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DRAFT GUIDELINES ON *IN VIVO* CONSERVATION OF ANIMAL GENETIC RESOURCES

Table of Contents

ME879

Box

Table

Figure

Abbreviations and acronyms

AI	artificial insemination
BCP	Biocultural Community Protocol
CBD	Convention on Biological Diversity (http://www.cbd.int/)
CV	conservation value
DAD-IS	Domestic Animal Diversity Information System (http://dad.fao.org/)
DNA	deoxyribonucleic acid
ΔF	proportional change in inbreeding per generation
f	coancestry
INTA	Institute for Agricultural Technology (Argentina)
MOET	multiple ovulation and embryo transfer
N_e	effective population size
NGO	non-governmental organization
PDO	Protected Designation of Origin
PGI	Protected Geographical Indication
RBST	Rare Breeds Survival Trust (https://www.rbst.org.uk/)
SNP	single nucleotide polymorphism
SWOT	strengths, weaknesses, opportunities and threats
USP	unique selling position

DRAFT GUIDELINES ON *IN VIVO* CONSERVATION OF ANIMAL GENETIC RESOURCES

FOREWORD

These guidelines present the basic concepts involved in the establishment and implementation of *in vivo* conservation plans for animal genetic resources for food and agriculture. The guidelines are intended for use by policy makers in the management of animal genetic resources, managers of animal breeding organizations, persons responsible for training in animal genetic resource management and any other stakeholders with a leading role in designing and implementing *in vivo* conservation of animal genetic resources. Although individual breeders and livestock keepers are not the direct target audience, the guidelines include background information that is relevant for all stakeholders involved in planning programmes for conservation of animal genetic resources.

The genetic diversity of the world's livestock species is in a state of continuous decline and the animal genetic resources that remain are often not used in the most efficient way. To address these problems, FAO's Commission on Genetic Resources for Food and Agriculture negotiated the *Global Plan of Action for Animal Genetic Resources* (*Global Plan of Action*)[1], which was adopted at the International Technical Conference on Animal Genetic Resources for Food and Agriculture held in Interlaken, Switzerland, in September 2007 and subsequently endorsed by all FAO Member Nations at the Thirty-fourth FAO Conference in November 2007.The implementation of the *Global Plan of Action* will contribute significantly to efforts to meet the Millennium Development Goals, particularly Goal 1: Eradicate extreme poverty and hunger and Goal 7: Ensure environmental sustainability.

The *Global Plan of Action* consists of 23 strategic priorities grouped into 4 strategic priority areas:

1. Characterization, Inventory and Monitoring of Trends and Associated Risks;
2. Sustainable Use and Development;
3. Conservation; and
4. Policies, Institutions and Capacity-building.

The main responsibility for implementation of the *Global Plan of Action* lies with national governments, but non-governmental and intergovernmental organizations are also expected to play a major role.

FAO's support to the implementation of the *Global Plan of Action* includes the preparation of a series of technical guidelines addressing specific areas of animal genetic resources management. To address Strategic Priority Area 3 of the *Global Plan of Action,* FAO commissioned a group of scientists to develop guidelines on *in vivo* conservation. This strategic priority area is also addressed by guidelines on *Cryoconservation of animal genetic resources,* which were endorsed by the Commission on Genetic Resources for Food and Agriculture in 2011.

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[1] http://www.fao.org/docrep/010/a1404e/a1404e00.htm

ACKNOWLEDGEMENTS

A wide range of experts in the *in vivo* conservation of animal genetic resources were consulted in the preparation of these guidelines. The following persons made up the team of primary authors of the guidelines:

Jesús Fernandez Martin (Spain); Gustavo Gandini (Italy); Balwinder Kumar Joshi (India); Kor Oldenbroek (Netherlands); and Phillip Sponenberg (United States of America).

The following persons generously contributed text boxes that describe certain concepts in more detail or present real-life examples of *in vivo* conservation activities:

Lawrence Alderson (United Kingdom); Elli Broxham (Germany); Coralie Danchin-Burge (France); Sabyasachi Das (India); Kennedy Dzama (South Africa); Ignacio García León (Chile); Gustavo Gutierrez (Peru); Sergej Ivanov (Serbia); Arthur Mariante (Brazil); German Martinez Correal (Colombia); Carlos Mezzadra (Argentina); Joaquin Mueller (Argentina); Keith Ramsay (South Africa); José Luis Riverso (Chile); Devinder K. Sadana (India); Alessandra Stella (Italy); Jacob Wanyama (Kenya); Kerstin Zander (Australia); and Pascalle Renee Ziomi Smith (Chile).

The guidelines were reviewed, tested, validated and finalized at a series of regional training workshops and expert meetings held around the world. The first workshop involved the Asia region and was hosted in October 2010 by the National Bureau of Animal Genetic Resources of India. In December 2010, the guidelines were introduced and offered for review at a joint workshop between FAO, the International Livestock Research Institute (ILRI) and the Association for Strengthening Agricultural Research in Eastern and Central Africa (ASARECA). The workshop was held at the ILRI campus in Ethiopia. In June 2011, the guidelines were tested and reviewed at a training workshop targeting Eastern Europe. The workshop was hosted by the University of Wageningen and the Centre for Genetic Resources of the Netherlands and was also supported by the European Regional Focal Point for Animal Genetic Resources and the Ministry of Economic Affairs, Agriculture and Innovation of the Netherlands. In November 2011, the guidelines were presented at a joint training workshop organized by FAO, ILRI and the Swedish Agricultural University. The workshop included a review by a panel of African experts. An expert panel from Latin America reviewed the guidelines at a meeting held in Santiago, Chile, in December 2011. Following the incorporation of recommendations from the various expert meetings and capacity-building workshops, the guidelines underwent a final review with a global audience. From January to March 2011, the Domestic Animal Diversity Network (DAD - Net) was used to conduct an electronic conference on the guidelines, during which each section was reviewed on a week-by-week basis.

More than 120 scientists, technicians and decision-makers attended one of the workshops or expert meetings. The electronic conference provided more than 1 600 subscribers to DAD-Net with access to the draft guidelines to. The following persons made contributions to the editing of the guidelines:

W. Akin. Hassan (Nigeria); Harvey Blackburn (United States of America); Salah Galal (Egypt); Rafael González Cano (Spain); Carol Halberstadt (United States of America); Christian Keambou Tiambo (Kenya); Ilse Köehler-Rollefson (Germany); Hans Lenstra (Netherlands); Bill Lyons (United Kingdom); Catherine Marguerat (Switzerland); Tadele Mirkena (Ethiopia); Siboniso Moyo (Mozambique); Hassan Ally Mruttu (India); K. Edouard N'Goran (Côte D'Ivoire); Chanda Nimbkar (India); Zabron Nziku (United Republic of Tanzania); Richard Osei-Amponsah (Ghana); Baisti Podisi (Botswana); Abdul Raziq (Pakistan); Violeta Razmaitė (Lithuania); David Steane (Thailand); Sonam Tamang (Bhutan); and Le Thi Thuy (Viet Nam).

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USER GUIDANCE

Introduction

According to the Convention on Biological Diversity (CBD, 1992), individual countries hold the main responsibility for conserving their genetic diversity on a long-term basis. The *Global Plan of Action* (FAO, 2007a) also recognizes that countries have the main responsibility for its implementation. Animal production is vital to humankind and conservation of animal genetic diversity is a way to secure food production from animals for our future. *In vivo* conservation of populations *in situ* is the preferred conservation method (FAO, 2007a). Oldenbroek (2007) writes:

> *"All objectives of conservation can be reached the best [with in situ conservation] and it offers ample possibilities for utilization. Besides, the development of a breed can continue and adaptation to changing circumstances is facilitated. However, the risks of inbreeding (caused by mating of relatives and leading to inbreeding depression: a decrease in fitness) and random drift (loss of alleles with a low frequency caused by random processes) has to receive full attention in the breeding scheme of these populations, that are merely of small size."*

Integration of *in situ* and of *ex situ* methods can, because of their complementarity, provide a powerful conservation strategy. *Ex situ* conservation usually implies *in vitro* cryoconservation of gametes in a gene bank. Cryoconservation can be supported by *ex situ – in vivo* conservation. This implies the conservation of a limited number of live animals in a small breeding herd or a zoo, where animals are kept outside their original production environment and adaptation to changing conditions is impaired.

The goal and structure of the guidelines

The objective of these guidelines is to provide technical guidance and a decision aid for the various available conservation options, along with concepts for the design and establishment of animal breeding programmes that conserve genetic diversity effectively and stimulate sustainable use, usually through the generation of increased income for the keepers of the livestock involved. The material presented is intended to be relevant to all species of livestock used for food production and in providing other products and services for humankind. Where appropriate, species-specific guidance is given.

These guidelines are intended to provide the necessary technical background needed by organizations or individual actors who want to set up, implement and monitor *in vivo* conservation programmes in a rational manner. It defines the tasks and actions that should be undertaken. The emphasis is placed on *in situ* programmes, because such programmes are likely to be the most relevant for short-term conservation objectives. The order of sections generally follows the chronological order of establishing a conservation programme. The subsections have a fixed format consisting of a rationale, an objective, the required input and the expected output, followed by a set of tasks and actions needed to obtain the desired objective.

Most countries have nominated a National Coordinator for the Management of Animal Genetic Resources (National Coordinator)[2] and established a National Focal Point for Animal Genetic Resources (FAO, 2011a). Many have also established a multistakeholder National Advisory Committee for Animal Genetic Resources. Although many *in vivo* conservation programmes will be established and implemented by various organizations working directly with livestock keepers, rather than by the government, the process of building a conservation programme should be realized with the full participation and awareness of the National Coordinator. The National Advisory Committee should also be consulted regularly. If no National Advisory Committee has been established, it is advisable to set up an ad hoc committee of relevant stakeholders and experts in the field of animal genetic resource management and that can be consulted during the process. Many groups of stakeholders are involved in the conservation of animal genetic resources (FAO, 2007b; Oldenbroek, 2007): national and regional governments, research and education institutes (including universities), non-governmental organizations (NGOs), breeders' associations, farmers and pastoralists, part-time farmers and hobbyists, and breeding companies.

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[2] http://www.fao.org/dad-is

Many countries have developed national strategies and action plans for animal genetic resources for the purpose of implementing the *Global Plan of Action* at National level or are planning to do so (FAO, 2009). Countries that have developed national strategies and action plans will probably have identified in broad terms their conservation needs and objectives and may have allocated responsibility for developing and implementing a conservation strategy. In such circumstances, the national strategy and action plan will provide the general framework within which the users of these guidelines operate. In the case of countries that do not yet have not a national strategy and action plan, the development this broader strategy and action plan for all aspects of animal genetic resources management and the development of a more detailed conservation strategy should obviously be approached in a coordinated way. Likewise, if countries have the advice offered in the guidelines on *Surveying and monitoring animal genetic resources* (FAO, 2011c), they will have taken the need for data to plan conservation strategies [see FAO guidelines on *Phenotypic* (2012) and *Molecular genetic characterization of animal genetic resources* (2011b)] into account in developing their strategies for surveying and monitoring and the planners of conservation strategies will not be starting from scratch.

Section 1 presents a brief overview of the importance of livestock, the state of animal genetic resources, the reasons for their loss, and objectives and options for their conservation.

Section 2 presents methods for identifying breeds that are at risk and are therefore candidates for conservation, including assignment of breeds to categories based on their risk status.

Section 3 describes methodologies that can be used to decide which breeds to conserve, assuming that financial resources for conservation preclude the conservation of all breeds. It describes the factors that influence the conservation value of a breed and methods for prioritizing breeds.

Section 4 describes how to choose the appropriate conservation method.

Section 5 describes the organization of the institutions required to implement programmes for *in vivo* conservation.

Section 6 deals with the design of effective conservation and sustainable use programmes, with special emphasis on the maintenance of genetic diversity within breeding populations.

Section 7 presents an overview of how to implement breeding programmes that combine conservation and sustainable use, largely by improving the productivity of the conserved breeds.

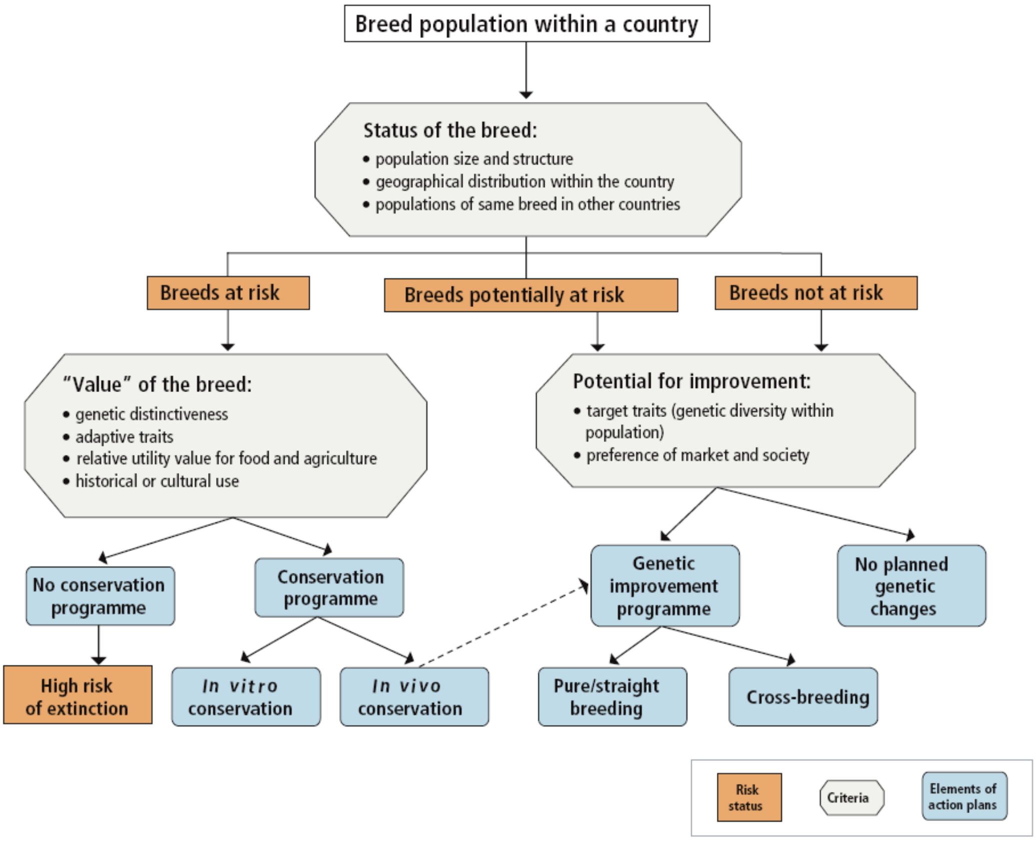
Section 8 outlines opportunities to increase the value of local breeds and their products in *in situ* conservation programmes.

A glossary of selected terms is included as an annex.

The guidelines follow the flow chart of activities shown in Figure 1, originally presented in *The State of the World's Animal Genetic Resources for Food and Agriculture* (FAO, 2007b): The (risk) status of a breed is identified by completing the tasks and actions described in Sections 1 and 2. The value of the breed is determined by completing the tasks and actions described in Section 3. Once it has been decided that a given a breed merits conservation, a decision must be taken as to the type of conservation programme to implement. Section 4 outlines and guides the choice between *in vitro* and *in vivo* approaches. Section 5 deals with the establishment of *in vivo* conservation programmes and Section 6 with the management of genetic diversity within such programmes. Genetic improvement programmes are addressed in Section 7. The tasks and actions described in Section 8 will help stakeholders add value to a breed or its products and will increase the sustainability of *in situ* programmes for the breed.

The guidelines recognize that geographic and economic conditions vary considerably across countries, as does the level of technical capacity. They also recognize that a similar goal can often be achieved in multiple ways. Therefore, most of the sections of the guidelines outline several different options for achieving the respective goals, including simple but effective strategies that can be applied in nearly any country. Countries are encouraged to identify and apply the approaches that are best adapted to their particular circumstances. Some countries may need outside assistance and advice if they plan to apply the more complex approaches described.

Figure 1. Flow chart for national management of animal genetic resources



Source: FAO (2007b).

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I. THE IMPORTANCE OF ANIMAL GENETIC RESOURCES AND OPTIONS FOR THEIR CONSERVATION

A limited number of species of mammals and birds are kept by humans and play an important role in agriculture and food production. These animals are the result of domestication processes that have been ongoing for almost 12 000 years. Over time, domesticated livestock species have evolved into more or less distinct subgroups or "*breeds*" (see Box 1 for definitions) through a variety of formal and informal processes.

Box 1

The definition of the term "breed"

A literature review by Woolliams and Toro (2007) concludes that the question "What is a breed?" is simple to state, but difficult to answer. The authors found the following definitions, from a variety of published sources, each relevant and pertinent to their particular stakeholders:

- "*Animals that, through selection and breeding, have come to resemble one another and pass those traits uniformly to their offspring.*"
- "*A breed is a group of domestic cats (subspecies felis catus) that the governing body of (the Cat Fanciers Association) has agreed to recognize as such. A breed must have distinguishing features that set it apart from all other breeds.*"
- "*A race or of men or other animals (or of plants), perpetuating its special or distinctive characteristics by inheritance.*"
- "*Race, stock; strain; a line of descendants perpetuating particular hereditary qualities.*"
- "*Either a sub-specific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species, or a group for which geographical and/or cultural separation from phenotypically separate groups has led to acceptance of its separate identity.*"
- "*A breed is a group of domestic animals, termed such by common consent of the breeders, ... a term which arose among breeders of livestock, created one might say, for their own use, and no one is warranted in assigning to this word a scientific definition and in calling the breeders wrong when they deviate from the formulated definition. It is their word and the breeders' common usage is what we must accept as the correct definition.*"
- "*A breed is a breed if enough people say it is.*"

The fifth definition (FAO, 2007b) notes that the breed concept involves cultural influences that should be respected. This perspective is also reflected in the final two definitions.

As livestock populations spread from their centres of domestication (via human migration, trade and conquest) they did so as small samples of the original populations. As these groups of animals encountered new ecological conditions, genetic drift and natural selection led to the emergence of distinct local populations. These local populations developed into distinguishable subgroups within the species, differentiated primarily on the basis of adaptive traits, but also through some selection for characteristics desired by their keepers. Because such breeds developed under the strong influence of their natural environments (i.e. the "land" in which they were developed), they are sometimes called "landraces" or "landrace breeds". The term "ecotype" is occasionally used to refer to populations within a breed that are genetically adapted to a specific habitat. However, the distinction between breeds and ecotypes within a breed is not very objective, and generally involves cultural rather than genetic factors.

As societies developed and diversified, new demands were placed on livestock, and knowledge and skills in husbandry and breeding were accumulated and led to the development of more specialized breeds and breeding lines. Performance and pedigree recording and human-controlled artificial selection of livestock in the past 250 years has led, particularly in more industrialized countries, to the development of individually uniform but collectively highly diverse, distinguishable populations, which are commonly called “standardized breeds”. The development of standardized breeds started in the middle of the eighteenth century with the activities of Robert Bakewell in England and was based on establishing an ideal (i.e. a breed standard), closing the population, recording pedigrees and using deliberate mating and selection to achieve the standardized ideal. In some cases, breeding companies have developed specialized lines with standardized breeds and selected them intensely for very specific production systems.

The interaction between landraces and standardized breeds has involved considerable give and take. On one hand, landraces played a basic role in the development of the standardized breeds; on the other, landraces were threatened by the expansion of the standardized breeds. In developing countries, landraces play an important role, especially in traditional production systems.

