Available online at www.sciencedirect.com
ScienceDirect
Livestock Science 120 (2009) 166 – 173
LIVESTOCK SCIENCE
www.elsevier.com/locate/livsci

Research opportunities in the field of animal genetic resources☆

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Abstract

Animal genetic resources are those animal species that are used, or may be used, for the production of food and agriculture, and the populations within each of them. The working unit of a database for farm animal genetic resources is the breed, a term taken in its widest possible sense to mean a population within the species, possessing a number of particular traits that permit the grouping of these animals under a common label and are associated to geographical areas and human groups. Research opportunities cover a wide range of thematic areas. The biggest gap in knowledge is animal breeding for local populations in harsh environments. There is also a lack of research in functional genetics and genomics of adaptation and disease resistance traits. By comparison, breed characterization, in particular molecular characterization, has been a more popular research subject. The same can be said for conservation, although some fundamental questions on genetic diversity and risk of its loss are still unanswered. Research is required to understand the socio-economic, infrastructural, technical and formal constraints that limit the operation of sustainable conservation programs in less developed countries. Information systems on animal genetic resources need input from research and data capture networks, in order to achieve a reasonable degree of completeness. Economic analysis and issues related to gene flow and access and benefit sharing should also profit from more research.

Keywords: Farm animal biodiversity; Domestic animal diversity; Breed characterization; Animal breeding; Conservation; Livestock diversity; Livestock breeds

1. Introduction

The global need to conserve and properly manage natural resources, among them livestock resources, had been discussed and emphasized 45 years ago in a publication by the United Nations on Science and Technology for Development (UN, 1963). It was a follow-up of a 1949 United Nations Scientific Conference on the Conservation and Utilization of Resources (UN, 1950). With terms that are today considered old fashioned, these reports are saying many of the same things we say today. One is tempted to ask, what is new? On the other end of this timeline, the year 2007 saw the presentation by a special agency of the United Nations, of the Report on the State of the World's Animal Genetic Resources for Food and Agriculture (FAO, 2007). Exponentially growing research has been published between these two time brackets. How can future research help fill in the knowledge gaps that still exist? Some ideas, concepts and opportunities for research in animal genetic resources are discussed in the present paper. The objective is to inform scientists about

☆ This paper is part of a special issue entitled Animal Genetic Resources, Guest Edited by Ricardo Cardellino.

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doi:10.1016/j.livsci.2008.07.002

this field and, perhaps, serve as an incentive to think about or conduct research in this area.

It is impossible within the scope of this paper to even attempt a complete bibliographical review of publications in the area of animal genetic resources. A few of the publications that helped shape animal genetic resources from the research and development side, not the political or policy side, will be mentioned. The World Dictionary of Livestock Breeds, Types and Varieties by I. Mason appeared in 1951 and is now in its fifth edition (Porter, 2002). It contains approximately 9000 entries and cross-references on breeds, sub-breeds, types, varieties, strains and lines of cattle, sheep, pigs, goats, horses, asses and buffalo. Documentation on breeds lost and at risk began to appear in books (for example, Alderson, 1978) which stimulated the formation of national and international societies, as well as non-governmental organizations dedicated to the various aspects of animal genetic resources but in particular to conservation. A few countries started setting up germplasm banks for their animal genetic resources.

The first edition of the FAO-UNEP (now only FAO) journal Animal Genetic Resources Information was published in 1983 and is now in its 42nd number (FAO, 2008a). A book on managing global livestock genetic resources was published in the USA (National Academy of Sciences, 1993). FAO produced several guidelines on the management of animal genetic resources (FAO, 2008b). There is more on animal genetic resources on the scientific literature now than before, as exemplified by a special issue of the journal Ecological Economics on valuing animal genetic resources (ISEE, 2003).

2. Terminology

The term “animal genetic resources” is the commonly accepted, abbreviated form for “those animal species that are used, or may be used, for the production of food and agriculture, and the populations within each of them” (FAO, 1999). Farm animal genetic resources and animal genetic resources for food and agriculture are also used. Domestic animal diversity is a term that has been used to mean the genetic differences among and within breeds of species used for food and agriculture. The term animal genetic resources is a broad one and allows for the expansion of the list of species used for food and agriculture, allowing also for regional differences and particularities.

