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IN SITU CONSERVATION OF LIVESTOCK AND POULTRY:
WHY IS IT NECESSARY? WHO WILL DO IT? WHO WILL PAY FOR IT?

Donald E. Bixby, DVM, American Livestock Breeds Conservancy
Robert L. Taylor, Jr., PhD, University of New Hampshire,

The past five years have demonstrated the ability of the National Animal Germplasm Program to begin to successfully capture and cryopreserve an impressive sampling of the genetic diversity of our livestock resources. That success has drawn attention to the need for in situ conservation to augment the genetic materials that can be saved by cryopreservation.

Cryopreservation is not the answer for all species nor does it reflect the conservation value of evolving, living populations. Cryopreservation is less than optimal for ova and embryos for swine or poultry. Poultry semen cannot be efficiently frozen and its preservation represents only half of the genome. Living populations continue to change because of genetic drift and selection pressures including changes in markets, management systems; environments; as well as scarcity of resources such as energy and water. Most importantly, animal scientists must see living animals to recognize needed traits.

The breed or strain level is the genetic unit of predictability. Taken together, the range of breeds and strains represent the genetic diversity within domesticated species. Several types of breeds/strains developed with characteristic degrees of human and natural selection: Landrace populations; Standard breeds; Industrial breeds and strains; Research strains; Long-term feral populations. In situ conservation issues loom largest for swine and poultry because of the constraints of cryopreservation technology, and for landrace and feral populations that are environment dependent for selection.

The successful conservation of genetic diversity is determined by how many people are involved and who is involved. Conservation can be done in a large centralized facility managed and overseen by USDA, a number of smaller satellite facilities with some level of central support and oversight, a centralized facility supported by smaller satellite locations, or in other structure.

Government and academic institutions have been important conservators in the past, but now we are seeing widespread abandonment of genetic collections because of economic restraints. Corporate entities have the need for genetic diversity to meet their future needs, but conservation is restricted by the short-term need for profitability. Other conservation structures might include a host of public and private institutions that have, and can contribute to in situ conservation. Finally, a way must be made to encourage farmers, ranchers and stockmen who were responsible for developing most of our breeds. These conservators have a vested interest in selection for their management systems. This range of selection and the number of people involved enhances genetic diversity.

Public and private benefit accrues from genetic diversity. That value must be demonstrated so that resources can be found. Only after years of discussion was the will to fund NAGP achieved. A similar will must be found to provide resources for all possible in situ conservators. Industry, government, and academia must find a way to value and conserve their genetic collections. Farmers and ranchers must be encouraged to continue their stewardship of genetic diversity. Finally, state and federal governments must find ways to recognize and support a wide range of in situ conservation systems to ensure a biologically, economically, and nutritionally secure food production system for the future.

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Historical Perspectives – Small Ruminants

Eric Bradford, UC Davis

Several factors have led to the development of a very wide range of breeds and types of sheep and goats in the world, including:

1. They are kept in a wide range of environments in terms of topography, climate and management systems and, compared to poultry, pigs, dairy cattle and to a lesser extent beef cattle, they are much
more dependent for their feed on the natural forage supply, with its large seasonal and annual variations.

2. They are raised to produce three products – meat, fiber and milk – usually two of these, in some cases all three.

3. Their smaller size and lower cost per individual (compared to cattle) facilitate development of new breeds.

The great diversity of breeds and types in these species presents certain problems, from the perspective of protecting and managing genetic resources.

Since total numbers within each species are not increasing and in fact are decreasing in many countries, many breeds are numerically very small. Markets in many developed countries emphasize uniformity of product, e.g. size of cuts of meat, fiber diameter of wool, thus contributing to a small number of dominant breeds and a reduction in numbers within many once more popular breeds. The latter are therefore lost, or maintained in small numbers with resulting risk of inbreeding. Even if they survive, such breeds lack the numbers necessary for an effective selection program based on modern genetic evaluation procedures, and thus over time become progressively less competitive with currently more popular breeds. As a result, genetic diversity is being lost. The above-mentioned lower cost per animal (compared to large ruminants) does permit the maintenance of herds and flocks by hobbyists, an important factor in maintaining genetic diversity in these species, but one that is not systematic nor necessarily dependable in the long term.

In developing countries, genetic diversity is subject to loss due to two major factors. One is loss of numbers and of production niches due to effects of human population increase, notably the conversion of grazing lands to arable crop production (often with undesirable environmental consequences as well). The second is the introduction, often indiscriminately, of ‘improved’ breeds, resulting in dilution or loss of adapted genotypes. Replacement by or crossing with imported breeds can on occasion be useful, but should be done only after life cycle comparison of total inputs and outputs for the traditional and ‘improved’ groups, under realistic environments and management practices. Often this is not done. This can result in a population less well adapted and less productive than the original stock, e.g. wool-hair sheep crosses compared to hair sheep in the tropics.