The composition of livestock populations has never been static; over time breeds emerged, were crossed to develop new breeds and disappeared. However, diversity prevailed. The process ultimately gave rise to the more than 8 000 reported breeds that exist today (FAO, 2012). These breeds represent the world’s animal genetic resources. They have been shaped by nature and by human interventions to meet demands in the relatively short term. However, over the longer term, they will need to be drawn upon to address changes in production environments (e.g. due to climate change) and in market demands.

In these guidelines, the use of the term *breed* generally follows the FAO definition used in The *State of the World’s Animal Genetic Resources for Food and Agriculture* (FAO, 2007b). However, from a practical perspective, “breed” is used to describe the *unit of conservation*, the specific population of animals that is to be conserved. The concepts described in the guidelines can apply to various populations, ranging from a village herd of animals to well-defined registered standardized breeds or specialized breeding lines. In general in the guidelines, breeds are divided into two categories, standardized breeds and non-standardized breeds; most of the latter could also be described as landraces.

The importance of livestock

Rationale

Within a country, the livestock sector has to balance a range of policy objectives. Among the most urgent are: supporting rural development and the alleviation of hunger and poverty; meeting the increasing demand for livestock products and responding to changing consumer requirements; ensuring food safety and minimizing the threat posed by animal diseases; and maintaining biodiversity and environmental integrity. As in the past, meeting these challenges will involve the establishment for a limited number breeds of breeding programmes for very specialized production goals, mixing breeds, and breeding individual animals with the qualities needed to meet the requirements of particular production, social and market conditions. However, matching animal genetic resources to specific development goals, threatens continued existence of some breeds. The loss of such breeds would result in genetic erosion: a decrease in the genetic variability within the species that exists thanks to genetic differences among breeds.

The capacity of a livestock population to adapt to future changes in environmental and market conditions is directly related to its genetic diversity. Therefore, if diversity is threatened, it is important that adequate measures to promote conservation and sustainable are put in place and that these measures are based on appropriate knowledge and skills. Within a species, the proportion of the genetic variation accounted for by differences among breeds typically ranges from 25 to 66 percent, depending on the trait (Woolliams and Toro, 2007).

Many livestock species have the ability to transform forage and crop residues that are inedible to humans into nutritionally important food products. Products such as meat, milk, eggs, fibre and hides from the more than 40 domesticated livestock species account for 40 percent of the value of world agricultural output. Livestock products provide one-third of humanity’s protein intake, as well as draught power and fertilizer for crop production, and thus are essential components in achieving sustainable food security. In some developing countries, particularly those where pastoral systems predominate, the contribution of livestock production is even more important. Livestock also serve as a very important cash reserve in many mixed farming and pastoral systems, thereby playing an important role in risk reduction. The genetic diversity of livestock is an essential resource in the dynamics of livestock production processes. Careful genetic management and use of breeds in these processes determine the effectiveness of the maintenance of the genetic diversity within the species.

The development of a national conservation programme for animal genetic resources starts with an overview of the country's livestock production systems including the species and breeds involved in different livestock functions. A starting point might be the country report[3] produced during the preparation of *The State of the World's Animal Genetic Resources for Food and Agriculture* (FAO, 2007b) as well as the information available in the Domestic Animal Diversity Information System (DAD-IS)[4].

Objective: To produce an overview of the relevant livestock species in the country or the region, the number of breeds within the species and of the functions of the different species and breeds.

Inputs:

1. The country report;
2. Any relevant information about national animal genetic resources that has been produced since the preparation of the country report; in particular, a national strategy and action plan for animal genetic resources, if available;
3. *Preparation of national strategies and action plans for animal genetic resources* (FAO, 2009a), assuming no such strategies and plan have been developed;
4. *Breeding strategies for sustainable management of animal genetic resources* (FAO, 2010); and
5. The knowledge of stakeholders involved in the management of animal genetic resources within the country (livestock keepers, pastoralists, farmers, veterinarians, breeding organizations, scientists, NGOs, regional governmental organizations for agriculture, etc).

Output:

- An overview of the species and breeds that are important in livestock production in the country or the region.

Task 1. Identify the breeds of livestock found in the country or in the region

Action 1. Establish a definition for the term "breed" that will allow for recognition of operational units of conservation

As described above (Box 1), the term "breed" has many possible definitions. Although "breed" is often regarded as a concept associated with industrialized countries and related production systems, it is imperative that each country have its own breed definition and applies the definition to its livestock populations. This step is a practical necessity because breeds serve as *units of conservation*, i.e. the distinct populations to which the concepts and actions described in these guidelines are applied. Ideally, the definition of the term will have a degree of harmony and homogeneity across countries. Therefore, it is recommended that the following definition be used as a guide: "*Either a sub-specific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species, or a group for which geographical and/or cultural separation from phenotypically separate groups has led to acceptance of its separate identity*." (FAO, 2007b)

In general, a breed is a population of animals whose members will be treated in the same way under the national programmes developed for management of animal genetic resources. With only rare exceptions (see Section 6), members of a conserved breed will only be mated with other animals of the same breed. Likewise, in most cases, the current members of a given breed will be the result of a multigenerational history of *inter se* mating. When introgression or any other crossbreeding is practised, the population of animals resulting should no longer be recognized as part of the original breed, and ideally a new breed should be established.

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[3] ftp://ftp.fao.org/docrep/fao/010/a1250e/annexes/CountryReports/CountryReports.pdf

[4] http://www.fao.org/dad-is

Some countries have a formal protocol for the recognition of breeds, with certain standards that must be met before the breed can be registered as a distinct population. In India, the National Bureau of Animal Genetic Resources is responsible for breed registration and has a precise and strict procedure for this purpose. A description of the procedure and requirements for breed registration is provided in Box 2.

Box 2

Registration of livestock breeds in India

The breed registration system in India is regarded not only as a tool with which to facilitate breed management, but also as a form of protection for local animal genetic resources under a *sui generis* system. The system of breed recognition is based on the FAO definition.

Under the breed registration system, any citizen of India can request the recognition of a breed by submitting a formal application to the National Bureau of Animal Genetic Resources, although the application must be approved by a state government official. Candidate breeds must have been bred pure for ten generations and scientific evidence of their uniqueness and reproducibility (e.g. scientific articles or research reports) must be provided. The application must be accompanied by a complete description of the breed using a standard set of species-specific descriptors, a detailed history of the breed and a list of characteristics that distinguish the breed from other populations. The applicant must also submit photographs of representative individuals of different sexes and ages, and a list of the registered animals that conform the breed standards. In addition, the applicant must submit letters from at least three different breeders or owners, indicating:

- why they believe it should become a recognized breed;
- how long they have been breeding the breed;
- the reasons for recognition of the breed as a separate identity;
- activities undertaken to establish this breed (e.g. breeding strategies);
- any suggestions as to how to further improve the breed in a long-term perspective; and
- characteristics that make this breed clearly different and distinctive from all other breeds.

The application is then reviewed and approved or rejected by a breed registration committee of National Bureau of Animal Genetic Resources, which maintains a permanent registry and database.

More information can be found at http://www.nbagr.res.in/Accessionbreed.html.

Provided by Balwinder K. Joshi.

Although precise protocols for breed recognition are an important part of an animal genetic resources management programme, they need to be complemented with policies for managing less-descript populations. These populations contain significant genetic variation and contribute significantly to food security and livelihoods. They must not be ignored. Neglecting them is likely to result in diminished genetic diversity in the species. Many important concepts in the management of large livestock populations are addressed in *Breeding strategies for sustainable management of animal genetic resources* (FAO, 2010).

Action 2. Prepare a protocol through which animals can be assigned to and/or excluded from a given breed

The history of *inter se* mating that is generally associated with the genetic development of a breed will usually have resulted in common observable heritable characteristics that allow an individual animal to be assigned to its breed even in the absence of breeding records. Assignment of animals to breeds will usually be important for conservation for a variety of practical reasons. For example, the identification of breeds at risk (see Section 2) is a function of population size and distribution. To count members of a breed, the animals must be clearly distinguished from those of other breeds. Similarly, in order to ensure that animals of the same breed are mated together, it is necessary to know which breed each animal belongs to.

Breed standards and protocols will usually be established by a breeders' association, if one exists. More details are given in Section 4. If no association exists, then the National Advisory Committee or other government body may need to establish criteria for breed assignment. Even if there is a breed association, the government may require a process of approval for the criteria, especially if breed associations are receiving public support (see Section 5).

Action 3. Review input documents to establish a baseline list of breeds and if necessary, undertake surveys to confirm the information in past reports and/or identify new breeds

In the early 2000s, most countries prepared a country report that included a list of their breeds. Many countries have subsequently updated their breed inventories in DAD-IS[5]. However, as breed formation is a dynamic process and breeds are continually created and lost, countries will periodically need to undertake surveys (FAO, 2011) to ensure that their inventories are up to date. If a new national definition of "breed" has been established (Action 1), it should be used as a basis for updating the national breed inventory.

Task 2. Evaluate the species and breeds of livestock present in the country or region along with their primary functions

Action 1. Study the input documents

As described in the user guidance section, if the country has a national strategy and action plan (FAO, 2009a) this will probably provide the framework for the development of a conservation strategy. It is likely to indicate the government's vision for the conservation of animal genetic resources, how this relates to general livestock and agricultural development plans, which animal species are important to the development of the country or to specific regions, and what objectives are considered most important in the conservation national of animal genetic resources.

Action 2. Consult the National Advisory Committee for Animal Genetic Resources and other relevant stakeholders

If a National Advisory Committee does not exist, then an *ad hoc* advisory committee on conservation of animal genetic resources should be created. The committee should be invited to provide advice on the review of species, breeds and functions and to provide a critical review of the outcomes. Other stakeholders, such as breed associations, NGOs and other organizations that deal with livestock breeds should also be consulted, as these organizations are likely to have even more detailed information on specific animal genetic resources than the National Advisory Committee.

Action 3. Summarize available information on locally available breeds and their functions

Produce a table for each species listing breeds and their functions. Include a short explanation of each. Submit the table to the National Advisory Committee for review. Functions of breeds comprise a wide range of services to humankind, which may include production of milk, meat, eggs, skins and fibre; provision of agricultural inputs such as draught power and manure; fulfilment of cultural roles such as participation in ceremonies and sporting events; provision of financial services such as savings and insurance; provision of social status for their owners; and provision of nature–management services such as conservation grazing to promote wildlife habitats.

The dynamics of the livestock sector

Rationale

Livestock systems are ever changing (FAO, 2007b). Drivers of change in livestock production systems include:

- population and/or economic growth and subsequent changes in demand for animal products;
- developments in trade and marketing;
- technological advances;
- environmental (including climate) changes; and
- policy decisions.

The outlook for a breed depends to a great extent on its present and future role in livestock systems. The decline of certain livestock functions is often a substantial threat to species and breeds that specialize in providing these functions. Perhaps the most obvious example is that throughout much of the world, the existence of specialized draught breeds is threatened by the expansion of mechanization

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[5] https://www.fao.org/dad-is

in agriculture. Similarly, breeds developed for wool and fibre production may be threatened by the availability of synthetic fibres. Availability of alternative sources of fertilizer or financial services also shifts the objectives of livestock keepers and may affect their breed choices. The emergence of new livestock functions and modification of existing roles challenge the use of a species and call for breeds specialized in these functions. Such specialization can only be realized if the relevant genetic diversity is available within the species, i.e. has been conserved in the past. Obvious examples of new or modified livestock functions are the use of horses exclusively for recreation and sport rather than work and the use of grazing species for nature management programmes. When a breed has significant genetic variability, it can be adapted through selection to fulfil a new role. If not, it risks being replaced by another breed.

The dominant trend within the global livestock sector is that rising demand for meat, dairy products and eggs is leading to the intensification, specialization and industrialization of production systems, which in turn narrows the range of animal genetic resources that can be used. Such systems are rapidly spreading in developing countries. Unfortunately, while this trend contributes greatly to increasing the supply of food of animal origin, it is a threat to the diversity of animal genetic resources. Many breeds are set aside because historically they have been selected for a range of traits rather than for a specific production trait. Within the breeds that are used in industrial systems, diversity is also decreasing due to the selection of a small number of superior individuals and families. This loss of diversity means the loss of important options for adapting production systems to future developments. Newly emerging market trends and policy objectives are continually placing new demands on the livestock sector. The prospect of further challenges such as adapting to global climate change underlines the importance of retaining a diverse portfolio of livestock breeds with large diversity in adaptive traits.

To identify the dynamics of the livestock sector and to detect opportunities and threats to a given livestock breed it is necessary to evaluate the livestock industry in the respective country or region, including the species and breeds used.

Objective: To evaluate the livestock industry and document the roles of the different animal species and breeds, threats to their sustainability and opportunities for their conservation and use.

Input:

1. The country report submitted to FAO during the preparation of the *State of the World's Animal Genetic Resources for Food and Agriculture*; and
2. An update of the statistics in the report.

Output:

- A description of ongoing and predicted future changes in the use of species, the number of breeds and the population sizes of each breed.

Task: Describe the dynamics of the species and breeds and their functions

Action 1. Describe the use of the different species and breeds in livestock systems

The basis for this may be available in the country report. However, the material will need to be updated.

Action 2. Describe the drivers of change of the livestock systems in your country and the dynamics of the livestock systems now and those to be expected.

The main drivers mentioned in the literature (Oldenbroek, 2007) are:

- growth of the human population;
- increased demand for animal products;
- increased regard for food quality and safety for safeguarding human health and animal welfare;
- increased interest of consumers in niche products and in sustainable use of resources;
- technological advances;
- environmental (including climate) changes; and
- policy decisions.

In developed countries there is an increasing demand for the nature management services provided by grazing livestock and for animals that are appealing to hobby farmers.

Action 3. Describe the trends

Describe observed and expected trends in the use of species and breeds as production systems change and the consequences of these changes for the species and breeds.

The national status and development of animal genetic resources

Rationale

As mentioned previously, about 40 animal species have been domesticated for food and agriculture. On a global scale, however, only five species – cattle, sheep, chickens, goats, and pigs – show widespread distribution and have large numbers of breeds. Cattle, sheep and chickens are widely dispersed across the global, whereas goats and pigs are less uniformly distributed. Goats are found in greatest numbers in developing regions and pigs are relatively uncommon in countries that are predominantly Muslim.

The *State of the World's Animal Genetic Resources for Food and Agriculture* (FAO, 2007b) reported on the distribution of the five major livestock species according to region and those results are summarized here:

Chicken breeds make up a large majority of the total number of avian breeds in the world. There are around 17 billion chickens, about half of which are in Asia and another quarter in the Americas. Europe and the Caucasus account for around 13 percent of the world's flock, followed by Africa with 7 percent.

Cattle are important in all regions and have a global population of over 1.3 billion animals, or about one for every five people on the planet. Asia and Latin America have 32 percent and 28 percent of the global herd, respectively, with Brazil, India and China accounting for particularly large proportions. Large cattle populations are also found in Africa (particularly Sudan and Ethiopia), and Europe and the Caucasus, with largest numbers in the Russian Federation and France. Cattle breeds contribute 22 percent of the world's total number of recorded mammalian livestock breeds.

The world's sheep population is just over one billion. About half are found in Asia and the Near and Middle East. China, India and the Islamic Republic of Iran have the largest national populations. Africa, Europe and the Caucasus, and the Southwest Pacific have around 15 percent each; and 8 percent are found in Latin America and the Caribbean. Sheep are the species with the highest number of recorded breeds (contributing 25 percent of the global total for mammals).

There are about a billion pigs in the world – one for every seven people. About two-thirds of the global population is found in Asia. China has the greatest number, but Viet Nam, India and the Philippines also have large national herds. Europe and the Caucasus have a fifth of the world's pigs, and the Americas another 15 percent. Pig breeds account for 12 percent of the total number of recorded mammalian breeds in the world.

There are about 800 million goats worldwide. About 70 percent of the world's goats are in Asia and the Near and Middle East, with the largest numbers in China, India and Pakistan. Africa accounts for just fewer than 15 percent, with about 5 percent being found in each of the Latin American and the Caribbean and Europe and the Caucasus regions. Twelve percent of the world's recorded mammalian breeds are goat breeds.

Less numerous species like horses, donkeys and ducks are also found in all regions, but they show a less uniform distribution than cattle, sheep and chickens. Certain species, such as buffaloes and various camelids, are very important in specific regions, but do not have a wide global distribution.

Around 20 percent of reported breeds are classified as at risk, but this statistic presents only a partial picture of genetic erosion. Breed inventories, and particularly surveys of population size and structure at breed level, are inadequate in many parts of the world. Population data are unavailable for about 30 percent of all breeds. Nevertheless, it can be concluded that the between-breed diversity within these livestock species is under threat. Moreover, among many of the most widely international transboundary breeds of cattle, within-breed genetic diversity is also being undermined by the use of few highly popular sires for breeding purposes. These two tendencies are leading to rapid and irreversible erosion of genetic diversity in livestock species.

Objective: To describe the dynamics of the livestock species in your country or region.

Input:

1. List of breeds found within the country;
2. Historical and present data on the number of animals per breed (e.g. from the country report, DAD-IS, for European countries, the European Farm Animal Biodiversity Information System – EFABIS, or the outputs of recent surveying and monitoring activities); and
3. National statistics and strategic and policy documents useful for predicting future breed population sizes.

Outputs:

- An estimate of the number of animals per breed now and prediction of population sizes in the future.

Task: Produce estimates of past, present and future numbers of animals per breed

Action 1. Obtain past and present numbers and analyse trends

A starting point might be the country report containing figures from around the year 2000. Many countries (Ministries of Agriculture or of Economic Affairs) produce annual statistics, although often not on a breed-by-breed basis. Annual reports of breeding organizations may also be available. Ministries, universities and research institutes regularly produce “outlooks to the future” that can be used to predict trends in the number of animals per species and possibly per breed. Ideally, part of national strategies and action plans will be to establish a programme for routine monitoring of breed population sizes, assuming such a programme does not exist.

Action 2. Predict the number of animals per breed in ten years from now

Based on the number of animals per breed ten years ago, the present number and the observed trends, the number of animals per breed ten years from now can be predicted (see Section 2).

When predicting future population sizes, it is good practice to consider different scenarios and produce two alternative figures: an optimistic estimate and a pessimistic estimate, which together present a realistic range.

Action 3. Consider general trends if breed population data are not available

In many countries, reliable multi-year information on breed population sizes is not available. In such cases, countries should consider the factors that affect diversity of animal genetic resources. Is importation of foreign livestock germplasm common and/or encouraged by the government? Is urbanization increasing as former livestock keepers or their adult-age children move to the city? Does the government provide support for development and conservation of animal genetic resources? Are farmers and breeders formally organized? Are there many international NGOs supporting production of local breeds of livestock? The answers to these questions may reveal whether livestock breeds are likely to be at risk, i.e. if the answers to the first two questions is “Yes” and the latter three “No”, then there is high chance that breeds may be at risk. If such trends suggest that animal genetic resources may be at risk, then implementation of a breed census should be given high priority.

