



Globaldiv

GLOBALDIV NEWSLETTER

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Editorial - Beyond GLOBALDIV

Dear reader,

here is the last Globaldiv Newsletter. The GLOBALDIV action 067, that received financial support from the European Commission, Directorate-General for Agriculture and Rural Development, under Council Regulation (EC) No 870/2004, has come to the end and I would like to make a few final comments and wishful thinking for the future. I will not comment all the deliverables produced by Globaldiv. They are substantial (Table 1) and I have to acknowledge the generous and passionate contribute of all Globaldiv participants for these accomplishments.

I would rather like to talk about the experience had in running such a project and on the value of AgriGenRes initiatives, as Globaldiv and others, and on issues needing further discussion.

Globaldiv operated in the present background of great uncertainty. The demand of animal products is increasing worldwide, particularly in emerging and developing countries, at a rate higher than the human population growth. Farm animal breeding is therefore expected to grow in numbers and market share to satisfy this demand. However, farm animals, ruminants in particular, contribute a non-negligible proportion of total greenhouse gases that play a part in climate change. The precise extent and consequences of climate change are difficult to predict, but undoubtedly higher temperatures, droughts, desertification, extreme climatic events and shortening of growing season will

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Globaldiv

mostly affect food security in the Southern and already poorer part of the world, where consequences will be more dramatic. This uncertain scenario calls for flexible solutions and, in terms of animal breeding, genetic diversity grants this flexibility. Conversely, the loss of Farm Animal Genetic Resources (FAnGR) is occurring at an increasing pace. To date 1 livestock breed out of 10 is extinct, 1 out of 3 is endangered and 1 out of 3 has unknown risk status (FAO, 2007).

In synthesis the husbandry system is facing the challenge to quickly produce more animal products with less input and less waste, to grant adaptation to changing environmental conditions and to drive selection towards new market requests... quite a challenge. Solutions can be explored exploiting new technologies and existing genetic diversity. Technologies are quickly evolving and can be rapidly replaced by better ones, therefore the real key for winning the challenge is genetic diversity, that unfortunately when lost is lost forever. This diversity can and will be better exploited tomorrow than today, also for industrial production (e.g. it is unlikely that all good alleles for milk production captured during domestication are now concentrated in the Holstein breed.....).

Together with other AgriGenRes initiatives, Globaldiv aimed at contributing to this debate, at raising awareness on FAnGR conservations issues and at training and disseminating knowledge on modern tools supporting conservation decisions. In particular it:

1. discussed advances in tools for breed characterization at the phenotypic and molecular level (genomics and other -omic technologies);
2. organised a meta-analysis of existing continental scale molecular data to gain a global view of available FAnGR diversity, reconstruct its origin and dispersal and define relationship between breeds (e.g. unrelated breeds may possess different and complementary alleles for a same relevant trait);
3. discussed the economic value of diversity, not completely captured by the market, and the effects of current EU policies on FAnGR sustainable conservation;
4. investigated methods of integrated analysis of data collected from different sources (e.g. geographic, socio-economic, genetic, environmental data) and of conservation prioritization in the present scenario of limited resources.

Results of these discussions have been presented in seminars and lectures, published in scientific and non scientific journals and collected in technical reports.

However, the last and possibly most relevant task of Globaldiv is the synthesis of a 4-year experience in a series of Recommendations for future actions, with a main focus on research, that I would like to submit to your attention:



Research

1. Phenotypic characterization and other data collection:
 - Develop standard protocols for phenotype recording and characterize many breeds in terms of their phenotypes, farming systems, geographical distribution, socio-economic and cultural significance;
 - Identify new relevant phenotypes for adaptation, production, disease resistance, fertility and welfare, and design corresponding monitoring tools;
 - Develop portable tools for the cheap and non-invasive recording of phenotypes.
2. Standardization of molecular analyses for characterization:
 - Make reference samples and datasets publicly available and strengthen the existing international cooperation to promote the adherence to common marker sets (e.g. FAO-recommended panels), the standardisation of results from existing and planned studies, the integration of national or regional datasets and the achievement of a global analysis of FAnGR diversity;
 - Make the advanced genomic tools accessible to researchers in developing countries and applicable also to extensively managed local breeds;
 - Improve methods and pipelines for the analysis of genomic data and develop simple user-friendly and flexible WebGIS-based tools to facilitate the integration, comparison and analysis and (geo)visualization of the data required for implementation of diagnostic tools, Early Warning Systems, and multivariate/multicriteria prioritization methods.
3. Use of new molecular technologies for characterization:
 - Implement panels of new markers (e.g. SNPs) for the characterization of diversity that avoid ascertainment bias and include genomic regions involved in functional diversity (e.g. adaptation, disease resistance or behavioural traits);
 - Target the original molecular diversity and the footprints of selection and of genome evolution by genomic sequencing of breeds most closely resembling the unselected early domesticates and breeds representing an array of selection histories, from the former to the highly selected lines;
 - Assess the effect of selective breeding on the loss of diversity versus the emergence of new sequence variants;
 - Anticipate the relevance of epigenetics and copy number variation for diversity studies.
4. Farm Animal Genetic Resources meta-analysis:
 - Analyse breeds from 'empty spots' on the current phylogeographic map as well as samples relevant for joining existing datasets;
 - Develop and validate meta-analysis of existing datasets as demonstrated already for cattle microsatellite and join existing dataset by re-analysis of the most relevant samples with common markers;





- Develop methods for combining datasets generated by established and new technologies, respectively.
5. Farm Animal Genetic Resources conservation:
- Connect national gene banks to create a European gene bank for the preservation of FAnGR biological material for conservation purposes and accessible to the scientific community for research purposes;
 - Aim at a scientific consensus with regard to the most practical and scientifically sound approaches for breed prioritization including genetic, demographic as well as socio-economic, socio-demographic and environmental criteria;
 - Collaborate with wildlife biodiversity specialists, to learn from management and prioritization methods in a different biological context;

Communication and dissemination

- Promote the communication between the scientists, policy makers, breeders and the development of a policy infrastructure to implement the use of scientific data in conservation and strategic decision-making, e.g. through GenRes actions;
- Centralize in Web platforms information on worldwide FAnGRs and facilitate the access to all categories of information on the management and conservation of FAnGR;
- Increase the awareness of the non-use value concept and raise social recognition of conservation efforts.

Training

- Train young scientists on the use of novel tools (molecular and statistical) and on interdisciplinary approaches (socio-economic analyses, Geographic Information Systems) applied to breeding and management of Farm Animal Genetic Resources.

Policy

- Provide benefits for farmers that conserve Genetic Resources as service to the society and ecosystem;
- Formulate for all countries national action plans, for the monitoring, characterization and sustainable conservation of local breeds; facilitation of the support to animal recording and breeding programmes;
- Implement transboundary collaborations. Actions are to be designed globally and taken locally, from training to application;
- Allocate research funding to multidisciplinary research on FanGR;



- Promote these policies by international and national organizations concerned with management of animal genetic resources, including the provision of training in their implementation and interpretation.

As geneticist I would like to include a comment on molecular technologies. These are powerful and informative for breeding and conservation and for this reason it is positive that the scientific community and decision makers interrogate and debate on their use and on the effects and side effects of their use. In this final issue you can read two papers describing different opinions on breed conservation and improvement on the basis of results obtained from the use of DNA technologies. This is an emblematic example of the contrasting needs of modern animal husbandry, on the one side conservation, on the other rapid improvement of production. These needs, together with that of reducing environmental footprints, are the challenges of the century in animal breeding. Systems are to be developed that imply coexistence between a very efficient, productive and industrialised animal husbandry model to feed the world, and more traditional farming models that maintain biodiversity for future use. How such models can be all made sustainable from an economic and environmental point of view is still puzzling, therefore the issue is to remain high in the agenda of the scientific and decision making communities.

