



GLOBALDIV NEWSLETTER

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Editorial - First GLOBALDIV Summer School

The first edition of the GLOBALDIV Summer School was hosted at the Università Cattolica del Sacro Cuore in Piacenza, Italy on September 8-11 2008. Lecturers were a selected sample of international experts (Figure 1) that presented basic aspects of the application of population genetics methods to the characterization of animal genetic resources, together with the major issues related to farm animal biodiversity valuation and conservation and on new technologies and data analysis methods. A total of 45 well qualified and motivated graduate students, post-docs and young researchers from 21 different Countries (Figure 2) were admitted to the School. In addition 15 students were permitted to attend a few lectures as auditors. Together, lecturers and participants represented a very heterogeneous sampling of human genetic and cultural biodiversity with common interests.

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Figure 1. Summer school lecturers.



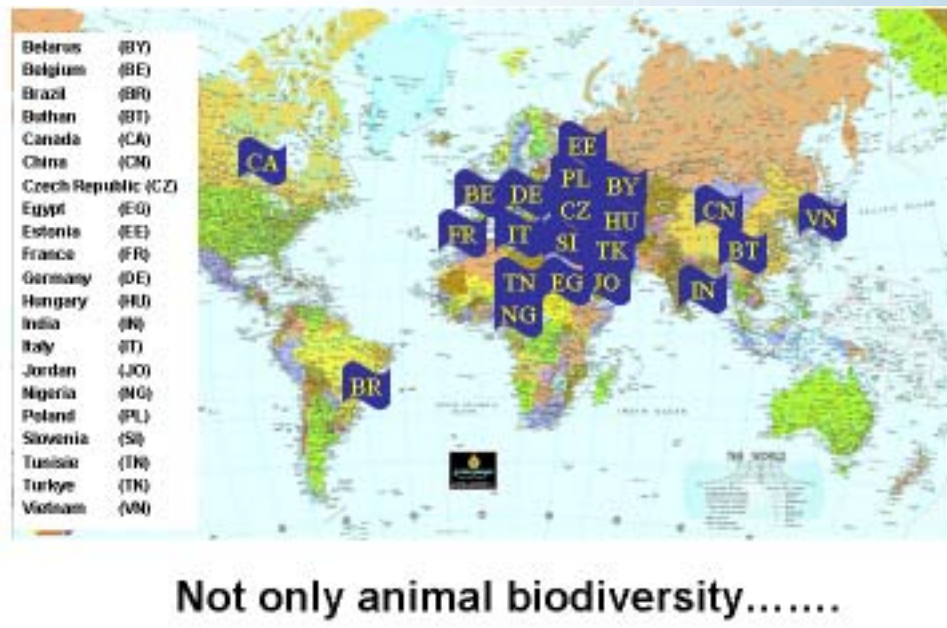


Figure 2. Summer school scholars.

Discussion was open and alive and frequently running well over time set for lecturing. The atmosphere was very friendly and collaborative (see some sample photos hereby).

The course started with a lecture on the description of farming systems and major threat to livestock biodiversity in Europe. Dr. Milan Zajc from the European Association for Animal Production (EAAP) made an historical overview of the trends in animal production and market demand of animal product in Europe, as well as in the public awareness of the importance of conserving biodiversity. Progress were described from the Rio the Janeiro Convention on Biological Diversity, to the FAO Report "The State of the World's Animal Genetic Resources for Food and Agriculture", approved by the Inter-governmental Technical Conference on Animal Genetic Resources in September 2007 in Interlaken, Switzerland. He described how farming systems changed in the last 50 years also as a result of changing Common Agriculture Policy measures and of specific actions dedicated to the conservation of Genetic Resources. The present main threats to biodiversity were highlighted, as the rapid spread of industrial production, local conflicts (e.g. as happened in the Balkan area), uncontrolled crossbreeding and disease outbreaks.



Figure 3. Participants to the summer school.