It is estimated that 90% or even more of the agricultural output comes from the following species distributed globally: pig, chicken, cattle, sheep, goat, buffalo, horse, ass and dromedary. Also widespread are: domesticated rabbit, turkey, domestic duck, Bactrian camel, the South American camelids (llama, alpaca, guanaco and vicuña), Guinea pig, domestic goose, Guinea fowl, quail, pigeon and ostrich. Less widespread are: pheasant, partridge, cassowary, ñandu, emu, pea fowl, mute swan, cormorant, little egret, some of which are not domesticated. Localized species, of which many are also not domesticated, include: banteng, mithan, yak, gaur, tamaraw, kouprey, anoa, wild rabbit, hare, agouti, capybara, coypu, giant rat, grasscutter, hutia, mara, paca, vizcacha, chinchillas, pacarana, springhare, rock cavy, salt-desert cavy, Solomon Island rodents, giant New Guinea rat, porcupines, kiore, soft-furred rat, giant squirrels, squirrels, color rat, spiny rat, bamboo rat, red deer, mouse deer, muntjac, water deer, duiker, lizards, green iguana, black iguana, elephants, bees, snails, crocodiles, silkworm, mink, fox, nutria (Rege and Gibson, 2003). Many of these localized species are grouped under the term microlivestock and have been described in detail in a book by the National Academy of Sciences (1991).

3. Animal genetic resource databases

DAD-IS is the FAO Domestic Animal Diversity Information System (DAD-IS, 2008) and today comprises the largest global specialized database with around 10,500 national breed records for mammalian species and 3500 for avian species, originating from 182 countries (data from 2006).

A database is as good as the quantity, quality and completeness of the information it contains. Data capture, including first-time information and regular updates, is relatively good in a number of developed countries but is rather deficient in most developing countries, exactly where having the information is crucial if a complete picture of the status of farm animal biodiversity is to be obtained. Until a global infrastructure is in place, the global FAO database will be incomplete, lacking an important component.

The working unit of a database for farm animal genetic resources is the breed. This term is taken in its widest possible sense. A generally accepted working definition of the term, in the context of databases and research on animal genetic resources, is that of a population within the species, possessing a number of particular traits that permit the grouping of these animals under a common label (the breed name) and is almost always associated to a geographical area and one or more human groups. The discussion on a precise definition of the term breed has been going on for a long time and will probably be endless, since it is highly dependent on the context in which the term is used. For example, in a legal sense in a Western European country, a breed has to have a precise standard and a recognized breeders' association, while previous to that stage, more loosely defined populations are considered to be in a pre-breed status. This western breed concept is meaningless for many developing countries of, for example, Africa. Several alternative definitions of the term breed that illustrate this point, are presented by Woolliams and Toro (2007).

The FAO global database uses a classification of breeds that partially avoids the problem of counting the breed more than once, if it is located in more than one country, a fact that distorted the early estimates of breeds at risk of extinction. Local breeds are considered those that occur in one country. Transboundary breeds are those that occur in more than one country. These are further divided into those that have regional dispersion, and those that have global dispersion, being considered international breeds. It may occur, though, that the same breed or equivalent populations are known by different names in different countries and are reported as such, and this may remain undetected.

Population figures are available for just a fraction of the recorded breeds. Using 2006 data from the global FAO database, it is estimated that 47.2% of breeds of mammalian species and 44.2% of breeds of avian species have at least some estimate of population data. This represents a high degree of incompleteness, affecting almost half of the breed records, not a very sure base on which to estimate rates of loss of domestic animal biodiversity. Table 1 shows this trend by regions.

The region with the lowest breed population data is Latin America and the Caribbean (13.15), followed by the Southwest Pacific (20.4%), Africa (30.5%) and the Near and Middle East (39.3%). The highest values of breed population information come from Asia (52.5%), Europe and the Caucasus (64.6%) and North America (69.3%). The average global figure is 46.5%.

