



Globaldiv

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Editorial: 2010: What does it mean for Farm Animal Genetic Resources? A perspective from the UK

On January 11th 2010, the United Nations launched the International Year of Biodiversity (IYB). This is seen as a landmark to launch a more urgent, serious and focus effort to conserve our biological heritage for future generations against a back-drop of rapid global environmental change^{1,2}. 2010 is also the deadline year for a series of aggressive measures that were put in place in order to halt or in some cases reduce the loss of biodiversity. The Gothenburg Declaration of 2001 [COM(2001)264] set the EU target to halt the loss of biodiversity by 2010, focusing on natural resources, agriculture, fisheries and development. In pursuance of this ambitious target, a series of 'Headline Biodiversity Indicators' was adopted, following international agreement at the CBD Conference of Parties in 2004 and a pivotal meeting at Malahide under the Irish Presidency. The Streamlining European 2010 Biodiversity Indicators (SEBI 2010) project was subsequently established under the European Environment Agency to oversee implementation of the framework at both a EU and pan-European level. The Malahide meeting established "*Trends in genetic diversity of domesticated animals, cultivated plants, and fish species of major socioeconomic importance*" as a Headline Indicator under the theme of Status and Trends of the Components of Biological Diversity and established a 'Genetics Group' to develop this area. The aim was to produce the first phase of the headline indicators by 2006. These indicators were specified in the Commission

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COM(2006)216 entitled "Halting the loss of Biodiversity by 2010 - and Beyond (Sustaining ecosystem services for human well-being)". By early 2008, 26 'specific indicators' had been further distilled, and included two with a quasi-genetic component, 'Livestock Genetic Diversity' (measured only as number of breeds) and 'Patent Applications Based on Genetic Resources' - interestingly, wild species, including wild relatives of livestock, were ignored.

It is now widely accepted that these measures have been insufficient, that many countries did not fulfil their obligations and that the 2010 targets have not been met in a substantive way³. Renewed efforts are underway to address this under-performance and the signs are encouraging that the world is beginning to take the problem of biodiversity loss seriously. However, relatively little discussion has taken place in the literature since the beginning of 2010 on the subject of Farm Animal Genetic Resources (FAnGR). For example, in the UK, the National Standing Committee on FAnGR has become a member of the IYB Partnership, but does not state how it intends to contribute to the IYB or indeed what the role of 2010 is in the UK's FAnGR policy development. However, the UK government's Department of Environment and Rural Affairs (Defra) commissioned a review of FAnGR genetic studies involving UK livestock which was carried out by Warwick University, the results of which have recently been published by Defra⁴ and which aimed to pinpoint breeds and populations which have been neglected or poorly studied during projects which have been carried out to date. The results were quite surprising. Current guidelines recommend that minimally 25% of breeds should be studied, with up to 50 unrelated individuals from each breed examined with a specified set of microsatellite markers. For cattle 15 breeds have been typed to date, and the authors recommended a further 11 native breeds for study including a minimum of five which urgently need to be studied to be able to draw strong conclusions about the genetic diversity of cattle in the UK. This means that only 57% of UK native cattle breeds have been genotyped in a substantial way to date. In sheep the situation is even worse where only 17 of 84 UK registered sheep breeds have been analysed, and the analysis has involved a variety of different marker panels (a common problem, of course, and a focus of Globaldiv). The authors recommended four additional breeds to be urgently studied to achieve a reasonable description of UK sheep breed genetic diversity. The situation is much better for pig diversity, with 12 of 15 breeds analysed to internationally recommended standards to date. However, UK goat and poultry breeds have been almost completely overlooked (0/8 and 1/46 breeds genotyped, respectively), as is also the case with waterfowl.

These results are surprising given the fact that there have been a number of groups active within the UK on FAnGR characterization for the last 15 years and that UK FAnGR is rather well-organised and understood compared to many countries. It could be argued that the UK has particular issues because of the large number of indigenous and introduced breeds, especially in sheep and poultry, but it remains surprising that the coverage so far has been so scant. It seems clear, therefore, that this review should be replicated for as many European countries as possible, so the scale of this problem can be assessed and recognized. If the results in the UK were to be any way replicated across the rest of Europe, then the implications are that molecular characterization studies are not as far advanced as perhaps some might think. It would also imply that FAO and ISAG should



think very carefully about how to manage the transition from microsatellite to SNP and even whole genome datasets. One could, on the one hand, argue that it would be foolish to switch to more expensive technologies when relatively simple methods have failed to be taken up. On the other hand, one could argue that if microsatellite datasets are not as ubiquitous and extensive as perhaps it was assumed, then switching to more data-rich and standardized methods might be a wise move sooner rather than later. This is a matter for discussion and may also be something Globaldiv should take a collective view on.