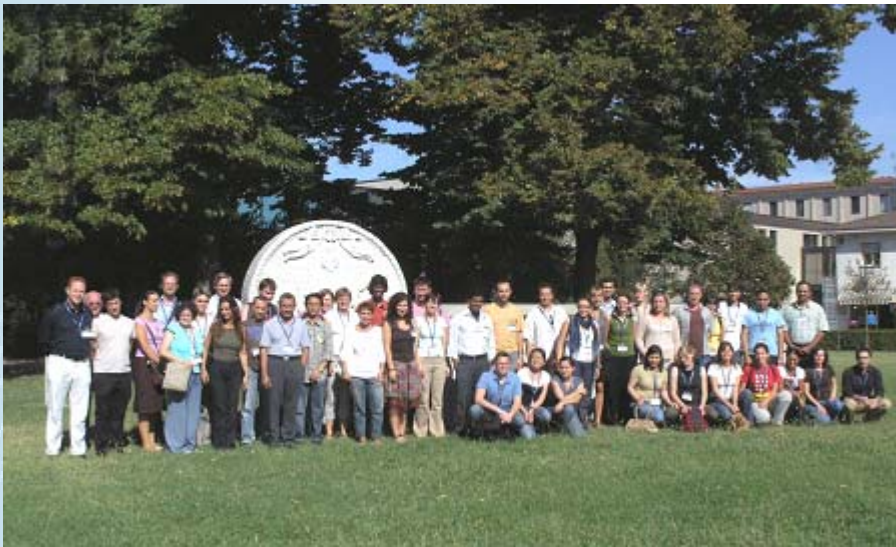


Figure 4. The whole group of students and teachers of the summer school.

Prof. José Fernando Garcia from São Paulo State University in Brazil held the second lecture. Prof. Garcia gave an overview of farming systems in South America, with a special focus on Brazil and on cattle. The presentation considered in particular the challenges that animal breeding and the marketing of animal products are facing in South America, from quality and safety requirements for export to the need for environmental-friendly farming system, through the risks of deforestation due to moving animal breeding from areas now increasingly dedicated to the production of bio-fuel. Prof. Garcia gave also an overview of molecular technologies used in Brazil for traceability purposes, breed characterization and molecular breeding as well of the objectives and perspectives of the Brazilian Conservation of Genetic Resources Programme.

Prof. Johannes A. Lenstra from Utrecht University in the Netherlands held the next lecture. Prof. Lenstra gave an historical overview of the use of different molecular marker types in animal breeding spanning from isozymes to genome-wide SNP panels. He also discussed new perspectives open by the use of 454 and Solexa high throughput sequencing. Also, he summarised changes in view on biological complexity and diversity, from the early "one gene one enzyme" dogma, to present knowledge on alternative splicing, microRNA regulation and role of copy number variations (CNVs).

The fourth lecture was presented by Prof. Paolo Ajmone Marsan from the hosting Institution Università Cattolica del Sacro Cuore, Piacenza, Italy. Prof. Ajmone Marsan discussed modern and upcoming technologies for genome analysis. In the lectures strategies for genetic and physical mapping and whole genome sequencing were reviewed together with new insights of the types of variation found in the human genome. Upcoming sequencing technologies were also reviewed in the light of the "1000 dollar genome" project recently launched by the US National Institute of Health. In addition, data on genome-wide Linkage Disequilibrium and genetic structure of cattle population were commented. These are the first results produced by the bovine HapMap project. Finally new opportunities for molecular breeding in farm animals were discussed, opportunities that presently seem to represent



an additional threat to the conservation of genetic resources but in the near future, with the whole genome sequencing at hand, may turn into new opportunities.

The fifth and sixth lectures focused on the methods of analysis of molecular data from nuclear DNA. The fifth was a “four hands” lecture prepared in a collaborative effort by Dr. Miika Tapio from the International Livestock Institute in Kenya and Prof. Juha Kantanen, from MTT Agrifood Research, in Finland. Lecturers discussed study design for breed characterization and described sampling strategies, number of animals to be collected, number of markers and highlighted importance of the use of recommended marker sets to facilitate the joining of independent datasets in a meta-analysis. Also methods and software for checking data quality prior to analyses were described, to avoid the use of markers affected by null alleles or breaking assumptions on neutrality and independence. In addition a critical overview of clustering methods and software was proposed, with particular attention to novel unsupervised Bayesian clustering methods.

Dr. Miika Tapio presented the sixth lecture. He critically discussed the analysis and quantification of within and between breed diversity with F and other statistics, the methods for estimating genetic similarity and distance between individuals and breeds under different mutation models and strategies for estimating the effective population size and the occurrence of recent bottleneck events. Finally Dr. Tapio presented methods for the graphical representation and interpretation on multivariate data, as trees, networks and multidimensional plots.