Reasons for loss of animal genetic diversity

There are several factors that place breeds at risk of loss and threaten domestic animal diversity (FAO, 2009b). In developed countries, the greatest cause of genetic erosion is, by far, the growing trend to a global reliance on a very limited number of international transboundary breeds suited to the needs of high input – high output industrial agriculture. The effect of this trend is that many breeds have fallen out of use and disappeared without notice. In developing countries, however, genetic diversity is potentially threatened by a variety of influences. In the literature, there is broad agreement regarding the general trends and factors threatening animal genetic resources in developing countries. For example, Rege and Gibson (2003) suggest that the use of exotic germplasm, changes in production systems, changes in producer preference because of socio-economic factors, and a range of disasters (drought, famine, disease epidemics, civil strife and war) are the major causes of genetic erosion. Tisdell (2003) mentions the following major causes: development interventions, specialization (emphasis on a single productive trait), genetic introgression of exotic breeds, the development of technology and biotechnology, political instability and natural disasters. For at-risk cattle breeds in Africa, Rege (1999) lists the following major threats: replacement by other breeds, cross-breeding with exotic breeds or with other local breeds, conflict, loss of habitat, disease, neglect and lack of sustained breeding programmes. Iñiguez (2005) identifies displacement by other breeds, and indiscriminate cross-breeding as threats to small ruminant breeds in West Asia and North Africa.

The increased demand for livestock products in many parts of the developing world drives efforts to increase the output of meat, eggs and milk for the market (Delgado *et al.*, 1999). Cross-breeding and subsequently the replacement of local breeds by a narrow range of high-yielding international transboundary breeds is a very widespread consequence of efforts to increase output. The rapid expansion of industrialized pig and poultry production systems in regions with a great diversity of local pig and chicken breeds gives rise in a great need for action to conserve the local breeds of these species. Trends in consumer demand can threaten breeds that do not supply products with the desired characteristics. For example, consumer preference for leaner meat has led to the decline of pig breeds that have carcasses with a higher fat content (Tisdell, 2003, EMBRAPA, 2006). Other threats to local breeds include climate change, lack of the necessary infrastructure and services for breed improvement, and loss of the labour force and traditional knowledge associated with livestock keeping because of the migration of livestock keepers to urban areas in search of employment (Daniel, 2000; Farooquee *et al.*, 2004).

These examples illustrate that there are a number of ways in which threats to animal genetic resources can potentially be classified. In The *State of the World's Animal Genetic Resources for Food and Agriculture* (FAO, 2007b), threats were grouped within the following three broad categories based on the different kinds of challenge they pose to the sustainable management of animal genetic resources:

- trends in the livestock sector;
- disasters and emergencies; and
- animal disease epidemics and control measures.

Before developing conservation programmes it is important to understand as fully as possible the threats facing animal genetic resources in your country or region.

Objective: To identify and describe the factors that threaten animal genetic diversity in your country or region.

Input:

1. A description of the drivers of change in livestock systems; and
2. Documents describing the likelihood of disasters and disease epidemics and the existence of emergency programmes combating the effects of disasters and diseases.

Output:

- A description of risk factors for genetic diversity in your country; and
- A general course of action to decrease the impact of the various threats.

Task: Estimate the risks associated with factors that threaten genetic diversity

Action 1. Analyse the drivers of change in livestock systems in your country or region

Assess the consequences of livestock production systems changes for the breeds presently used these systems. For example, when intensification of animal production is widely adopted as the primary strategy for meeting increased demand for food of livestock origin, breeds not fitting these systems because of their low production potential will be set aside.

Action 2. Analyse the chances of disasters and disease outbreaks

Disasters in this context are events such as wars and floods that may destroy whole populations of animals in a short period of time. An attempt should be made to identify the extent of the threat that such events pose to animal genetic resources within the country or region. Political instability, for example, increases risks associated with military conflict and civil disorder. Data on previous climatic or geophysical disasters can provide an indication of which areas are particularly threatened. In many countries, veterinary departments produce annual reports that provide overviews of the disease situation within the country and the threats posed by transboundary diseases. As well as the threats posed by diseases themselves, it may also be relevant to examine the institutional policies that are in place for dealing with disease outbreaks. In many countries, disease eradication procedures may be a real threat to breeds, especially breeds with small populations concentrated in a specific geographical region and on a small number of farms. For this reason, and because of the threat posed by other geographically concentrated disasters, it is important to determine the geographical distribution of breeds within the country or region.

Action 3. Describe the risk factors for local breeds and consider corresponding preventive measures

Based on the outcome of Actions 1 and 2, the risk factors for breeds in the country of region can be summarized. This summary should cover:

1. the risk of a breed being set aside because of to economic drivers, resulting in a continual decrease in the breed’s numbers; and
2. the risk of a rapid and severe decline in a breed’s population size or its extinction because of a disaster or a disease outbreak.

To address the first type of risk, long-term rural development, breed improvement and/or marketing programmes may be needed (see Sections 7 and 8). To address the second type of risk, policies with regard to disease control may need modification. Measures to expand the area of distribution of geographically concentrated breeds may also be considered. Cryoconservation will be a useful complementary activity in both cases (see below).

Objectives for conservation

Rationale

The early 1980s saw an increased awareness of the important role of animal genetic diversity in the various production systems of the world and of the fact that this diversity was contracting. As a result, a number of countries established national conservation efforts. Depending on the country, these activities involved either *in situ* or *ex situ* conservation or a combination of the two. In all cases, it became apparent that any conservation activity would require substantial involvement with livestock owners and a diverse group of public and private sector organizations. While at first, most emphasis was placed upon *in situ* conservation, in recent years, increasing attention (albeit relatively less) has been given to the establishment of *ex situ* programmes, gene banks in particular.

In many developed countries, people interested in the maintenance of local breeds founded national breed conservation associations. These organizations, which were often non-governmental, recognized the cultural and historical value of national breeds. They initiated *in situ* conservation activities for local breeds with an ecological or historical–cultural value and called for action by governments, breeders’ organizations and breeders. Many of these national organizations collaborate at the global level in the NGO Rare Breeds International[6].

There are a number of reasons why animal genetic resources should be conserved. In developed countries, traditions and cultural values are accepted objectives for conservation, which ensure the development of conservation measures for breeds at risk and promote the emergence of niche markets for livestock products. In developing countries, however, the immediate concerns are more for food security and economic development.

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[6] http://www.rarebreedsinternational.org/

Objectives for conservation of animal genetic resources fall into five categories:

Economic: Domestic animal diversity should be maintained for its potential economic contributions. Increased genetic diversity will allow for greater response to selection and faster adaptation to changes in climate, production systems, market demands and regulations, or the availability of external inputs. Diversity in livestock also contributes to diversity of diets and hence improved nutrition.

Social and cultural: Domestic animal diversity has an important social and cultural role. Livestock breeds reflect the historical identity of the communities that developed them, and have been integral parts of the livelihoods and traditions of many societies. Loss of typical breeds, therefore, means a loss of cultural identity for the communities concerned, and the loss of part of the heritage of humanity.

Environmental: Domestic animal diversity is an integral part of the environment, in terms of both the natural environment and man-made production systems**.** The loss of this diversity would contribute to greater risk in the production system, and reduced ability to respond to changes and degradation of the environment. Livestock can provide basic environmental services such as weed control and seed dispersion. As the human population and demand for livestock products grows, marginal areas and low-to-medium input production systems will likely increase in importance for food production in developing countries. In developed countries arable areas are sometimes given back to nature and well-adapted grazing animals play an important role in the development and maintenance of such areas. In both developed and developing countries, maintenance and development of adapted breeds are of critical importance in ensuring that these objectives can be achieved sustainably without adverse environmental impact.

Risk reduction: Domestic animal diversity is an important form of insurance that enables responses to as yet unknown future requirements. It is risky to rely on only a few breeds: concentration on a small number of breeds results in losses of genes and gene combinations that are not relevant at present, but which could become relevant in the future. Breeds may differ in their level of resistance and resilience to emerging disease challenges. Conserving domestic animal diversity reduces risks and enhances food security.

Research and training: Domestic animal diversity should be conserved for use in research and training. This may include basic biological research in immunology, nutrition, reproduction, genetics and adaptation to climatic and other environmental changes. For example, genetically distant breeds can contribute to research into disease resistance and susceptibility, helping to achieve a better understanding of the underlying mechanisms and thus to develop better treatments or management of the disease. Having a wide range of breeds available can aid in the precise localization of mutations responsible for particular characteristics (see Box 3) and livestock can serve as animal models for the study of genetic diseases in humans.

Box 3

Colour sidedness: an example of genetic diversity conserved for genetic research

Colour sidedness is a dominantly inherited phenotype of cattle characterized by pigmented areas on the flanks, snout and ear tips. It is also referred to as “lineback” or “witrik” (which means white back), as colour-sided animals typically have a white band along their spines. In several countries, animals are specifically bred for this colour pattern and thus the trait is conserved. Colour sidedness has been documented at least since the Middle Ages and is presently segregating in several cattle breeds around the world, including Belgian Blue, some Nordic breeds, Dutch Witrik, American Randall Lineback and Brown Swiss. By genotyping animals from several colour-sided breeds and comparing the data to those from a breed lacking this trait, scientists in Belgium were able to determine that colour sidedness in cattle is caused by segments of the genome that have been duplicated and exchanged between the Chromosomes 6 and 29 (Durkin *et al.*, 2012).

This study marked the first example of a phenotype determined by duplicated genes found on separate chromosomes. The maintenance of several cattle breeds with the colour pattern facilitated the detection of this genetic mechanism previously unknown in mammals.

Provided by Kor Oldenbroek.

Gandini and Oldenbroek (2007) summarized these five categories into two main objectives:

1. Conservation for sustainable utilization of rural areas, including economic activities, socio-cultural roles and environmental services.
2. Conservation of the flexibility of the genetic system, including reduction of risk and maintenance of opportunities for research and education.

The first objective can only be fully met through *in vivo* conservation programmes (with cryoconservation as a safety net). The second objective is most efficiently met by cryoconservation (with *in vivo* conservation as a facilitating mechanism speeding up the reconstruction of a breed).

Because the conservation objectives determine the appropriate conservation method, it is necessary to establish which conservation objectives relevant to the breeds under consideration for inclusion in a conservation programme.

Objective: To determine national objectives for conservation by species.

Inputs:

1. Governmental livestock development policy documents;
2. List of potential conservation objectives; and
3. If available, the national strategy and action plan for animal genetic resources.

Output:

- Relevant objectives for conservation of different species and breeds.

Task: Describe the objectives for conservation that apply in the different species and breeds under consideration

Action 1. Analyse by species and breed the relevant objectives for conservation

For a given species or breed, several objectives may apply. A breed can have a cultural value, fulfil an economic function and have a unique characteristic.

Action 2. Produce tables of species × objectives

Two tables should be created to distinguish between the two sets of objectives:

- the five different objectives listed above; and
- the two summarizing objectives, i.e. sustainable utilization of rural areas and maintenance of the genetic flexibility of the system.

Determine the position of each breed and develop a strategy for the future

Rationale

As described above, many breeds are set aside from the commercial production systems or are not involved in such systems. This creates the risk that the number of breeding animals within such breeds will decrease and in extreme cases that the breeds will become extinct. The present situation of such a breed in its production system and a strategy for the future can be determined by performing a SWOT (strengths, weaknesses, opportunities, threats) analysis (EURECA, 2010).

A SWOT analysis is an approach for evaluating an entity on the basis of its Strengths, Weaknesses, Opportunities and Threats, and for making decisions on future strategies and activities. SWOT analysis was developed in the 1960s by Dr Albert Humphrey of Stanford University in the United States of America. Although SWOT analysis was originally used for evaluation of businesses and is often applied in that context, it is now used in many fields. With respect to animal genetic resources, SWOT analysis is an individual or group activity that can be used to evaluate the status of breeds and to identify conservation strategies by analysing the characteristics of the breed and its relevant stakeholders, along with the possibilities and challenges facing them.

SWOT analysis for breeds consists of four steps (Martin-Collado *et al.,* 2012):

- Definition of the system to be analysed, i.e. defining the internal and external components of the system in which the breed has its primary position. The stakeholders and entities to involve in the process should be first identified. The stakeholders should be asked to list the breed's strengths, weaknesses, opportunities and threats.

- Identification of the strengths, weaknesses, opportunities and threats.
    - *Strengths* are positive characteristics of a breed, the owners or the breed organization that improve the breed's value and competitiveness, especially with respect to other breeds.
    - *Weaknesses* are negative characteristics of a breed, the owners or the breed organization that hinder the breed's competitiveness and thus the sustainability of the breed and place it at a disadvantage with respect to other breeds. Some weaknesses may be common to all breeds; e.g. susceptibility to some diseases, so relative weaknesses should be emphasized.
    - *Opportunities* are external conditions or possibilities that affect the breed, the owners or the breed organization and may offer particularly favourable circumstances for exploiting the breed relative to other breeds.
    - *Threats* are external challenges that affect the breed, the owners or the breed organization, which may have to be overcome to safeguard the viability of the breed.
- Ranking of the driving factors: analyse and compare the strengths, weaknesses, opportunities and threats and limit them to the most important (maximum of about three).
- Identification and prioritization of conservation strategies by combining strengths with opportunities, weaknesses with opportunities, strengths with threats or weaknesses with threats (see below).

One of the main objectives of a SWOT analysis is to determine the current status of a breed and to consider what the future may hold, with and without intervention. The present status of the breed is determined by strengths and weaknesses, which are "internal" factors, particular to the breed. The future is determined by "external" factors, which consist of opportunities and threats. The internal factors can often be directly managed. The external factors create the challenges for a breed.

A SWOT analysis may serve as a decision-making tool for use in planning strategies for future breed management. A common approach is to emphasize two of the four categories. For example, strategies may be based on:

1. using the strengths to take advantage of the opportunities (SO-strategy);
2. using the strengths to reduce the likelihood and impacts of the threats (ST-strategy);
3. overcoming the weaknesses by using the opportunities (WO-strategy); or
4. avoiding the likelihood of disastrous outcomes that may arise because of the combination of the weaknesses and the threats (WT-strategy).

Objective: To develop a conservation and sustainable use strategy for a breed.

Inputs:

1. A description of the characteristics of the breed, its history, knowledge about its functions and products and characteristics of the production system(s) where it is used.
2. An analysis of the present and potential stakeholders of the breed, trends in land use, livestock systems and the patterns of the human population in consumption of livestock products and services.

Output:

- Alternative strategies for breed conservation and use.

Task: Determine the future conservation and use of a breed

Action 1. Undertake a SWOT analysis of the breed and its stakeholders in its present system based on the characteristics of the breed and a stakeholder analysis

The strength of a breed might be, for example, its genetic uniqueness, its adaptation to a production system or its past and present function in human culture. Another strength might be an effective breeding organization with sound programmes for registration of pedigrees and performance of individual animals. The weaknesses of a breed might be, for example, low production of commodities such as meat, milk or eggs, a small population size, a concentrated geographical distribution or owners with a high average age. Another weakness of the breed might be that the population genetic knowledge required for conservation activities is not available. Examples of opportunities may include consumer interest in breed-specific products, government support for nature management or other ecosystem services, or an increasing number of persons interested in hobby farming. Threats might include the importation of high-output animals belonging to an international transboundary breed or a governmental focus on production of livestock products for commodity rather than local markets. Boxes 4 and 5, respectively, provide examples of SWOT analyses for a European cattle breed and a chicken breed in the United States of America.

Action 2. Prioritize the strengths, weaknesses, opportunities and threats

Once strengths, weaknesses, opportunities and threats have been identified, various approaches can be taken to developing strategies based on them. One option is to translate the most important strengths and the most important opportunities into a strategy for a breeding programme and for the sustainable use of the breed. Another approach is to confront the weaknesses of the breed with the opportunities and propose a strategy, including a management plan that overcomes the weaknesses by taking advantage of the opportunities.

Box 4

SWOT analysis of Eastern Finncattle in Finland

History

Eastern Finncattle have a distinct phenotype, including a red colour-sided coat pattern with a broad white band on the back. They have been officially recognized as a distinct breed in Finland since the 1890s and a breeders' association was formed in 1898. The activities of the association were initially focused on establishing a base registry of animals, and visible breed characteristics were stressed when selecting animals for breeding. From the 1920s onwards, the emphasis shifted to economically important traits and selection on recorded milk production was introduced. The breed registry included more than 15 000 animals by 1930. The Second World War had a disastrous effect on cattle numbers, reducing the breed to fewer than 5 000 animals. After the war, the decline continued, primarily because of breed substitution by Ayrshires and Friesians. The size of the population dropped to its lowest point in the 1980s, at which time only about 50 cows and fewer than 10 bulls remained. Fortunately, various conservation programmes were initiated and now the number of pure-bred cows is around 800 and slowly increasing.

Strengths: Unique and symbolic germplasm in Finland.

Weaknesses: Low milk yield

Opportunities: Special features exploited in product development; "green care" farms

Threats: Many breeders lack the expertise (new farmers) or interest (hobby farmers) to apply selection to improve milk production

Breeding, conservation and promotion

The proportion of recorded cows is about 30 percent. The artificial insemination (AI) organization has 75 000 doses of semen from 48 bulls and 100 embryos from 18 cows (12 sires) stored in the national gene bank. The breeders' organization recommends matings for each cow on the basis of genetic relationships within the population. Some breeders have been able to market their milk and meat by cooperating with restaurants. The farmers raising Eastern Finncattle also receive a subsidy from the government.

Source: EURECA (2010).

Action 3. Formulate the different alternative conservation and use strategies and evaluate them for viability

It is important to be aware that some conservation strategies may work more efficiently for some breeds and species than others. For example, a strategy that involves using livestock to improve the livelihoods of rural women may be more appropriate for poultry or small ruminant breeds than for cattle, as these species will require a smaller initial investment and less use of other resources such as feed and housing.

Comparison of conservation options

Rationale

Conservation strategies can be categorized as *in situ* (conservation through continued use by livestock keepers in the production system in which the livestock evolved or are now normally found and bred) or *ex situ* (all other cases). The latter can be further divided into *ex situ in vivo* conservation (a limited number of animals kept outside their original production environment) and *ex situ in vitro* conservation (cryoconservation in a gene bank).

Box 5

SWOT analysis of the Java chicken in the United States of America

History

The name suggests otherwise, but the Java chicken was developed in the United States of America; foundation stock were of uncertain Asian origin. Java chickens were once common mid-level production birds in the country, but declining numbers in the face of the industrialization of poultry production reduced the breed to a relic status in need of targeted conservation programmes if the breed was going to survive, especially with any of its productive potential intact. A SWOT analysis revealed strategies forward.

Strengths: Historic status as a productive range-raised meat bird with desirable carcass characteristics and flavour.

Weaknesses: Reduced growth rates and size. Existence of only two breeding lines of the birds. Diminished fertility and vitality.

Opportunities: Increased interest of consumers in extensively raised poultry meat from identifiable traditional breeds. Improved breeding and population management could reduce inbreeding depression.

Threats: Inbreeding depression (if not managed). Low numbers in few locations.

Breeding, conservation and promotion

These factors were combined to develop a programme of crossing the two existing bloodlines, and then selecting the result for growth rate, fertility, and conformation. The boost from crossing the two relatively inbred populations restored the previous production level of the breed. A new breeders’ organization expanded the number of sites at which the breed was kept, which further enhanced the goal of reducing the risk associated with the loss of any one population. Splitting the population into several sites also subdivided the risk of uniform genetic drift and inbreeding in the entire breed. Increased production levels led to increased interest on the part of producers interested in alternatives to industrial production, which reversed the steady decline of the breed in both numbers and vitality.

Provided by Phil Sponenberg.

