



# Globaldiv

## GLOBALDIV NEWSLETTER

ISSUE N. 15 – 20<sup>TH</sup> JULY 2010

### Editorial: 2010: The second GLOBALDIV Workshop

The second GLOBALDIV Workshop took place in Rome on May 5-6, 2010 in the form of a joint meeting organized by the GLOBALDIV and EURECA European GenRes projects.

The event was hosted by the Food and Agriculture Organization of the United Nations (FAO), and was attended by a total of 96 people which included scientists, students and other stakeholders coming from 24 different countries. Besides the participants to the two European projects fostering the event, also delegates of other European projects (FP7 CONGRESS, ELBARN, EFABISNet, HERITAGESHEEP) and of several International Institutions were present: the International Livestock Research Institute (ILRI), the International Atomic Energy Agency (IAEA), the European Association for Animal Production (EAAP), the World Association of Animal Production (WAAP), the International Committee for Animal Recording (ICAR), the United States Department of Agriculture (USDA).

All participants received a certificate of attendance, the last two issues of the GLOBALDIV newsletter and a copy of the Special Issue of the journal *Animal Genetics* containing review papers authored by GLOBALDIV partners and experts. The special issue is open-access and can be freely downloaded from the journal website ([www3.interscience.wiley.com/journal/123356073/issue](http://www3.interscience.wiley.com/journal/123356073/issue)). All slides presented during the workshop are available at the GLOBALDIV website ([www.globaldiv.eu](http://www.globaldiv.eu)).

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Dr. Olivier Diana, from the General Directorate for Agriculture and Rural Development of European Commission opened the Workshop. He presented an overview of the animal genetic resources in EU Council regulation (EC) No 870/2004 and the programmed actions through year 2011. These aim at promoting *in situ* and *ex situ* programs for the conservation of genetic resources for the microbial, animal and plant species useful in agriculture through the implementation of web-based inventories, the sharing of information, the dissemination of knowledge, the definition of national priorities and the promotion of cryo-conservation programs involving the whole European Community.

In the first part of his talk, Prof. Paolo Ajmone Marsan, from the University Cattolica del Sacro Cuore of Piacenza, Italy, and Globaldiv coordinator, presented the project and its objectives. In particular, he pointed out how dissemination was carried out successfully through the project website (more than 27,000 downloads of the Newsletter per year), the recent publication of review papers jointly written by Globaldiv partners and experts during the past two years (Animal Genetics, vol. 41, May 2010), the 2008 and 2009 Summer Schools held in Piacenza (Italy), the Bydgoszcz (Poland) workshop in march 2009 and the contribution given by Globaldiv members to the latest version of FAO recommendations for the Molecular Characterization of Animal Genetic Resources for Management and Conservation. In the second part of his contribution, Prof. Ajmone-Marsan described how the project is constituted, by detailing the specific missions of the different Work Packages: molecular tools for characterization of FaNGR diversity, meta-analysis approach for integration of independent studies on diversity, the socio-economic aspects of farm animal conservation and the integrated analysis of livestock genetic data with socio economic and environmental information.

Dr. Tad S. Sonstengard from USDA, ARS, Bovine Functional Genomics Laboratory of Beltsville, USA, discussed on novel genomic tools for breed characterization. Currently the Illumina BovineSNP50™ is the state of the art technology for cattle breed characterization, management and selection and to carry out selection signatures analyses and genome wide association studies. Still, Dr. Sonstengard evidenced that the actual opportunities need further improvement, to eliminate time consuming and cost demanding progeny tests and take full advantage of the last whole genome sequencing technology to increase accuracy in genetic prediction, facilitate across breed genomic selection, enhance QTL mapping precision and develop chips for cheap application. He announced the set up of higher density SNP chip and presented all the underlying issues for the development of such platforms, the ongoing collaborations and projects pursuing this objective, together with the latest data produced by USDA.