Acknowledgments

I have to sincerely acknowledge:

- The extraordinary contribution of all Globaldiv Partners and Experts. Working with them has been a privilege and a pleasure.
- People from the Animal Genetics group at the Università Cattolica in Piacenza. They have always participated enthusiastically to the organization of Globaldiv Summer Schools, some also as lecturers, becoming a key for School success: Licia Colli, Riccardo Negrini, Raffaele Mazza, Marco Pellicchia, Ezequiel Louis Nicolazzi, Lorenzo Bomba, Fatima Chegiani, Francesca Sibella, Giordana Lucente, Marco Milanese, Marcin Rezpuz.
- Elena Murelli, that deserves a special mention. She has been the core manager of the project. With her contribution coordinating Globaldiv was easy and pleasant.
- Polish friends from the University of Technology and Life Sciences of Bydgoszcz, for having hosted the first Globaldiv Workshop and in particular Prof. Marek Bednarczyk, Prof. Maria Siwek, Dr. Katarzyna Kasperczyk and Dr. Anna Slawinska.
- FAO for having hosted the second Globaldiv Workshop in Rome, and in particular Irene Hoffmann, Paul Boettcher, Beate Scherf and Badi Besbes.
- EPFL for having hosted the final Globaldiv Conference in Lausanne, and in particular Dr. Stephane Joost, Prof. Marc Parlange, Dean of the ENAC faculty, and Dr. Sylvie Stucki; in addition, also François Pythoud, Head of International sustainable agriculture Unit, FOAG Switzerland that co-financed the event.



- All summer school lecturers for the excellent work done. None of them received any compensation other than trip and lodging support.
- Olivier Diana and the GenRes team in Bruxelles, always following the project in a supporting mode.

Finally I would like to wish all the best to the new ESF project Genomic Resources (website: www.esf.org/activities/research-networking-programmes/life-earth-and-environmental-sciences-lesc/current-esf-research-networking-programmes-in-life-earth-and-environmental-sciences/advances-in-farm-animal-genomic-resources-genomic-resources.html) and to all Newsletter readers.

Sincerely,

*Paolo Ajmone Marsan
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| DELIVERABLE | DESCRIPTION | NOTES |
|---|--|---|
| Involvement of the Scientific Community | 35 scientists from 11 European countries and 5 International Organizations | |
| Summer schools | 3 Globaldiv Summer School held in Piacenza, Italy in September 2008, 2009 and 2010. A total of 109 students from 32 countries and 5 continents | Very good feedback from students very satisfied for lectures and for the set up of new connections and collaborations |
| Training material | 94 Summer school and workshop presentations freely downloadable from the website www.globaldiv.eu | |
| Meta-analyses of existing continental scale datasets | In cattle, sheep, chicken and goats | Selected breeds were genotyped with selected markers to create datasets bridging existing ones |
| Scientific papers | 1 open access Special issue in Animal Genetics and other publications in peer reviewed scientific papers | Papers in the special issue were the 1st, 2nd, 3rd 5th and 13th most downloaded Animal Genetics papers in 2010. |
| Communication towards the scientific community | Many posters/communications/seminars | |
| Communications towards the general public | Many seminars | |



| DELIVERABLE | DESCRIPTION | NOTES |
|---|---|--|
| Communication towards the scientific community | Different posters/communications/seminars | |
| Communications towards the general public | YY seminars | |
| Website | more than 1500 visits per month (56 per day) | |
| Newsletters | 19 issues, more than 67,000 downloads | |
| Documents | Technical guidelines and recommendations | |
| Collaboration with International Agencies | FAO, IAEA, ILRI, EAAP, WAAP | Active contribution to FAO guidelines for the molecular characterization of Animal Genetic Resources |
| Collaboration with other AGRIGENRES and FP7 projects | Eureca, Heritage Sheep, Elbarn, Efabis-Net, NextGen | |
| Spin-off of other projects | ESF Genomic Resources | |

GLOBALDIV FINAL WORKSHOP, EPFL. LAUSANNE, (SWITZERLAND) FEBRUARY 8-9, 2011

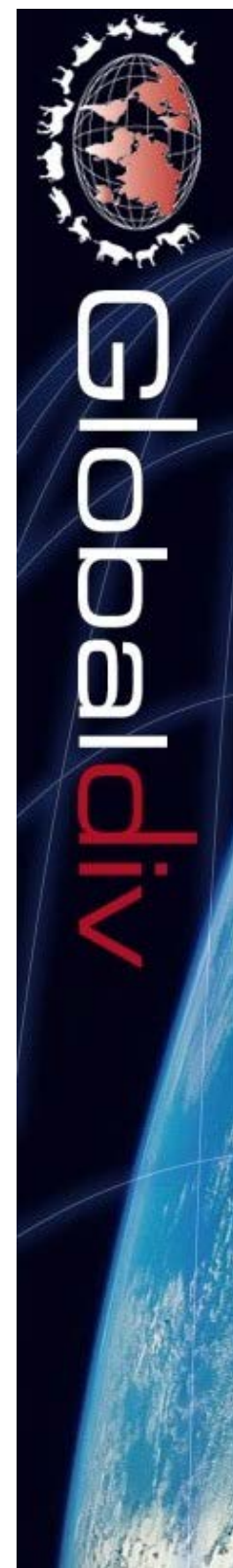
An international workshop Co-organized by the GLOBALDIV project (www.globaldiv.eu) and the ESF GENOMIC-RESOURCES project (www.esf.org/genomic-resources) will be held in Lausanne, at EPFL premises, Switzerland, on February 8 and 9, 2011.

The theme of the workshop has been "A global view of livestock biodiversity: experiences and lessons from wildlife biodiversity management".

This 2-days joint workshop was addressed to policy makers, scientists, NGO's and representatives of industry and received a good audience with 80 participants from different countries.

The workshop opened with a description of the very positive initiatives for Livestock diversity conservation implemented by our host Country, Switzerland, followed by an overview of the impact of EU policies on FAnGR. Following lectures described challenges, opportunities and case studies of characterization and maintenance of domestic and wildlife species, considering technological progress and maintaining a worldwide sight.

The second day the Workshop continued with a description of the results obtained by the joint collaborative effort of a large number of scientists within the GLOBALDIV project. Lectures focused on novel genomic tools for FAnGR characterization, examples of meta analysis of diversity, socio-economic aspects of FAnGR management, priority setting for conservation



and GIS based integrated analyses. Finally, an agenda for future research activities was proposed and discussed. The final part of the day was dedicated to the public kick-off of the new project GENOMIC RESOURCES. This project, coordinated by the local host, Stephane Joost, is ideally the continuation and advancement of GLOBALDIV, and focuses on the options offered by next generation sequencing and genotyping technologies in the livestock sector. Accordingly, the opening lecture of this project was on human genetics, the sector where to date new technologies have been applied the most.

Below are some details into presentations made during the workshop.

The Workshop was opened by **Prof. François Pythoud, Head of the International sustainable agriculture Unit, FOAG Switzerland** that gave a speech on Conservation of Farm Animal Genetic Resources in Switzerland. Prof. Pythoud described the different values (direct and indirect use, heritage, non-use and insurance values) associated to FAnGR and progress in developing synthetic indicators to attribute a total economic value to genetic resources. Then he presented the status of native Swiss breeds, the Swiss policy and regulatory framework for conservation of Farm AnGR and the on-going projects on national genetic resources conservation. Finally he stressed the importance of international collaboration and described the fully operative level of implementation of the FAO National Plan of Action in Switzerland.