Important needs, particularly but not only in developing countries, include determination of genetic distances between identified breeds or types, to assist in developing a strategy for maintaining maximum genetic diversity with minimum total numbers, and more complete characterization of the productive potential of the highest priority stocks.

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ANIMAL GENETIC RESOURCES IN THE POST GENOME SEQUENCING WORLD

Noelle E. Cockett, Utah State University

Availability of the full genome sequence will no doubt advance the discovery of underlying genes and mutations affecting important traits in livestock animals. It is truly phenomenal that the full genome sequence is now known for three domesticated species. The vast amount of data that we now have is being analyzed for generalizations about the number of genes, regions of similarity and dissimilarity among species, mechanisms of protein diversity, etc. Sequence comparisons across species will allow better characterization of chromosomal regions of interest, and will also lead to inferred function of putative genes.

The mapping of traits to chromosomal regions is often done using populations of animals segregating for desirable and less desirable alleles. For example, studies with the Chinese pig x Large White crosses identified genes for reproduction, growth, feed efficiency and carcass traits, all which differed significantly between these two breeds. While the important favorable alleles identified in these studies had already been fixed in commercial populations, genes involved in fundamental biological pathways were revealed. Creation of very broad crosses, as well as those between commercially favorable breeds or lines, are critical for identifying markers suitable for genetic selection, as well as information on the underlying biological mechanisms. These animal resources will allow us to Atease apart@ the phenotypes rather than being satisfied with large
confidence intervals around QTLs, which can contain tens to hundreds of genes. Optimally, the causative mutation(s) for economically traits will be discovered and incorporated into genetic tests. However, only a few markers are currently available for marker assisted selection (MAS). Although the intention of MAS is to identify animals used for breeding, current application has been for designating which animals are moved into progeny tests.

Cataloging phenotypes of breeds and lines, as well as some measurement of genetic variation, will provide the needed information for determining which crosses will have the most impact and lead to the discovery of interesting genes. One possibility is to gather standard phenotypic measurements on all breeds included in the National Animal Germplasm Program, such as coat color, size and growth parameters, blood work, muscle and bone measurements, behavioral and performance assessment. Also, the vast biodiversity that exists in other countries, particularly in Asia, provides alternative alleles to those currently available in populations within the United States. Crosses including these unusual breeds will lead quickly to regions of biological interest.

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What happens to special/unique livestock if there were an outbreak of FMD in the United States? Disease, Risk, Opportunity

Barbara Corso, Ann Seitzinger

The recent outbreak of Foot and Mouth Disease in the United Kingdom reminded everyone of the potentially catastrophic consequences of such an outbreak. The response plans in place in the UK proved inadequate to battle the outbreak, and the economic and social consequences included aspects not seen in the past. All countries that are free of FMD are updating their response plans for such an outbreak.

Preparations in the United States include a number of efforts. The Department of Agriculture has been working for a number of years on updating our plans. This work includes development of a disease simulation model that can be used to approximate the spread of disease through a population (including introduction of various controls measures), development of economic models that use the output from the epidemiological models to assess the costs and economic benefits of various situations and response activities, and development of indemnity procedures that will be in used in an outbreak.

The disease simulation model was used to estimate the impact of an outbreak of FMD in the United States. Results from the disease simulation model were used in a multi-sector agricultural demand systems model to estimate the impacts of FMD on the U.S. agricultural industry. The FMD outbreak simulated was limited to the livestock population in the state of Minnesota. Minnesota was chosen because of the availability of farm locations within the state. Both cattle and swine herd with superior genetic value are located within MN and were included in the model estimations.

Special/unique livestock would be compensated at a higher rate in the event of a FMD outbreak in MN, but FMD would affect these animals in the same way as animals with commercial or terminal value. The FMD spread model does not differentiate disease impacts based on livestock value. Economic impacts of the disease impacts for special/unique animals are also similar to the impacts all livestock producers experience in the event of a disease impact, though some additional costs may be incurred when repopulating special/unique animals.

Two types of economic impacts, direct and indirect, are experienced in the event of a disease outbreak. Direct impacts are those related to the fighting of the disease and include the value of the animals that are depopulated, and cleaning and disinfection. Indirect impacts include the value of lost trade, lost access to markets, reduced reproductivity of surviving animals, higher cost of replacements when regional supply is affected, and lost genetic diversity. Indirect impacts can exceed direct impacts, and usually the bulk of indirect losses result from restricted export markets for affected U.S. livestock products.