In the following presentation, Prof. Johannes A. Lenstra from Utrecht University, the Netherlands, and Dr. Steffen Weigend from the Friedrich Loeffler Institut (FLI), Germany, explained the current status of the evaluation of genetic diversity in livestock breeds focusing on chicken and cattle biodiversity. In particular, Dr. Weigend showed how a multilocus clustering based on a batch of 30 microsatellites, suggested by FAO, divides the chicken gene pool of 85 population into 3 main group and that mtDNA analysis suggests an Indian sub-continental origin for the European breeds,



while commercial lines are of admixed origin. Dr. Lenstra described how mitochondrial (mtDNA), autosomal and Y chromosome markers are able to reconstruct cattle origin and domestication and to describe the present diversity in this species. The parallel analysis of uniparental and autosomal genomes indicates that zebu and taurine cattle were domesticated independently and that African cattle is of admixed origin. Data on mtDNA indicate that European taurine animals mostly originate from South West Asia ancestors, but that a contribution from local auroch populations is possible. Y chromosome data indicate a clear North-South Europe contrast and suggest a nordic expansion of lowland dairy cattle and a southern expansion of alpine cattle.

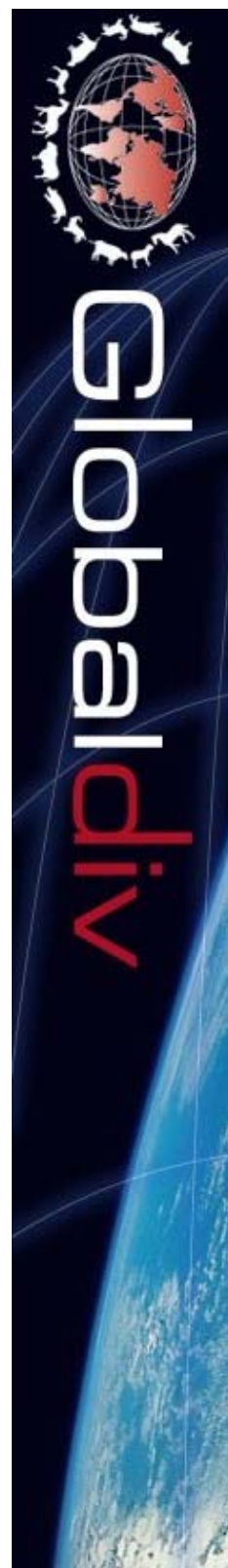
The last presentation of the morning session was given by Dr. Massoud Malek from the International Atomic Energy Agency (IAEA), Vienna, Austria. He related on the commitment of IAEA to conduct applied research in the field of animal production and health with the main objective of contributing to increase livestock production through improvement of breeding and feeding strategies and control of important animal diseases. IAEA, in collaboration of FAO, develops bioinformatics and genomic tools, some of them already deployed, and organizes training. Among the achievements, a laboratory information management system (LIMS) and a research and management platform for developing countries.

## Second Session

During the second session Dr. Simon Mack Senior FAO Officer from the Livestock Production Group (AGA) presented "The state of food and agriculture 2009", FAO's major annual publication. He gave an overview on structural change in livestock production systems in a world with an increasing demand for livestock products. He underlined the contribution of livestock to livelihoods and food safety and the underlying economical and political implications. The most forthcoming task in the changing scenario will be to balance different objective for the sector, such as livelihood, food security, environmental impact and human health.

The following presentation was given by Dr. Irene Hoffman chief of the Animal Genetic Resources Branch at FAO. She presented the Global Plan of Action for characterization, breeding and conservation of animal genetic resources. She underlined that climate change will have its major impact in developing countries and that biodiversity is of critical importance for the selection of new breeds in response to environmental changes causing physiological, thermal, nutritional and disease stress to livestock. Farming will have to evolve and develop systems for the adaptation of livestock production to new conditions, which can only be performed by taking advantage of the new technologies and the characterization and conservation of animal genetic resources.

Prof. Eildert Groeneveld from the Institute of Farm Animal Genetics of the Friedrich Loeffler Institut (FLI), Germany, presented the EFABISnet project, an integrated network of decentralized country biodiversity and genebank databases. In particular, EFABISnet promoted national inventories of animal genetic resources in 12 countries and established national inventories of



national gene bank collections in 10 countries. Moreover it allowed the development of permanent management structure of the European network of animal genetic resources.