Mr. Olivier Diana from DG AGRI RES GEN, European Commission explained in his talk the EU policy context on conservation and use of animal genetic resources. He first described how the EU Biodiversity Policy developed, starting from Göteborg declaration in 2001, and illustrated all on-going EU activities and actions under the EU Biodiversity Strategy Conservation and use of genetic resources. Mr Diana stressed the importance of the opportunities offered by these action and in particular by the three Axes of the Rural Development Programme (Axis 1: Competitiveness; Axis 2: Environment and Land Management and Axis 3: Diversification and quality of life) for the conservation and sustainable use of genetic resources in agriculture at national and regional levels. Then Mr. Diana discussed challenges facing Common Agricultural Policy in the near future (2014-2020). He also described EU financial instrument for research involving animal genetic resources, in particular collaborative projects in the Area "Food, Agriculture, Fisheries and Biotechnology" and Life + projects in the Area "Environment" of FP7. He finally described the achievements and communication policy of the first two Community Programmes for the conservation of genetic resources in agriculture and the targets of a possible future third program, still under discussion.

Prof. Henner Simianer (Georg-August-University Goettingen) gave a talk on "Animal breeding in the genomics era: challenges and opportunities for the maintenance of genetic diversity". His talk critically discussed options offered by genomic selection in small populations. He indicated that using high density SNP arrays, genomic based genetic improvement will likely be possible in small populations when these are related to larger populations and jointly used to estimate marker effects. He also showed that selection based on Genomic Enhanced Breeding Values (G-EBVs) should lead to a smaller increase of inbreeding compared to selection on pedigree-based BLUP breeding values, particularly in low heritability traits and that the



additional genetic progress that can be obtained through Genomic Selection can be used to increase selection pressure towards functional traits. He concluded that Genomic Selection provides good opportunities to maintain genetic diversity but that since most of the results so far available are based on simulations, more research is needed to verify models on real data.

Dr. Irene Hoffmann (FAO, Food and Agriculture Organization) explained the complexities of monitoring biological diversity in livestock. She pointed out that besides having to take into account the three levels addressed by the Convention of Biological Diversity (CBD, i.e. ecosystems, species and genes), in livestock it also needs to take into account the breed concept, an entity often defined on the basis of cultural aspects as much as morphology or genetics. Hoffmann stressed the difficulties that livestock community is facing, including the uneven availability of information and tools for characterization, inventory and monitoring of livestock biodiversity at the gene, species and ecosystem level. Despite the effort spent during the last years, characterization at the agro-ecosystem level still remains a big challenge, as it requires interdisciplinary approaches and the evaluation of complex long-term ecological relationships. Such analysis is very much needed for future sustainable ecosystem management, particularly related to emerging diseases and zoonoses often deriving from wild or domesticated animals. A key element is also the collection of information on breed phenotypes and performance to create linkages to the gene level of diversity. For molecular genetics, livestock characterization is far more advanced than in nearly other non-human, non-model animal species: molecular tools are at the forefront of genomic research and efforts have been made to establish standards and to create global databases to run meta-analyses of diversity. Due to its deep cultural and ethical significance, preserving livestock resources also becomes an institutional/public service rather than a purely scientific challenge. Because of the multifaceted drivers and threats affecting breed diversity, it is therefore crucial to monitor equally both agro-ecosystem and gene level drivers.

The importance of genetic monitoring for wildlife conservation was highlighted by the contribution of **Prof. Fred Allendorf (University of Montana, USA)**. He pointed out that, on one hand, the recent rapid advances in molecular techniques made genetic monitoring relatively easy and inexpensive to quantify temporal changes in the genetics of populations over tens or even hundreds of years. But on the other hand, the existing plans for the implementation of CBD at the national level only rarely recognize the need for monitoring the levels of genetic variation through time. This, besides undermining efforts to maintain genetic diversity at all levels, also endangers the economically exploited wildlife species through genetic risks associated to population augmentation, and hampers the recognition of ongoing processes of adaptation to changing climates, selective harvesting effects and human-driven landscape alterations. Instead, monitoring is foreseen for these adaptive responses as a future valuable tool in conservation biology, for identifying populations unable to evolve at sufficiently high rates and for identifying possible donor populations for genetic rescue. The realization of these potentials will be further augmented by technological advances, notably next generation sequencing technologies that may allow for monitoring at the level of whole genomes.



The same message, i.e. the importance of recognizing adaptive genetic variation, was emphasized by **Dr. Aurélie Bonin (LECA, Université Joseph Fourier, Grenoble, France)** through the description of a Population Adaptive Index (PAI). PAI accounts for the adaptive uniqueness of a given population among a set. Its estimation relies upon a population genomics approach which aims to detect loci with atypically high population differentiation compared to the rest of the genome, as a distinctive signature of divergent selection. Bonin illustrated the use of PAI in two case studies, one on the common frog (*Rana temporaria*) and the second on the threatened plant Austrian dragonhead (*Dracocephalum austriacum*) and the investigation of four different conservation strategies to identify the one most suitable to protect the maximum amount of either neutral or adaptive genetic diversity. She also stressed that a range of empirical case studies are now required to assess the impact of different parameters on PAI estimation before the index can be used to steer management decisions in wildlife or in livestock conservation.

The usefulness of genomic data to evaluate the adaptive potential of livestock breeds was also highlighted by **Prof. Olivier Hanotte (University of Nottingham)** during his presentation. He presented an approach for which the basis - landscape genomics - was developed at the intersection of livestock and wildlife sciences, illustrating the powerful potential of joining efforts to develop new methods to study adaptation. Hanotte stated that livestock landscape genomics offers a new start for the sustainable improvement of African livestock productivity. Combined with selection based on genome-wide analyses, this approach might offer the opportunity to tailor individual indigenous African livestock genotypes to current needs, while taking into account future environmental conditions. In this respect, livestock may represent an unique model for the study and the understanding on how animal species may be adapted to future changes of the environment such as climatic ones. This new field of livestock landscape genomic selection is building-up on the outcomes of past research aiming to characterize and to understand the distribution of indigenous livestock diversity, illustrating the importance of such work in the today context of the study of adaptation. Interestingly, genome wide screening of polymorphisms will provide also a fine map of genome introgression pattern in crossbreeds taurine x zebu, populations commonly found across most of sub-Saharan Africa. It may provide an interesting model for the understanding introgression pattern across the genome which follows hybridization of wild species.

The risk due to introgression also affects wildlife species, as **Dr. Iris Biebach (University of Zurich, Switzerland)** pointed out. Together with her colleagues, she investigated the Major Historic compatibility Complex (MHC) a gene family known to be important for the immune response in vertebrate, in Alpine ibex, *Capra ibex*, and Iberian ibex, *Capra pyrenaica*. Both species showed low genetic diversity at this gene, which is likely to be a consequence of their recent demographic history. Populations of both ibex, in fact, experienced severe bottlenecks due to strong hunting pressure during the last century and were subsequently subject to reintroduction/restocking starting from the few nuclei of individuals still surviving in the wild. Similarly, the two species exhibit low genetic diversity at neutral microsatellites loci and, unexpectedly, possess alleles that were identical to those found in domestic goats. According to Linkage Disequilibrium analyses, a likely



explanation for this is introgression between domestic goat and ibex which probably took place by chance during the recent evolutionary past of both ibex species.