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Article of the month - Current strategies to characterize Farm Animal Genetic Resources

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In all farm animal species, focusing on a few high-output breeds or lines in breeding increases the risk of erosion of genetic resources. Given that genetic variation in traits of interest is the basis for future breeding programs measures need to be taken to promote conservation and sustainable utilization of farm animal genetic resources (FAnGR). This requires comprehensive evaluation of these resources.

Domestication of animals was an essential step in human demographic and cultural development. A long history of migrations, in combination with the evolutionary forces of mutation, selective breeding, adaptation, isolation



and genetic drift has resulted in enormous genetic diversity within farm animal species, reflected in the existence of a large number of different strains and breeds. Conservation and sustainable use of farm animal genetic resources (FAnGR) requires, *inter alia*, demographic characterization, recording of production environments and effective data management. Modern genomics may facilitate sustainable management of these resources and ensure their exploitation for human benefits. Within the framework of the EC project Globaldiv, a consortium of scientist from various institutions reviewed the current state of knowledge in the characterization of FAnGR (cattle, yak, water buffalo, sheep, goats, camelids, pigs, horses and chickens). The findings and conclusions of the study have been set out in a review paper (Groeneveld *et al.*, 2010¹) and are summarized below.

Databases, demographic characterization and production environment

Effective management of FAnGR requires comprehensive knowledge of breeds` characteristics, including data on population size and structure, geographical distribution, the production environment, and within- and between-breed genetic diversity. Integration of these different types of data will result in the most complete representation possible of biological diversity within and among breeds.

Data collection and information dissemination are fundamental components in monitoring, conservation and utilization of FAnGR. FAO's Domestic Animal Diversity Information System (DAD-IS www.fao.org/dad-is) is widely known internationally. It is based on the EAAP (European Association for Animal Production) database initiated in the 1980s which contains a large number of factual data items on breeds from all over Europe. Redesign of DAD-IS led to FABISnet, a worldwide network consisting of communicating national and regional databases of which the current DAD-IS is the global node. Compared to other FAnGR databases, the FABISnet databases are the most comprehensive, with data from 198 countries and territories on more than 14,000 populations from 37 species, including descriptions of morphology, performance, reproduction and demographic data. Several other websites, particularly breed society websites, describe specific breed populations, while a few national websites cover breeds considered to be national heritage. Demographic data, such as the size and structure of the population, the risk status of a population depending on current, and predicted future, population trends and its geographical distribution, are fundamental to the assessment of the risk status of livestock breeds. Data obtained at the national level need to be considered in the context of the global demographics of the breeds in question. In a recently developed classification (FAO 2007b), breeds present in only one country are termed "local breeds" and those present in more than one country are termed "transboundary breeds", the latter being further differentiated into "regional"

¹L.F. Groeneveld, J.A. Lenstra, H. Eding, M.A. Toro, B. Scherf, D. Pilling, R. Negrini, E.K. Finlay, H. Jianlin, E. Groeneveld, S. Weigend, and the GLOBALDIV Consortium. *Animal Genetics* 2010 (in press)



and "international" depending on their distribution. In 2008, 7040 local breeds, 500 regional transboundary breeds and 551 international transboundary breeds were recorded in DAD-IS (FAO 2009). Data on the geographic distribution of breed populations is limited. However, efforts to improve the situation are underway - textual data describing breed distribution that have been entered into DAD-IS are being converted into georeferenced coordinates; more comprehensive georeferencing is regarded a priority and will be part of the implementation of a set production environment descriptors within DAD-IS.