Indirect impacts may be particularly harmful to the special/unique livestock industry after the outbreak. Developing genetic value is time-consuming, and owner costs associated with large-scale depopulation of genetically rare animals will exceed the fair-market compensation value paid to livestock owners. Additionally,
replacement animals may not be attainable when an animal is significantly unique, and the time associated with recreating that genetic uniqueness, assuming it is possible at all, will exceed expected compensation.


**Status of Utilizing, Preserving, and Collecting Animal Genetic Resources:**

**Beef Cattle**

Larry V. Cundiff  
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Diversity among breeds used for beef production is important to exploit effects of heterosis on efficiency of production by crossbreeding and to optimize performance levels and match genetic potential with the climatic environment, feed resources, and consumer preferences for lean and tender beef products. Inbreeding continues to accrue within beef breeds at a rate of about .5% per generation. Depressing effects of inbreeding production efficiency can be recovered by crossbreeding. Effects of heterosis increase production per cow about 20 to 25 percent in *Bos taurus* crosses (e.g., Angus X Hereford) and at least 50 percent in *Bos indicus* X *Bos taurus* breed crosses (e.g., Brahman X Hereford). In temperate environments, genetic potential for retail product and marbling are more nearly optimized in cattle with 50:50 ratios than in cattle with higher or lower ratios of Continental to British inheritance. To limit costs of production and improve efficiency of production a strong influence of tropically adapted germplasm is needed in subtropical regions of the U.S. In hotter more humid climates of the Gulf Coast cattle with 50% tropically adapted germplasm may be optimal. In more intermediate subtropics, cattle with 25% tropically adapted germplasm may be optimal. The relative influence of diverse breeds of British, Continental European, and Tropical origins used in U.S. beef production over the past 40 years will be discussed based on registrations in breed associations. Results from the U.S. Meat Animal Research Center (MARC) Germplasm Evaluation Program indicate that differences between Continental and British breeds are considerably less today than they were evaluated 25-30 years ago. However, differences between Continental and British breeds in retail product percentage, marbling score, and percentage grading USDA Choice remain to be about the same to day as they were earlier. It is important to conserve this genetic diversity by storing semen and embryos in a National Repository. Significant progress has been made in establishing a beef cattle germplasm repository at ARS, USDA facilities in Fort Collins, Colorado. The current inventory at the central repository in Fort Collins includes semen from 28 breeds and embryos from three breeds. Experimentation and backup inventories include semen from 29 breeds at MARC and semen from seven and embryos from four breeds at the Subtropical Agricultural Research Station, Brooksville, Florida.

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**The Use of Embryonic Stem Cells for Genetic Conservation**

Robert J. Etches, PhD, DSc

In most species of domestic food animals, genetic diversity is diminishing as breeds that were once preferred by local breeders are replaced by more productive stocks. In addition, genetic resources that were developed for research purposes have been abandoned during the past 40 years as financial resources to maintain these stocks is withdrawn by universities and research institutions. The high cost of maintaining populations of animals that have no immediate value is unlikely to be reduced and therefore, new technologies for the preservation of rare and unusual genetic resources need to be developed.

The mouse is an instructive model for the storage and retrieval of genetic resources because the biomedical research community has developed and supported the infrastructure to maintain and distribute genetic resources. In part, the acquisition, cataloging and distribution of murine genetic resources is made possible by the availability of cryopreserved embryonic stem cells and embryos.
The tools for successful storage of genetic resources within each of the species of domestic food animals are only partially developed. In cattle, sheep, pigs and goats, embryos can be frozen and could be distributed from institutions supported by national or international funding agencies. In addition, there is a need to develop embryonic stem cell technologies and refine nuclear transfer technologies for these species to facilitate storage of existing genetic resources and the development of new genetic variation. In poultry, freezing of embryos is fraught by technical difficulty and is unlikely to become available. However, primordial germ cells can be used to store genetic resources in poultry and chicken embryonic stem cells may become available for this purpose.

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Development of Information Systems to Link Genetic, Phenotypic and Environmental Information

Scott C. Fahrenkrug, Ph.D.
University of Minnesota, Department of Animal Science

There is a high degree of conservation in the anatomy, physiology, and genetics of all vertebrates. With the sequencing of many genomes completed or underway, we face a great challenge in capturing and analyzing data, let alone converting this information into value for animal agriculture. We have undertaken the development of a relational database for livestock genomics. The schema for this database is based on that developed at the USDA Meat Animal Research Center (Keele et al, 1994; Harhay and Keele, 2003) that was primarily developed for handling genetic data. Continued improvement has resulted in a data model that also integrates molecular and gene expression data and serves as a laboratory information management system for livestock molecular genetics, the Minnesota Animal Genome and Ontology (MANGO) database. MANGOd currently manages data from functional genomics research being conducted at the Beckman Center for Transposon Research, with special emphasis on handling insertional mutagenesis and gene-knockdown data. MANGOd also currently serves as the backbone for a shopping-cart (SeqCart) based system for DNA sequence analysis using both public (Primer3, Polypred, Consed, Overgo4.0, BLAST and BLAT) and proprietary tools.

