-rich science. The ongoing increasing number of web-based databases provide an exceptional portal of access to the large amount of data which are organised at different level of detail and specificity. Each database has its own format and user interface which are strongly dependent on the objective it aims to. Storing and retrieving information as well as integrating data from different sources and species are complex tasks that affect the efficiency with which the researchers can access and analyse the data. Genome browsers like the UCSC genome browser, NCBI Map Viewer and Ensembl are the most widely used multi-species databases that collect and integrate information from various sources and display many customizable features alongside the genome in an efficient way. This presentation will mainly focus on the Ensembl genome browser and is intended to provide an overview of the capabilities of the browser to investigate genes across a number of organisms in comparative studies, analyse variations and function and access to the large set of information available through external links.

“Convergence between wildlife and livestock conservation”, P. Taberlet - Laboratoire d'Ecologie Alpine, France

Senior scientist at CNRS (Centre National de la Recherche Scientifique). Director of the Laboratoire d'Ecologie Alpine in Grenoble (France). He is mainly interested in conservation genetics, both for wild and domestic animals and studied the domestication process in sheep and goats. He is currently coordinating the European project "NextGen", dealing with conservation of biological resources in cattle, sheep and goats, based on whole genome data.

Short syllabus of the course

The first part of the talk deals with the domestication process, and the link between the domestic species and their respective wild ancestors. We will focus on sheep and goat domestication, and will briefly review the origin of other farm animals. The second part concerns the concept of effective population size and the 50/500 rule. We will examine the influence of small populations on genetic drift, with emphasize on the extinction vortex, first for wild animals, and then for domestics. The third part presents the selection process and its influence on genetic diversity. Finally, we will contribute to the controversy of using neutral versus selected genetic markers in conservation. We will present the population adaptive index, and give examples in wild and domestic animals.

CASE STUDIES

During the session dedicated to the students case studies, 16 participants presented the results or the main objectives of their own research projects, taking advantage of the lecturers willingness to give suggestions or to answer specific questions.

TIMETABLE	FULL NAME	CASE STUDY
Biotech	Waleid Mohamed E. M. Shakweer	Sperm mediated gene transfer
Breeding	Tadele M Keba	Community-based alternative sheep breeding plans to genetically improve and conserve indigenous breed in Ethiopia
Breeding	Anamarija Frkonja	estimation of level of crossbreeding/admixture in cattle population
Breeding	Valerio Paini	Nero of Parma swine population
Breeding	Julian Echeverri	Genetic Improvement of dairy cattle in Colombia
Diversity	Samia Kdidi	1) genetic diversity of Tunisian dromedary camel as revealed by microsatellites 2) genetic polymorphism of the Alpha-S1 casein gene in Tunisian native goat
Diversity	Deyana Gencheva Hristova	genetic diversity of local sheep breeds using DNA-marker, especially microsatellites.
Diversity	Kozet Avanus	Casein gene polymorphisms among sheep breeds in Turkey

TIMETABLE	FULL NAME	CASE STUDY
Diversity	Erika Zakar	genetic diversity of different honey bee
Diversity	Saif-Allah Hassan Ahmed Agha	goat and bovine diversity data
Diversity	Marie Vranová	genetic diversity in MHC cassia gene in 3 populations of donkeys
Diversity (plants)	Nader El-Badry	the genetic diversity for drought tolerance in barley by exploiting a cultivars collection previously phenotype for yield performance under different water regimes
Nutrition	Núria Tous	Diet Dietary factors affect pig fat deposition and composition and their contribution in IMF in terms of meat quality
Phenotypes	Gemeda Duguma Jaleta	methodologies to identify community based objective traits identification (with raw data)
Phenotypes	Pulane Sebothoma	Alternative methodology that could be followed in characterization of indigenous genotypes

CONCLUSION

After the conclusion of the lectures, the attendants were asked to rate their level of satisfaction by answering an anonymous questionnaire regarding both the scientific contents and the organization and the logistic aspects of the School. The results were satisfactory and the level of enjoyment ranged from “good” to “excellent” on average.

A GLOBALDIV Summer School Certificate of attendance was distributed to all the students, while two ECTS credits from the Università Cattolica, spendable in any European University, were acknowledged to those who passed the examination by answering the 60 multiple choice questions prepared by the lecturers.

All the material of the Summer School is available at: http://www.globaldiv.eu/Summer_School_2010/Presentations/Files.html

Due to the highly satisfactory results achieved by both the 2008, 2009 and 2010 the ESF GENOMIC RESOURCES project co-financing the GLOBALDIV 2010 edition, is evaluating the possibility to replicate the event in the following years.