The seventh and eight lectures were held by Dr. Licia Colli from the Università Cattolica del Sacro Cuore, Piacenza, Italy and by Dr. Anna Olivieri from the Università di Pavia, Italy. The focus of these lectures was on the methods of analysis of molecular data from mitochondrial DNA. In the first part of her lecture, Dr. Colli briefly presented the main characteristics of mtDNA and reviewed the traditional molecular diversity indices for mitochondrial data. In the second part, several methods for mtDNA data analysis were introduced, spanning from Analysis of Molecular VARIance, mismatch distribution, estimates of population expansion and admixture analysis to the most commonly used techniques for the reconstruction of trees from sequence data. For each method of analysis, Dr. Colli also provided a list of freely downloadable software packages and literature references list.

Dr. Anna Olivieri explained the advantages of the use of uniparental markers for the study of parental lineages and further explored the methods (sample selection, sequencing strategies, database creation, reconstruction of high-resolution phylogenetic trees) and software for analyzing mitochondrial sequence data by presenting three specific case studies:

1. the phylogenetic study of the human M haplogroup;
2. the study of the phylogeny of modern cattle using the same level of molecular resolution as for humans, and
3. a population study on modern Tuscans.

Dr. Paul Boettcher from FAO conducted the software session, explaining the main features and the interpretation of results obtained from the software packages PHYLIP, for basic population genetics analysis and dendrogram



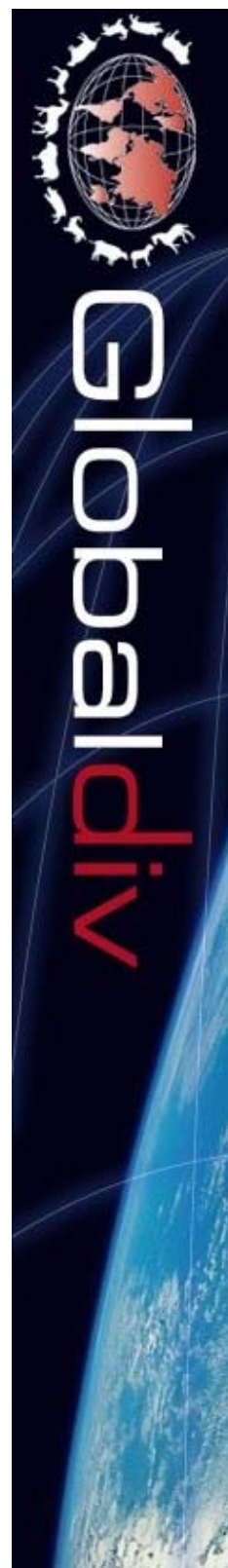
construction, STRUCTURE for the unsupervised clustering of molecular data and the investigation of genetic structure and admixture of populations, and DISTRUCT, for the representation of Structure results.

Dr. Ercole Zerbini from Cargill prepared his presentation in collaboration with Dr. Olivier Hanotte from ILRI, Kenya. He gave an overview of the main drivers affecting animal breeding and biodiversity with particular focus on Africa and Asia. In the first part of his presentation trends were described of human population growth and demand in animal product, in yield of cereals and animal products and of efficiency of feed conversion. Dr. Zerbini highlighted the existence of competition between the production of food, animal feed and biofuels and the consequent increase of food prices and malnutrition. Also he discussed the problem of water shortage that together with land availability represents a limit to animal production. The pro and cons of intensification and de-intensification of agriculture were also discussed. In the second part Dr. Zerbini addressed the challenges and approaches to maintain animal biodiversity in the developing world by *in situ*, *ex situ* and *in vitro* conservation strategies.

Dr. Linn Fenna Groeneveld, from the University of Göttingen/German Primate Center focused her talk on the biodiversity of wild fauna. In particular, Dr. Groeneveld studied the endemic, nocturnal lemurs of Madagascar with the aim of characterizing the genetic diversity of the genus *Cheirogaleus*. Both genetic markers (mitochondrial and nuclear) and morphological data were used to reconstruct the phylogenetic relationships and the taxonomic status of the populations sampled. Of great interest was the discussion about the species concept inside the genus: how many taxa do exist within *Cheirogaleus*? Where is the species boundary? Then, an extensive survey was presented on the distribution in space and time of the different taxa, using the existing bio- and phylogeographic hypotheses for Madagascar.