Even though there is no complete agreement on the issue, it is generally accepted that introgression may represent a factor of endangerment from the point of view of the conservation of genetic diversity. This was exemplified by **Prof. Mike Bruford (University of Cardiff, UK)** through the description of the recent events which led to the removal of the ban to the bull semen import to the island of Jersey. Besides highlighting the risks of genetic erosion in similar cases, Bruford also highlighted the underlying lack of implementation of recommendations using real genetic data in conservation actions. According to his view, there is a general and widespread antipathy towards genetic data in the conservation community. This probably derives from the lack of a clear legislative and policy framework for genetic diversity in countries outside of North America and negatively affects both wildlife and livestock conservation efforts. As Bruford explained, to help improve this situation in the European Union, an EU FP7 support action project, CONGRESS "Conservation Genetic Resources for Effective Species Survival", has recently been launched to provide information and resources for biodiversity managers and policy makers to encourage the use of genetic data in biodiversity projects.

An overview of farm animal history has been presented by **Dr. Pierre Taberlet (CNRS/University of Grenoble, France)**. Cattle, sheep and goats were domesticated in the Middle East about 10000 years ago, spread out of the domestication centers, and gave many populations well adapted to the local conditions. After a period of soft selection during thousands of years, the situation changed dramatically 200 years ago with the emergence of the breed concept. The selection pressure strongly increased, and the reproduction among breeds was seriously reduced, leading to the fragmentation of the initial gene pool. About 50 years ago, the selection pressure was increased again via the use of artificial insemination, leading to a few industrial breeds with very high performances, but with low effective population sizes and the associated risk of genetic drift and inbreeding. Beside this performance improvement of industrial breeds, genetic resources are being lost, first because of the replacement of traditional breeds by high performance industrial breeds at the worldwide level, and second because of the loss of genetic diversity in these industrial breeds. Many breeds are already extinct, and genetic resources in cattle, sheep, and goats are thus highly endangered, particularly in developed countries. The recent development of next generation sequencing technologies opens new avenues for properly characterizing the genetic resources, not only in the very diverse domestic breeds, but also in their wild ancestors when they still exist. Based on sound genetic characterization, urgent conservation measures must be taken to avoid an irremediable loss of farm animal genetic resources, integrating economical, sociological, and political parameters.

The second day was opened by **Prof. Prof Paolo Ajmone Marsan (Università Cattolica del Sacro Cuore)** and GLOBALDIV Project Coordinator, that gave a general presentation of the GLOBALDIV project that focuses on the characterization and conservation of livestock genetic diversity. After the presentation of the background in which Globaldiv has



operated, he presented the objectives and the organization of the project. A total of 35 researchers from different countries, contributed as Partners or Experts to the project. They participated in Working Groups reviewing different issues of Animal Genetic resources: i) FAnGR characterization, with particular focus on new genomic technologies; ii) meta analysis of existing molecular data on FAnGR diversity; iii) socio economic aspects of FAnGR conservation; iv) integration of interdisciplinary data related to FAnGR and prioritization methods; v) future research needs. He also described Globaldiv training initiatives and communication strategies that reached a remarkable high number of stakeholders worldwide.

Dr. Steffen Weigend (Institute of Farm Animal Genetics of Friedrich Loeffler Institut - FLI) described the tools for FAnGR characterization. During his talk he presented a wide overview of both the traditional and the most advanced molecular methods adopted for the characterization of FAnGR. In particular Dr. Weigend focused on how to analyze multilocus genetic data to fully exploit the information they provide and, thorough the description of some relevant case studies on chicken diversity, he illustrated the methods for statistical data analysis, for a model-based clustering of individuals and for detecting selection signatures through a population genomics approach. Dr. Weigend also showed how varying the number of loci can influence the power of genetic analyses and affect the results.

Dr Johannes Arjen Lenstra, (Institute for Risk Assessment - Utrecht University), during his speech explained that meta-analysis of genetic diversity data sets may multiply the usefulness of separate studies on farm animal genetic resources by establishing relationship of livestock breeds from different regions, thus adding a global dimension to our view of genetic diversity. He showed a successful combination of the Econogene goat microsatellite data with data from Berne on Swiss and African breeds, analyzed with the same panel of markers. The separate position of the African breed suggests that the Econogene goat breed panel represents only part of the global genetic diversity of goat. Further he described a new Dutch project in which several Nordic goat breeds will be analyzed with the Econogene microsatellite panel. The genotyping will be carried out for 1000 euro per 16 animals. Anyone who would like to add a goat breed to the growing number of breeds (Econogene - Swiss - Nordic) is welcome to send in samples and obtain genotypes for the same price. He especially welcomed African, Asian and American breeds, which so far are underrepresented..

For sheep the Econogene microsatellite showed a less clear phylogeographic structure. Meta-analysis with Northern European, Asian and African breeds with a subset of the Econogene markers are underway. Meanwhile, the International Sheep Genomic Consortium has published a study on several breeds analyzed with 1536 SNPs and is working on the analysis of 74 breeds from Europe, Asia, Africa and America analyzed with 49034 SNPs. Meta-analysis of both datasets via 474 common markers was straightforward and successful. Comparison of the SNP genotypes of domestic and wild sheep suggested that the Southern-Italian sheep are more closely related to the wild sheep than domestic sheep from southwest Asia near the domestication site. He proposed an origin of wool sheep in South Italy, which in the Roman period were crossed into other European, Asian and African populations.



Dr. Janlin Han (International Livestock Research Institute) explained how the meta-analysis of genetic diversity with microsatellites can help to improve the characterization of FAnGR at a global scale. Due to the lack of standardization in microsatellite marker panels used so far in FAnGR diversity studies, the merging of the different dataset available to date represents an important though challenging task. The process of merging datasets requires the standardization of alleles between datasets generated in different laboratories or by adopting different experimental methods. When effective, this approach provides several advantages but requires a minimum number of common samples - the so called "standard samples" - to be genotyped in every facility. Dr. Han also described the most useful software for the meta-analysis of microsatellite data and illustrated the effectiveness of this approach through a case study specifically developed during the course of Globaldiv project: the merging of goat microsatellite dataset produced by the EU funded Econogene project and the FAO/IAEA CRP Asian goat project.

Prof. Philippe Baret (Université de Louvain) explained the role of socio-economics in FAnGR management and stressed the need for a timely paradigm shift in agricultural knowledge, science and technology. This will be necessary to meet the goals of development and sustainability and to respond to changing priorities and circumstances. The implementation of socio-economics into livestock management would contribute to the development of new economic models, such as the "prosperity without growth" one which should reduce the dichotomy between the production sector and the implications at the social, nutritional, animal health and environmental level. To effectively mend this gap, it is necessary to develop a diversity of options to cope with future uncertainties and a new paradigm for agriculture and food systems which takes into account e.g. agro-ecology, organic farming and low-input agriculture. To achieve such goal, on the one hand the socioeconomic issues should be translated into scientific questions and on the other hand, the recommendations given by scientists should be translated into action. To think FAnGR in the perspective of future systems, we need to keep options open, understand the diversity of options in agriculture and share methods with social scientists.

Dr. Paul Boettcher (FAO-AGAG) gives a talk on Priority Setting for Conservation of Animal Genetic Resources. For national management of animal genetic resources (AnGR), comprehensive planning and organization are critical. These activities help to ensure that most valuable AnGR are maintained, increase the efficiency of resource utilization and, when done properly, consider the interests of all stakeholders. A first step in this process is to make an inventory of breeds and their population sizes to determine which breeds are at risk and are thus candidates for conservation. Unfortunately, the number of breeds at risk often exceeds the number for which conservation resources are available; therefore, prioritization is necessary. Various factors may influence conservation priority, including risk of extinction, genetic variability, production and adaptive traits and historical and cultural importance. Because multiple factors can be important, the process of ranking breeds may be complex. Various approaches to prioritizing breeds have been proposed, including simply ranking breeds according to extinction risk, performing SWOT or other breed comparison analyses, subjectively voting and applying formal objective approaches that use advanced quantitative procedures to simultaneously account for all factors. Regardless of the approach used, several issues need to be



addressed: 1) having a clear conservation objective, 2) involving the relevant stakeholders, 3) obtaining and using the most accurate information possible and 4) reaching a consensus that all stakeholders can support. Finally, the results of the prioritization procedures must be shared with the livestock keepers and policy makers and the conservation plans have to be implemented.