An assessment of risk of extinction in the main eight species of mammals in the global database is presented in Table 2. The percentage of breeds at risk is 16.2%, but almost 34% of them, that is 1823 breeds, have no population data and therefore no risk factor is available. The extreme values are for rabbits (72%) and ass (59%). If it were assumed that the group of breeds with unknown status have the same risk percentage as the group with population data, it would mean that 446 more breeds are at risk, a total of 24.4%. This is simply speculation but it shows that the basis for assessing the status of domestic animal biodiversity will be shaky until data are more complete.

Table 1
Percentage of breeds with population data in the different world regions and class (*Mammalia, Aves*) in the global database

	Class [a]	Number of breeds	Percent of breeds with population data
Africa	M	1596	32.5
	A	351	21.4
	M+A	1947	30.5
Asia	M	1931	55.9
	A	600	41.3
	M+A	2531	52.5
Europe and the Caucasus	M	3488	67.2
	A	1482	58.4
	M+A	4970	64.6
Latin America and the Caribbean	M	1640	12.9
	A	358	13.7
	M+A	1998	13.1
Near and Middle East	M	299	42.5
	A	60	23.3
	M+A	359	39.3
North America	M	326	61.3
	A	91	97.8
	M+A	417	69.3
Southwest Pacific	M	398	22.1
	A	132	15.2
	M+A	530	20.4
World	M	9678	47.2
	A	3074	44.2
	M+A	12752	46.5

Data from 2006 (FAO, 2007).
[a] M=mammals; A=birds.

A similar data structure is shown in Table 3, regarding six of the most important species of birds. The average percentage of breeds without population data is 39.9% with the highest value for Guinea fowl (59%). Assuming equal distribution of risk classes in the breeds without population information as in those with population data, the total is augmented by 395 breeds, and thus the percentage of breeds at risk in all bird species for food and agriculture would go up to 52.1%.

Recently two questions were posted in the domestic animal diversity network (DAD-Net, 2008) directed to national coordinators for animal genetic resources and scientists in the different countries: 1. Does your country have a system to assess changes in the population size and structure of national breed populations? 2. Does your country have a systematic approach to respond to such changes? If yes, please describe your national approach. With few exceptions, the common answer from developing countries to these two questions was no. This means that unless a program to support the implementation of national structures for animal genetic resource data capture in developing regions is quickly launched and followed up, the global database will remain deficient.

Table 2
Assessment of risk of extinction in the main eight species of mammals in the global database

	Unknown [a]	At risk [b]	No risk	Extinct	No. of breeds
Ass	58.6	16.7	21.0	3.7	162
Buffalo	35.0	8.0	56.9	0.0	137
Cattle	30.0	16.0	38.1	15.9	1311
Goat	33.8	13.6	49.5	3.1	618
Horse	34.6	23.0	31.3	11.1	786
Pig	30.4	18.0	32.6	18.9	739
Rabbit	71.6	20.3	7.3	0.9	232
Sheep	29.6	12.7	44.9	12.8	1409
Total	33.8	16.2	38.1	11.9	5394

Data from 2006 (FAO, 2007).
[a] no population data.
[b] at some risk = critical + endangered.

Another animal genetic resource database is DAGRIS (2007), an information system designed to facilitate the compilation, organization and dissemination of information on the origin, distribution, diversity, present use and status of indigenous farm animal genetic resources based on research results. This system aims at providing elements for developing breed improvement and conservation programs. It contains information on breeds and ecotypes of cattle, sheep, goats, chicken and pigs. Its current geographic scope is Africa and selected Asian countries. Population data and risk status of breeds in this database are rather limited.

4. Animal breeding

Terms such as sustainable utilization of animal genetic resources and sustainable intensification, have been used for what is plainly known as animal breeding, especially of local breeds or populations.