Dr. Stephane Joost is Research and Teaching Associate at GIS Laboratory (LASIG) of the Ecole Polytechnique Fédérale de Lausanne (EPFL). His talk aimed at introducing the present GIScience approaches to link genetics and geography. Genetic information is embedded within a geographic context, which should be considered in trying to understand genetic resources (the "landscape genetics" concept). Interestingly, the combination of GIScience with molecular biology lead to the development of a spatial analysis method to detect signatures of natural selection within the genome. To find out these signatures, spatial analysis takes advantage of the evolution of genetics toward genomics and of the subsequent availability of large data sets generated by large genome scans. This permits to compute many simultaneous univariate logistic regression models and to identify specific regions of the genome which are selected by environmental parameters.

Dr. Marco Pellecchia is a Postdoc from the Università Cattolica del Sacro Cuore of Piacenza. The core of his presentation focused on livestock and their domestication history. A detailed phylogeography of bovines and swine allowed biologists and anthropologists to reconstruct past human migrations. In fact, since the early Neolithic, human populations move away together with their own domestic animals: while the complex genetic history of *Homo sapiens* often masks the faint tracks of the past, genetic signals still detectable in livestock' genome help in unravelling the forgotten human events. This is the case of Italian *Bos taurus* from Tuscany, which definitively shed light on the Eastern origin of the ancient Etruscan civilization.



Prof. Pierre Taberlet, from the Laboratoire d'Ecologie Alpine of CNRS and the Université Joseph Fourier, in Grenoble, France was the last lecturer. Prof. Taberlet gave a comprehensive background on the domestication process and described the last results produced in his laboratories on sheep and goat domestication. Parallel analysis of mitochondrial DNA sequences from large numbers of wild and domestic sheep and goats permitted new insight on the domestication dynamics of these species. In particular sheep data indicate *Ovis orientalis* as the sole wild ancestors of domestic sheep, confirmed the existence of a large domestication centre in Eastern Anatolia and Northwestern Iran and excluded a previously hypothesized domestication site in the Indus valley. Goat data revealed signatures of early genetic management of wild *Capra aegagrus* and that in this species domestication has likely been a long process that occurred on a large geographic area in Eastern Anatolia and Northern Zagros. In both species domestication appears to have been a large-scale process involving no strong genetic bottlenecks, contrary to what observed in other species (e.g. cattle).

Two sessions, chaired by Prof. Tixier-Boichard and Dr. Negrini were dedicated to the discussion of 9 case studies selected among those proposed by participants. These were selected by chairs to represent different species, countries and environments. In the first session case studies were on sheep in Turkey, presented by Dr. Evren Koban from Middle East Technical University, Ankara, Turkey; cattle in Jordan, presented by Dr. Raed Al-Atiyat from Mutah University, Amman, Jordan; pigs in Bhutan, presented by Mr. Karma Nidup from University of Sydney, Australia; poultry in Vietnam, presented by Ms. Kim Cuc Ngo Thi from Georg-August University, Göttingen, Germany. In the second session case studies focused on ancient and modern Chinese pig, presented by Ms. Ran Ran Liu from China Agriculture University; on Poultry conservation in Egypt, presented by Mr. Mostafa Nassar from Humboldt University of Berlin, Germany; on European domestic dog, presented by Dr. Gregoire Leroy from AgroParisTech/INRA, France and on Hungarian Grey cattle morphology by computerized image analysis system, presented by Mr. Agos Maroti from Szent Istvan University, Budapest, Hungary. Finally a method for the Cryo-conservation of poultry was presented by Ms. Katarzyna Kasperczyk from Technology and Life Sciences in Bydgoszcz, Poland

In summary the Summer School touched, with a global view, farm animal farming systems, local and general trends and major drivers in biodiversity losses, the basic population genetics theory together with traditional and new technologies for the characterization of genetic diversity and reconstructing the evolutionary history of animal species and a number of examples and case studies that help in understanding the present day diversity of some of the main livestock species. How to use these and other information to evaluate and set up conservation priorities will be the target of the next GLOBALDIV Summer School.