Dr. Stéphane Joost (EPFL, Ecole Polytechnique Fédérale de Lausanne) and **Dr Christine Flury (Swiss College of Agriculture)** gave a talk on GIS data integration and multicriteria analysis for the assessment of breeding activities sustainability. In fact, the management and conservation of livestock genetic resources can take great advantage from the integration of multidisciplinary data. The prioritization of breeds to preserve needs the simultaneous evaluation of several factors and criteria, e.g. population and evolutionary genetics, animal husbandry practices, socio-economics and socio-demographics of the regions where animals are bred, environmental information (climate, geophysics etc.), political and administrative boundaries. This multidisciplinary approach can help to identify hidden relationships and to calculate synthetic indicators, thus allowing the depiction of complex scenarios and supporting decision-making for conservation and prioritization of breeds. The high potential of this integrated approach was highlighted through the case study of a Swiss autochthonous cattle breed, the Swiss Original Braunvieh.

At the end of the GLOBALDIV session, **Prof. Paolo Ajmone Marsan (UCSC)** presented the setting the agenda for future research activities in FanGR, explaining the recommendations given above in the editorial of this newsletter.

The final GLOBALDIV workshop concluded with a session dedicated to the new GENOMIC-RESOURCES project, a 4 years (2010 - 2014) European Science Foundation (ESF) Research Networking Programme that may be considered as GLOBALDIV's project follow-up. **Dr. Stéphane Joost (EPFL)** presented this new ESF action and **Dr. Panagiotis Deloukas (Wellcome Trust Sanger Institute - Hinxton, Cambridge - UK)** who gave a talk on "Genomic Approaches in Human Genetics" to explain to the participants the current advances in human genomics that should soon become available for application to animal science. Dr Deloukas presented examples of genetic studies of cardiometabolic traits, functional annotation, and gave an overview of next generation sequencing tools and related implications in human genomics.



ARTICLE OF THE MONTH N. 1. CATTLE FROM THE ISLE OF JERSEY: A PERFECT STORM FOR CHANGE

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More than a year has passed since a brief presentation for the case “to keep Jersey Island herd book closed” was given by Dr. Mike Bruford at the 2010 GlobalDIV workshop on biodiversity held in Rome, Italy. The topic of focus was brought about by a change in Jersey legislation put forward by the Royal Jersey Agricultural & Horticultural Society (RJA & HS) in 2008, which strongly supported the importation of Jersey semen onto the island after nearly 219 years of breed isolation. Arguably, this importation could be considered the most significant “depurification” of well-known globally popular breed that had established much of its notoriety from breed purity and special product branding in the marketplace.

The point of this commentary is to provide a contrasting viewpoint to this event tagged as undesirable. We intend to establish this as an event rich in economic and scientific opportunity, rather than focusing on the termination of possibly the longest running in situ-in vivo breeding experiment for cattle in the world. We assert that the importation of semen onto the Isle of Jersey was “a perfect storm” with technology, cryopreservation and economics all playing a role in making this important change possible. The genetic improvement of Jersey Island cattle provides a case study of potential opportunities and challenges that scientists and policymakers will face. This inevitable conflict will arise from opposing goals of implementing well-planned breed conservation efforts versus maintaining economic viability of livestock production and meeting the increasing global demand for livestock derived food. This paradigm will be typical of future scenarios of breed extinction caused by more extensive socio-economic pressures.

The events leading to the opening of the Jersey Island herd book are not surprising considering that the in situ conservation of a breed or population of livestock can only exist where the production system is profitable to the producers. As such, the 2008 legislation to allow importation of semen from bulls with high genetic merit for production should be considered quite pragmatic. The legislation is also somewhat ironic. Understanding this irony requires a step back into the origins and development of Jersey Island cattle, and the impact this breed had on dairy farming since first being recognized as a distinguishable type of animal in the mid 17th century.

The original Jersey cattle seem to be derived from rigid selection practices used by most island farmers on a limited local population of animals. These cows were thought to be mostly descended from 500 brown cattle given



as a tribute by the King of France to a group of Danish Vikings to leave the region around Nantes¹. This hypothetical origin of Jersey cattle has yet to be substantiated by high-density single nucleotide polymorphism (SNP) assays. Such SNP genotyping results could, possibly, identify conserved haplotype signatures between Jersey cattle and Nantaise oxen from the Normandy region. Nonetheless, by the mid-17th century, selection had resulted in a type of cattle recognized for special characteristics that included moderate stature, docility, and an ability to produce rich milk from modest amounts of forage.

Jersey selection practices were considered a success, because these cattle, when exported to other countries, were easily distinguishable from other cattle based on production quality. Exports became frequent as Jersey cows commonly crossed the Atlantic with sea captains to meet important nutritional needs during the journey. Upon reaching America, these animals could be sold for a premium. This productivity and constant migration caused Jerseys or "Alderneys", which they were sometimes called, to gain notoriety among farmers and breeders in America and England². The rising popularity coincided with a time in history when livestock breeding was just beginning to be recognized as a science, which also helped to thrust Jersey cattle to the forefront with prominent breeders.

Thus, the Isle of Jersey became known as a source of high-quality cattle, and the demand for Jersey genetics based on this reputation would remain high for more than two centuries. The demand was so great, in fact, that prior to 1763 both entrepreneurs and farmers exploited the reputation of "Alderney" cattle by passing animals from Normandy through Jersey to sell them duty-free in England. This flow of cattle agitated some of the native breeders. However, movement of counterfeit Jerseys through the island did not subside until legislation prohibiting this practice was finally passed in 17893. This legislation effectively ended the open pedigree of Jersey cattle. Subsequent regulations on importation were so strict that cattle from Jersey transported to competitions in England were not allowed return.

At the same time, producers that had imported genuine Jersey cattle recognized the need to protect the identity and value of these cattle procured at great cost. This realization led to the development an independent herd book to record pedigrees, track undesirable phenotypes, and stop fraudulent representation of the breed. The members of the RJA & HS did not adopt this idea of a formal recording of the pedigree until 18663. Shortly thereafter, the American Jersey Cattle Club was formed in 1868 to record and register pedigrees for cattle in the U.S.

The breeders from the Island of Jersey continued to reap the benefits of the genetics they developed by merchandising tens of thousands of cattle over the next 100 years. Again, this long tradition of exporting some of the most desirable dairy genetics lasted until the middle of the 20th century. Jersey cattle exports to the U.S. begin to decline after WWII, most likely because a premium was being paid for milk volume. This change in the dairy production market also meant a reactionary change by producers for a different type of dairy animal, and most U.S. producers considered Holsteins the premium. Of course, many U.S. and Canadian dairymen remained loyal to the Jersey breed, and large populations also existed in New Zealand and Denmark. Over the next 45 years, the national genetic evaluation programs of these larger Jersey populations led to a rapid rise in



the milk yield, production efficiency, and component traits of the typical registered Jersey cow. In contrast, the average production for native Jerseys remained static until the early 1980s, when an evaluation program was initiated. However, the gains in production were still significantly lower than the larger foreign herds, and the numbers of Jersey Island cattle continued to decrease as exports and profitability waned. The differences in average production between Jerseys from different national herds is exquisitely shown and described in a detailed report prepared for the RJA & HS by Dr. M. Bichard⁴.