There is no doubt that animal breeding for the major international breeds has led to genetic gains for many important production traits. More emphasis, however, has been put on speed than on direction, meaning that research has been more on how to achieve genetic gains than on selection objectives. Today it is recognized that more relative importance has to be given to the so called functional traits such as anatomy of feet, legs and udders (in dairy cattle), metabolic stress, fertility, longevity, health, disease resistance, behavior and others.

Breeding programs for local breeds kept by small farmers in developing countries are a major challenge. Animal recording of pedigree and performance under conditions of subsistence livestock farming is difficult or next to impossible. This means that standard genetic evaluations, as well as selection and planning of matings based on estimates of the animals' genotypes, cannot be done at any level in the population of the target breed or genetic group. So the desired or potential speed of genetic change, in comparison with the international major breeds, cannot be realized. This may be a blessing in disguise: what assurance do we have, from the western/developed animal breeding point of view, that a standard intervention in such populations will not make matters worse? What is known, for example, about genetic and non-genetic variation for production traits in those harsh environments? What is known about genotype–environment interactions in unfavorable environments? Which are the crucial adaptive traits? How big is the risk that standard breeding interventions will get the population off its adaptation equilibrium and thus make matters worse? These challenges represent major knowledge gaps that research may be able to fill.

These problems, however, are not new. More than 50 years ago a special symposium was held in Texas on breeding cattle for unfavorable environments (Rhoad, 1955). Aspects such as heat tolerance, effects of climate on reproduction, animal health, climate stress, low plane of nutrition and production, crossbreeding and the improvement of indigenous breeds, were brought to light. Although today's tools for speeding up genetic improvement were not available then, the observations on breeding objectives under harsh environments are still valid and relatively up to date.

Considerations on breeding objectives and strategies for small ruminants in the tropics, relevant also to other species, have been given by Kosgey (2004). The Indian experience on breeding services for small dairy farmers is amply described by Chacko and Schneider (2005).

An important factor in the success of animal breeding programs for local breeds is the interaction of people and animals—of indigenous breeds and local communities.

Table 3
Assessment of risk of extinction in the main eight species of birds in the global database

	Unknown [a]	At risk [b]	No risk	Extinct	No. of breeds
Chicken	38.7	32.9	25.2	3.1	1273
Duck	43.0	26.5	29.1	1.3	223
Goose	36.3	30.2	33.5	0.0	179
Guinea	59.3	9.3	27.8	3.7	54
Pigeon	47.1	32.4	20.6	0.0	68
Turkey	39.8	34.0	24.3	1.9	103
Total	39.9	31.3	26.3	2.5	1900

Data from 2006 (FAO, 2007).
[a] no population data.
[b] at some risk = critical + endangered.

Without this dual component, programs have no continuity because when the external source of financing is gone – in general a time-limited project as part of bilateral or multilateral development aid – almost all activities stop. Examples from many parts of the world on how communities cope with threats to their animal genetic resources and look for sustainable ways to improve them, are given in Tempelman and Cardellino (2007). The importance of indigenous knowledge in animal breeding has been discussed and exemplified by Sansthan and Köller-Rollefson (2005).

5. Conservation

Conservation of animal genetic resources is one of the most controversial issues in this field, basically because of decisions on what breeds to conserve, how to do it and who will pay for it. The rationale behind conservation of farm animal diversity is that humankind may need to keep this specific genetic biodiversity to face future (unknown) challenges such as changes in demand for livestock products, spread of new diseases, reducing environmental impact and climate change (Woolliams et al., 2008). This biodiversity would be the source pool for genes that confer disease resistance, specific product qualities like fatty acid composition or milk composition, resistance to draught and high temperatures, and production traits to be combined in newly formed breeds or crossbreds. There are also less production-oriented arguments in favor of conservation, such as cultural values and the preservation of rural landscapes (Mendelsohn, 2003).

Conservation of animal genetic resources, in economic terms, would be the maintenance of use and non-use value to humans. Use values are those directly derived from food, fiber and other products and services, and indirectly as a contribution to landscapes and ecosystems. Another use value is the option value, defined as the flexibility to cope with unexpected future events. Non-use values are given by the satisfaction of individuals or societies arising from the existence of domestic animal biodiversity. Several open questions remain. Among them, since the basic unit of all databases is the breed, what is the correlation between loss of breeds and loss of domestic animal biodiversity? What is the definition of a breed at risk? What information is needed to assess the probability of breed loss?