The level of student satisfaction was evaluated through an anonymous questionnaire addressing logistic issues (location, travel, accommodation, services) and the scientific program (topics, lecturers, material and case studies). Results were extremely positive for all aspects and very few criticisms. Suggestions indicated the wish for more extensive software



sessions and for longer time dedicated to the discussion of case studies. Details on the results of the questionnaire can be downloaded from the GLOBALDIV website.

Lecturers were as well very satisfied of the level of discussion and involvement of the participants. With their consent, pdf versions of the presentations are now freely downloadable from the GLOBALDIV website (www.globaldiv.eu)

Participants received a GLOBALDIV Summer School Certificate of attendance. In addition 11 of them applied to sustain the GLOBALDIV Summer School examination consisting of 60 questions prepared by lecturers. All of them successfully passed the exam and gained two ECTS credits from the Università Cattolica, to be spent in any European University.

GLOBALDIV is now preparing the next events, the 1st GLOBALDIV Workshop to be held at the University of Technology and Life Sciences, Bydgoszcz, Poland on 18-19th March 2009 and the second edition of the Summer School, that will be organised in Piacenza in September 2009. More details will be distributed with the next Newsletter in January 2009.

I would like to thank sincerely the GLOBALDIV Summer School Organising Committee (Licia Colli, Paola Crepaldi, Elena Murelli, Riccardo Negrini, Marco Pellecchia) and all students that generously contributed with their work to the organisation of the initiative, in particular Lorenzo Bomba, Giordana Lucente, Rosanna Marino, Raffaele Mazza and Francesca Sibella; all lecturers, for their commitment to transmit their knowledge without restriction (and remuneration...) and all scholars, for their will to learn and active participation that stimulated interesting discussions within the group and contributed to create the right mood for standing long and tiring days of work. Finally I would like to thank Dr. Kor Oldenbroek for having made freely available to GLOBALDIV Summer School students copies of his book "Utilisation and conservation of farm animal genetic resources" Wageningen Academic Publishers (2007).

Thanks a lot!
Paolo Ajmone Marsan
(GLOBALDIV coordinator)

Article of the month: Towards self-sustainable European, REgional Cattle breeds

During the past decades, native, local/regional cattle breeds in Europe have extensively been replaced by specialized, high productive breeds. Local breeds are however recognized as important elements of agrobiodiversity, of agroecosystems and of our cultural heritage in Europe.



For such breeds a relevant question is which strategy would be effective to make/keep the particular breed successful.

The EURECA project will provide answers to this question and is aimed at assisting conservation, development and sustainable use of local/regional cattle breeds in Europe. Action EURECA 012 AGRI GEN RES 870/2004 receives financial support from the European Commission, Directorate-General for Agriculture and Rural Development, under Council Regulation (EC) No 870/2004.

Self-sustainability

The most secure conservation strategy for those breeds is to promote measures which contribute to self-sustainability of the breed. The main objective of EURECA is to provide guidelines for improved (conservation) strategies and breed self-sustainability. Profitability remains a key factor in maintenance of local breeds, which could be achieved, for example, by linking local breeds and their typical products or identification and promotion of the value of local breeds for their environmental services. Moreover, the contribution of the breed to the multifunctional character of agriculture (e.g. maintenance of rural cultural diversity, rural development and tourism, etc.) could be emphasized. And, we should not forget to organize conservation and breeding programs in an effective and efficient way, further strengthening the distinct and profitable characteristics of the breed.

State of the art knowledge and 'good practices' on conservation, development and sustainable use of local/regional cattle breeds will be exchanged between partners of the project and will be disseminated to a wider audience.

EURECA project halfway

The first year of the project was mainly dedicated to data collection on national level. The project partners carried out detailed breed assessments in their country. Breed assessment means that we collected information available about breed demography, the factors behind the trends, about breeding and conservation actions, and for each breed we carried out a 'strengths, weaknesses, opportunities and threats' analysis (SWOT). For 15 breed cases across Europe we have now detailed information available, collected from literature and from farmer/stakeholder interviews. This breed-specific data is in the process of analysis across countries at the moment.

Another work package was on the analysis, organization and status of cryopreservation activities related to local/regional cattle breeds in 5 selected countries.

Thirdly, parallel to the breed assessments and analysis of cryopreservation work, we explored available methodologies and software for the management of genetic variation within populations. During the next EAAP conference in Barcelona, we will dedicate (part of) a workshop program to this topic.