During this last 30 years, there also was a growing concern among Island breeders that an intensification of selection based on a few elite animals could lead to a sharp rise in inbreeding. A diversity study completed on a sampling of animals across the island by Chikhi and colleagues clearly showed there was enough diversity within the population to sustain a closed herd⁵. This report also went on to conclude that imports of semen were not justified, and could lead to a further reduction in effective population size by overuse of popular sires. This conclusion is reasonable, but only in consideration of maintaining diversity in situ and assuming no overuse of popular native sires. Based on the reports by both Bichard and Chikhi and colleagues, it was clear that Island breeders still must decide what traits of Jersey cattle had more value^{4,5}. Was the goal to maintain economic sustainability through rapid genetic gain available in foreign Jersey genetics, or was there more value in maintaining uniqueness as a closed population with full pedigree recording?

The decision on whether to allow the importation of semen rested with the Jerseys legislature, known as the "States of Jersey." This body conducted an inquiry, or "scrutiny," of the issues involved⁶. The advent of cheap SNP-based beadchip assays that interrogate thousands of markers across the genome possibly helped tipped the scale of this decision towards economic sustainability in 2008. With these tools, Jersey Island breeders could effectively introduce new and superior production genetics from foreign Jersey herds. A historic repository of semen would provide a failsafe vault for conservation, and the original diversity could be re-constructed with the aid of these tools, if necessary. In addition, the SNP tools could be used to monitor the change in diversity as Jersey Island animals were enhanced with foreign Jersey chromosomes. The IlluminaSNP50 tool has already proved invaluable in quickly stopping the introduction of an impure Jersey bull, which upon being genotyped was identified to be carrying a fraction of non-Jersey genome. By using these genomics tools, the purity of the Jersey breed was maintained, while facilitating genetic improvement through the use of global germplasm.

In conclusion, these authors firmly believe that long-term sustainability of cattle production on the island of Jersey was undoubtedly enhanced through the importation of superior Jersey germplasm. Through genomics; the purity, diversity, and inbreeding levels of this island breed can be monitored and manipulated as seen fit. We believe that the decision made by the States of Jersey was one based on sound science and will prove to enable the continuation and conservation of a thriving dairy industry on the island.



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ARTICLE OF THE MONTH N. 2. POPULATION GENETICS OF THE ISLAND JERSEY CATTLE BREED: DATA, MANAGEMENT AND POLITICS

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In 1999, with funding obtained from the UK Department of Environment, Food and Rural Affairs (then the Ministry of Agriculture, Fisheries and Food) we carried out a genetic survey of UK cattle and sheep breeds and develop new statistical approaches to analyse molecular data for rare and minority breed conservation. As part of this project a study was carried out by MWB, Lounès Chikhi, Benoit Goossens and Alan Treanor (Ministry of Agriculture, States of Jersey), to assess the genetic diversity and structure of the island Jersey cattle breed. We were ably assisted by the Royal Jersey Agricultural and Horticultural Society (RJA & HS) who allowed us to access many of the island's herds to enable one of the first comprehensive studies of the genetic structure of a cattle breed across its entire native range. The Jersey had at that time become a popular breed across large parts of the world, but off-island populations had substantially changed from the indigenous population on the island of Jersey, which had been isolated from any imports of cattle from the rest of the world, including England and France, since 1789. As geneticists, this study presented an excellent opportunity to examine the structure of an isolated, island breed, where we could rule out the effects of recent introgression from other breeds as a source of genetic variation. Furthermore unusually, very detailed pedigree records have been maintained for much of its history, potentially providing information of the breed's dynamics and its changes over time and giving context to the results we would gain.



We examined the genetic diversity and structure of the island Jersey, and compared our estimates to those obtained for other breeds at the time. We also hoped to examine a longstanding problem in livestock genetic diversity by addressing the effects of differing sampling design (across the entire island, within parishes, and farms) on estimates of genetic diversity. By doing so, we also tested for evidence of inbreeding (a perceived problem within the breed which previous pedigree-based studies had attempted to quantify) and assessed the correlation between genetic differentiation and geographic separation among parishes. We carried out microsatellite genotyping for 12 loci in 223 individuals representing all of Jersey's parishes (church districts) except one. The results (reported in Chikhi et al 2004) were surprising. We found relatively high levels of genetic diversity across the island ($HE = 0.64$) a value that, at the time, was comparable to many continental breeds that had not undergone documented upgrading. Furthermore, although limited (and statistically significant, in some cases) genetic structure was detected among parishes and some farms, Bayesian partition analysis strongly supported the notion that the breed was a single genetic unit (Probability of $K = 1$ was 0.98). Finally, we could not detect evidence for inbreeding in the molecular data, and we inferred that gene-flow across the island to have been sufficient to overcome local genetic drift in nearly all comparisons.

In the context of discussions ongoing at the time, we concluded that the level of genetic diversity and its distribution within the island was substantial enough to provide the raw material for ongoing and future selection programs, including marker assisted selection, and concluded that it was therefore unnecessary to import unrelated genetic material to the island to mitigate against perceived low genetic variation. The genetic distinctiveness of the island Jersey breed had been demonstrated in several molecular studies (e.g. Wiener et al 2004) and there was evidence, including from molecular data (e.g. Hansen et al 2002) that this distinctiveness is less pronounced in Jersey cattle off-island, which implied that introgression (upgrading) from other breeds has occurred at some time in the past. Further, selection regimes even in putatively non-introgressed continental populations are known to have differed substantially from on-island management practices (particularly in terms of male effective population size).

In 2007, the RJA & HS decided, however, to apply to remove the 1952 State legislation preventing the importation of cattle semen onto the island, following a vote where 79% of registered milk producers participating favoured the proposition (representing 62% of the total dairy farmers on the island). Scientific evidence in favour of commencing importation of semen centred around work carried out by Dr Maurice Bichard, which concluded that *"the Island herd is some 15% to 20% behind the genetics of Jersey herds internationally in terms of average milk yields. It also demonstrates that genetic progress from 1988 to 2007 has been slow (0.6% per annum) principally because of the small cattle population and lack of uptake by producers. In addition ...the effect of the dairy industry restructuring in 2002 which reduced the population (from 4,500 cows to 3,300) to a level where even genetic maintenance, because of inbreeding, may not be achievable in the medium to long term (cited in States of Jersey, 2008).*



Unsurprisingly, perhaps, the evidence from our study in 2004 was not cited in the applications since it indicated very low levels of inbreeding in the island Jersey population. However, it was also stated in the application that *"To safeguard the pedigree of the Island breed the RJA&HS Council have resolved to only register the offspring of bulls with a pedigree that shows that all its forebears have a pure Jersey pedigree for at least 7 generations"*. It is now a matter of historical record that the review of the Corporate Services Scrutiny Panel of the States of Jersey ruled in favour of removing the importation ban on 16th July 2008, paving the way for the subsequent importation of genetic material into this population, with the proviso that *"the storage of a complete set of current local genetics off-Island as a precursor to any importation"* would be required.

During the consultation process, along with other organisations, we were allowed to submit evidence from our study on the genetic diversity and inbreeding status of the island population. The transcripts from the review document affirm that some elements of inbreeding considerations were discussed. These specifically addressed the potential negative consequences of using a limited number of imported sires, and links to a study carried out by GLHA in 2000 which showed that the list of active Jersey bulls on UK mainland has a strong North American influence; the North American population at the time being characterized by a small cohort of related dominant sires. However, our molecular data are not explicitly referred to in the transcript of the discussions on genetic diversity and how it may change as a consequence of the importation – in effect our results seem largely to have been overlooked or simply ignored.