The basic concept of saving farm animal biodiversity for future need does not go unchallenged. Large companies that produce poultry and swine genetics for the predominantly industrial production in these two species, have over the years eliminated old lines and strains because of high costs of keeping this material. A small part of it has presumably ended up in a very limited number of national germplasm banks. There are no known examples of breeders needing a breed for their production-oriented work, only to discover that it has gone extinct. Hill and Zhang (2004) concluded that rates of progress continue to be high in livestock and that variability can be maintained over long periods despite intense selection in populations of limited size. The role of conserved populations would unlikely be that of source of variation in commercial populations, but mainly to preserve our culture and to fill particular niches.

Choosing the conservation strategy, measuring the genetic uniqueness in livestock, selecting breeds for conservation, establishing a conservation scheme, operation of conservation schemes and development of an expert system for conservation, have been discussed by several authors in Oldenbroek (1999). A comprehensive collection of papers addressing topics related to conservation of animal genetic resources can be found in Simm et al. (2004). Managing inbreeding in selection and genetic conservation schemes of livestock has been the subject of a thesis by Sonesson (2002).

Some European countries, Brazil and the USA have programs of *ex situ in vitro* conservation. Diverse issues on cryopreservation, such as methods, advances by species, physical and information management of gene banks, access and sanitary protocols, among others, have been addresses by Hiemstra (2003) and Planchenault (2003).

6. Multidisciplinary research projects

Several projects illustrate the multidisciplinary nature of a relatively novel approach to the management of farm animal genetic resources. They also show the interaction and positive synergy among different areas of research and different types of research teams dealing with the subject in several institutions.

Pig Biodiversity I (Delgado et al., 2003) involved technical aspects of sampling, AFLP and micro-satellite marker genotyping, statistical analysis of genetic profiles and calculation of genetic distance, dissemination of data and legal aspects of the intellectual property of the genetic material and its associated information. Pig Biodiversity II (European Commission, 2008) extended the research to 50 Chinese pig breeds, including sampling and storage of DNA to study genetic diversity by micro-satellite markers, characterizing type I loci and QTL regions, mtDNA and Y-chromosomal DNA, and using DNA marker data to identify genes involved in functional differences among breeds.

The project ECONOGENE (European Commission, 2008) combines molecular analysis of biodiversity, socio-economics and geostatistics to address the conservation of sheep and goat genetic resources, and rural development in marginal agrosystems in Europe.

It maps populations deserving high conservation priority, investigates socio-economic conditions where breeds are raised, maps development perspectives and areas with high chance of success, estimates the economic value of biodiversity for these species in order to justify specific management or conservation actions, and arrives at guidelines and actions for economically viable conservation of local breeds. Its continuation is the project GLOBALDIV (European Commission, 2008) that has the objective of disseminating current advanced methodologies for the characterization and conservation of livestock genetic resources and developing software for integration of specialist knowledge from disciplines as different as management, genetics, sociology, economics and geographic information systems.

In the framework of the Iberoamerican cooperation for the conservation and utilization of farm animal genetic resources, a research and training network has been active for the last 10 years and has produced a great deal of research results mainly in the Americas and the Iberian peninsula (Delgado et al., 2005).

7. Research priorities reported by countries

What follows is a summary of the research priorities that have been identified by countries and that were reflected in the report on the State of the World's Animal Genetic Resources (FAO, 2007). As originally presented, it was supposed to give research directions for filling current knowledge gaps in animal genetic resource management. In other words, subjects that need

Table 4
Research priorities for animal genetic resources in information systems, characterization, genetic diversity, functional genetics and animal breeding