Interfacing MANGOd with the Generic Model Organism Database provides for facile integration with other model organism databases, access to tools and viewers being developed by the Open Source community, and access to developing biological ontologies. This platform also provides access to a rapidly expanding “experiment” ontology (MGED) with current importance in describing microarray experiments, and future importance to the development of phenotype ontologies. The development of phenotype ontologies for livestock is critical to our ability to connect heterogeneous data types back to animal performance. Although much of the anatomical ontology from other mammals can be leveraged, detailed trait ontologies for livestock will only arise from Animal Scientists. Commodity groups and funding agencies should invest in the development of effective livestock phenotype ontologies.

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Animal Genetic Resources….The Next Steps

Denny Funk, ABS Global, DeForest, WI

The United States has made tremendous progress in the preservation of genomic resources in the last 5 years. To continue this progress will require coordinated efforts in the following key areas: Awareness, Involvement, Technology, Utilization, Globalization, and Funding. Public awareness is needed in order to ensure that genetic diversity remains a priority issue for funding at the government, university, and industry level. Large population size does not necessarily mean genetic diversity, and simple examples can help heighten awareness. An important first step in determining what should be preserved is to assess the genetic diversity within species, as preserving genetic material from every single breed will be expensive and administratively very difficult. Cryopreservation is probably the most affordable way to conserve genetic resources, although more research is needed to improve efficiencies of cryopreservation for some species. A major challenge, once extensive
libraries of genetic resources has been established, will be the protocols for utilization of the genetic material, but the highest priority must be given for maintaining viable genetic material that can be used to re-infuse critical genes back into living populations. The United States can provide leadership in the global efforts to preserve genetic resources from less developed countries.

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**SAMPLING POPULATIONS FOR GENETIC CONSERVATION, GENE DISCOVERY, VALIDATION, KNOWLEDGE & EXPLOITATION**

Dorian J Garrick, Colorado State University

In this context, a population is sampled when some DNA (or RNA) is collected and maintained. Such DNA can be put to various uses. The manner in which sampling took place will influence the suitability of the DNA for these various uses.

The possible uses for samples include:

**Genetic Conservation.** This involves collection of DNA to ensure the continued existence, evolution and availability of a population to future generations. Many individuals in a population share the same genes in common. Closely related individuals share more genes in common than those animals that are more distantly related. The challenge in sampling is in ensuring one samples the rare polymorphisms and gene combinations with as small a sample as possible. Pedigree knowledge assists in identifying clusters of less closely related animals and phenotypic information ensures that animals with outlying levels of performance are sampled.

**Gene Discovery.** This comprises the use of phenotypic and genotypic information to identify gene sequences that are associated with differences in performance. There are a number of different strategies to discover genes and each strategy has different sampling issues. These strategies include: approaches based on pedigree and performance (without DNA) to identify segregation; methods based on comprehensive coverage by anonymous DNA such as markers; methods based on RNA and expression profiles that are tissue specific; and methods based on candidate genes.

**Validation of Discoveries.** The process of validation is demonstrating that a discovery in a previous experiment can be repeated. This is critical to industry benefit from the adoption of a new test. The limiting factor in sampling is often access to phenotypic rather than genotypic information.

**Gaining Knowledge of the Population from a Genetic Perspective.** This involves determining the gene frequency and some aspects of population dynamics. For example, it involves undertaking a gene test on legacy sires in an industry to determine the source of the mutation and to trace its selection in the population. It also provides for determination of any other effects the gene may have based on existing phenotypic data. Furthermore, it can facilitate in-silico genotyping of a wider population than that contained in the sample.

**Exploiting Discoveries to Improve the Population.** This involves sampling particular animals to aid in selection of current candidates. This is one form of final commercial application of gene discovery.


**SOCIO-ECONOMIC VALUATION OF GENETIC RESOURCES**

Douglas Gollin, Williams College and Yale University

Genetic resources have many sources of intrinsic value, but from an economic perspective, they are primarily important as an actual or potential source of useful traits. These are traits that might confer economic benefits to producers or consumers (or both). Genetic resources might have value from their direct use in varietal improvement programs, but they may also contribute indirectly. For example, scientists may make use of large
collections of genetic resources as they attempt to identify a particular gene or to understand a biological mechanism.