Paul Boettcher, from the Animal Production and Health Division, FAO, reported on the methods for prioritization in conservation of animal genetic resources. He emphasized the importance of conservation and listed the factors influencing conservation priorities. He then presented the main methods used to set conservation priorities on the basis of extinction probabilities, within and between breed diversity. Most of these methods still have limited application because of a lack in molecular and phenotypic characterization which have to be promoted together with population monitoring, diversity measure and software development.

Dr. Catherine Marguerat, from the Federal Office of Agriculture (FOAG), Switzerland, described the strategies to support endangered livestock breeds in Switzerland. She presented a survey of endangered species and a series of legal binding and disposition of the Swiss Government. She gave examples of projects aiming at the conservation of animal genetic resources in horse, cattle, chicken, sheep and goats.

Dr. Stephane Joost from the GIS Laboratory (LASIG), Ecole Polytechnique Fédérale de Lausanne (EPFL), Switzerland, reviewed the methods for the prioritization of breeds for conservation and on integration of data from different sources, with a specific focus on the use of geographical information for complex spatial data representation, mining and analysis. He presented an interesting case study in which different types of information (social, economic, demographic and environmental) were integrated in a GIS to assess the sustainability of Original Brown Swiss husbandry in Switzerland, highlighting regions of highly sustainable breeding activities.

The feedbacks we received from the audience were very positive: the participants not only followed with great interest and attention the speakers' presentations, but also actively took part in the final "wrap-up" discussion which concluded the workshop.

The next events organized by GLOBALDIV will be the third edition of the Summer School which will take place in Piacenza, Italy, on 6-9 September 2010, and the conclusive workshop that will be held in Lausanne, Switzerland, on February 8-9, 2011.

The 2010 School syllabus will focus 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 will be given on conservation strategy applied to wildlife that may be of interest for livestock management. To stimulate interaction between students and teachers, the attendants will be proposed to bring their own case studies, some of which will be presented, analysed and discussed.



We sincerely thank the Food and Agriculture Organization of the United Nations (FAO) for hosting the second GLOBALDIV Workshop, all the members of the Organizing Committee (Prof. Paolo Ajmone Marsan, Prof. Sipke Joost Hiemstra, Dr. Elena Murelli, Dr. Licia Colli, Dr. Riccardo Negrini, Dr. Rita Hoving and Dr. Kafia FassiFihri) and all the people who contributed to the organization of the event from FAO (Dr. Irene Hoffmann, Dr. Paul Boettcher and Dr. Beate Scherf) and - last but not least - all the speakers and the participants for sharing their own experiences and points of view on the conservation of farm animals.

Thank you!

***Giordana Lucente, Raffaele Mazza and Paolo Ajmone Marsan***

## **Article of the month: RBST/Roslin Institute - UK Poultry Genetic Diversity Project**

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### **Introduction**

Many breeds of chicken were created in the UK but relatively little is known about the genetic relationships between them. Some very rare breeds have been saved through the efforts of the Rare Breeds Survival Trust (RBST) on an ad hoc basis but there has not been a systematic programme of preservation of chicken breeds in the UK. To provide a rational basis for safeguarding rare and traditional breeds RBST and the Roslin Institute initiated a project in 2006 to determine which breeds were particularly valuable from a genetic perspective and identify those breeds that needed special protection or monitoring. A second objective was to combine the resulting information with the large European Aviandiv data set to contribute to the EU-wide programme to protect and conserve remaining genetic variation in chickens.

We established a list of more than 25 traditional breeds with a bias towards those that were created, or had been widely used, in the UK: two such breeds are illustrated in Figure 1. Flock owners were identified, using the extensive knowledge of Dr Dawn Teverson at RBST, and asked to provide fertile hatching eggs for the scheme. These were sent to Roslin for incubation for 7 days and the resulting embryos and stored in two portions ("head" and "tail") at -80oC for subsequent extraction of DNA. Extraction of DNA





Figure 1. Two traditional breeds: Maran (right) and Cornish Game (right).

from 7 day embryos is relatively easy and produces large yields of good quality DNA. The aim was to collect a total of at least 5 samples from 5 flocks to make up a total of 30 samples of each breed.