Information systems	Upgrading of existing AnGR information systems
	Data on population size and structure
	Geographical referencing of animal genetic resources (GIS)
Characterization	Adaptation and performance traits of indigenous populations
	Methods for phenotypic characterization
	Environment descriptors to evaluate G × E interactions
Genetic diversity	Definition and determination of risk of extinction
	How to monitor population status
	Measures to halt the decline of genetic diversity
	Assessments of genetic diversity using molecular genetic markers
	Development and supply of international reference samples
	Integration of phenotypic and molecular data
	Worldwide identification of gene variants for important traits
	Methods to assess the extent of genetic dilution of a breed
	Indicators for farm animal genetic diversity
Functional genetics	Understanding the genetic basis of adaptive traits
	Genetic basis of disease resistance and host– pathogen interactions
	Genetic basis of adaptation to difficult environments and efficiency
	New tools for conventional and transformative genetic improvement
Animal breeding	Whether to implement genetic improvement programs
	Genetic impact assessment
	Simulation to predict the consequences of introducing exotic breeds
	Breeding strategies in low external input environments
	Breeding strategies with little or no organizational infrastructure
	Stable crossbreeding systems with a role for native breeds
	Selection for disease resistance if specific genes have been identified
	Implement DNA-based selection without compromising production
	Definition of welfare traits
	Measurement of stress/psychological status (aggression, discomfort)
	Selection methods for temperament and less foot and leg problems
	Selection for increased efficiency of feed utilization
	Genetic variance in nutrient (e.g. amino acid) requirements
	Genetic variance in digestion of specific amino acids and phosphorus

Based on country reports, State of the World's Animal Genetic Resources (FAO, 2007).

Table 5
Research priorities for animal genetic resources in conservation, economic analysis, access and benefit sharing

Conservation	*In situ in vivo* conservation to maximize livestock keepers' livelihoods
	Sustainable *in situ in vivo* conservation with development objectives
	Self-sustaining *ex situ in vivo* conservation in developing countries
	Ex situ in vitro cryoconservation of gametes and embryos
	Sampling and storage of germplasm as backup for breeding programs
	Somatic cloning to improve safety and cost-effectiveness
	Blueprints for national and multinational genebanks
	Legal and sanitary frameworks for storage and access
	Criteria for optimization of resource allocation in conservation
	Early warning/response mechanisms with defined triggers and actions
Economic analysis	Analytical methods to define global benefits of conservation
	Costing of conservation alternatives in diverse situations
	Field-test promising valuation methods across production systems
	Traits used by farmers for local breeds under some production systems
	Market analysis for livestock breeds and their products
	Cost–benefit analysis of breeding programs
	Ex ante analyses of effects on livelihoods of using alternative breeds
Access and benefit sharing	Relationship between access and trade in livestock germplasm
	Need for and impacts of frameworks for access and benefit sharing
	Assessment of public and community use of biodiversity
	Significance of national regulations/animal disease control protocols
	Current and future benefits from global flows of livestock germplasm
	Assessment of scenarios that change flows and the share of benefits

Based on country reports, State of the World's Animal Genetic Resources (FAO, 2007).

input from the basic and applied science and development side. The list of research priorities is divided into main headings according to thematic areas, and presented in Table 4 (information systems, characterization, genetic diversity, functional genetics and animal breeding) and Table 5 (conservation, economic analysis, access and benefit sharing).

8. Conclusions

Research opportunities in the field of animal genetic resources are plenty and cover a wide range of thematic areas. Perhaps the biggest gap in knowledge is in the area of animal breeding for local populations in harsh environments. Researchers seem to be rather reluctant in addressing the problems in this applied area. Related to this, there is also a lack of research in functional genetics and genomics of adaptation and disease resistance traits. By comparison, breed characterization, in particular molecular characterization, has been a more popular research subject. The same can be said for conservation, although some fundamental questions on genetic diversity and risk of loss of this diversity are still unanswered. There is little experience in sustainable conservation programs in less developed countries. Research is required to understand the socio-economic, infrastructural, technical and formal constraints that limit their establishment and operation. Information systems on animal genetic resources need input from research and data capture networks, in order to achieve a reasonable degree of completeness. Economic analysis and issues related to gene flow and access and benefit sharing should also profit from more research.

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