In plant breeding, the value of genetic resources has long been understood, and for several centuries, there has been organized effort to protect "original" or farmer-selected cultivar types (landraces), mutants, sports, and related wild species. Ex situ collections of these original materials have been established for most important crops. The proportion of original materials that have now been conserved in collections is quite high for most crops. The "gene banks" in which these materials reside are supported as an integral part of national and international plant breeding programs.

A comparable system for animal genetic resources, where resources embodied in animal breeds are collected and preserved in institutionally supported collections, has not historically been supported. Many breeds have instead been maintained for commercial purposes, and rarer breeds have often been maintained in in situ collections (herds) that depend on support by private individuals and groups, rather than a more formal institutional mechanism. These collections may be vulnerable if support changes. Ex situ collections include zoos and other live animal parks away from the native habitat of the animals in question. Other forms of ex situ collections have taken on increasing importance as technology has improved, including cryopreservation of sperm, ova, and embryos. In recent years, new techniques of cryopreservation, and declining costs, have begun to encourage ex situ conservation approaches for animal genetic resources.

In the competitive marketplace, no private sector actor has strong incentives to collect or conserve animal genetic resources. Commercial interests in animal agriculture are likely to view the benefits of conservation as vague, distant, and diffuse (i.e., widely shared), while the costs of collecting and conserving germplasm are immediate and real. As a result, this is a classic "public goods" problem, from the perspective of economic theory: no individual actor has a market incentive to take an action that would be socially valuable (or to act on a sufficiently large scale). In such situations, some kind of public investment or cooperative arrangement is normally desirable.

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Some Background of Interest Prior to the Development of an Animal Genetic Resources Management Program

Notes by: Keith E. Gregory, MARC-ARS


   1. Role of U.S. Development Assistance in Maintaining Biological Diversity in Developing Countries.
   2. Grassroots Conservation of Biological Diversity in United States.
   4. Technologies to Maintain Biological Diversity.


13. 1989. Board on Agriculture, National Research Council, National Academy of Science. Committee on Managing Global Genetic Resources, Sub Committee on Animal Genetic Resources. John Pino, Michael Strauss, and Brenda Bellachy. This study was at the request of ARS, USDA in 1986, Terry Kinney, Administrator. This effort may not have resulted in a report. If so, it was not given wide distribution. ARS, USDA, funded much of this effort. John Pino started on this effort in 1986. Terry Kinney left the role of Administrator, ARS in 1988.

14. 1989. Report of Work Group on U.S. Strategies for Conservation, Management and Utilization of Livestock Genetic Resources. 38 pp. Prepared by: K. E. Gregory, G. E. Dickerson and John A. Acree. This report was provided to group listed under Item 13. I am not sure how it was used by this group. Also, this report was provided to ARS Administrator and other ARS officials.


Additional Background Materials

Keith E. Gregory, MARC, ARS

January 23, 1989
REPORT OF WORK GROUP ON
U.S. STRATEGIES FOR CONSERVATION, MANAGEMENT
AND UTILIZATION OF LIVESTOCK GENETIC RESOURCES

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Note: This report was prepared by Keith E. Gregory, Gordon E. Dickerson and John A. Acree.

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Species Committee Reports: Dairy Cattle

Les Hansen, University of Minnesota

The dairy cattle committee of the NAGP has been comprised of 10 members – two from land-grant universities, two from USDA-ARS, three from the A.I. industry, one from a breed association, and two ex officio members from USDA. The committee has met once or twice annually since its inception.

The committee’s major concern has been the loss of genetic diversity within the six established dairy cattle breeds in the U.S. A measure of genetic diversity is an estimate of “effective” population size, and the most recent estimates from increases in average inbreeding (covering the period from 1997 to 2003) are: Ayrshire – 79, Brown Swiss – 32, Guernsey – 40, Holstein – 60, Jersey – 30, and Milking Shorthorn – 238. Milking Shorthorn has a much larger effective population size than the other breeds because it is a composite breed that has had considerable genetic migration into the population. The average inbreeding of females in each breed for 2004 are: Ayrshire 5.7%, Brown Swiss 5.6%, Guernsey 6.2%, Holstein 5.0%, Jersey 7.2%, Milking Shorthorn 4.9%. Despite an absolute population size of 8 million cows in the U.S., the Holstein breed has an amazingly low effective
population size. The Jersey breed has reached a point of relationship within the breed such that functionality of cows could become compromised.