Descriptions of breeds' production environments are important for many aspects of FAnGR management. They can be used to make inferences regarding the breeds' characteristics, based on the assumption that being exposed to particular climates, feed resources and pathogens will over time have led to genetic differences in adaptation to environmental conditions. While descriptions of the production environments of individual breeds - varying in their focus and level of detail - can be found, comparisons are difficult; and too often breeds are considered in isolation from their production environments. Efforts have therefore been made to develop a recognized set of "production environment descriptors" to be used throughout the world as common framework for describing production environments and to provide a basis for recording more detailed production environment data within DAD-IS. Under the proposed framework a production environment is divided into two main domains, the management environment and the natural environment. These domains are further broken down into a hierarchy of criteria. Most of the measures required for the natural environment domain (with the exception of the distribution of diseases and parasites) are now available on global high-resolution maps. Overlaying these data with georeferenced breed distributions will allow more comprehensive descriptions and analyses of the production environments.

Molecular markers help to identify ancestors of domesticated species

During the last two decades, our understanding of genetic diversity in FAnGR has been deepened significantly by technological progress in molecular genetics. Blood groups, enzyme polymorphisms, transplantation antigens and hybridisation techniques (as for example RFLPs) have been succeeded by mtDNA and Y-chromosomal haplotypes and autosomal microsatellites. For all domestic species, mtDNA has elucidated the relationships with wild ancestor species, and for most species it is also informative at the intercontinental level. In combination with archaeological data, it has shown that the most important areas for domestication events of the main livestock species and chickens are in Asia and Europe, with the South American camelids representing an exception. There is evidence of multiple domestication events for most species, often involving more than one ancestor species or subspecies and repeated introgression events of closely related ancestor species.



Sheep, goats and taurine cattle are presumed to have been domesticated in Southwestern Asia. The Indus valley (western part of the Indian Subcontinent) has been proposed as the site of domestication of indicine cattle and river buffalo, while the swamp type of water buffalo is thought to have originated in the Yangtze valley (China). The domestication of pigs is considered to have happened across Eurasia and Eastern Asia in at least seven separate events involving both European and Asian subspecies of boar. The yak is presumed to be the result of a single domestication event in China/Tibet, with at least three maternal lineages contributing to the ancestral yak gene pool. Domestic chickens are thought to be the result of multiple domestication events, predominantly of Red jungle fowl (*Gallus gallus*) in Southeastern Asia and possibly also involving *Gallus sonneratii* and maybe *Gallus lafayettii*. Horses were domesticated in a broad area across the Eurasian steppe, and in this species the husbandry style has left considerable signatures. It is presumed that mares were domesticated numerous times, but that only a few stallions contributed to the genetic make-up of the domestic horse. The last finding illustrates the use of Y-chromosomal haplotypes as a marker for mammalian patriline. This is still limited by the identification of haplotypes, but probably has the same potential as in human population genetics.

Molecular markers revealed great genetic diversity in FAnGR

Autosomal microsatellites have been the most frequently used molecular marker in genetic diversity studies in FAnGR over the last 10 years. A consistent finding with all molecular markers is that genetic variability declines with increasing distance from the domestication centres. This has been shown for pigs, sheep, goats, cattle and chickens. Insight into the extent of diversity in several species of FAnGR has been gained using microsatellites in numerous studies. Relationships between breeds have often been represented schematically via trees, networks, coordination plots or clustering diagrams. Microsatellite genotypes allow reconstruction of migration routes, reveal patterns of diversity, and allow breeds to be grouped according to their geographic origin based on model based clustering algorithms. The interested reader may find further details in the special issue of the Globaldiv project published in Animal Genetics ("A Global View of Livestock Biodiversity and Conservation" - Guest Editor: Paolo Ajmone-Marsan. - Volume 41 - Supplement 1 -May 2010 ANIMALGENETICS Immunogenetics, Molecular Genetics and Functional Genomics - ISBN 0268-9146).

One drawback of these studies, however, is that several of them use different microsatellite panels, which precludes the combination of datasets. Only a minority of the research institutes use the FAO-standardized microsatellite markers (see www.globaldiv.eu/docs/Microsatellite%20markers.pdf) for surveys. This seriously hinders comparison of breeds from different datasets, although a meta-analytic approach may be feasible. In recent years, single



nucleotide polymorphism (SNP) has been discussed as a very promising class of molecular markers. Efforts are needed to develop a standardized set of SNP markers for future biodiversity studies within FAnGR species.