In situ conservation

In the context of livestock diversity, *in situ* conservation is primarily the active breeding of animal populations for food and agricultural production such that genetic diversity is best utilized in the short term and maintained for the longer term. *In situ* conservation includes activities such as performance recording and development of breeding programmes with special emphasis on maintaining the genetic diversity within the breed. *In situ* conservation also includes ecosystem management and use for sustainable agriculture and food production of food.

Ex situ conservation

In the context of livestock diversity, *ex situ* conservation means conservation away from the production systems where the resource was developed or is now normally found and bred. This includes both maintenance of live animals (*ex situ in vivo)* and cryoconservation.

Ex situ in vivo conservation

This type of conservation is maintenance of live animal populations in environments that are not their normal management conditions - e.g. in zoological parks or governmental farms - and/or outside the area in which they evolved or are now normally found. For financial and practical reasons, animals are often kept in very limited numbers. Because the animals are kept in outside their normal production environments and their numbers are small, natural selection is usually no longer effective in its role of ensuring the adaptation of the population to these environments. It is strongly recommended that *ex situ in vivo* conservation be complemented with cryoconservation.

A key question with regard to *ex situ in vivo* conservation is whether or not long-term financial commitment is available to maintain generations of animals to the standards required for successful conservation.

Cryoconservation is the collection and deep-freezing of semen, ova, embryos or tissues, which may be used for future breeding or regenerating animals. Cryoconservation is also referred to as *ex situ in vitro* conservation. A key question for cryoconservation is whether, in the short term, the facilities and expertise required for the collection of the samples can be financed and put in place. The logistics and costs of providing and maintaining storage facilities will need to be addressed before the cryoconservation is carried out.

The roles of in situ and ex situ conservation

Table 1 shows the relationship between conservation techniques and conservation objectives. This information can be used to find the appropriate conservation technique for meeting the conservation objectives for a breed. From the table it can be concluded that *in situ* conservation is the method of choice for most situations. *In situ* and *ex situ* strategies differ in their capacity to achieve the various conservation objectives. Cryoconservation is the method of choice when the flexibility of the genetic system is seen as the only objective for conservation. *Ex situ in vivo* conservation has little to add to cryoconservation, except in particular situations. For example, it may facilitate the regeneration of a breed with frozen semen by ensuring the presence of a few living females from which to start the regeneration process.

In situ and *ex situ* conservation are not mutually exclusive. The Convention on Biological Diversity (CBD, 1992) emphasizes the importance of *in situ* conservation and considers *ex situ* conservation as an essential complementary activity to *in situ*. *In situ* conservation is often regarded as the preferred method because it ensures that a breed is maintained in a dynamic state (FAO, 2007a). This may be true when the adaptation and genetic change of a breed is slow and involves adaptation to a variety of demands, which helps to ensure the maintenance of genetic variability. However, commercially important breeds often suffer from high selection pressure associated with high levels of inbreeding (a few top sires fathering many offspring). Commercially less important breeds often have a small population size and are threatened by genetic drift and extinction (see Sections 2 and 6). In these two examples, standard *in situ* management may not be sufficient to conserve genetic diversity. Likewise, e*x situ in vivo* conservation will not always guarantee the maintenance of the original genetic diversity of a breed because the animals are not kept in their original production environments. Therefore, it is preferable that *in vivo* conservation, whether *in situ* or *ex situ*, be complemented by cryoconservation of germplasm (see also Section 4).

Table 1. Conservation techniques and objectives

	Technique		
Objective	*In situ*	*Ex situ in vivo*	Cryoconservation
Flexibility of the genetic system, as			
• insurance against changes in production conditions	yes	yes	yes
• safeguard against diseases, disasters, etc.	no	no	yes
• opportunities for research	yes	yes	yes
Genetic factors			
• continued breed evolution / genetic adaptation	yes	poor	no
• increase knowledge of breed characteristics	yes	poor	poor
• limit exposure to genetic drift*	yes	no	yes
Sustainable utilization of rural areas			
• opportunities for rural development	yes	poor	no
• maintenance of agro-ecosystem diversity	yes	limited	no
• conservation of rural cultural diversity	yes	poor	no

*The extent of genetic drift will depend on the population size *in situ* and the number of animals sampled for cryoconservation.
Source: adapted from Gandini and Oldenbroek (2007).

Objective: To determine the appropriate conservation method for the breeds of a given species.

Input:

1. List of breeds and species to be conserved; and
2. Description of the theoretically applicable conservation methods.

Output:

- Description of the conservation options applicable for each species in your country.

Task: Describe the relevant options for conservation of the species and breeds in your country

Action 1. Determine if the various methods for conservation are feasible given the existing or realistically-obtainable infrastructure and resources

An *in vivo* programme can often only be organized effectively when an association of breeders exists or when governmental and non-governmental institutions have farms that can be used for this purpose (see Section 5). Cryoconservation can only be executed when it is possible to collect, to freeze and to store semen and other materials reliably and safely.

Action 2. Describe the conservation options that can be used for each species

It may be useful to construct a table with rows for the species and breeds and columns for the conservation methods. It may be worthwhile to distinguish *in situ*, *ex situ in vivo* and cryoconservation.

Action 3. Determine what needs to be done to implement the relevant conservation methods in the relevant species

The feasible conservation options were identified by *Action 1*, but some “feasible” options may not be immediately accessible. By evaluating the current status and future needs, the most appropriate options can be identified. Plans for implementing these options, including needs for training and facilities, can then be drawn up.

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II. IDENTIFICATION OF BREEDS AT RISK

Completing the actions described in Section 1 will provide an overview of information on the country's livestock breeds and their functions, within the broader framework of the dynamics and trends of the livestock sector and opportunities for conservation of animal genetic resources. This section discusses the methodology for identifying breeds that are at risk of extinction, i.e. the breeds need to be targeted by conservation programmes. The risk of extinction of breeds can be assessed on the basis of the results of censuses and other surveys. Not all breeds at risk will have the same conservation value, and in some countries funds may be insufficient to conserve all at-risk breeds. Determining the conservation value and prioritizing breeds for conservation are dealt with in Section 3.

Determining the risk status of national animal genetic resources

Rationale

The Convention on Biological Diversity (CBD, 1992) specifies the need for monitoring biological diversity, with particular attention to components of biodiversity requiring urgent conservation measures (Article 7). The importance of monitoring the level of risk of animal genetic resources is underlined in the *Global Plan of Action for Animal Genetic Resources* (FAO, 2007a): "Complete national inventories, supported by periodic monitoring of trends and associated risks, are the basic requirements for the effective management of animal genetic resources". In the *Global Plan of Action* countries agreed to establish or strengthen country-based early warning and response systems. Assessing the risk status of the country's breeds is an essential element of such systems. Cooperation among countries is necessary for monitoring the risk status of transboundary breeds.

We can define the degree of risk of a breed as a measure of the likelihood that, under current circumstances and expectations, the breed will become extinct in a specified period of time, and/or that it will lose through time its genetic variation at a non-sustainable rate (Gandini *et al.*, 2005), leading to a high proportion of monomorphic loci (i.e. regions in the genome with no genetic variability and genes with only a single allele), a greater occurrence of genetic defects and a loss of fitness and adaptability. The two aspects of breed extinction, loss of animals and loss of gene variants, are deeply interconnected. However, for a general treatment of the problem, we can frame the issue separately in genetic and in demographic terms.

Population size and rate of population change (for declining population sizes in particular) are the most important factors influencing a breed's risk of extinction. Obviously, the smaller a breed's the population size, the greater is the risk that it will be wiped out by a series of negative circumstances (e.g. low proportions of female offspring, poor fertility or survival) or a single catastrophe (e.g. war or disease outbreak). Breeds with continually decreasing population numbers will eventually reach a critically small size at which risk of extinction becomes high. Box 6 details how future population sizes can be predicted given the current population size and an estimate of the rate of population growth or decline.

Some complexity in this framework comes from the difficulties involved in accurately predicting the population growth rate over several years. Few countries have available the time series census data required for estimating the growth rates of their breed populations. Most importantly, the growth rate will usually not have a constant value but will change unpredictably over time. Growth rate might change, for example, because a breed's profitability, and consequently farmers' interest in keeping it, is affected by changes in the market, competition with other production sectors or the introduction of new regulations. As noted in Section 1, when reliable breed population data are not available, general trends in the livestock sector have to be used to determine whether animal genetic resources are likely to be at risk. Estimates obtained using from general trends are likely to be imprecise, so breed-based surveys should be given high priority.

Box 6

Growth rate and the dynamics of population size

Consider that N_0 represents the size of a population of breeding females of a breed at a given time and that r represents the multiplicative growth rate per year (e.g. $r = 1.01$ corresponds to an increase of 1 percent per year). When $r = 1$ population is stable, $r > 1$ and < 1 correspond respectively to positive and negative (decline) rates of growth. After one year, the new population size, N_1, will be equal to N_0 multiplied by r (i.e. $N_1 = N_0 r$) and after t years N_t will be equal to N_0 multiplied by r^t (i.e. $N_t = N_0 r^t$). The table below shows several examples of 5-year population size estimates for different values of N_0 and r.

Example of growth dynamics in five years with different initial population sizes and growth rates

Initial population size (N_0)	Growth rate (r)	Population after five years (N_5)	Trend
250	1.21	648	+
1 000	0.92	659	-
2 000	0.80	655	-

In these three examples, the initial population numbers vary greatly, but after five years all three populations have a similar size – about 650 breeding females. This example demonstrates the strong impact of growth rate, which is a parameter that can be influenced by the existence and effectiveness of conservation programmes.

A limit of this simple prediction model is that population growth rate is assumed to be constant, with no variance across years, whereas smaller populations are more likely to be affected by random variation in survival and reproductive rates. Nevertheless, this simple model gives us important information with which to plan conservation actions, for example on the expected period of time within which we have to act if population extinction is to be avoided.

In addition to population size and trends, other demographic factors can influence risk. Concentration of the population in a restricted area or in a limited number of herds may place it at greater risk of extinction. Another element to take into account is the possible presence of controlled or uncontrolled cross-breeding. For each cross-bred mating, the breed population size is effectively decreased by one-half of an individual from a genetic point of view and by a whole individual from the perspective of maintaining a pure-breeding population.

To analyse risk in terms of the loss of genetic variation, it is necessary to understand that breeding populations undergo random fluctuations in the content of the gene pool (genetic drift) from one generation to the next, depending on the sample of animals that are chosen as the parents of the next generation. When populations are smaller, these fluctuations tend to be larger. This process also tends to reduce genetic variation because the probability that alleles will be lost from the population is increased. Genetic variation is necessary for the adaptation of the population to changes in the production environment and in market demands, as well as to guarantee response to selection programmes. This topic is discussed in more detail in Section 6.

A variety of parameters can be used to measure genetic variation. The average coancestry (typically expressed as “f”) of a population (i.e. breed) is the most appropriate proper measure of its genetic variation. Nevertheless, the inbreeding coefficient (typically expressed as “F”) is the most commonly used parameter for monitoring genetic drift and the consequent loss of genetic variation. Section 6 discusses the relationship between inbreeding and coancestry, including those cases in which the inbreeding and coancestry parameters provide different information. Another commonly used parameter is the effective population size (N_e), which is defined as the number of breeding individuals in an idealized population that would show the same amount of random genetic drift or the same amount of inbreeding as the population under consideration. An idealized population is a randomly mated population with equal numbers of males and females with a uniform probability of contributing progeny, and not subjected to other forces that change genetic variability, such as mutation, migration and selection. The idealized population is primarily a theoretical concept, rather than a reality, especially for livestock. In livestock populations, N_e is usually smaller than the actual (*census*) population size because of a smaller number of breeding males than females, large differences in the number of progeny per animal (particularly among males) and the presence of selection. Inbreeding increases at a rate per generation that is inversely proportional to the N_e, as $\Delta F = 1/(2\times N_e)$. A larger N_e thus is considered advantageous because it is associated with more genetic variation and less inbreeding.

Box 7

Basic rules for computing effective population size (N_e)

The effective population size (N_e) is the number of breeding individuals in an idealized population that would show the same amount of random genetic drift or the same amount of inbreeding as the population under consideration. Livestock populations obviously differ from such an idealized population, which has equal numbers of males and females, among other characteristics. There are different models for computing N_e, that take into account various aspects in which real populations deviate from the idealized population.

The simplest model (Wright, 1931), takes into account the fact that numbers of breeding males and breeding females are usually not equal, as $N_e = (4*N_M*N_F)/(N_M+N_F)$, where N_M and N_F are the numbers of breeding males and females used as parents. Because half the genetic information is transmitted by each gender, the scarcer gender is the limiting factor that primarily influences N_e.

For example:

Population A: 5 breeding males and 995 breeding females, for a total of 1 000 breeding animals.

$N_e = (4 \times 5 \times 995) / 1\,000 = 19.9$

Population B: 20 breeding males and 980 breeding females, also 1 000 breeding animals.

$N_e = (4 \times 20 \times 980) / 1\,000 = 78.4$

As inbreeding increases at a rate per generation that is inversely proportional to the N_e, $\Delta F = 1 / (2N_e)$, population A is exposed to a ΔF almost four times greater than population B, although both populations comprise the same number of breeding animals.

It is important to recall that the above N_e model assumes random mating, with no selection and no variance in the number of progeny produced by each breeding animal. If selection is present, even simple mass selection (i.e. selection based on phenotype), the Wright formula overestimates N_e and consequently leads to an underestimation of ΔF. Given that mass selection is practically always present to some degree in livestock populations, it is advisable to account for selection according to the model proposed by Santiago and Caballero (1995). Their model for accounting for selection is to decrease the estimated N_e by 30 percent (adjusted N_e = original $N_e \times 0.7$). Applying the adjustment to the above example, for population A, $N_e = [(4 \times 5 \times 995) / 1\,000] \times 0.7 = 13.9$; and for population B, $N_e = [(4 \times 20 \times 980) / 1\,000] \times 0.7 = 54.9$.

If information from related animals is used for the estimation of breeding values (e.g. with family-based indices, or the method of best linear unbiased prediction – usually abbreviated as “BLUP”), adjustment factors even smaller than 0.7 should be used unless inbreeding restriction strategies are implemented. In general, methods to control and monitor inbreeding should be used whenever selection is applied, but this is particularly important for small populations such as those in conservation programmes (see Section 7).

Even in the case of no selection, the stochastic (random) variability of the number of progeny may be high and affect N_e. This factor is not taken into account here, but it is discussed in Section 7.

The rate of inbreeding has a predictable form, and has a very important relationship with the loss of variation: if σ_g^2 is the genetic variation, then the loss per generation is: $\Delta\sigma_g^2 = \Delta F * \sigma_g^2$. Excessive ΔF might also result in decreases in fertility and productivity (this phenomenon is called *inbreeding* *depression*; see Section 6 and particularly Box 31) as well as increases in the occurrence of genetic abnormalities.

The well-known formula of Wright (1931):

$$N_e = (4*N_M*N_F)/(N_M+N_F),$$

where,

N_M = number of males, and

N_F = the number of females

provides a simple estimate of N_e, gives a useful general idea of the dynamics of genetic variability within a given population. In livestock, other approaches for calculating of N_e are more precise because Wright's formula assumes several conditions that are rarely met in livestock populations (see Box 7).

Therefore, we have two major criteria for evaluating the risk status of a population:

1. demographics (parameter: number of breeding females), and
2. genetic criteria (parameter: N_e).

In assigning populations to risk categories, these two criteria are assumed to be independent, although the genetic and demographic parameters are obviously correlated.

In addition to future inbreeding, it is also necessary to consider inbreeding accumulated in the population during the recent past. High ΔF in the past may correspond to low current genetic variability in the population and therefore poor fitness and adaptability. Cumulated inbreeding can be estimated from the demographic history of the population, such as the presence of bottlenecks (periods of time when there were particularly low numbers of breeding animals) or can be computed from pedigree information, if this is available, following standard techniques (e.g. path analysis and tabular methods – Falconer and Mackay, 1996). The reliability of pedigree-based estimates of inbreeding depends on the number of generations of ancestry recorded. To obtain meaningful estimates, a minimum of five generations is recommended.

Breed risk status is a complex issue, first because numerous factors are involved (see Section 1), but also because all the information needed to estimate the parameters necessary for predicting risk status is rarely available. Various parameters and procedures of varying complexity have been proposed for estimating risk status and some are in use (for reviews see Gandini *et al.*, 2005; Alderson, 2009; Alderson, 2010; Boettcher *et al.*, 2010). FAO has selected some simple parameters that can be obtained in many situations, thus allowing most countries to categorize breeds according to risk (see Task 2, Action *1* of this section). In countries where more information is available, additional more accurate estimates can be obtained. However, it is strongly recommended that, in such cases, countries also calculate the simple estimates in order to allow harmonization of risk status figures internationally.

Objective: To obtain objective information about the risk status of each breed.

Inputs:

1. List of breeds within the country (from the tasks of Section 1);
2. Existing information about population sizes, the composition of the populations, trends and the geographical distribution of breeds;
3. Existing information on the same or similar breeds in other countries; and
4. *Surveying and monitoring of animal genetic resources* (FAO, 2011b).

Outputs:

- New information about population size and trends and geographical distribution;
- List of breeds with their respective risk status; and
- Methodology with which to update the risk status regularly.

Task 1. Determine the population size, structure, trend, geographical distribution, and cross-breeding activities in all the breeds under consideration

Action 1. Review the information available about breed population sizes

Many countries lack formal systems for surveying of breeds and routine monitoring of population sizes. If no such systems are in place, the availability of data from other sources should be reviewed. FAO guidelines on *Surveying and monitoring of animal genetic resources* (FAO, 2011b) are a valuable resource for establishing such systems.

Action 2. Form a task force to conduct breed surveys

An entity with the responsibility of determining the level of risk of national animal genetic resources should be identified. This entity might be the National Advisory Committee for Animal Genetic Resources or equivalent body, a specific task force established by the National Advisory Committee or any other body that has sufficient knowledge of animal genetic resources and their management. *Surveying and monitoring of animal genetic resources* (FAO, 2011b) suggests the establishment of a strategy working group for surveying and monitoring of animal genetic resources, which might directly conduct data collection or might coordinate and oversee subcontractors carrying surveys. The National Coordinator for Management of Animal Genetic Resources should be part of these entities or collaborate closely with them. In many cases, information and expertise on breeds will be scattered in many places, including officially and unofficially recognized breed associations, NGOs, elite breeders, breed experts, research centres and universities. Potential sources of information should be mapped thoroughly and a wide range of stakeholders should be involved in planning and implementing data-collection activities.

Action 3. Gather information about each breed population

Adequate planning of data collection is important in ensuring the success of surveys and the quality of results (FAO, 2011b). Planning should include accurate definition of the parameters to be collected and the methodology of collection, identification of sources of reliable information, identification of collaborators and obtaining financial support. As information different breeds may be obtained from many different sources, it is advisable, as a first step, to define clearly a common set of parameters that need to be collected in order to estimate risk status. This will help to ensure that the risk-status estimates of different breeds are comparable.

The base set of parameters required in order to compute risk status following FAO risk categories are:

- total population size or total number of breeding females (registered and not registered, if possible);
- total number of breeding males (registered and not registered, if possible);
- percentage of females bred to males of the same breed, as females used for crossing do not contribute to renewal of the population;
- trend of population size, classified as stable, decreasing, increasing, or, whenever possible, measured by an estimate of growth rate during recent years (see Box 8);
- presence of conservation programmes, and/or of populations maintained by commercial companies or research institutions, under strict control;

and whenever relevant and possible:

- distribution, measured as: (a) length (km) of the maximum radius of the area within which approximately 75 percent of the population lies, (b) number of herds and trends in these figures;
- degree of introgression through the use of cross-bred animals as breeding stock.