Contributions of frozen semen to the NAGP collection was initiated with a system of routine contribution from a number of cooperating A.I. organizations, with one out of 10 young Holstein sires entering A.I. organizations as well as all young sires entering A.I. for the other breeds. This routine contribution of bulls born beginning in the very late 1990’s has been supplemented by 1500 units of frozen semen from the 1964 control line of Holsteins from the University of Minnesota. Furthermore, sizeable contributions of frozen semen from collections maintained at Iowa State University, Virginia Tech, and Colorado State University have dramatically improved the representation across time for the latter half of the 20th century of the NAGP collection. Also, 158 frozen Holstein embryos, which are F1 crosses of 1964 control line females with A.I. sires born in the 1990’s, were contributed to the collection by the University of Minnesota.

ABS Global will be contributing a vast collection of frozen semen in the near future. The contribution includes 350,000 units of semen from 10,000 bulls representing 52 breeds. Although the majority of bulls are Holstein, this collection contains all six dairy breeds as well as many beef breeds. Birthdates of bulls range from the 1950’s to 2000’s. For dairy cattle, retrospective studies have documented that no effective selection for milk production occurred until the 1960’s. Therefore, the semen collection from ABS Global will cover virtually the entire period from the advent of progeny testing in the U.S. to the present time.

The dairy cattle committee nominated one live (in situ) population for the National Registry of Genetically Unique Animal Populations of NAGP – the 1964 control line of Holsteins at the University of Minnesota (maintained as 30 lactating cows) – and the nomination was approved. Tasks for the committee include thinning of the frozen semen collection following the contribution of ABS Global, potentially altering the rate of routine semen contributions from young sires, and reviewing requests for withdrawals from the NAGP dairy cattle collection on an ongoing basis.

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The Dutch AnGR Conservation Program & Collaboration Within Europe

Sipke J. Hiemstra, Centre for Genetic Resources, the Netherlands

On a European level, biodiversity, including conservation and sustainable use of AnGR, is a priority policy area. National co-ordinators for AnGR collaborate within the European network ERFP (European Regional Focal Point). The main objectives of the ERFP are enhancement of collaboration between countries and exchange of information and knowledge regarding AnGR policies, conservation and management.

Recent strategic policy documents of the government of the Netherlands include priorities on further development of a cryopreservation program for AnGR, promoting in situ conservation initiatives and enhancement of international collaboration. A gene bank for farm animals is managed by the Centre for Genetic Resources, the Netherlands (CGN). CGN is also (technically) supporting in situ management of AnGR and gives policy advice to governments, NGO’s and the private sector.

So far, Dutch gene bank collections consist of genetic material from cattle, sheep, pigs, poultry and horses. Both semen of rare/endangered breeds and back-up-samples of commercial lines/breeds are stored in the gene bank on two locations. Over 100,000 doses of semen is in storage. More than 75% of the semen doses is bull semen.

The objectives of the cryopreservation program in the Netherlands for the period 2004-2008 are 1) to store a sufficient amount of genetic material of all endangered breeds in the gene bank to be able to re-establish the breed; 2) to store a back-up of all (Dutch) commercial lines or breeds in the gene bank and 3) to support small/critical populations by providing semen from the gene bank. Different stakeholders play a role in the cryopreservation program and both government and private sector contribute financially.
CGN is continuously looking for improvement of efficiency and efficacy of conservation methods. Two examples are presented. For rare Dutch (heath) sheep breeds successful collection of semen from the epididymus after slaughter has been undertaken. CGN decided to start collection of ram semen after the FMD outbreak in 2001 and will continue this action because of the risks associated with the scrapie eradication program. Another recent major improvement is on cryopreservation of rooster semen, which gives good opportunities for future conservation of poultry breeds.

Regular evaluation and rationalization of in situ and ex situ conservation strategies is necessary, taking into account advances in (bio)technology. Many initiatives have started on a national level, but it is recommended to enhance international (regional/global) collaboration.

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Farm Animal Genetic Resources in Canada - An Overview

S.K. Ho, Agriculture and Agri-Food Canada

Most of Canada’s animal agriculture is intensive. Changing requirements of the consumer is providing opportunities for specialized animal products, stimulating interest in use of more breeds of animals. The recent animal health events and the effect they have on the livestock and poultry industry underscore the importance of maintaining genetic resources for food security and supply.

The Rio Summit, FAO’s Global Strategy for the Management of Farm Animal Genetic Resources and the associated preparation of country reports, etc. have and are continuing to raise awareness of the decline of farm animal diversity and the need for action.

Canada is in the process of establishing a national program in animal genetic resources conservation and sustainable utilization. It is expected that this program will have the involvement of all stakeholders. International collaboration is seen as one of the important approaches.