What's next

Next year, first results will be published and guidelines, best practices and policy recommendation will be developed and disseminated. For a number of selected breed cases we will continue working – in close collaboration with the major stakeholders – on strategy development towards breed (self)sustainability.

We will also carry out a Europe-wide survey on the status of (all) local/regional cattle breeds in Europe. A limited number of questions were selected from the breed case assessments and the analysis of the cryopreservation activities. This wider survey, in addition to the 15 breed cases, is expected to provide useful new data about the status of European cattle breeds, which may result in recommendations to further improve the regular breed monitoring system and recommendations for policy makers.

Website

At the project website: www.regionalcattlebreeds.eu you can find information about the project, about the partners in the project, the project description and the work packages. On our project website, we also published a series of 'breed of the months'. As an example of one of the breeds targeted in this project, we provide information about the Eastern Finncattle in this GLOBALDIV newsletter, which had dramatic low numbers in the 1980's, due to the choice for more milk producing breeds.

S.J. Hiemstra
Project Co-ordinator
Centre for Genetic Resources, the Netherlands

The breed of the month: Eastern Finncattle

Herdbook foundation: 1898

No. Breeding females: about 450

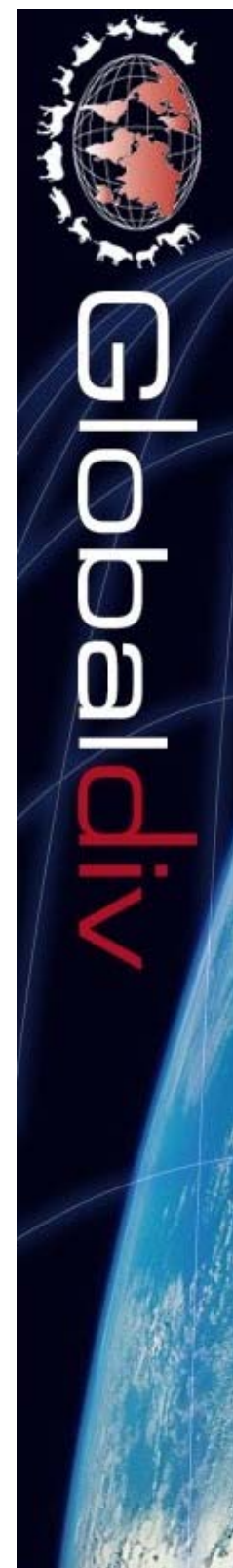
Trend: upward

Location: Mainly Eastern Finland

Local name: Itäsuomenkarja, Kyyttö

History from breed recognition to modern functions in rural society

The Eastern Finncattle cows were recognized as a separate breed in the 1890's. There was a need to improve milk production. The recognition of breeds was part of the development work. The general interest in well-characterized breeds coincided with strong nationalistic feelings at the time. The eastern part of the country – especially Karelia and Savo - was less



affected by imported cattle breeds compared to the areas in the western and southern part of the country. The keepers of the Eastern Finncattle founded a breed society in 1898 at the cattle show in Kuopio (Savo). This was the first cattle breeding organisation in Finland. The Northern Finncattle society was started in 1905 and that for the Western Finncattle in 1906.

The herdbook for the Eastern Finncattle began in 1914 and by 1927 there were 4 620 bulls and 14 650 cows registered by 4 233 society members. First attention in selection was given to breed characteristics. The cows in remote villages were considered as the most pure bred ones and breed description used words like handsome and gentle. From the 1920's onwards the emphasis on exterior traits made way to selection on recorded production.

The wartime hit dramatically the Eastern and Northern Finncattle. People from the lost eastern part moved with their Eastern Finncattle cows to different parts of the country. Along the declining cow numbers the three Finncattle societies resorted to collaboration and were amalgamated in 1946. At that time there were some 5 000 Eastern Finncattle in the herd book.

The Ayrshire cattle spread to eastern and northern parts of the country in the 1950's. Another blow to local breeds was to use Finncattle cows in crossing with imported Friesian semen in the 1960's. Consequently the less productive indigenous cows were abandoned as out-dated and unfashionable. The Eastern Finncattle sank to the bottom lowest numbers in the 1980's having only some 50 cows and less than 10 bulls left.