In conclusion, improvement of our knowledge about mechanisms underlying genetic diversity may assist in the reconstruction of domestication events, determination of relationships between populations, and assessment of genetic variation within populations. In the near future, new technologies such as high throughput SNP typing or even whole-genome sequencing are likely to revolutionize our insight into the diversity and uniqueness of breeds, with the ultimate objective of gaining a fuller understanding of the molecular basis of functional diversity. Molecular genetic tools will provide information that is an essential prerequisite for effective conservation and management of genetic diversity within farm animal species.

The breed of the month - Finnsheep: A Northern Speciality

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The Finnsheep is the native sheep breed of Finland. Because of its special characteristics, the breed is a globally important genetic resource.

History of Finnsheep

Evidence on the Neolithic animal husbandry in Finland during the period of the Corded Ware Culture (in Finland 5000 - 4200 BP) is still incomplete but other younger archaeological findings clearly indicate that the sheep has belonged to the Finnish domestic fauna at least since the Bronze Age (in Finland 3500 BP). We can assume, however, that these oldest sheep stocks once brought to Finland are the ancestors of the native sheep breed of Finland, the Finnsheep.

Finnsheep has a unique domestication history. Recent studies show that sheep entered to Europe from the original domestication sites in the south-western Asia via more than one migratory episode. Finnsheep, like several other North European native sheep breeds, originates from the earliest domesticated sheep imported to Europe. During the prehistorical times, the earliest sheep populations were nearly entirely replaced by the later importations and a great majority of the present-day Eurasian sheep breeds descend from these younger stocks.

The genetics of Finnsheep has been investigated by comparing molecular genetic data of this breed with that of several European and Asiatic ones. These studies have indicated that the genetically closest relatives to the Finnsheep are the Karelian landrace populations in western Russia. Analyses of mitochondrial DNA (mtDNA) sequences have in turn showed that the most common ovine mtDNA haplogroups A and B are present in the





Figure 1. A flock of Finnsheep.

Finnsheep and several mtDNA haplotypes in the group A may have been "imported" to Northern Europe from the East. In addition, the Y-chromosome data suggest that the Finnsheep breed displays haplotypes which are not common in other European sheep breeds

Breed characteristics

The Finnish Sheep Breeders Association was established in 1918. Animals from eastern parts of Finland were mainly used as founders for the breed because sheep in the eastern parts of the country were considered heavier and bigger than those originating from the western regions. Originally, the Finnsheep was used mainly for serving domestic needs for wool and fur, but since the 1950s the main use has shifted to a multipurpose use of the breed mainly for meat, but also for handicraft wool, furs, and landscape management.

The Finnsheep is one of the most fertile sheep breeds, exhibiting several favourable fertility traits, such as early sexual maturity, high ovulation rate and large litter size. Finnsheep ewes may have quadruples or quintuplets, and the record is eight lambs. Finnsheep ewes have excellent mothering instincts and it is very rare for a ewe to reject her lambs. They also have a



remarkable milk production. Unlike most sheep breeds, the Finnsheep can breed any time of the year. In accelerated lambing systems, ewes lamb three times in two years.

The largest Finnsheep rams weigh over 120 kg and large ewes weigh almost 100 kg. The Finnsheep has a short tail, and no docking is needed in order to avoid hygiene problems. The animals are nowadays typically polled.

The meat of Finnsheep lambs is tender, fine-textured and has a mild taste. Finnsheep lamb carcasses do not easily become fat because the body fat reserves are held around the internal organs. From there, fat is easily removed, resulting in a very lean carcass.

Finnsheep wool is considered medium quality wool. It is typically soft, lustrous and elastic, and the fibre is highly crimped. Finn-wool is available in a variety of natural colours including white, black, brown and grey. It is considered to be one of the best wools for felting.

Different from many other sheep breeds, the Finnsheep is not very sensible to copper toxicity.

A low level of inbreeding

The demographic trends in the Finnsheep breed in terms of the status of inbreeding, effective population size, and coefficients of relationships between individuals have been explored. The study showed that average inbreeding



Figure 2. Finnsheep grazing.



coefficients by birth year for animals born between 1989 and 2005 ranged from 0.63% to 2.95%. Based on the rate of increase in inbreeding per generation and average generation interval (2.85 yr), an effective population size of 119 animals (overlapping generations not considered) or 122 animals (overlapping generations considered) was estimated for Finnsheep.