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Status of Utilizing, Preserving, and Collecting Animal Genetic Resources Small Ruminants

David R. Notter, Virginia Tech

The Small Ruminant Subcommittee of the National Animal Germplasm Program (NAGP) oversees the inventory, collection, and characterization of U.S. sheep and goat genetic resources. NAGP activities in support of small ruminant genetic resource conservation and use include:

- **Cryopreservation of semen and embryos of sheep and goat.** The collection currently includes over 27,500 units of semen from 293 rams representing 19 sheep breeds and nearly 2,600 doses of semen from 137 bucks representing eight goat breeds, as well as nearly 450 frozen embryos from selected lines of Targhee sheep. In sheep, the collection includes representative samples of material from currently popular wool breeds such as the Dorset, Finnsheep, Rambouillet, Suffolk, and Texel; hair sheep composite breeds such as the Katahdin and Dorper; and rare and endangered breeds such as the Gulf Coast Native, Navajo Churro, and Warhill composite. Meat (Spanish, Boer, and Myotonic), fiber (Angora), and dairy (Alpine and Lamancha) breeds are each represented in the goat collection by five or more sires.

- **Development of methods for cryopreservation of sheep and goat semen.** In the U.S., facilities and expertise for collection and freezing of semen from sheep and goats and for artificial insemination using frozen semen are limited. Research has been undertaken to develop improved techniques for on-farm collection
of ram and buck semen and for shipping of chilled semen to the central repository for freezing. Effects of different extenders and freezing rates on post-thaw semen characteristics have also been evaluated.

- **Support for in situ conservation of rare and endangered breeds.** In sheep, activities have concentrated on the Gulf Coast Native and Navajo Churro breeds. The Gulf Coast Native exhibits a high level of genetic resistance to intestinal roundworms. The Navajo Churro produces wool used to make traditional Navajo weavings and is culturally linked to the Navajo people. In goats, focus has been on the Angora and Spanish breeds, both of which have declined in numbers because of lower mohair prices and increased crossing with other breeds.

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**Cryobiology – The Reality**

William F. Rall, National Institutes of Health

The National Animal Germplasm Program (NAGP) seeks to ensure that genetic diversity in agricultural and aquaculture animal species is maintained to provide future generations of Americans with high-quality food and fiber of animal origin. The general strategy for accomplishing this goal is to establish banks of spermatozoa and embryos for those species with optimized cryopreservation procedures, and maintain living populations of species which do not yet have effective cryopreservation protocols.

Current cryopreservation protocols are empirically-derived using general cryobiology concepts of cryoprotection and cryoinjury. Generally, semen cryopreservation protocols must be optimized for each species, presumably due to differences in the physiology and characteristics of the spermatozoa. It is interesting to note that embryo banking requires fewer species-specific modifications, with one notable exception (porcine embryos).

One area of special concern is the inbreeding of livestock species due to genetic selection for increased productivity traits or small population size. The banking of inbred strains of rodents is complicated by wide variations in the quality of embryos and sperm. The current inbreeding coefficients (5-7%) of dairy cattle are reported to have deleterious effects on some production traits (e.g., fertility and milk production), but there is no evidence of a reduction in semen or embryo quality. The high level of genetic relationship (>10%) among animals within each breed of dairy cattle requires careful selection of matings by dairy producers to reduce inbreeding in the resulting progeny. Monitoring of germplasm quality is warranted in light of the continuing trends to higher inbreeding and genetic relationships within dairy breeds.

Immediate research needs include the development of optimized procedures to cryopreserve sperm and embryos for species lacking a cryopreservation option and/or strong industry infrastructure. Long-term research needs include: 1) assessment of intra-cytoplasmic sperm injection, spermatogonial stem cells, and somatic cell nuclear cloning as tools for rederiving breeding stock, and 2) the development of alternative preservation procedures such as freeze-drying, vitrification, and high-temperature storage.

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**Animal Genetic Resources in the Post Genomic Sequencing World**

Lawrence B. Schook, Institute for Genomic Biology, University of Illinois at Urbana-Champaign
Harvesting the ‘genomic promise’ provided by the Human Genome Initiative (HGI) is still a major goal and challenge. One clear message has emerged from the HGI. That the relationship between genetic diversity and resulting phenotypes will challenge our collective investigative efforts. From the outset, the linkage between germplasm preservation and genomics have been viewed as the “two-headed coin” within the agricultural research community. However, because of the major windfalls of the HGI, livestock genomics has rapidly progressed. Today the dream of the cattle genome being sequenced is a reality. Now, it is critical that we return our attention to defining the animal resources that will be essential if we are to capture the genomic sequence information.