The collection of additional parameters will improve understanding of the factors driving breed dynamics and improve risk-status estimates (see Task 2, Action *2*). These additional parameters include the following:

- number of registered breeding females: registered females constitute the part of the population that can be monitored in terms of age structure, reproduction capacity, accumulated inbreeding, mating structure, gene introgression from other breeds and can actively participate in selection programmes;
- number of females registered each year: the annual number of registered female replacements has been suggested as a more accurate measure of population dynamics,

mainly because it reflects the current interest of breeders in keeping the breed (Sponenberg and Christman, 1995; Alderson, 2009);

- number of males used in AI: when AI is practised, the contribution of males to the next generation can be highly heterogeneous, accelerating the ΔF in future generations (see Section 6);
- presence of selection and the type of selection practised (mass selection, index selection based on best linear unbiased prediction (BLUP), optimum contribution selection, etc.): selection will usually accelerate inbreeding rate if methods to control inbreeding are not implemented effectively (see Section 6 and 7);
- presence of past bottlenecks (severe restrictions in the number of males or females in a past generation): bottlenecks usually result in depletion of genetic variability, thus affecting the genetic variation currently present in the population;
- presence of active breeders' associations (this is expected to increase the resilience of the breed);
- average age of farmers keeping the breed, as an indication of generational transfer of herds and an early indicator of future breed dynamics;
- cultural attachment of farmers to their breed (a high level of attachment is expected to increase the resilience of the breed);
- economic competitiveness of the breed relative to other breeds and/or economic activities in the area (population decline has been often associated with a lack of economic competitiveness);
- national and regional trends in animal production;
- national gross domestic product and the proportional contribution of agricultural products;
- economic and political stability of the country/region;
- risk of catastrophes, such as epidemics, drought, floods, and contingency plans for dealing with them; and
- presence and status of other populations of the same breed in other countries.

In general, the base set of parameters required for calculating risk status according to FAO categories are single data points per population per year. The exception is the trend in population size, which involves calculations if a numerical estimate of growth rate is desired (i.e. rather than simple categorization of trend as increasing, stable or decreasing) or if trend is to be determined by using more than two observations of yearly population size (see Box 8). For the additional parameters listed above, a common methodology within the country should be put in place for all breeds, thus allowing across-breed comparisons. Several of the parameters are not quantitative in nature and, therefore, the use of a classification system is recommended. For example, presence of selection or recent bottlenecks could be categorized as "yes" or "no". The cultural attachment of livestock keepers to their breeds could be classified as "high", "medium" or "low". In addition, the systems used should be harmonized as much as possible across countries that may be collaborating in conservation activities. In this respect, communication and collaboration among national advisory committees from neighbouring countries is advisable.

Finally, collecting the data required to determine risk status is a costly and time-consuming exercise. It is therefore important that the provision of adequate human and financial resources is thoroughly addressed during the planning phases (FAO, 2011b).

Action 4. Analyse and interpret data

Once data have been collected, they must be analysed and interpreted in order to estimate as accurately as possible breeds' degree of risk and identify and understanding the factors influencing the degree of risk.

Box 8

Estimation of population growth rate

The estimation of population growth rate (r) requires at least two censuses at a time interval of at least several years or about one generation interval for the respective species. The parameter of particular importance is the number of breeding females, although the same equation can be applied to other parameters, such as total populations size.

Rate of growth per year (r) is estimated by means of the following equation:

r = anti-log[(log N_2 − log N_1)/t],

where N_1 and N_2 are, respectively, the number of breeding females from first and the second census and t is the time interval in years between the two censuses. If more than two sets of census data are available, regression analysis can be used to obtain predicted values of N_1 and N_2 based on the trend across the multiple data points.

Example

Data: Year 1 = 2 000 and N_1 = 1 000 breeding females; Year 2 = 2008 and N_2 = 800 breeding females; t = 8 years.

Note that time is measured in years in this example, rather than in a genetic unit, such as number of generations. For horses the time period between the two censuses encompasses about one generation interval, while for poultry it encompasses about eight generation intervals, although this does not change the value of r.

Calculation: r = anti-log[(log 800 − log 1 000) / 8] = 0.988.

The growth rate r is <1, and the population size, measured as number of breeding females, has been decreasing.

Following the method described in Box 6, the population size that can be expected after another 20 years (in 2028) if the growth rate does not change can be calculated as follows: $N_{20} = 800 \times (0.988^{20}) = 628$.

As underlined in Box 6 this prediction assumes that the growth rate will remain constant in the coming years. In situations characterized by uncertainty (a high level of economic and political instability, high risk of catastrophes, low rates of generational transfer of herds, weak cultural attachment to breeds, etc.), the population size and growth rate should be monitored continuously over the years.

Data analysis should be preceded by accurate editing of the information collected. This should be done as soon as possible after data collection. Providers of data may be asked to provide accompanying notes that facilitate the interpretation of the data. The estimates for certain parameters can be verified by comparing them to information from other sources. For example, the number of breeding males in a population where natural insemination is used should correspond logically to the number of herds and the number of females; population trends should be compared to previous estimates; the total number of females registered each year should be compatible with the number of breeding females registered. Data analysis may indicate the need to collect additional information that can contribute to a better understanding of breed dynamics and risk status. Data collection and analysis are discussed in detail in *Surveying and monitoring of animal genetic resources* (FAO, 2011b). Conservation of animal genetic resources involves many different disciplines, ranging from conservation biology to sociology and economics. Discussion with experts in these disciplines may provide useful insights into the data and the consequences of the trends observed. Box 9 provides an example of how various data can be interpreted.

Box 9

Analysis of population data: an example

The following hypothetical example shows how statistical analysis can provide an understanding of trends of breed populations and insights into the factors affecting population dynamics.

Data on a hypothetical breed distributed across eight herds

Herd code	Herd size (no. of breeding females)	Reproduction	Farmer's age (years)
A	8	natural	73
B	10	artificial	70
C	60	artificial	55
D	15	natural	70
E	175	artificial	45
F	70	artificial	40
G	12	natural	66
H	310	artificial	42

The following statistics can be calculated from the raw data:

Herd size: mean = 82.5; standard deviation = 107.8; range 8 to 310.

Herd size distribution: <50 females/herd (50 percent), 50–100 (25 percent), >100 (25 percent).

Farmer's age: mean = 57.6; standard deviation = 13.8; range = 40 to 73.

Correlation between herd size and farmer's age = -0.76.

Frequency of AI = 62.5 percent.

Frequency of AI as a proportion of herd size = <50 females/herd, 25 percent; ≥50/herd, 100 percent.

The analysis shows that mean herd size provides limited information because the number of breeding females varies widely across the herds (standard deviation > mean). There is a clear correlation between the age of the farmer and the herd size; the greater the age, the smaller the herd; this might be explained by the fact that older farmers invest less in farming activities. AI is used more frequently in large herds than in small herds. The prospects for the survival of small herds (50 percent of herds have fewer than 15 females and their owners are all more than 65 years old) should raise some concern.

Task 2. Identify breeds eligible for conservation activities

Action 1. Assign breeds to categories according to risk status

From a conservation point of view, one of the most important outcomes of a breed survey is the categorization of breeds according to their risk status. This facilitates the monitoring of livestock biodiversity at national level, helps in the planning of conservation actions and contributes to reporting and analysis at international level (e.g. FAO, 2011a). A limited number of parameters are sufficient for obtaining an indication of risk, but the collection of additional information can refine the analysis by detecting underlying trends and causes.

The risk categorization system proposed in these guidelines combines, in terms of criteria and thresholds, the previous system used by FAO (FAO, 2007b) with more recent proposals (Gandini *et al.*, 2005; Alderson, 2009; Alderson, 2010).

The categorization is primarily based on three major parameters:

1. numerical scarcity (number of breeding females);
2. inbreeding rate (ΔF); and
3. presence of active conservation programmes.

Numerical scarcity is most accurately measured based on the number of females in the breeding population, and preferably also the proportion of females mated to males of the same breed (i.e. not cross-bred). When these data are not available, the total population size can be used as a proxy.

When possible, the rate of population growth/decline should be estimated or at least the general trend should be identified.

The ΔF is estimated based on the numbers of breeding males and females, following the approach described in Box 7. The scarcer gender, usually males in livestock populations, is the factor that primarily influences N_e.

Conservation programmes, both *in vivo* and *in vitro,* are implemented for the purpose of increasing a breed’s chances of survival (i.e. decreasing the risk of extinction). The categorization system recognizes this fact by including subcategories for breeds that are included in conservation programmes. These subcategories are particularly important for the purpose of reporting to DAD-IS and for monitoring the diversity of animal genetic resources at global level.

The three parameters listed above are used to assign breeds into the following five categories (and two subcategories), listed in descending order of risk:

- extinct,
- critical (including the subcategory critical-maintained),
- endangered (including the subcategory endangered-maintained),
- vulnerable, and
- not at risk.

In addition, a sixth category, unknown, is used to describe breeds for which precise information on their population size is lacking. Breeds that are categorized as critical, endangered or vulnerable are grouped together in the broader category, “at-risk”.

Assignment to risk-status categories is based on the least favourable parameter, i.e. breeds are allocated to the highest-risk category for which they qualify. For example, if the number of females in a breed is small enough to indicate that it should be assigned to the critical category, then it is assigned to this category even if the number of males is large enough to suggest that it should be classified as endangered. A breed cannot be assigned to two different categories.

Species differ greatly in their reproductive capacities, measured as the expected number of breeding females produced by each female during her life. Even if the census size is equal, populations belonging to species with low reproductive capacity, such as the horse, are at relatively greater risk than populations belonging to species with high reproductive capacity, such as the pig. This is because in species with lower reproductive capacity, recovery from a population decline will take more time and more generations of breeding. For example, because female pigs can produce ten or more offspring per litter and multiple litters per year, a pig population may easily double its census size within a single year, whereas the same process would require many years for a horse population.

For the sake of simplicity, when assigning breeds to risk status categories FAO has previously not used different thresholds for different species (FAO 1998, 2007b). In these guidelines a refinement of this type is introduced, but in a simplified form. Species are assigned to two groups, the first group comprises species that have high reproductive capacity, such as pigs, rabbits, guinea pigs and avian species, and the second comprises species that have low reproductive capacity, i.e. those belonging to the taxonomical families *Bovidae*, *Equidae*, *Camelidae* and *Cervidae*. For the reasons described above, the species in the low reproductive capacity group have thresholds for the number of breeding females and for overall population size that are three times greater than those used in the high reproductive capacity group (this applies to all risk-status categories) (Alderson, 2010). Thresholds for the number of males (i.e. for ΔF) are the same for all species, as the reproductive capacity of a species is primarily determined by the reproduction capacity of the females. Table 2 shows the reproductive capacity classification for all species recorded in DAD-IS.

Table 2. Reproductive capacity of livestock species recorded in DAD-IS.

High reproductive capacity		Low reproductive capacity	
Cassowary	Chicken	Alpaca	Ass
Chilean tinamou	Dog	Bactrian camel	Buffalo
Duck	Emu	Cattle	Deer
Goose	Guinea fowl	Dromedary	Goat
Guinea pig	Ñandu	Guanaco	Horse
Ostrich	Partridge	Llama	Sheep
Peacock	Pheasant	Vicuña	Yak
Pig	Pigeon		
Quail	Rabbit		
Swallow	Turkey		

Risk status classification

Extinct: A breed is categorized as extinct when there are no breeding males or breeding females remaining. The categorization refers to live animals. Even if genetic material that would allow recreation of a breed has been cryoconserved, the breed will nonetheless be classified as extinct. If countries have breeds that have no live animals but have genetic material stored in a gene bank, they are encouraged to indicate in DAD-IS that a cryoconservation programme is active. Such breeds can then be reported as cryoconserved by FAO. However, the interpretation of these data may be difficult, as the ability to reconstitute an extinct breed depends on the amount of and type of stored material.

From a practical point of view, extinction may occur well before the loss of the last animal or genetic material, because a small number of living animals or small quantity of stored germplasm represents a very small amount of genetic information, which may be insufficient to keep the breed viable in the long term.

Critical: A breed is categorized as critical if:

- the total number of breeding females is less than or equal to 100 (300 for species with low reproductive capacity); or
- the overall population size is less than or equal to 80 (240) and the population trend is increasing and the proportion of females being bred to males of the same breed is greater than 80 percent (i.e. cross-breeding is equal to or less than 20 percent);
- the overall population size is less than or equal to 120 (360) and either the population trend is stable or decreasing, or the percentage of females being bred to males of the same breed is equal to or less than 80 percent (i.e. cross-breeding is greater than 20 percent);
- or the total number of breeding males is less than or equal to five (i.e. ΔF is 3 percent or greater).

If the population trend is unknown, then it is assumed to be decreasing. Likewise, if the proportion of females bred to males of the same breed is unknown, it is assumed to be less than 80 percent.

Breeds for which demographic characteristics suggest a critical risk of extinction, but that have active conservation programmes (including cryoconservation) in place, or populations that are maintained by commercial companies or research institutions are considered to be “critical-maintained” for reporting purposes.

Endangered: A breed is categorized as endangered if:

- the total number of breeding females is greater than 100 (300 for species with low reproductive capacity) and less than or equal to 1 000 (3 000); or
- the overall population size is greater than 80 (240) and less than 800 (2 400) and increasing in size and the percentage of females being bred to males of the same breed is above 80 percent; or
- the overall population size is greater than 120 (360) and less than or equal to 1 200 (3 600) and either the trend is stable or decreasing or the percentage of females being bred to males of the same breed is equal to or less than 80 percent; or
- the total number of breeding males is less than or equal to 20 and greater than five (i.e. ΔF is between 1 and 3 percent);

Once again, if the population trend is unknown, then it is assumed to be decreasing. Likewise, if the proportion of females bred to males of the same breed is unknown, it is assumed to be less than 80 percent.

Endangered breeds will be assigned to the subcategory “endangered-maintained” if active conservation programmes are in place or if their populations are maintained by commercial companies or research institutions.

Vulnerable: A breed is categorized as vulnerable if:

- the total number of breeding females is between 1 000 and 2 000 (3 000 and 6 000 for species with low reproductive capacity); or
- the overall population size is greater than 800 (2 400) and less than or equal to 1 600 (4 800) and increasing and the percentage of females being bred to males of the same breed is greater than 80 percent;
- the overall population size is greater than 1 200 (3 600) and less than or equal to 2 400 (7 200) but decreasing and the percentage of females being bred to males of the same breed is equal to or below 80 percent; or
- the total number of breeding males is between 20 and 35 (i.e. the ΔF is between 0.5 and 1 percent).

Unknown population trends and proportions of females bred pure are assumed to be decreasing and less than 80 percent, respectively.

Not at risk: A breed is categorized as not at risk if the population status is known and the breed does not fall in the critical or endangered categories (including the respective subcategories) or the vulnerable category. In addition, a breed can be considered not at risk even if the precise population size is not known, as long as existing knowledge is sufficient to provide certainty that the population size exceeds the respective thresholds for the vulnerable category. Nevertheless, for such breeds the implementation of a survey to obtain a more precise estimate of population size is strongly recommended (FAO, 2011b).

Unknown: This category is self-explanatory and calls for urgent action. A population survey is needed; the breed could be critical, endangered or vulnerable!

Table 3. Risk categories according to numbers of breeding females, numbers of males and species reproductive capacity*

Reproductive capacity	Males (n)	Breeding females (n)						
		≤100	101 - 300	301 - 1 000	1 001 - 2 000	2 001 - 3 000	3 001 - 6 000	>6 000
High*	≤5	■	■	■	■	■	■	■
	6 - 20	■	▨	▨	▨	▨	▨	▨
	21 - 35	■	▨	▨	░	░	░	░
	>35	■	▨	▨	░	□	□	□
Low**	≤5	■	■	■	■	■	■	■
	6 - 20	■	■	▨	▨	▨	▨	▨
	21 - 35	■	■	▨	▨	▨	░	░
	<35	■	■	▨	▨	▨	░	□

■ = critical, ▨ = endangered, ░ = vulnerable and □ = not at risk.

* High reproductive capacity species = pigs, rabbits, guinea pigs, dogs and all poultry species.

**Low reproduction capacity species = horses, donkeys, cattle, yaks, buffaloes, deer, sheep, goats and camelids.

Table 3 shows the risk classification system graphically, as a function of numbers of breeding-age females, numbers of males and the reproductive capacity of the species. Note that in each case, a low value for the least favourable parameter is sufficient to result in the breed being allocated to the higher risk-status category. For example, if the population includes only five males, the breed is allocated to the critical category even if the number of breeding females exceeds 6 000.

Tables 4 and 5 are similar to Table 3, but they show the risk categories when the size of the entire population is used rather than the number of breeding females, along with the population trend and the proportion of females mated to males of the same breed. Table 4 presents results for populations with high reproductive capacity and Table 5 presents results for species with low reproductive capacity.

Table 4. Risk categories for species with high reproductive capacity[*], according to total population size and trend, numbers of males and proportion of pure-breeding

Population trend and pure-breeding proportion[**]	Males (n)	Population size (n)						
		≤80	81 - 20	121 - 800	801 - 1 200	1201 - 1 600	1601 - 2 400	>2 400
Increasing trend and >80% pure-breeding	≤5	■	■	■	■	■	■	■
	6 - 20	■	▓	▓	▓	▓	▓	▓
	21 - 35	■	▓	▓	░	░	░	░
	>35	■	▓	▓	░	░	□	□
Decreasing trend or ≤80% pure-breeding	≤5	■	■	■	■	■	■	■
	6 - 20	■	■	▓	▓	▓	▓	▓
	21 - 35	■	■	▓	▓	░	░	░
	>35	■	■	▓	▓	░	░	□

■ = critical, ▓ = endangered, ░ = vulnerable and □ = not at risk.

*High reproductive capacity species = pigs, rabbits, guinea pigs, dogs and all poultry species.

[**] When trend and proportion of pure-breeding are unknown, trend is assumed to be decreasing and pure-breeding is assumed to be <80 Percent.

Table 5. Risk categories for species with low reproductive capacity[*], according to total population size and trend, numbers of males and proportion of pure-breeding

Population trend and pure-breeding proportion[**]	Males (n)	Population size (n)						
		≤240	241 - 360	361 - 2 400	2 401 - 3 600	3 601 - 4 800	4 801 - 7 200	>7 200
Increasing trend and >80% pure-breeding	≤5	■	■	■	■	■	■	■
	6 - 20	■	▓	▓	▓	▓	▓	▓
	21 - 35	■	▓	▓	░	░	░	░
	>35	■	▓	▓	░	░	□	□
Decreasing trend or ≤80% pure-breeding	≤5	■	■	■	■	■	■	■
	6 - 20	■	■	▓	▓	▓	▓	▓
	21 - 35	■	■	▓	▓	░	░	░
	>35	■	■	▓	▓	░	░	□

■ = critical, ▓ = endangered, ░ = vulnerable and □ = not at risk.

[*] Low reproduction capacity species = horses, donkeys, cattle, yaks, buffaloes, deer, sheep, goats and camelids.

[**] When trend and proportion of pure-breeding are unknown, trend is assumed to be decreasing and pure-breeding is assumed to be <80 percent.