### Data collection

After the first year (2007) we assessed which breeds were still needed and tried to complete the collection in 2008 and 2009. The total numbers of eggs, fertile eggs and embryos collected are presented in Table 1. We had collected over 1.400 samples of DNA but selected a maximum of 5 from at least 6 flocks, wherever we could, for genotyping. The selected breeds and numbers of flocks are presented in Table 2. We did not collect enough samples from Polish or Malay birds and separated Light Sussex from the

Table 1 Numbers of batches, hatching eggs set, fertile eggs and DNA samples from rare and traditional breeds of chickens by year.

Year	Batches	Eggs set	Fertile	Samples
2007	166	1732	1006	799
2008	62	666	414	347
2009	64	648	337	270
Total	292	3046	1768	1416

Table 2. Breeds and samples selected for genotyping with the number of supplying flocks and colour variants.

Breed	Samples	Flocks/Lines	Colours
Appenzellor	30	9	3
Araucana	30	7	3
Brahma	28 (30) <sup>1</sup>	6 (7) <sup>1</sup>	4
Buff Orpington	30	10	1
Cochin	30	6	2
Coloured Leghorn	30	7	4
Coloured Sussex	30	6	3
Croad Langshans	30	8	1
Derbyshire Redcap	30	9	1
Dorking	30	7	4
Game	30	9	4
Hamburg	30	10	3
Ixworth	30	6	1
Light Sussex	30	6	1
Lincolnshire Buff	30	6	1
Maran	30	6	2
Marsh Daisy	30	8	1
Norfolk Grey	19 (30) <sup>1</sup>	4 (5) <sup>1</sup>	1
OEPF	30	9	1
Rhode Island Red	30	7	1
Scots Dumpy	30	6	1
Scots Grey	30	6	1
Silkie	30	6	3
Spanish	30	7	1
White/coloured Sussex	30	7	4

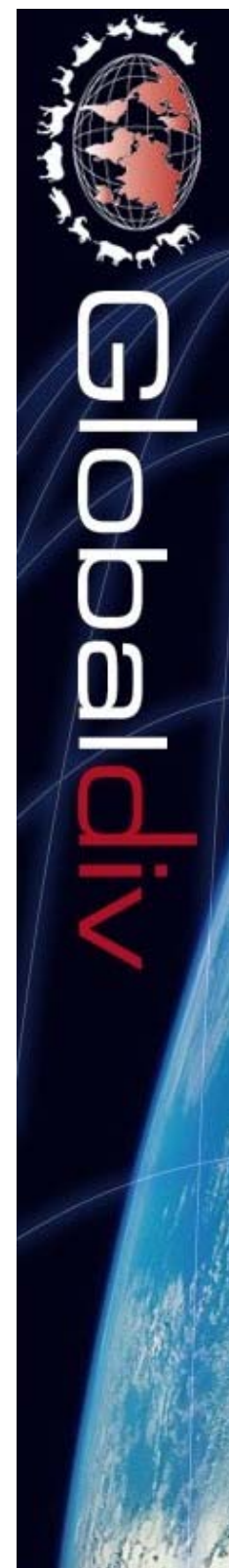
<sup>1</sup> Total after additional collection in 2010.

other Sussex colours to make a 25th breed. We received information on different colours or lines within several breeds and these data are included in the last column of Table 2.

## Genotyping

We used the Aviandiv common set of 30 microsatellite markers and also genotyped a control set of 9 DNA samples from the Aviandiv project as a check on allele sizes. Genotyping was conducted by ArkGenomics and completed in March 2010 for all 750 samples. Genotyping was effective for over 95% of the samples for all but 2 microsatellite markers (MCW020 and MCW123) (Figure 1).

A PhD student, Samantha Wilkinson, will be analyzing the data to ascertain relationships between breeds and to identify which breeds are most variable, those that are more distinct or genetically similar. It is well known that crossing breeds to enhance or recreate specific phenotypes for show



purposes, or to introgress new colours into a breed is widely practiced, and we took care to sample flocks that followed dedicated breeding of particular lines. The genetic analyses should therefore provide a measure of breed differentiation among genuine breed representatives.

### Fertility and embryo survival

We have analyzed the data for an estimate of fertility and 7-day embryo survival. The statistical model included fixed effects for Breed, Year (2007, 2008, 2009) and "season" (February-April, May, June, July-September) and random effects for supplier. Analyses were conducted with the Generalized Linear Mixed Model procedure of Genstat with binomial errors.