Experimental approaches developed to initially support the HGI initially focused on model organisms (flies, worms and mice). It is clear that the methodologies used to study these organisms may not be sufficient to adequately address genetic diversity in livestock species. Thus, it is critical that we answer fundamental questions regarding germplasm and how genomics assists in germplasm priorities. These answers have clear implications for addressing broader biological, biomedical; and agricultural future needs. We need to elucidate criteria for selection of specific animals (e.g., champions, populations, clones). Also, it will be critical that we identify “background” genetics to assess phenotypic variance as a function of allelic substitution. Finally, if we are to harvest the full potential, we will need to overcome technological hurdles that will require the global scientific community to integrate methods of cryopreservation, defining diversity, and genomic tools to permit the ability to capture nature’s diversity, maintain it and reconstruct the past while preserving the future. Databases and appropriate bioinformatics will be essential if we are to understand genetic diversity to its fullest in order to preserve diverse life.

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**SWINE GERMPLASM UTILIZATION AND PRESERVATION (SGUP)**

Terry Stewart, Committee Chairman
Animal Sciences, Purdue University, West Lafayette, IN 47907

The US swine population consists of 8 commercially active breeds, about 10 sources of privately controlled commercial lines and 6 to 8 publicly held research lines that would be distinctly different from commercial breeds, 10 heritage breeds and several novel populations noted for a specific phenotype. The total number of swine produced in the US has remained constant for the past 40 years but because of increases in reproductive technologies and consolidation in the structure of the industry, the number of breeds or lines and the number of sires per line used has steadily decreased. The threat to these populations is loss of diversity because of decreasing population sizes and consolidation of production goals more than that from extinction. Preservation technologies available in swine are currently limited to cryopreservation of semen, and even then, post thaw motility of porcine semen is considerably less than that of bovine semen. Limited quantities of swine semen have been frozen by the industry since the 1980s. An in-vitro fertilization study was conducted to evaluate the effect of storage time on semen viability. There were no differences associated with storage time found for any semen quality characteristics. This is encouraging that long-term cryopreservation is feasible and is supported by studies of storage time on bovine semen. Embryos have been successfully frozen in research laboratories but the protocols need considerable improvement before they can be applied.

Food and Agriculture Organization guidelines for quantities of frozen semen were used as a basis to determine the quantity of semen stored to secure a population. Our goal is to sample 100 sires distributed across a breed and secure 30 doses of frozen semen per sire. Considering that swine are a litter bearing species, this should provide sufficient semen to reconstruct the variation of a population at the time of sampling. The Goal is to sample two populations per year and to resample populations every 3rd or 4th generation.

Breed organizations and sire owners has been very cooperative, commercially active breeds and lines have a large number of sires available in studs for sampling and will be relatively easy to secure. Fresh semen is used extensively in commercial artificial insemination programs so sires are available for sampling. Heritage breeds and novel lines present logistical challenges because sires are widely dispersed and not typically trained for semen collection. Another concern is the poor characterization of either the phenotype or genotype of lines and individual sires for traits beyond growth and litter size.
Current committee members are: Archie Clutter, Wayne Singleton, Fields Gunsett, Kirt Zuelke, Tim Safranski, Terry Stewart, Mark Wilson, Darrell Anderson, Mark Boggess, Rodger Johnson, Joe Cassidy, Tom Rathje, and Dave Guthrie.

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Genetic Improvement and Protection
and/or
Protection and Management of Genetic Resources

Hein van der Steen, Sygen International

Breed and line development has been and is the role of breed societies and breeding organizations and, in general, serves a commercial purpose. Society is interested in maintaining genetic diversity for present and future use of genetic resources. Objectives of breed societies and breeding organizations do not necessarily overlap with those of society as a whole. A coordinated approach is problematic in several species due to the lack industry or general funds, the immaturity and/or fragmented nature of the industry and a lack of consensus about what the best strategy is.

Serious investment in genetic improvement programs and new technology by breeding companies can only be justified if a return on this investment can be expected. This increasingly requires ‘genetic protection’, i.e. the ability to prevent the leakage of genetic improvement to the competition. The question is whether the commercial purpose and need for genetic protection is in conflict with the societal objective of maintaining genetic diversity.

The conflict is, in general, less than perceived as:
- genetic diversity is required to generate genetic improvement
- today’s programs need to take future objectives into consideration
- genetic diversity supports future line development

and
- commercial value facilitates maintenance of a genetic resource
- preservation is, to a large extent, based on commercially relevant information
- preservation is, in the end, more important than who owns the germplasm

Genetic protection is required to sustain genetic development and investment in technology. This is the case for all species where genetic development is required, although issues vary between species. Commercial genetic protection will lead to a certain degree of preservation of genetic resources and responsible management of genetic resources, as it makes good commercial sense. Additional public support will be required to protect genetic resources where the potential for commercial in the future use is less obvious.

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