Action 2. Refine the categorization of risk

The thresholds presented in Tables 3 to 5 for assignment of breeds to risk categories in DAD-IS were developed for general application on a global level. They should be used judiciously at national level. They provide a basis for ranking breeds within a country according to degree of risk. They should prompt the need for additional data collection and breed monitoring. Studying similarities among breeds in the same categories may also help to identify factors acting upon the degree of risk for local animal genetic resources, now and in the future. They should not be applied uncritically, however.

For example, simply to assume that all populations with more than 1 000 females (>3 000 for species with low reproductive capacity) and 15 males are not endangered may be risky. Historical bottlenecks or inappropriate mating and selection systems may have resulted in an average relationship and ΔF in the population that are much greater than expected based on numbers of breeding males and females. In such cases, the need for action is as urgent as in the case of breeds assigned to higher risk-status categories. One option for addressing this issue is to calculate *ΔF* by using a more sophisticated approach (see Section 6) and reclassify the breed according to the *ΔF* thresholds provided rather than according to the DAD-IS criteria based on numbers of males.

Potential factors to be considered in refining the DAD-IS risk categories:

- Population trend is not considered in the assignment of DAD-IS risk status when the number of breeding females is used as the population size parameter. For breed management at national level, a more informative approach is to estimate population growth and assign risk status based on the projected population size ten years into the future.
- Concentration of a major part of the population in a restricted geographical area or in a few herds will usually place the breed at greater risk from the consequences of catastrophic events (i.e. events that occur rarely but that greatly reduce the size of the livestock population in the affected area) such as disease outbreaks, natural disasters and political upheavals. When the occurrence of such events is considered possible, breeds with a concentrated distribution should be upgraded to the next (higher) risk-status category (e.g. from vulnerable to endangered). Such an approach has been developed for the United Kingdom (Alderson, 2009). The thresholds in this case are based on the maximum radius of a circle in which 75 percent of the population of a breed is found: if the radius is less than 12.5 km, then the breed is assigned to the critical category; and if the radius is between 12.5 km and 25 km the breed is assigned to the endangered category.
- Although the DAD-IS risk classification does not consider proportion of pure-breeding females when the number of breeding females is used as the population size criterion, countries should calculate the proportion of cross-breeding that occurs. Females used for cross-breeding do not contribute to population renewal. In addition, it is important to monitor the degree of introgression from other breeds in both the females and the males of the population (i.e. if cross-bred animals are used for mating, rather than simply marketed in a terminal crossing system – see Section 7). Continual cross-breeding and introgression of genetics from other breeds will erode the original genetic variation of the population. Levels of 12.5, 7.5 and 2.5 percent introgression per generation have been suggested as thresholds for considering a population critical, endangered and vulnerable, respectively (Alderson, 2010). For the sake of simplicity, this factor has not been taken into account as a risk criterion in these guidelines. However, it should be considered when taking action at national level.
- In the above discussion of the genetic aspects of risk (i.e. *ΔF*) the generation is used as the unit of time. Genetic changes in a population occur at the transmission of genes from parents to progeny. The *ΔF* should be low enough to avoid expression of deleterious alleles (i.e. genetic defects and inbreeding depression – Meuwissen and Woolliams, 1994) and their accumulation in the long term. However, in planning a conservation programme, it is necessary to consider actions and consequences in terms of years. To account for this, we can convert *ΔF* per generation to a yearly rate by dividing *ΔF* by the average generation interval (in years). Generation interval varies according to the species and the breeding system. Average generation intervals in major livestock species are approximately as follows:
    - at least one year for avian species;
    - 1 to 2 years for pigs;
    - 4 years for sheep and goats;
    - 6 years for cattle, buffalo, llamas and alpacas; and
    - 8 years for horses, asses and camels.

  The differences in generation intervals imply that populations exposed to similar *ΔF* per generation but belonging to different species will accumulate different amounts of inbreeding in a given time period. For example, a pig population (generation interval of two years) with *ΔF* of 1 percent will accumulate 15 percent inbreeding in 30 years, while in the same time period a cattle population (generation interval of six years) will accumulate 5 percent inbreeding. Although generation interval will not affect risk status at any single moment in time, this factor should be kept in mind in making plans for the future, especially in situations when is not possible to increase the population size rapidly to above the critical or endangered threshold (such limited animal housing facilities in an *in vivo ex situ* programme). Breeding approaches to avoid inbreeding (see Section 6) will be particularly important in such cases.

- When more information is available, and in particular when a breed is on the borderline between risk categories, additional analysis should be undertaken in order to refine the state of knowledge about the breed's degree of risk, reasons for this degree of risk, and how to conserve the breed. For example, the demographic and inbreeding aspects of risk can be more precisely evaluated by considering the numbers (and year-to-year trends) of registered females, number of males used in AI, number of herds, and the trends. Pedigree data and information about historical bottlenecks will yield information about genetic variability.
- As described above, populations should be assigned to risk categories according to the least favourable parameter, i.e. if one parameter indicates a high degree of risk the breed should be assigned to a high-risk category even if other parameters correspond to a lower degree of risk. For example, populations consisting of several hundred females and a very limited number of males are not uncommon. For example, consider a breed population consisting of 3 400 cows, which is stable in size and in which five bulls are used for AI. This population should be categorized as critical, based on the low number of males, even though the number of females would qualify the breed as vulnerable. In such cases, it is important to underline the fact that the breed is in a high risk category because of suboptimal management. By simply increasing the number of males from 4 to 25, the breed could be moved up into the vulnerable category.

Action 3. Interpret results of the risk classification and contemplate the consequences for each breed

The genetic and demographic consequences associated with the different risk categories are shown in Table 6: the higher the risk category, the more unfavourable the genetic and demographic consequences and the more urgent the need for action (see Section 3). If the risk category is high, the breed suffers greater loss of diversity due to inbreeding depression and loss of alleles and faces greater risk of extinction due to random events, such as disease outbreaks, natural disasters and even low fertility rates or unequal sex ratios among the offspring.

Table 6. Genetic and demographic consequences associated with risk categories

	Genetic consequences		Demographic consequence
Risk category	Loss of diversity	Genetic defects	Susceptibility to random events
Critical	++++	++++	+++
Endangered	+++	++	+
Vulnerable	++	+	
Not at Risk	+	+	

Note: the number of + signs corresponds to the severity of the negative consequence.

Note that even populations that are classified as not at risk are subject to loss of genetic diversity and expression of deleterious alleles. However, this occurs with less intensity than in breeds in the at-risk categories.

Alternative systems of risk categorization

As described above, various procedures have been proposed and are used for estimating degrees of risk and for categorizing breeds according to their risk status (for reviews see Gandini *et al.*, 2005; Alderson, 2009; Alderson 2010; Boettcher *et al.*, 2010). Some methods emphasize population demography (e.g. EC Commission Regulation 445/2002[7]), others, such as that proposed by the European Federation of Animal Science (EAAP), emphasize genetic erosion based on estimates of N_e (e.g. EFABIS – http://efabis.net). When countries have more information available than is needed for categorizing breeds according to the worldwide FAO system, they may wish to develop national criteria and thresholds for risk categories. If countries develop their own approaches, it is strongly recommended that they base them on the general demographic and genetic principles presented above

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[7] http://eur-lex.europa.eu/LexUriServ/LexUriServ.do?uri=CELEX:32002R0445:EN:NOT

and seek, as far as possible, to use criteria similar to those used elsewhere, as this will facilitate comparisons of risk status on an international scale.

Specific risk criteria can also be developed at regional level, taking into account the levels of data availability common to the countries of the region. Such criteria are, for example, used to classify European transboundary breeds recorded in EFABIS. In the case of breeds that are kept in more than one country, degree of risk should be calculated first at national level; then, in collaboration with the other countries in which the breed is present, it should be calculated at regional or global level. DAD-IS offers users the possibility to visualize simultaneously the risk status of national populations of transboundary breeds and also calculates risk status on an international level. When exchange of animals or germplasm (semen and/or embryos) among country populations is large enough, these populations can be considered subgroups of a single large population. In such cases, if national populations are at risk due to their small sizes, it is essential that countries collaborate and manage their national populations as a large single population. Programmes for common management of country populations should be implemented in particular for breeds in the critical and endangered categories, with the aim of controlling or reducing their risk status.

Population sizes and breed utilization

The categorization systems described above are based on population numbers required to reduce genetic erosion and decrease the risk of extinction. Larger population sizes may be necessary for practical reasons, such as to guarantee the fulfilment of breed roles such as provision of cultural, environmental or social services, or to develop niche products (see Section 8). In addition, larger breed populations have more scope for combining increased selection with the maintenance of genetic diversity (see Section 7).

Because the categorization system used by FAO is designed specifically for use in assessing genetic erosion and risk of extinction rather than for assessing breeds’ contributions to a wider range of national and regional needs and objectives, the system is not recommended as a basis for breed subsidy programmes.

Action 4. Disseminate information about risk to stakeholders

The degree of risk provides an indication of the time that is available to evaluate options and to act to save the breed before it becomes extinct. Therefore, once a breed’s risk status has been established, it is important to communicate this outcome to all relevant stakeholders as soon as possible. Ideally, the information will stimulate the stakeholders to act. *Surveying and Monitoring of Animal Genetic Resources* (FAO, 2011a) provides detailed information on how report and communicate the results of surveys and indicates the importance of providing stakeholder groups with information that is tailored to their needs. It also provides advice on how identify appropriate messages and communication methods.

Effective dissemination of information on breeds’ risk status can also raise awareness among policy makers and the general public. This may facilitate the raising of funds to support breed conservation activities. One approach that can be adopted at national level is to develop and publish a “Red List” of breeds at risk of extinction.

Although dissemination of information at national level is of primary significance, exchange of information about breeds at risk is also important at international level. National Coordinators should ensure that all relevant breed population data available at national level is entered into DAD-IS or (for European countries) EFABIS. It is also important to communicate to both national authorities and international collaborators the difficulties encountered in population monitoring and information dissemination so that they can be taken into account in the planning of subsequent investigations.

Task 3. Design and implement interventions according to the risk category

Different risk categories require different conservation measures. With the exception of implementing a formal selection programme (which is not recommended for small populations), the actions should be similar for all categories, but the stress and urgency put on each will vary from one risk category to another. The interventions must also consider the country’s livestock development objectives, available resources and technical capacity, as well as the needs and wishes of stakeholders, particularly the livestock keepers.

Action 1. Identify the most appropriate interventions, based on risk status

Table 7 outlines the relative emphasis that should be given to four different types of intervention – enlarging the population, managing diversity, selection for productivity and cryoconservation; according to risk category.

Table 7. Relative importance of different animal genetic resources management objectives for populations in different risk-status category

Risk category	Enlarging the population	Managing diversity	Selection for productivity	Cryoconservation
Critical	+++	++		+++
Endangered	++	+++		++
Vulnerable	+	+	+++	+
Not at risk			+++	

Populations categorized as critical will have already lost a major part of their original genetic variation and require urgent attention. Two basic requirements are 1) to determine the genetic status of the populations (e.g. accumulated inbreeding and/or amount of introgression from other breeds) and 2) to assess the likelihood of the breed recovering from the critical status. If recovery is deemed possible, efforts should be directed primarily towards increasing the real population size of the breed while controlling inbreeding through judicious mating. In such populations, enlargement of real population size is the first objective. This means that if possible, all animals should remain in the active breeding population even if they are closely related to other animals in the population. The use of advanced reproductive technologies such as superovulation and embryo transfer may also be justified. Increasing the census size will help increase the N_e. If possible, semen and/or embryos should be cryoconserved to help insure against breed loss in the short term and to improve management of genetic variation in the long term.

For populations categorized as endangered, the objective of interventions should be to prevent them from falling into the critical category and ideally to raise them to vulnerable status. Emphasis should be placed on increasing the N_e as well as the census size. Relative to critical breeds, endangered breeds offer more opportunity for managing genetic diversity, such as by targeting specific animals in population expansion activities (i.e. targeting individual animals that are less related to the general population than others – see Section 6). Cryoconservation to complement *in vivo* conservation is recommended.

Vulnerable populations should be managed so as to prevent them from falling into the endangered category, and thus selection for production is paramount, although it should be optimized with maintenance of genetic diversity (see Section 7). The dynamics of vulnerable populations should be continuously monitored so as to understand the factors threatening the breed's viability. Programmes to increase the breed's economic competitiveness should be implemented if possible (Section 8). Preventing vulnerable breeds from reaching the higher risk categories is preferable to applying remedial actions. Vulnerable populations should be subject to genetic improvement measures, but measures to maintain a sufficiently large N_e (i.e. at least 50) should also be implemented along with actions designed to increase the census size. Although the need for cryoconservation will not be as great as in critical and endangered breeds, banking of genetic material from vulnerable breeds is recommended, especially if it can be simply implemented as part of a conventional artificial programme.

The absence of a + sign in a cell in Table 7 does not mean that the corresponding activity is irrelevant. For example, increasing the population census size is always desirable, even for not-at-risk breeds. However this will not be a priority in management plans for such breeds. Some selection for production to help improve profitability may be desirable for any breed, but is very unlikely to be feasible for critical and endangered populations without compromising genetic variability. Cryoconservation can always be beneficial, but its benefits exceed its costs by a greater margin when extinction risk is higher.

Although not shown in Table 7, populations categorized as "unknown" should not to be ignored. These breeds need urgent analysis to determine their risk status. Breed surveys should be undertaken as soon as possible.

Action 2. Implement the interventions

Whichever interventions are proposed, they should be undertaken in a timely and efficient manner. Details about implementing specific interventions are presented in Sections 4 to 8.

Task 4. Update risk status.

Livestock production systems in many areas of the world are being transformed rapidly. These changes may affect demographic trends and the genetic status of breeds within short periods of time. It is therefore advisable to establish within each country a methodology for regularly updating the risk status of breeds, as well as early warning and information systems capable of monitoring changes in the nature and intensity of the major factors affecting negatively breed risk. For example, cross-breeding activities should be strictly monitored, as should the number of males and their use, especially in populations where AI is widely practised. Efficient monitoring and analysis of population data is a prerequisite for the timely implementation of conservation measures.

The methods used for surveying the status of animal genetic resources and the threats facing them may change over time as new techniques become available and production systems change. In such cases, the change from one method to another needs to be carefully analysed before the adoption of the new method in order to ensure consistency between older and newer data. For further advice on this and other aspects of planning a national monitoring strategy for animal genetic resources, see FAO (2011b).

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III. DETERMINING THE CONSERVATION VALUE OF A BREED

Upon completion of the activities described in Section 2, a country will have a measure of the risk status of each of its breeds. All breeds in at-risk categories can be considered candidates for conservation activities. Ideally, a conservation programme would be developed for all at-risk breeds. In most countries, however, the costs required to conserve all breeds at risk will be greater than the resources available for conservation. Depending on the goal of the conservation programme, the conservation of all breeds may anyway not be justifiable. Some breeds may be judged to have no particularly unique or valuable characteristics worth conserving, either for the immediate or the longer term, and have little historical or cultural significance. In other cases, breeds may be very similar to each other genetically, meaning that a large proportion of the genetic diversity of the total population can be captured by conserving only a subset of breeds, or in some cases by making a composite population by combining multiple closely related breeds. Countries will need to decide how the resources available for conservation should be utilized and which breeds should be conserved.

A wide range of approaches for prioritizing breeds for inclusion in conservation programmes is available. These approaches vary considerably in the types of information and data used and in their complexity and precision. This section is therefore broken into two subsections that differ in terms of complexity. Specifically, the second subsection describes methods that use genetic markers for evaluating genetic variability, whereas the first subsection involves techniques that do not require genetic markers. The approaches described generally increase in complexity and in the amount of information required as one reads further into each subsection.

Before choosing a prioritization method, countries should consider the level of precision they require and the state of capacity to implement various options. In some cases, the National Advisory Committee will need to collaborate with local researchers and other experts to implement the prioritization methods. The more complex approaches described below will not be feasible for some countries because of a lack of molecular genetic data or technical capacity. If this is the case, the simple approaches outlined in the following subsection are perfectly acceptable. However, both phenotypic and molecular genetic characterization should receive due consideration in a country’s national strategy and action plan for animal genetic resources to help ensure that prioritization can be as accurate as possible.

Accounting for factors other than risk status in prioritizing breeds for conservation

Rationale

Risk status is generally considered the most important criterion for determining whether a breed should be subject to conservation activities. As a simple approach, breeds can be ranked according to their risk status, and those at the greatest risk given the greatest priority for conservation. However, other factors may influence a breed’s conservation value, and countries may wish to consider these as well. Among the factors that may influence the conservation priority of a breed are the following (Ruane, 2000).

- **Species**

  In general, breeds belonging to species that are more economically or culturally important to a country will merit a greater priority in conservation strategies. In addition, species should be given high conservation priority in the countries where they were originally domesticated, especially if the species are not common in other parts of the world. For example, in Peru, the alpaca has a high conservation value for all the above reasons.

  Practical considerations may also influence conservation priorities among species. *In vivo* conservation programmes for small animals, such as poultry, rabbits and even small ruminants, are likely to be less costly than programmes for larger species such as cattle or horses. Thus, if all other factors (e.g. economic, cultural, etc.) are equal, the smaller species may merit greater priority because more breeds can be conserved per unit of resources spent on conservation. On the other hand, larger animals may have more value per animal unit.

Most formal, objective procedures for prioritization of breeds for conservation (see below) are applicable for use within species rather than across species.

- **Genetic diversity of the breed**

  As described above, genetic diversity is critical to the conservation of animal genetic resources. Two aspects of genetic diversity can be considered in conservation decisions:

  Genetic uniqueness of the breed. Maintaining breeds that are genetically distinct is often a high priority for national conservation programmes. At-risk breeds that are distinct from each other and from the breeds in the not-at-risk category are particularly valuable from a genetic point of view, as they may be more likely to have unique alleles and gene combinations (see Box 10). Understanding the genetic history of a particular breed will assist in determining its uniqueness.

  Genetic variation within the breed. Genetic variation gives an animal genetic resource the capacity to adapt and allows for genetic response to selection. Conserving the most genetically diverse breeds is the most efficient way to conserve the diversity of a given species.

Box 10

Unique alleles allow the Araucana chicken of Chile to produce natural "Easter eggs"

The Easter egg hunt is a traditional holiday event in many predominantly Christian countries. Children search in parks and gardens for painted eggs that were supposedly hidden by a mythical rabbit. However, breed of chicken is able to provide coloured eggs year-round, by a totally natural process.

The Araucana hen is an endangered chicken breed from Chile. It is recognized for its particular phenotypic characteristics, the presence of "earrings" (straight feathers coming from the neck, right down their ears, like earrings) and blue-shelled eggs. These features occur because of the existence of the gen Et and gen O alleles in the breed's genome, which are unique in the species. The Araucana hen is also well-known in its local area for its high rusticity. It is capable of withstanding extreme temperatures and tolerating locally present diseases. The eggs and laying hens can command very high prices, which may even be twice as high as those of commercial breeds. The breed is associated with the Mapuche, an indigenous Chilean community, who uses it in traditional ceremonies and raise it in extensive systems. Today, the Chilean Government and other stakeholders are developing research programmes involving the conservation of Araucana genetic material and its use by the indigenous community.

Provided by Ignacio Garcìa Leòn and Pascalle Renee Ziomi Smith.

- **Phenotypic characteristics of the breed**

  Traits of economic importance. Clearly, if a breed has exceptional economic productivity this is likely to be due in part to superior genetics. Thus, action should be taken to ensure these genes are available for breeding programmes. Both the current and potential future importance of particular characteristics should be considered. Of course, breeds whose economic value is currently high are less likely to be currently at risk.