There was a significant interaction of year and season ( $P < 0.01$ ) for fertility (fertile eggs/eggs set) that was associated with large differences in the last two seasons of 2009 probably as a result of small sample size. In general, fertility declined as expected from early spring to late summer: average fertility was 64, 63, 51 and 39% respectively for the 4 seasons.

The proportion of eggs that were fertile averaged 53% (unweighted average of breed means). Breed differences were significant ( $P < 0.01$ ) with a range from 21 to 74% for flocks with at least 5 batches of eggs. The worst performing breed was the Silkie (10 batches) and the best was the Appenzellor (14 batches). About 10% of the variation in fertility was associated with flock. For comparison, over 95% of broiler eggs, for example, are fertile and the overall mean in our eggs was disappointingly low. The results suggest that research to find out why some flocks have relatively poor fertility is warranted.

Off the fertile eggs that were incubated, 22% of embryos were dead in shell (breed range 8 to 37%) and 13% of the variation was associated with the supplying flock. The range of dead-in-shells in week one of incubation in commercial flocks is 2 to 4% and our high rate is likely to be the result of an extended storage time and rough handling during transfer

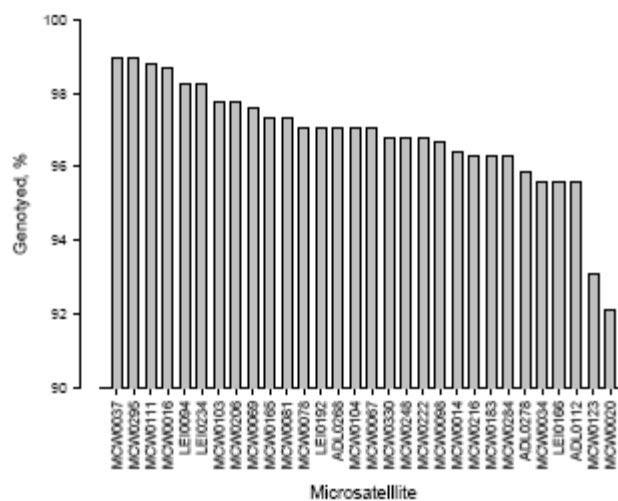


Figure 2. Proportion of samples successfully genotyped with the Aviandiv set of chicken DNA markers.



to Roslin: some supplying flocks sent eggs that had been stored for 14 days. As for fertility, breed x season interactions were significant ( $P < 0.05$ ) but unlike fertility, the remaining fixed effects were not.

It will be interesting to discover if low breed fertility is related to low genetic diversity and vice versa or whether it is due to management of these traditional breeds e.g. breeding from older birds. Overall fertility of little more than 50% is very poor compared with commercial hybrids and was unexpected. It had been assumed that small groups of hens mated with one or two males would have near maximum fertility. It is possible that small groups are not inherently fertile e.g. it is known that hens can be choosy. If the reasons for this observation could be identified and overcome, the management of breeding birds in traditional flocks would become considerably more predictable and efficient, and possibly contribute to the effective preservation of genetic diversity. In terms of data collection, a yield of only 41% (samples per 100 eggs set) was disappointing!

### A large data resource

These DNA samples will contribute to the international chicken genetic diversity project. The results will assist RBST to develop conservation programmes, where necessary, based on genetic evidence from UK breeds.

Some of the DNA samples have also been used for unrelated research by scientists interested in genes affecting normal development of the limbs and immune responses. These samples represent a valuable resource for research workers in a number of fields that make use of the large breed differences in phenotype among traditional breeds of chickens.