But how important are these considerations? It is without question that a strong majority of milk producers on the island placed a greater priority on the perceived rapid improvement of the breed over its genetic distinctiveness. It is also evidently the case that livestock production is first and foremost a business. The Unique Selling Point of Jersey cattle has traditionally been 'Gold Top' milk, the luxury creamy product that is still marketed with a strong regional focus today. Interestingly, the following statement can still be found on the marketing website for this product: *"The Islands of both Jersey and Guernsey have, for decades, prohibited any other breed of cattle from their land to ensure that the blood line and off-spring are kept pure. Channel Island milk is rich and creamy yet is still only 5% fat. It tastes delicious as a drink in its own right, and anything made with Channel Island milk also takes on this superiority."* (www.gold-top.co.uk). It seems, therefore, that marketing of Jersey cattle products still values the distinctiveness of these island breeds, even in light of the decision of 2008, which, it could be argued, renders this marketing ploy obsolete.

If one examines the implications of this dilemma in the context of global Farm Animal Genetic Resources (FAnGR) policy and recommendations and if, in particular, one examines the UK national report for the FAO's State of the World's Animal Genetic Resources in 2002, the following statements are to be found:



4.2.2 **Distinctive breeds** (designated D in Appendix 3) are important because distinctiveness is identified by FAO as a high priority criterion and because of its cultural interest. Native breeds at risk with special morphological characteristics, performance characteristics or great genetic distance should be identified and prioritised in conservation programmes. Such breeds are of particular interest under the Convention on Biological Diversity (CBD). Their genetic importance may justify incentive payments without the qualification of environmental factors, and they should have priority in characterisation studies.

And in Recommendation 5.1.3.2:

Breeds at Risk (Locally Adapted, Distinctive and Rare). National cooperation is recommended in the following areas:

- **Use of biological impact studies.** Assessment of the possible effect of substitution of native AnGR by exotic breeds by the application of genetic (biological) impact studies (Rare Breeds International 2001) preceding importation, including the evaluation of incoming genetic material is considered advisable.

The above definition and recommendation is broadly in line with FAnGR policy enacted by the FAO and many other countries in the context of conserving locally distinct genetic resources. In Appendix 3 of the UK Report, the Jersey (Island) breed is recorded as **D** (Distinctive) and **L** (Locally Adapted). It can, of course, be debated as to whether the evidence base for the breed designations used by the UK in the SOWAnGR Report are sufficiently robust to justify these designations and whether, by extension, what has occurred in Jersey contravenes these recommendations. It is also the case that the autonomy of the States of Jersey renders the applicability of these recommendations rather questionable. However, in our opinion, there is little doubt that the actions carried out in 2008 are contrary to the spirit of the UK report. At the very least, it we would argue that additional research on characterization of locally adapted traits should have been carried out prior to the importation of semen (following 4.2.2). In a sense, this example shows the need to demonstrate such local distinctiveness in a sound scientific manner, to provide evidence for or against actions such as occurred in 2008.



In 2007 Rare Breeds International released the following policy statement on British cattle breeds: "*Breeds and populations that are at risk are recognised by Rare Breeds International (RBI) through the application of three primary indicators, namely numerical scarcity, geographical concentration and genetic erosion. The severity of risk is categorised in three steps of Critical, Endangered and Vulnerable.*

A significant number of breeds or populations in Britain are at risk, but the exceptional importance of a few merits a high prioritisation for their conservation. The highest priority currently is placed on three cattle populations, namely Vaynol, Chillingham and Jersey (Island). Vaynol cattle are found only in one herd and have a breeding population of only one bull and circa twenty cows. The herd originated about 100 years ago. Chillingham cattle are a semi-feral group found in one closed herd in Northumberland with a small reserve group in Scotland. The population has been closed since the eighteenth century and numbers less than 100 animals. Jersey (Island) cattle have been a closed population since the late nineteenth century, and are the source of all other Jersey populations. The priorities are to increase the numbers of Vaynol cattle and to protect the integrity and distinctiveness of the closed populations of Jersey (Island) and Chillingham cattle."

While the Island Jersey cattle breed is not numerically scarce [although it may be classified as 'rare' under criteria currently being discussed by FAO and ERFP], the importation of semen and the inevitable change in the genetic structure of the breed on the island, may change its status in the medium-term. There are many examples where introgression of genetic material from other populations or breeds has altered the status of a breed seemingly irretrievably (even in cases where original breed semen is available) and from our perspective, the potential irreversibility of the loss of distinctiveness of a population is a vital consideration. The production ethic that has driven, for example, the surge of the Holstein in locally adapted breeds across the globe has already changed the genetic landscape of the world's domestic cattle in a potentially irreversible manner, and many local FAnGR are in danger of being lost as a consequence. It is our contention, therefore that while the decision to wed the Island Jersey to this process may seem attractive in the short term, but we would argue that it may prove counter-productive in the medium term, and then it may be too late or be perceived as being too difficult to undo.

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ARTICLE OF THE MONTH N. 3. MONITORING GENETIC CHANGE IN WILD POPULATIONS OF FISH AND WILDLIFE.

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Genetic monitoring is a valuable tool for the management and conservation of fish and wildlife populations. Recent rapid advances in molecular genetic techniques make it relatively easy and inexpensive to quantify temporal changes in the genetics of populations over tens or even hundreds of years (Schwartz et al. 2007). We co-direct a Working Group entitled "Genetic monitoring: Optimal design and development of tools for data analysis" that is jointly funded by the US National Center for Ecological Analysis and Synthesis (NCEAS) and the US National Center for Evolutionary Synthesis (NESCent).

Genetic diversity is the foundation for all biological diversity; the persistence and evolutionary potential of species depend on it. World leaders have agreed on the conservation of genetic diversity as an explicit goal of the Convention on Biological Diversity (CBD). To assess the extent to which genetic diversity is currently recognized in national biodiversity policy programs, we used information available at the convention's website to review National Biodiversity Strategy and Action Plan of a subset of countries party to the CBD (Laikre et al. 2010a). Our aim was to investigate whether individual parties state in their strategies and action plans that genetic variation of wild animals and plants is to be conserved in their country and whether they explicitly recognize the need for developing monitoring programs for this diversity. Existing national plans for implementation of the CBD genetic diversity goal clearly are insufficient. Less than half of the reviewed countries have included explicitly the goal of conserving genetic variation of wild animals and plants, and only 20% recognize the need for monitoring this level of variation. Failure to maintain genetic diversity undermines efforts to maintain diversity at all other levels. International support and effort are urgently needed to monitor all components of diversity, including genetic diversity.



Large-scale exploitation of wild animals and plants through fishing, hunting and logging often depends on augmentation through releases of translocated or captive raised individuals (Laikre et al. 2010b). Such releases are performed worldwide in vast numbers. Augmentation can be demographically and economically beneficial but can also cause four types of adverse genetic change to wild populations: (1) loss of genetic variation, (2) loss of adaptations, (3) change of population composition, and (4) change of population structure. While adverse genetic impacts are recognized and documented in fisheries, little effort is devoted to actually monitoring them. In forestry and wildlife management, genetic risks associated with releases are largely neglected. We outline key features of programs to effectively monitor consequences of such releases on natural populations.