  Agricultural economists have proposed a system with which to describe the values for animal genetic resources that mirrors approaches used to describe other types of resource (see Box 10). The system facilitates the comparison of attributes that can be immediately marketed (such as milk or meat) with those that cannot (such as genetic variation).

  Unique traits. Breeds with special behavioural, physiological or morphological traits should be given high priority for conservation, as these traits are likely to have a genetic basis and be associated with unique alleles (see Box 11).

Box 11

Botfly resistance in the Blanco Orejinegro cattle of Colombia

The Blanco Orejinegro is a Colombian Creole cattle breed distinguished by its white coat and black ears. The breed descends from the cattle introduced by the Spanish conquistadores in the fifteenth century and was developed in the central foothills of the Andes, the region of the country known for its coffee production. Also endemic to this region is the botfly (*Dermatobia hominis*, or "nuche" in Spanish), a parasite of cattle skin. Botfly infections cause huge economic losses, not only because of the damage caused to hides by the movement of the botfly larvae under the cattle’s skin, but also because of the weight loss that occurs because of discomfort and secondary infections caused by lesions produced when the larvae penetrate the skin at the start and the end of their lifecycles. At El Nus Research Station, located in Antioquia, Colombia, many studies on cattle–botfly interactions have been carried out since 1948. Studies have shown that the progeny of animals that were not parasitized (i.e. that showed resistance) were also resistant. This led researchers to conclude that this resistance has a genetic origin, most likely controlled by one or a few genes acting in a non-additive (dominant) manner. The presence of these genes makes the Blanco Orejinegro a valued genetic resource for livestock production in this area of Colombia, and possibly in other countries where the botfly is endemic.

Provided by German Martinez Correal.

Adaptation to a specific environment. The adaptation of breeds to specific environments is likely to be under some genetic control. Thus conservation of breeds showing such adaptations may be important. Environmental adaptations will be especially important if the conditions to which the breed is adapted are likely to become more common in the future (e.g. warmer conditions under predicted climate change scenarios).

- **Cultural or historical value**

  Breeds were developed in part by human intervention and thus can be regarded as part of the cultural or historical heritage of a give region or population that has been passed down the generations and thus should be passed on to future generations (Ruane, 2000). Therefore, breeds with greater cultural importance should receive greater conservation priority. In many areas of the world, traditional grazing over many centuries has contributed to the creation and maintenance of agro-ecosystems of high biodiversity value. Similarly, many landscapes have been shaped over time by traditional farming systems. The results of co-evolutionary processes among locally adapted breeds, traditional framing systems and the natural environment retain their character and richness as long as the breed and production system are maintained. For example, grazing livestock maintain the distinctive features of alpine meadows. A breed’s role in maintaining a unique ecosystem may be a reason for giving it a high priority for inclusion in a conservation programme. Methods for estimating the cultural value of a breed are available (Gandini and Villa, 2003; Simianer *et al.*, 2003).

- **Probability of success in conserving the breed**

  The main reason for prioritizing among breeds is to ensure that available resources are invested as wisely as possible. The future sustainability of a conserved breed must therefore be considered during the prioritization. Factors such as the existence of a breeders’ association, organized record keeping, the existence of a stock of semen from males of previous generations, or evidence of interest and cooperation among breeders often indicate a greater chance that the breed will be able survive with only a relatively small amount of formal assistance from outside. On the other hand, breeds in a critical state of risk whose population has declined to only a few animals (and that has no other resources such as cryopreserved semen or embryos) may never regain a large and diverse gene pool, regardless of the interventions undertaken.

- **Status of a breed at regional level**

  When only local breeds are considered for a national conservation programme, prioritization is simplified because only the factors listed above need be considered. The situation is more complex when transboundary breeds are candidates for conservation. Such breeds can be at-risk in one country and not at risk in another country or not at risk on a regional basis if all national populations are considered. DAD-IS assigns a global risk status to transboundary breeds, but this should be regarded simply as an estimate. The relevant countries should collaborate to establish a more definitive risk status for each transboundary breed.

  An individual country may give a transboundary breed low conservation priority under the assumption that another country will conserve it. This creates the risk that some breeds will end up being conserved by no country. The best solution is discussion, prioritization and planning for conservation of such breeds at regional level. A similar approach could be applied at the global level, for international transboundary breeds at risk.

Objective: To determine the conservation value for each breed based on non-demographic factors.

Inputs:

1. List of breeds at risk; and
2. Sources of information (including stakeholders) about factors influencing conservation value.

Outputs:

- Information about factors affecting the conservation value of each breed; and
- Ranking of breeds on the basis of conservation value.

Task 1. Assess the conservation priority of breeds according to non-demographic factors

Action 1. Assign responsibilities for prioritization of breeds

An entity with the responsibility for determining the conservation value of breeds must be established so that a clear and unambiguous decision can be made. This responsible entity may be the National Advisory Committee on animal genetic resources (see Section 1), a special conservation task force, a specialized NGO that works with keepers of breeds at risk, or even a single individual with sufficient knowledge of the animal genetic resources within the country. For simplicity, the discussion in this section will always refer to the “National Advisory Committee” as the entity responsible for prioritizing breeds for conservation. Whatever entity is given this task, participatory approaches to prioritization should be used and representatives of all major stakeholders should be consulted.

Action 2. Determine the factors upon which the calculation of conservation value will be based, according to the desired conservation strategy

The first activity of the responsible entity will be to evaluate the conservation objectives for each species (see Section 1) and, based upon these objectives, agree upon the factors to be considered in determining the conservation value of the breeds, as well as their relative importance.

The thought process required in order to obtain a list of specific factors for use in assessing conservation value based on a general conservation objective may be facilitated by considering the overall strategy for conservation of animal genetic resources in a country. Bennewitz *et al.* (2007) outlined three strategies to consider.

1. **Maximum risk strategy.** This strategy considers only the degree of endangerment, and can be justified if the main objective of the country is primarily to prevent the near-term loss (within ~10 years) of breeds at high risk of extinction.

2. **Maximum diversity strategy.** This strategy considers only the genetic diversity of a breed relative to the amount of diversity of other breeds that at are risk and as a complement to the diversity of the breeds that are not at risk. This strategy may be optimal where a fixed amount of financial support is available for conservation activities and the goal is to capture as much genetic diversity as possible for the funds available.

3. **Maximum utility strategy.** This strategy considers factors beyond risk of endangerment and genetic variability. Although this strategy may be applicable in many situations, it should particularly be used if conservation programmes are expected to be partially or fully economically self-sustainable.

The choice of the strategy, the factors influencing priority and the relative importance of each factor are decisions that merit serious thought and discussion. The choice of breeds to be targeted may vary greatly depending on the strategy and factors chosen, especially when there are many breeds at risk and few resources for their conservation. Some factors that may influence conservation priority are antagonistic, and breeds that excel for one may rank poorly for another. For example, breeds at the greatest risk of extinction (and thus deserving of the highest priority with the maximum risk strategy) will often be low in genetic diversity (maximum diversity strategy) and/or genetic value for economic or special traits (maximum utility strategy). Also, the probability of success of the conservation programme is often lowest for the breeds at the greatest risk of extinction.

In some cases, two or more factors may be closely related. For example, the cultural importance of a breed may be tied to its genetic uniqueness or presence of a special trait. In such cases, consideration of all these factors may result in their over-emphasis in determining conservation priority.

If quantitative methods are going to be used to rank breeds (see below in this section), the National Advisory Committee should agree on numerical weights for the factors used to determine conservation value that are proportional to their relative importance. Various approaches have been proposed to aid in the process of assigning weights. A simple participatory and visual approach is called “participatory piling”, whereby members of the group charged with assigning weights are each given a certain number of small objects (stones, marbles, beans, etc.) and asked to distribute them across the various factors based on their perceived importance. The results are then averaged across the participants to obtain overall weights.

In a more objective but more complicated approach, economists have suggested assigning the values of breeds to different classes and estimating values in monetary terms. Box 12 describes an approach for classifying values that may be applied to breeds or other animal genetic resources.

Box 12

Values of animal genetic resources

From a formal economic perspective, animal genetic resources can have various different types of values for conservation. These values can be categorized as follows (Drucker *et al.*, 2001; FAO 2007):

Direct use value – results from benefits obtained from the utilization of animal genetic resources, such as the production of milk or meat;

Indirect use value – results from the provision of support or protection to other activities that produce benefits, such as through the provision of regulating and supporting ecosystem services;

Option value – results from the potential benefits of having a given resource available for the future; for example, having genetic variability available that can be used to respond to market and environmental changes;

Bequest value – results from benefits that might be obtained from the knowledge that others may derive benefits from the animal genetic resource in the future;

Existence value – derived only from the satisfaction of knowing that a given animal genetic resource exists, even if no other type of value can be derived from it.

In most instances, indirect use and option values will be the most important for at-risk animal genetic resources, as these are values in which locally adapted breeds are likely to excel over other breeds. Increasing, the direct use value will contribute to economic sustainability of a breed and therefore, the potential success of conservation activities (see Sections 7 and 8). Bequest and existence values are likely to apply only in particular situations.

A method known as “choice modelling” can be used to obtain quantitative data for the values listed in Box 12. In brief, choice modelling uses a survey or questionnaire to evaluate the preference of respondents (e.g. farmers or other stakeholders) for a set of alternative outcomes (i.e. profiles describing breeds or types of animals). Each of the alternative outcomes is defined by a set of attributes with different levels (i.e. traits of breeds). Then, a statistical model is used to determine the importance of a given value based on the frequency with which the profiles excelling in that value were chosen by the respondents. Some examples of the application of choice models to animal genetic resources are presented in Box 13. Clearly, the success of choice modelling will depend greatly on the appropriateness of the design of the survey and the statistical analysis. Therefore, applying such an approach will generally require consultation with a statistician or other scientist with experience in choice modelling.

Box 13

Using choice models to value and rank breeds for conservation

Choice models can be used in order to understand the full range of values livestock can have for people and to express these as a Total Economic Value. The Total Economic Value includes a whole range of values held by breeds, ranging from the value of the goods they produce (use values) to landscape/recreational, adaptive, cultural or simply existence values. Non-use values cannot be assessed from market transactions and are often undervalued if not assessed properly. In choice models, people are asked to state their preferences for hypothetical animal profiles that describe the traits of breeds. People choose their preferred profile, which allows calculation of how much they might be willing to pay for particular traits. Analysis of choice data reveal the values of traits relative to each other and allows ranking of the traits. Choice models have been used widely for valuing livestock breeds in developing countries, mostly in Africa and mostly applied to cattle breeds (e.g. Zander and Drucker, 2008), but also to breeds of small ruminants (e.g. Omondi *et al.*, 2008), chickens (e.g. Faustin *et al.*, 2010) and pigs (e.g. Scarpa *et al.*, 2003). The evaluation can often be used to identify farmers who prefer the traits of traditional breeds and may therefore be willing to conserve them with minimal external incentive payments.

Recently, choice model studies have been carried out on European endangered cattle breeds in order to understand synergies between the use of the animals and conservation management (Fadlaoui *et al.*, 2006). Results showed that the European public would be willing to pay substantial amounts simply to ensure the existence of some breeds for their own sake, but the public also appreciated the role of some at-risk locally adapted breeds as components in traditional landscapes, in cultural events and as sources of premium food products.

Results from choice modelling can be combined with measures of genetic distinctiveness and the costs of conservation, allowing conservation programmes to be ranked according to their efficiency (Weitzman, 1998; Zander *et al.*, 2009). In countries where farmers already get paid to keep at-risk breeds, choice model results can help maximize the efficiency of such breed conservation programmes, by matching conservation payments to the value of each breed to the public.

Provided by Kerstin Zander.

Action 3. Gather the information necessary to determine the conservation priority

Once a decision has been made with regard to the factors influencing conservation priority, research should be undertaken, if necessary, to determine the status of each breed with respect to each factor. For example, if the phenotypic characteristics of each breed are going to be considered, then this information should be obtained for all or a representative sample of animals. For traits of economic importance, breed averages should be obtained. The presence of unique traits or of adaptation to a particular environment should be noted if these qualities are recognized as important for prioritization. Pedigrees or genetic markers can provide insight into genetic variation (this topic is discussed in more detail in Section 5). Any historical or cultural significance of the breed should be noted.

Ideally, countries will have already characterized their breeds phenotypically and genetically prior to undertaking decision making on conservation (see *Phenotypic characterization of animal genetic resources* – FAO, 2012 and *Molecular genetic characterization of animal genetic resources* – FAO, 2011). If breeds have been characterized, then most, if not all, of the information required will have been gathered through that process. If characterization has not been undertaken, then the most efficient approach would be to combine characterization and gathering of data for conservation decision making. If this is not possible, then the members of the National Advisory Committee or other persons responsible for collecting and organizing the information required may need to consult a number of sources. Ideally, the persons chosen to collect the information will have some existing familiarity with the breeds. Data for phenotypic traits may be available in local or international scientific literature or in local "grey" literature, such as technical reports. Various stakeholders (e.g. farmers and breeders, local historians) can be consulted to obtain information about other factors such as unique traits and breeding history in order to obtain insight into the uniqueness and cultural significance of the breeds.

Information about genetic diversity can be obtained from a variety of sources, which may differ in terms of their accuracy. For standardized breeds with recorded histories and pedigrees, determining the origin of the breed and the extent to which it has been influenced in the past by other breeds (introgression) likely to be more straightforward than for non-standardized breeds. Pedigree data can be used to estimate the level of inbreeding and its trend over time (ΔF) and therefore N_e. As discussed in more detail in the next subsection, genetic markers can be used to evaluate genetic diversity within breeds and genetic relationships among breeds. In the absence of such sources of information, consultation with stakeholders that have knowledge of the history of breeds can yield valuable data. Past population bottlenecks (severe reduction in population numbers) will have led to lower variation in the current population. Past cross-breeding can be expected to have decreased the uniqueness and distinctiveness of a breed. Widespread use of AI will likely have decreased N_e, by increasing the imbalance in the ratio of male versus female parents.

Action 4. Discuss and evaluate the advantages and disadvantages of the breeds

Section 1 describes the use of a SWOT analysis to describe the roles, functions and dynamics of livestock species and assist in establishing conservation objectives. The information from the SWOT analysis, along with the information gathered under *Action 3* can serve as the basis for a discussion on the values of each breed and its contributions to the various conservation objectives. Ideally, this discussion should be undertaken by the members of the National Advisory Committee. The merits and disadvantages of each breed should be noted. The results of the discussion and evaluation should be summarized in written form, so that the committee can, if requested to do so, easily explain their decisions to policy makers.

Action 5. Rank breeds for conservation priority

Based on the group discussion and analysis, breeds should be ranked for conservation priority. Either subjective or quantitative approaches can be used.

At the close of the discussion undertaken in Action *4,* it may be possible for committee members simply to arrive at a clear consensus on a priority order for the breeds at risk. If a consensus cannot be reached, a vote can be taken to obtain a final decision. Alternatively, all committee members may be asked to rank the breeds in priority order and then the rankings can be averaged to yield a final order. If the responsible entity is a single person, a subjective ranking may be used. However, in such cases, the person should document the logic he or she followed in the decision-making process in order to inform policy makers and other stakeholders.

For a quantitative approach, the attributes for each breed for each factor influencing conservation priority must be expressed numerically. Statistics, such as breed averages for economically important traits will automatically be expressed in numerical terms, but not this is necessarily the case for factors such as presence and absence of special traits or cultural importance. For presence and absence of unique or adaptive traits, presence can be scored as 1 and absence as 0. When multiple special traits are considered, then results can be summed for each breed. For more heterogeneous characteristics, such as historical and cultural significance, two options may be considered:

1. Breeds can be ranked for the characteristic of interest, and then assigned scores corresponding to their ranking. For example, for cultural significance among a group of three breeds, the breed with the most importance can be assigned a score of 3, the second a score of 2 and the third a score of 1.

2. Breeds can be rated for the characteristic of interest in a process similar to that described above for overall conservation priority. For example, members of the conservation committee can each be asked to rate every breed for its cultural importance on a 1 to 10 scale, with 10 being “very important” and 1 being “not important”. The committee members’ ratings can then be averaged for each breed.

Even when the maximum diversity and maximum value strategies are used, risk status will usually be an important consideration and the breeds at the greatest risk of extinction should generally receive the highest priority. Therefore, decisions should be made separately within each risk category. When there is only a single non-demographic factor upon which to base conservation priority, the decision is straightforward. Breeds can simply be prioritized (within risk category) based on their ranking for the single factor.

When multiple factors influence conservation priority, then a simple multifactor index can be used to prioritize breeds. The following formula can be used to establish priority according to *conservation values*:

$$CV_i = w_{F1} \times (F1_i - \mu_1)/\sigma_{F1} + wF_2 \times (F2_i - \mu_{F2})/\sigma_{F2} + ... + w_{Fn} \times (Fn_i - \mu_{Fn})/\sigma_{Fn}, \text{ (Equation 1)}$$

where,

CV_i = is the conservation value of Breed *i*,

w_{F1} = is the weight (i.e. relative importance) of Factor 1 (e.g. genetic uniqueness),

$F1_i$ = is the value for Factor 1 for Breed *i*,

μ_{F1} = is the average of all breeds for Factor 1,

σ_{F1} = is the standard deviation of all breeds for Factor 1,

and so forth for the rest of the factors to be considered. Box 14 presents an example of a situation in which three hypothetical breeds must be prioritized for conservation.

Box 14

Use of a simple index to prioritize three breeds for conservation

This example shows how a simple index based on four factors can be used to prioritize breeds for conservation. The table shows the values assigned to three hypothetical dairy cattle breeds for each of the four factors, along with the relative weights assigned to each factor.

Breed values, population averages and weights for four factors to be considered in conservation prioritization

	Effective population size	Genetic uniqueness	Milk yield (kg/year)	Cultural importance
Breed 1	60	2	1 000	0
Breed 2	100	3	700	0
Breed 3	50	1	500	1
Overall mean	70	2	733.33	0.33
Standard deviation	26.46	1	251.66	0.58
Weight in index	3	1	2	1

In this example, the four factors under consideration are effective population size (N_e), genetic uniqueness, annual milk yield per female and cultural importance. It is an example the use of the maximum value strategy for evaluating breeds. Two of the factors, N_e and genetic uniqueness, are both measures of genetic diversity. The National Advisory Committee for Animal Genetic Resources has decided that N_e is the most important factor, and it is therefore given the greatest weight (w = 3). N_e and milk yield are estimated and measured quantitative factors, respectively, whereas genetic uniqueness and cultural importance are based on ratings.

Each of the three breeds is superior to the others in one of the four factors: Breed 1 has the greatest milk yield; Breed 2 has the most genetic diversity (for both measures); and Breed 3 is the only breed considered to have any particular cultural importance.

The table below shows intermediate calculations and final results for the conservation value index for each breed. Standardized values are the factor values minus overall mean, divided by standard deviation. Weighted values are standardized values times weights. Conservation values are the sums of weighted values for each breed.

Standardized and weighted values and overall conservation value and rank for three breeds.