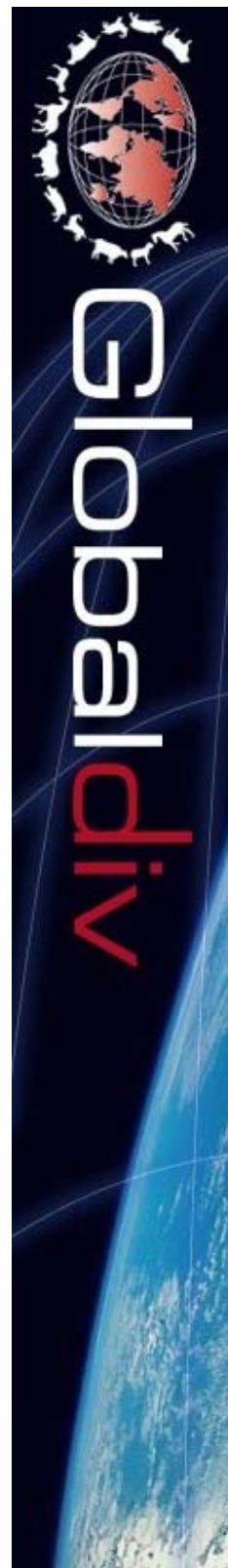
## The Breed of the month: Swiss Original Braunvieh

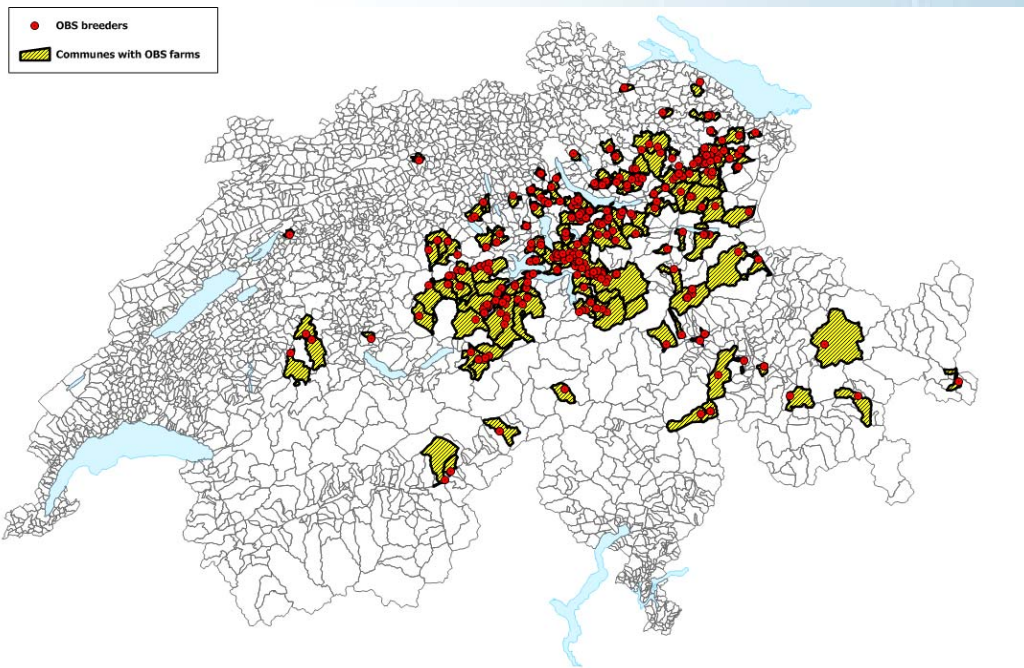
**Bapst Beat**

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### Swiss Original Braunvieh

The country of origin, the cradle of the Braunvieh is, of course, Switzerland. Documentary evidence shows that the Benedictine monks residing at the Einsiedeln Monastery started breeding this cattle as early as approx. 1'000 years ago. In the beginning of the 19th century, different types of Brown Cattle had still been kept in Central and East Switzerland. The interchange of the different types by and by resulted in today's uniform Swiss Brown Cattle. The inclement environmental conditions and keeping the livestock up in our alps, left their mark on the Swiss Braunvieh and as a result of the natural selection and the breeding work of our mountain dwellers, an excellent breed resulted, much appreciated and in demand in foreign countries as well. It found its way into the neighbouring alpine