We have evaluated the ability of a linkage disequilibrium estimator of effective population size (N_e) and a simple capture-recapture estimator of abundance (N) to quantify the size and trend of stable or declining populations, using simulated Wright–Fisher populations (Tallmon et al. 2010). In general, monitoring N_e proved a more robust means of identifying stable and declining populations than monitoring N over most of the parameter space we explored, and performance of the N_e estimator is further enhanced if the N_e/N ratio is low. However, at the largest population size ($N = 10,000$), N estimation outperformed N_e . Both methods generally required more than five generations to pass between sampling events to correctly identify population trend.

Widespread environmental changes including climate change, selective harvesting and landscape alterations now greatly affect selection regimes for most organisms. How animals and plants can adapt to these altered environments via contemporary evolution is thus of strong interest. We have considered how adaptive responses can be studied by genetic monitoring via repeated analysis of the same populations over time (Hansen et al. in revision). After describing monitoring designs we develop explicit criteria for demonstrating adaptive responses. These include testing for selection and establishing clear links between genetic and environmental change. We reviewed a few exemplary studies that explore adaptive responses to climate change in *Drosophila*, selective responses to hunting and fishing and contemporary evolution in *Daphnia* using resurrected resting eggs. We further reviewed a broader set of studies to assess how well they meet the proposed criteria. Only 9% fulfill all criteria. Many (57%) fail to rule out the alternative hypothesis of replacement by a different, better adapted population. Likewise, 55% of studies based on phenotypic variation fail to test for selection as opposed to drift. These shortcomings can be addressed via improved experimental designs.

We foresee monitoring of adaptive responses as a future valuable tool in conservation biology, for identifying populations unable to evolve at sufficiently high rates and for identifying possible donor populations for genetic rescue. The realization of these potentials will be further augmented by technological advances, notably next generation sequencing technologies that may allow for monitoring at the level of whole genomes.



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THE BREED OF THE MONTH. JERSEY CATTLE

Jersey cattle, or Jerseys, (also with the corresponding lower-case spellings), are a breed of small dairy cattle. Originally bred in the Channel Island of Jersey, the breed is popular for the high butterfat content of its milk and the lower maintenance costs attending its lower bodyweight, as well as its genial disposition. Possibly the best known example of the breed outside the United Kingdom is Elsie the Cow, the famous mascot of Borden, Inc., in the United States. Her face is portrayed on cans of Eagle Brand Sweetened Condensed Milk, cheeses, fresh and shelf-stable milk.

The Jersey cow is quite small, ranging from only 360 to 540 kg (800 to 1200 pounds). The main factor contributing to the popularity of the breed has been their greater economy of production, due to:

The ability to carry a larger number of effective milking cows per unit area due to lower body weight, hence lower maintenance requirements, and superior grazing ability.

Calving ease and a relatively lower rate of dystocia, leading to their popularity in crossbreeding with other dairy and even beef breeds to reduce calving related injuries.

High fertility

High butterfat conditions, 6% butterfat and 4% protein, and the ability to thrive on locally produced food.[1] Bulls are also small, ranging from 540 to 820 kg (1200 to 1800 pounds), and are notoriously aggressive.

Castrated males can be trained into fine oxen which, due to their small size and gentle nature make them popular with young teamsters. Jersey oxen are not as strong as larger breeds however and are generally out of favor among competitive teamsters.





Due to the small size, docile and inquisitive character and attractive features of the Jersey cow, small herds were imported into England by aristocratic landowners as adornment for aesthetically landscaped parks.

Jerseys are adaptable to hot climates and are bred in the hottest parts of Brazil.

Jerseys come in all shades of brown, from light tan to almost black. They are frequently fawn in color. All purebred Jerseys have a lighter band around their muzzle, a dark switch (long hair on the end of the tail), and black hooves, although in recent years color regulations have been relaxed to allow a broadening of the gene pool.

They are calm and docile animals, but tend to be a bit more nervous than other dairy cow breeds. They are also highly recommended cows for first time owners and marginal pasture.

Unfortunately, they have a greater tendency towards postparturient hypocalcaemia (or "milk fever") in dams and frail calves that require more attentive management in cold weather than other dairy breeds due to their smaller body mass and greater relative surface area.

EVENTS CALENDAR

- 1) 37th ICAR session on "New technologies and new challenges for breeding and herd management », Bourg en Bresse, France (22 - 24 June 2011) <http://www.icar2011.fr/>



- 2) 62nd Annual Meeting 2011 - Stavanger, Norway (29 August - 2 September 2011 - <http://www.eaap2011.com/index.php>)
- 3) Eighth International Symposium on the Nutrition of Herbivores (ISNH8) - Aberystwyth, Wales UK, 6 - 9 September 2011 - www.isnh8.org
- 4) 8th (RBI) Global Conference on the Conservation of Domestic Animal Genetic Diversity to be held in Tekirdag (TÜRKIYE) in October 2011 <http://rbiglobalconf2011.nku.edu.tr>
- 5) Socio-economic and Cultural Values of Farm Animal Breeds. 7- 9 September 2011 in Reykjavik, Icelan. Organised by NORDGEN (The Nordic Genetic Resource Center) and The Agricultural University of Iceland
- 6) Summer school. "Animal breeding meets social sciences". 26-29 September 2011, Vienna, Austria. BOKU-University of Natural Resources and Life Sciences, Vienna, Austria. www.boku.ac.at

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178 partners located in 25 Member States and 12 non EU countries, and a total EU co-funding of EUR 8.9 million. The projects and overarching framework are available on the following links of the web site of DG AGRI:

http://ec.europa.eu/agriculture/genetic-resources/publications/index_en.htm

http://ec.europa.eu/agriculture/genetic-resources/actions/index_en.htm

- A Global View of Livestock Biodiversity and Conservation Special Issue of *Animla Genetics* - Co-ordinators: Paolo Ajmone-Marsan and Licia Colli.- Journal compilation © 2010 Stichting International Foundation for Animal Genetics
- European Livestock Breeds Ark and Rescue Net (ELBARN) Area Action Plans - ELBARN European Project 2010
- Farm animal breeding, identification, production recording and management - 37th ICAR Biennial Session (Riga, Latvia 31 May - 4 June 2010) Editors: E. Skujina, E. Galvanoska, O. Leary & C. Mosconi
- Joost, S., Colli, L., Bonin, A., Biebach, I., Allendorf, F., Hoffmann, I., Hanotte, O., Taberlet, P., Bruford, M. and the GLOBALDIV Consortium (accepted) Promoting collaboration between livestock and wildlife conservation genetics communities, *Conservation Genetics Resources*
- CONSERVATION BIOLOGY FOR ALL - Free conservation biology textbook

" Oxford University Press makes conservation biology textbook by some of the world's most prominent ecologists and conservation biologists available as free download *Conservation Biology for All* provides cutting-edge but basic conservation science to a global readership. A series of authoritative chapters have been written by the top names in conservation biology with the principal aim of disseminating cutting-edge conservation knowledge as widely as possible. Important topics such as balancing conversion and human needs, climate change, conservation planning, designing and analyzing conservation research, ecosystem services, endangered species management, extinctions, fire, habitat loss, and invasive species are covered. Numerous text boxes describing additional relevant material or case studies are also included.

The global biodiversity crisis is now unstoppable; what can be saved in the developing world will require an educated constituency in both the developing and developed world. Habitat loss is particularly acute in developing countries, which is of special concern because it tends to be these locations where the greatest species diversity and richest centers of endemism are to be found. Sadly, developing world conservation scientists have found it difficult to access an authoritative textbook, which is particularly ironic since it is these countries where the potential benefits of knowledge application are greatest. There is now an urgent need to educate the next generation of scientists in developing countries, so that they are in a better position to protect their natural resources".



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