Prof Kalle Maijala at MTT Agrifood Research Finland paid as early as in the late 1960's attention to the erosion of the breed spectrum. He was one of the initiators for the EAAP working group on animal genetic resources started in 1980, for the Nordic Gene Bank which started as a working group in 1980 and as an independent entity supported by Nordic Council of Ministers in 1991, and for the respective national committee in Finland which has been functioning in different forms since 1983.

A very unique feature of the Finnish programme is the collaboration with the prison farms, which at one time housed cows of all the three Finncattle breeds. There is now a society for Indigenous breeds and the breeding organisation Faba Breeding is carrying out registration and advisory work also for the rare Finncattle breeds. Since joining the EU, Finland has been actively supporting farmers raising rare local breeds. Persons from different parts of the society have taken part in rescuing herds threatened to die out. Also the media is eager to report news on Finnish rare breeds and the general public knows all the indigenous breeds.

The widely available molecular genetic techniques have been used to give a general picture on the relationships between the cattle breeds and the state of the genetic variation within the breeds. The Eastern Finncattle breed has a high conservation value with a considerable deviation from the pool of cattle breeds and with a substantial amount of within breed variability.

The systematic work by enthusiastic and stubborn persons has proved fruitful. The cow register recognizes now the indigenous breeds. In 1997 the number of purebred cows exceeded a hundred both in the Eastern and Northern



Finncattle. At the moment in the Eastern Finncattle the number of purebred (down to four generations) cows is around 450. The number is slowly growing. The AI cooperatives have several bulls stored. In choosing the breeding cows and bulls, a special attention is given to the development of coancestries in the population. As an ex situ scheme, embryos and semen doses are annually deposited in the cryo-bank.

The breed is currently enjoying healthy popularity. There are few restaurants in major cities offering products made of milk and meat of Eastern Finncattle. They are also used in landscape management and even in modern therapy practices.

Breed description

Animals are typically red coloursided with broad winding band on the back. The zigzag band has made people to call animals with a name kyyttö, a local nickname to adder living also in Eastern Finland. When animals were first registered in the 1910's, majority had horns. By the 1920's most of the animals were polled. The bulls weigh about 600 kg and are 135 cm high. The figures for cows are 118 cm and 440 kg.

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Events calendar

- 64th British Cattle Conference, 2009. Telford, England. 19-21 January 2009; (www.cattlebreeders.org.uk/conference/index.php5).
- ANA World Conference "Animal nutrition: preparedness for the challenge". New Delhi, India. 14-17 February 2009. www.anft.org or else; (www.anaworldcon2009.in).
- Joint International Agricultural Conference 2009. Wageningen, NL. 6-8 July 2009; (www.jiac2009.nl).
- 1st GLOBALDIV Workshop - University of Technology and Life Sciences, Bydgoszcz, Poland - 18-19th March 2009
For more information soon at: www.globaldiv.eu

Bibliography

- Breed variation and genetic parameters for growth and body development in diverse beef cattle genotypes R.A. Afolayan, W.S. Pitchford, M.P.B. Deland and W.A. McKiernan.
<http://cup.msgfocus.com/c/14XWSvuknKigbn7SM>
- A study of heterogeneity of environmental variance for slaughter weight in pigs N. Ibanez-Escriche, L. Varona, D. Sorensen and J.L. Noguera.
<http://cup.msgfocus.com/c/14XWX5UGafZWL901E>



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- Bayesian prediction of breeding values for multivariate binary and continuous traits in simulated horse populations using threshold-linear models with Gibbs sampling
K. F. Stock, O. Distl and I. Hoeschele
<http://cup.msgfocus.com/c/14XWZo7R3vQN31W65>
- Mouse models for identifying genes modulating fertility parameters
P. Laissue, D. L'Hote, C. Serres and D. Vaiman - a review
<http://cup.msgfocus.com/c/14XX1GI1WLHDkUSaw>
- Incorporation of genotype effects into animal model evaluations when only a small fraction of the population has been genotyped
E. Baruch and J. I. Weller
<http://cup.msgfocus.com/c/14XX3YycQ1ytCNOeX>
- Recent advances in the regulation of milk fat synthesis
K.J. Harvatine, Y. R. Boisclair and D. E. Bauman - a review
<http://cup.msgfocus.com/c/14XX6gLnJhpjUGKjo>

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