*Geographical distribution of Swiss municipalities where the Swiss Brown Original is reared (yellow areas). In red are shown the localities if the 302 SBO breeders. Source: Swiss Brown Cattle Breeders' Federation.*

countries hundreds of years ago and the first exports of Braunvieh to the United States of America and other countries can be traced back to 1869. After the foundation of the Swiss Braunvieh Breeding Association in 1897, the breed has been standardized and improved still further. At that time breeding still had three objectives: a cow needed that could provide milk and meat, and could be used as a draught animal. Thus, an animal with an all-round nature developed: robust, a prolific breeder, long-lived, strong,



adaptable, and very well-balanced in build and colour. Her strong limbs and claws make it possible for her to find fodder on difficult terrain as well with meagre grass growth and a limited number of watering places. Her strong skin with dense, brown hairy coat and her dark-blue eye pigmentation helps her to resist extreme solar radiation (statistical data is available from tropical countries, based on practical experience). Her double utility, providing a good milk and meat output performance enables the owner to hold his own in any type of production. In the late sixties, animals with an increased milk output and stronger build came into demand. In order to achieve these objectives much faster, many Braunvieh breeders reached for "Brown Swiss"-Genetics from America for pairing. Convinced breeders of original Braunvieh however stuck to their pure breeding ideas and improved the milk production performance by strong selection within the original Braunvieh population under strict maintenance of the meat output rate.



### The Situation today

Around 500 breeders of original Braunvieh have organized themselves within the framework of an Association. Their animals are entered into the official herd book of the Swiss Braunvieh Federation in Zug, Switzerland as an



Swiss Original Braunvieh, and are marked, as soon as they satisfy the examiners that they are pure-bred. Swiss Original Braunvieh-cows perform well, produce 5'500 kg (12'100 lb) milk and more per lactation and produce offsprings that are eminently suitable for fattening at any age level. Thus, Original Braunvieh calves are in great demand by meat producers as they guarantee a daily weight increase between 1'200 and 1'300 g (2 lb 10 oz to 2 lb 14 oz), representing high productivity coupled with excellent meat quality.

### Monitoring

The OBS is not classified among endangered breeds but it is under observation in Switzerland (OFAG, 2002). The Herdbook of the Brown Cattle Breeders' Federation in Zug gives today evidence of 12'000 head of Original Braunvieh, out of which 6200 cows. Breeding is done with some 100 head of Original Braunvieh sires. It is essential to monitor the evolution of the population because, beyond the skills in terms of production capacity, the Swiss Original Braunvieh has a genetic heritage of great value that is internationally recognized. This breed was exported to North America over 100 years ago with an original population consisting of only a few females. From this starting point, American breeders developed the herd and exported the Brown Swiss all over the world. Nevertheless, in the past decade, genetic anomalies were detected in these animals mainly in the United States. With respect to this issue, it is very likely that several genotypes of OBS in Switzerland are still single and that they have never been exported outside the country. Therefore, it is imperative for Switzerland to maintain and enhance this unique gene pool.

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## GLOBALDIV Events

Dear Colleagues,

The Project Secretariat reminds you that the application for the 3rd GLOBALDIV Summer school to be held in Piacenza, Italy (6-9 September 2010) within the EU Project "GlobalDiv" is OPEN and some grants are available:

- 9 grants for accommodation (hotel and lunches paid directly by the organization) are available for students from Asia, Africa, Latin America and Eastern Europe;



- 4 grants with a lump sum of 350 euro in total are available from the European Science Foundation for students from UE (27 countries), Switzerland, Norway and UK

**Application is restricted to PhD students and junior researchers.**

Deadline for application is as following:

- Students requesting the grant and need VISA should apply within **25th July 2010**
- Students that does not need VISA and would like to apply for grants or not, should apply within **15th August 2010**

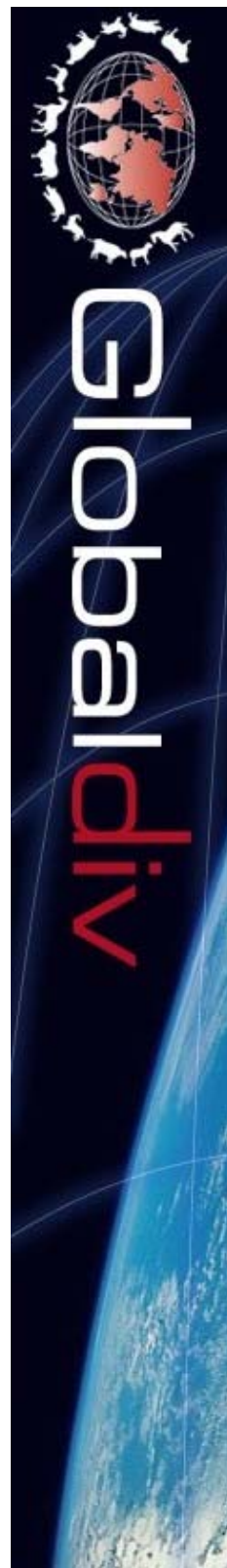
The 2010 School focuses on the use of genomics for the characterization of genetic resources and on methods and software for large molecular data-set management and analysis. In addition, an update will be given on conservation strategy applied to wildlife that may be of interest for livestock management.