These results suggest that the Finnsheep breed has a healthy population structure and potentiality for continued genetic gain. Also molecular genetic data have indicated that the breed displays relatively high within-population diversity.

Important genetic resource

Because of its special traits, Finnsheep breed has been exported to over 40 countries in five continents. Used either as sire-breed or dam-breed in crosses and in the formation of new synthetic breeds, the gene pool of Finnsheep has improved the profitability of sheep farming in the world. The Finnsheep is the best-known Finnish breed globally and Finland has a national responsibility to conserve this multi-purpose breed.

Finland actively supports the conservation of Finnsheep genetic resources. For example, a living gene bank (comprising 270 ewes) for Finnsheep has been established on the Pelso prison farm in northern Finland. A cryo-banking of genetic materials has also been started.

GLOBALDIV EVENT

Livestock Biodiversity Workshop - FAO, Rome, May 5-6, 2010

Which policies and strategies are required to successfully maintain our European Farm Animal Genetic Resources? What are the opportunities of the latest methodologies to characterize and prioritize livestock breeds? During the past two years, the GLOBALDIV and EURECA projects have been focused on these questions. GLOBALDIV and EURECA are both GENRES projects which are co-funded by the EU AGRI GENRES program. This program aims to contribute to a better characterization of farm animal genetic resources and to strengthening of conservation efforts.

The GLOBALDIV and EURECA projects are pleased to announce a joint 2-days workshop for policy makers, scientists, NGO's and representatives of industry. Outcomes and recommendations from GLOBALDIV, EURECA and other GENRES projects will be presented. Lecture topics will span from genomics to socio-economic issues in biodiversity conservation.

More information is available:

www.globaldiv.eu/Livestock_Biodiversity_Workshop/index.html

REGISTRATIONS ARE CLOSED! On-site registration is NO MORE possible!



Events calendar

- 3-4 May, 2010. The 2010 Arthur B. Chapman Lectures in Animal Breeding and Genetics at the University of Wisconsin-Madison will be presented by Prof. Daniel Sorensen, Department of Genetics and Biotechnology, University of Aarhus, Denmark.
www.cattlenetwork.net/2010.htm
- 16-18 May, 2010. China Animal Husbandry Expo and Feed Industry Expo (CAHE) will be held on in Beijing, China.
www.caaa.com.cn/2010/en.php
- 17-18 May, 2010. The 14th QTL-MAS workshop organised by the Poznan University of Life Sciences, Department of Genetics and Animal Breeding, in collaboration with the Wroclaw University of Environmental and Life Sciences.
<http://jay.up.poznan.pl/qtlmas2010>
- 19-21 May, 2010. AAP2010 - International conference Adapting animal production to changes for a growing human population - University of Lleida, Spain (UdL). Auditorium Centre de Cultures (capacity 350).
www.aap2010.udl.cat/index.html
- An International Network for Capacity Building and Research in Climate Change Adaptation and Mitigation for Food Security.
www.iccamnet.org
- 31 May-4 June, 2010. 37th Session of ICAR - Riga, Latvia.
www.icar2010.lv/en/id3_1.php
- 31 May-2 June 2010. Animal Genomics for Animal Health International Symposium - "Maison de la Chimie", Paris, France.
<https://colloque.inra.fr/agah2010>
- May 31 - June, 2010. Bioinformatics Summer Course 2010: Analyzing Next Generation Sequencing Data. Kellogg Biological Station, MSU.
<http://bioinformatics.msu.edu/ngs-summer-course-2010>
- 7-11 June, 2010. Course on Quantitative Genetics of Response to Selection by Bruce Walsh at Wageningen University, The Netherlands
www.cattlenetwork.net/docs/training/quantitative.pdf
- 8 - 11 June, 2010. Stochastic Modeling Techniques and Data Analysis International Conference (SMTDA2010). Chania, Crete Greece
www.smta.net
- 14-30 June, 2010. Summer Institute in Statistics and Modeling in Infectious Diseases, Seattle, Washington, USA
www.biostat.washington.edu/suminst
- 27-30 June 2010. TWOWS Fourth General Assembly and International Conference "Women Scientists in a Changing World" ? Beijing China.
www.twows.org



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- 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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