More information are available on the web at: [www.globaldiv.eu/Summer\\_School\\_2010](http://www.globaldiv.eu/Summer_School_2010), or please consult Elena Murelli at: [elena@globaldiv.eu](mailto:elena@globaldiv.eu)

You are also invited to spread the information to potential candidate in your institution

## Events calendar

- 26-30 July 2010 - ISAG 2010 - Edinburgh  
<http://www.isag2010.org/>
- 26-30 July 2010 at Nairobi, Kenya and October 11-15 at Thika, Kenya. - Project Planning, Monitoring & Evaluation -  
[ftp://ext-ftp.fao.org/ag/reserved/dad-net/ProjectPlanning\\_m\\_E.pdf](ftp://ext-ftp.fao.org/ag/reserved/dad-net/ProjectPlanning_m_E.pdf)
- 1-6 August 2010 - WCGALP 2010 Lieptiz, Germany  
<http://www.wcgalp2010.org/>
- 16-20 August 2010 - 9th IVIS - 9th International Veterinary Immunology Symposium at Tower Hall Funabori (Edogawa-ku) in Tokyo.  
<http://9th-ivis.jtbcom.co.jp/greeting.html>
- 16-20 August 2010 - Second International Conference on Climate, Sustainability and Development in Semi-Arid Regions -  
[www.agrobiodiversityplatform.org/blog/?p=2944](http://www.agrobiodiversityplatform.org/blog/?p=2944)
- 23-27 August 2010 - 61st Annual Meeting of the EAAP - Crete.  
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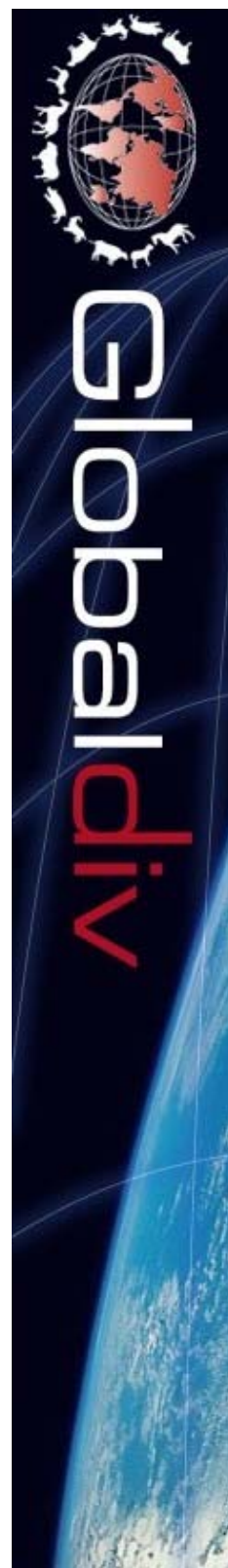
- A global view of livestock biodiversity and conservation - GLOBALDIV - P Ajmone-Marsan
- Genetic diversity in farm animals - a review - LF Groeneveld, J A Lenstra, H Eding, MA Toro, B Scherf, D Pilling, R Negrini, EK Finlay, J Han, E Groeneveld, S Weigend
- Climate change and the characterization, breeding and conservation of animal genetic resources - I Hoffmann
- Integrating geo-referenced multiscale and multidisciplinary data for the management of biodiversity in livestock genetic resources -S Joost, L Colli, PV Baret, JF Garcia, PJ Boettcher, M Tixier-Boichard, P Ajmone-Marsan
- Objectives, criteria and methods for using molecular genetic data in priority setting for conservation of animal genetic resources - PJ Boettcher, M Tixier-Boichard, MA Toro, H Simianer, H Eding, G Gandini, S Joost, D Garcia, L Colli, P Ajmone-Marsan

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