	Breed 1	Breed 2	Breed 3
Standardized values			
Effective population size	-0.38	1.13	-0.76
Genetic uniqueness	0	1	-1
Milk yield	1.06	-0.13	-0.93
Cultural importance	-0.58	-0.58	1.15
Weighted values			
Effective population size	-1.13	3.40	-2.27
Genetic uniqueness	0	1	-1
Milk yield	2.12	-0.26	-1.85
Cultural importance	-0.58	-0.58	1.15
Conservation value	0.41	3.56	-3.97
Rank	2	1	3

According to the conservation value index, Breed 2 merits the greatest priority for conservation, mostly because of its superiority in genetic diversity, the most important factor. Breed 3 ranks last despite its high cultural importance, because this factor is not considered as important as genetic variability or milk yield, for which this breed is inferior.

Note that the choice of factors used in this case is intended as an example rather than as a recommendation. Each country should determine its own criteria, based on local objectives. Although milk yield was considered in this example, alternative factors such as functional traits or a more complex measure of milk productivity that also considers the cost of production may be preferable. Also, this example has four factors, but a country may consider more or fewer factors. The weights assigned to the various factors are also for example purposes only. Each country should establish its own weights for prioritization.

Task 2. Disseminate information to stakeholders

Stakeholders involved in implementing or financially supporting conservation programmes must be informed about both the results of the breed prioritization and the logic used in the prioritization.

Action 1. Prepare a report on breed prioritization

The results of the breed prioritization should be summarized in a written report that is distributed to stakeholders. The report should also include an explanation of the procedures used and a summary of the information used to support the analyses.

Action 2. Hold meetings with stakeholders to explain the results of the prioritization

Stakeholders should be given an opportunity to discuss the results of the prioritization activities and to voice any concerns they may have about the final ranking of breeds. Concerns should be taken seriously and addressed thoroughly, because the efforts made in prioritization will be wasted if stakeholders refuse to accept them and implement programmes according to the recommendations.

Use of information from genetic markers to account formally for genetic diversity in conservation prioritization

Rationale

The importance of maintaining diversity and genetic variation in animal genetic resources is described in the preceding sections. Genetic variability allows for adaptation and genetic improvement and protects against the detrimental effects of inbreeding, such as increased occurrence of genetic defects and decreases in fecundity and viability. Genetic diversity and variation should thus be considered in the planning of conservation programmes and in the prioritization of breeds for conservation activities.

The previous section described approaches to prioritization that consider genetic diversity on the basis of measures of N_e based on pedigree or population structure and/or knowledge of genetic uniqueness. This section describes the use of genetic markers based on DNA to estimate diversity both within and across breeds and the use of these estimates in prioritizing breeds and making conservation decisions. When breeds have been subject to genetic characterization and molecular genetic data are therefore available, formal methods can be used to account objectively for genetic variability within and among breeds along with other factors when assigning priority to breeds for conservation.

Objective: To evaluate the genetic diversity of breeds by using genetic markers and account for this diversity in decision-making regarding which breeds to include in conservation activities.

Inputs:

1. Information on the general conservation objectives to be addressed;
2. List of breeds to be considered for inclusion in conservation programmes;
3. For each breed, information on the factors that affect conservation value; and
4. The molecular genetic information needed to evaluate breed diversity.

Outputs:

- Quantified analysis of the genetic diversity of breeds in each species under consideration; and
- List of breeds prioritized for conservation.

Task 1. Gather the data needed to apply objective methods of breed prioritization

Action 1. Obtain molecular genetic data on breeds

Genetic characterization is a recommended step in the evaluation of breeds for improvement of their management and for development of programmes for sustainable use and conservation. Genetic characterization includes the collection and analysis of DNA from a sample of animals from each breed of interest, in order to evaluate genetic variability at molecular level and determine relationships among breeds (Box 15). Guidelines on molecular characterization (FAO, 2011) are available to assist countries in this activity.

For reliable results, DNA should be collected from at least 40 animals, including at least 10 of each sex. Animals should represent the geographical and genetic distribution of the breed, which generally means that very close relatives should be avoided. Animals should be genotyped by using the most informative system of genetic markers available given the financial constraints. Current recommendations are to use the panels of 30 species-specific microsatellite markers compiled by the ISAG-FAO Advisory Group and listed in the FAO guidelines *Molecular genetic characterization of animal genetic resources* (FAO, 2011), but newer genotyping platforms such as SNP chips may be considered, based on costs and overall objectives. Ideally, genetic characterization data should be obtained not only for the breeds at risk, but also for the not-at-risk local and transboundary breeds in the country. High genetic similarity to not-at-risk breeds indicates low distinctiveness and thus diminishes a breed’s conservation priority. Box 16 gives an example of how genetic markers were used to make inferences about populations of pigs and chickens in Southern Africa.

Box 15

Genetic markers

Molecular genetic markers are sites of variability in the sequence of DNA that have a statistical association with a characteristic of different cells, individuals or populations. Various types of markers exist. They differ in the types of variation evaluated and the laboratory procedures used. Markers can be “neutral” or affected by the process of selection. Neutral markers are recommended for measuring genetic diversity and population genetic statistics. Selective markers are associated with phenotypic traits. In the last two decades, molecular markers have been widely used to investigate the genetic diversity of livestock populations. In the late 1980s to early 1990s the use of short tandem-repeat DNA sequences, known as “microsatellites”, became popular because of their high polymorphism, high information content, speed of assay, low cost and suitability for analysis in automatic sequencers. They have also been used extensively for investigating the evolutionary history and diversity of livestock species.

As a result of whole genome sequencing and HapMap projects, millions of single nucleotide polymorphisms (SNP) have recently been identified in several livestock species. From these, panels including tens of thousands of validated SNPs are already available to the scientific community (e.g. in cattle, sheep, chickens and pigs) or will likely be available in the near future (e.g. in goats, horses), permitting genome-wide scans at a very low cost per data point. SNP panels open new perspectives in livestock genetics, in particular for the investigation of genome diversity within and among individuals and populations, population structure and inbreeding, and for the identification of signatures left by selection. This last application provides an attractive prospect for the identification of genomic regions influencing traits that are very difficult to record and are directly associated with conservation value of an animal genetic resource.

With the continual rapid advancement in DNA sequencing technology, whole genome data are a realistic target for population and conservation studies in the very near future. Technology provides new methods of assaying adaptive variation in the genome of threatened populations, enabling prioritization protocols to use unique adaptive variants as well as neutral, demographically mediated variation, and even to test the association of this variation with environmental variables and thereby identify geographic regions of priority (e.g. Bonin *et al.*, 2007; Joost *et al*., 2007). By examining all regions of the genome and through genome-specific coalescent analysis, the effects of mutation, drift, selection and admixture can be distinguished at a fine scale. Therefore, for example, locally adapted variants can be distinguished from ancestral polymorphisms and long-term selection can be distinguished from admixture.

Provided by Alessandra Stella.

Action 2. Agree upon specific genetic objectives for maintenance of genetic diversity

The general objective of conserving genetic diversity may have a more specific goal and this goal will affect the definition of molecular genetic diversity to be used to prioritize breeds. The appropriate approach to the assessment of genetic diversity depends on the specific type of genetic diversity to be conserved. For example, the specific goal may be to maintain the maximum amount of diversity across breeds. Alternatively, conservation of genetically distinct breeds may be the primary objective. In other cases, ensuring the maintenance of specific alleles or gene combinations may be important. In most cases, a balance between conserving specific breeds and across-breed diversity will be the most logical objective.

If relationships among breeds are not considered important, then a simple quantitative measure of diversity such as heterozygosity or marker-based N_e (see Box 17), can be calculated. This measure of diversity can simply be inserted into the Conservation Value (CV) equation described under Task 1, Action 5 of the preceding subsection. However, ignoring relationships among breeds is not optimal, and thus using a more complex objective approach, as described Actions 3 to 7 below is preferable.

Box 16

Use of genetic markers to study the diversity of chickens in Southern Africa

Southern Africa is the home of a number of local chicken populations. The importance of these animal genetic resources has been recognized, and specialized institutional flocks have been developed for their conservation. There has always been some uncertainty, however, about whether these populations are distinct breeds or just ecotypes within the same breed and whether the genetics of the local chickens are well-represented in the conservation flocks. A research project was therefore undertaken to answer these and other questions regarding the chicken populations in Southern Africa. DNA was sampled from three village chicken populations, as well as from four conservation flocks and several reference populations. The countries with chicken genetic resources represented in the analysis were Malawi, Mozambique, Namibia, South Africa and Zimbabwe. The project followed FAO guidelines for characterizing animal genetic resources (FAO, 2011 and FAO, 2012), whereby the production environment was first described via questionnaires and surveys, followed by genetic analyses of the populations using both microsatellite DNA markers and mitochondrial DNA.

The analyses yielded several conclusions. First, from a genetic perspective, the three populations of village in chickens from across the subregion were all part of a single large population. However, slightly different ecotypes had been developed through breeding within isolated geographic regions The differences among ecotypes were primarily observable at the phenotypic level (e.g. plumage or coat colour and in some cases production performance). In addition, cluster analyses indicated that the village populations were genetically distinct from the conservation lines, even in the case of the village populations that were reportedly used to form particular lines. The village populations were found to be more genetically diverse than the conserved lines, based on the numbers of alleles for the genetic markers. Inbreeding within the conservation lines was less than within the village populations. Mitochondrial DNA revealed multiple maternal lineages; South African chicken populations shared three major haplotypes, which were presumed to have originated from China, Southeast Asia and the Indian subcontinent.

The overall findings increased awareness of the importance of genetic management and utilization of the local chicken genetic resources of Southern Africa. In addition, the study provided a baseline dataset to support the decision-making process for the design of conservation strategies. Among the main conclusions of the study were that the conserved lines were being managed well, inbreeding was being kept low, but the initial sampling may have been too small and failed sufficiently to represent the genetic variability of the village populations. Resampling to capture this diversity was therefore suggested.

Provided by Kennedy Dzama. For further information, see Mtileni *et al.* (2011a, 2011b).

Action 3. Choose the objective method to be applied based on the genetic objectives and the definition of molecular diversity

The application of objective approaches to account for molecular genetic diversity in the prioritization of breeds for conservation has been reviewed by Boettcher *et al.* (2010). Various options exist. The choice of which to apply will vary according to the definition of genetic diversity that is being used. The Weitzman (1992) approach measures genetic diversity according to genetic distances among breeds (Box 18) and therefore considers exclusively the genetic differences among breeds while ignoring the genetic variation within breeds. This approach should be applied when only uniqueness of breeds is considered important and crossing of breeds is not expected to be undertaken in the future. The prioritization procedures of Caballero and Toro (2002) and Eding *et al.* (2002) define diversity according to kinship (Box 19) and are suitable when within-breed diversity is of primary importance. This approach will capture the most genetic information across a selection of breeds and is ideal for maintaining the maximum species-wide diversity. Such an approach is justified if the individual breeds are not considered important and crossing of conserved breeds is expected to be common in the future. In most situations, future activities will emphasize the maintenance of distinct breeds, with some cross-breeding. In such cases, the definitions of diversity used in the prioritization methods of Piyasatian and Kinghorn (2003) and Bennewitz and Meuwissen (2005a), which consider an intermediate balance of within- and across-breed diversity, will be the best option (Meuwissen, 2009).

Box 17

Estimating within-breed molecular genetic diversity

The simplest measure of within-breed genetic diversity is heterozygosity. Increased heterozygosity is associated with greater genetic diversity. An animal is heterozygous at a given locus if its two alleles differ. Two measures of heterozygosity exist: observed and expected heterozygosity. Observed heterozygosity (H_o) at a given locus is calculated simply by observing the genotype of each animal sampled, counting the number of heterozygous animals and dividing by the total number of animals. Expected heterozygosity (H_e) at a given locus is calculated by determining the frequency of each allele present and then applying the following formula:

$$H_e = \sum_{i=1}^{n}(1 - p_i^2) \quad \text{(Equation 2)}$$

where n is the number of loci and p_i is the frequency of allele i. Heterozygosity measures should be calculated for each locus and averaged across loci. Most computer software for molecular genetic analysis will compute both H_e and H_o. All breeds should be evaluated using the same loci.

For prioritization of breeds, H_e is preferable, as it indicates the amount of genetic diversity "available" assuming random mating. In fact, H_e is also known as "gene diversity". H_o may differ significantly from the H_e if some type of non-random mating has occurred in the previous generation. Inbreeding or mating of similar animals decreases (assortative mating) H_o, whereas mating of non-similar animals (disassortative mating) increases H_o.

Molecular markers may also be used to estimate N_e. Various approaches to doing this have been proposed, several of which are described by Cervantes *et al.* (2011). Many of the approaches require multistage sampling of animals, which may not always be feasible. For a single sample of genotyped animals, N_e can be estimated based on linkage disquelibrium. Various software for computing molecular N_e exist:

NeEstimator (Ovenden *et al.*, 2007) is based on theoretical expectations (Hill, 1981; Waples, 1991) of differences between observed and expected gametic frequencies. It can be downloaded free of charge from http://www.dpi.qld.gov.au/28_6908.htm. Registration is required.

ONeSAMP (Tallmon *et al.*, 2008) applies an approximate Bayesian formulation to obtain an estimator similar to theoretical expectations that is expected to increase precision relative to the NeEstimator software. Calculation is performed online at http://genomics.jun.alaska.edu. The user inserts values for various parameters (numbers of individuals and loci) and provides the path to the input file. Results are sent by e-mail.

Box 18

The use of genetic markers for estimating genetic distances among breeds

Genetic distance is a quantitative measure of genetic divergence between two sequences, individuals, breeds or species. For a pair of livestock breeds, genetic distance provides a relative estimate of the time that has passed since the two breeds existed as part of a single, panmictic population. Divergence between the two breeds over time is measured through changes that have occurred through allelic substitution, resulting in different allelic frequencies among breeds.

Many methods for estimating genetic distance exist. One that is considered particularly appropriate to account for short-term genetic differences, such as those that arise during breed formation, is that proposed by Reynolds *et al.* (1983).

$$\text{Reynold's genetic distance} = \frac{1}{2} \cdot \frac{\sum_k (p_{xk} - p_{yk})^2}{\sum_j \left(1 - \sum_k p_{xk} p_{yk}\right)} \quad \text{(Equation 3)}$$

where, for j different loci and different alleles for each locus and two breeds *x* and *y*, p_{xk} and p_{yk} are the frequencies of allele k in breeds x and y. Various software are available free of charge for estimating genetic distances from genetic-marker data, including TFPGA (http://www.marksgeneticsoftware.net/tfpga.htm – Miller, 1997) and PHYLIP (http://phylip.com – Felsenstein, 2005).

Box 19

The use of genetic markers for calculating kinships among breeds

The kinship or the "coefficient of kinship" (also known as coancestry) between two individuals is defined as the probability that single alleles drawn from the same locus of each of the two individuals are identical by descent from a common ancestor. Kinship is used as a measure of genetic diversity, and increased kinship indicates decreased genetic diversity. Kinships can be estimated by using pedigrees if the data are sufficiently complete to trace pedigrees back to common ancestors. However, such detailed pedigree data are not available for many breeds, and pedigree data for estimating of kinships across breeds are almost universally absent. Genetic markers can be used, however, to obtain estimates of kinship between individuals and average kinships both within and across breeds.

For a single locus with K different alleles, a simple measure of kinship between two breeds can be calculated using the following equation:

$$\text{Simple kinship} = \sum_{k} p_{xk}p_{yk} \quad \text{(Equation 4)}$$

where p_{xk} and p_{yk} are the frequencies of allele *k* in breeds *x* and *y*, respectively. To obtain a full kinship matrix M, this kinship should be calculated for each locus for all combinations of breeds (including for the case in which breeds *x* and *y* are the same) and averaged across loci. The following example is based on three breeds:

$$M = \begin{bmatrix} m_{11} & m_{12} & m_{13} \\ m_{21} & m_{22} & m_{23} \\ m_{31} & m_{32} & m_{33} \end{bmatrix} \quad \text{(Equation 5)}$$

m_{11} is the average simple kinship across all loci for breed 1 and itself, m_{12} is the average simple kinship between breeds 1 and 2, and so forth.

Note that this method for estimating of kinship is simple and based on some genetic assumptions that will generally not be true in livestock populations. Eding and Meuwissen (2001 and 2003) described methods to account for this additional complexity in estimating kinships. The software Molkin (http://www.ucm.es/info/prodanim/html/JP_Web.htm) can be used to compute average kinships of groups of breeds (Gutierrez *et al.*, 2005).

Action 4: Estimate extinction risk

As noted above, extinction risk is usually the most important factor in the prioritization of breeds for conservation. The prioritization approaches discussed above account for this implicitly by recommending that breeds are prioritized within each risk category and that breeds within the higher-risk category be given greatest priority. The objective methods of prioritization with molecular genetic information imply the use of a numerical estimate of extinction risk.

There are several ways to approach quantitative measurement of extinction risk:

- First, if the National Advisory Committee is satisfied with the assumption that risk is equal within each risk category and does not wish to consider prioritization across categories (i.e., so that all breeds within a given risk category are assumed to have greater conservation value than all breeds from categories of lower risk, regardless of non-risk factors), the objective approach can simply be applied within risk category, and all breeds can be assigned an equal risk of extinction (0.25, for example), regardless of risk category.
- Second, if the committee is willing to assume extinction probability is equal within risk category, but would like to allow for prioritization across risk categories, then reasonable estimates of the probability of extinction can be established for each category, and breeds within the same category can be assigned the same risk value. For example, extinction probabilities of 0.50, 0.25, and 0.10 may be reasonable for Critical, Endangered and Vulnerable categories, respectively.
- Third, a specific extinction probability can be estimated for each breed (i.e. and risk category will not be directly considered). Three general approaches can be used to estimate extinction

probability. The first approach is to identify factors assumed to affect breed extinction and use them as parameters to define endangerment categories to which breeds are assigned (Reist-Marti *et al.*, 2003 – see Box 20). The second approach is to predict the trend in extinction probability over time through mathematical modelling of population dynamics (Bennewitz and Meuwissen, 2005b). The third approach is to use loss of genetic variation through time as a proxy for extinction (Simon and Buchenauer, 1993). In general, the second and third approaches require historical census and pedigree data, respectively, which may limit or preclude their application in many countries.

Action 5: Determine non-genetic factors to include in prioritization

As explained earlier in this section, many factors in addition to genetic variability and extinction risk may influence the conservation priority of a breed. Many of the objective methods allow for the consideration of such factors in prioritization. The information collected in Actions 3 and 4 in the preceding subsection should be incorporated into objective approaches for prioritization. However, given that genetic markers will account for diversity, genetic factors such as N_e and distinctiveness should not be included.

Action 6: Prioritize breeds for conservation

Methods have been developed for combining data on molecular genotypes, phenotypic characteristics, risk of extinction, and cultural and social factors to yield a single value for each breed that can serve as a final criterion for prioritization. Examples of such a comprehensive approach to objective prioritization of breeds for conservation have been presented by various authors (e.g. Reist-Marti *et al*., 2003; Tapio *et al*., 2006; Gizaw *et al*., 2008). These procedures involve a reasonably high level of arithmetic and computational complexity and thus require appropriate expertise in genetics and matrix algebra. Expert assistance may be necessary. An adapted version of the approach of Reist-Marti *et al.* (2003) and Gizaw *et al.* (2008) is summarized step-by-step in Box 20.

Task 2. Disseminate information to stakeholders

Regardless of the prioritization procedure, the stakeholders of conservation programmes must be informed about the priority assigned to breeds. Actions equivalent to those described in Task 2 of the preceding subsection are thus required.

Box 20

A step-by-step example of an objective method prioritizing breeds

Step 1: Estimate extinction risk. Following the framework of Reist-Marti *et al.* (2003), extinction risk can be estimated by assigning values to each breed for various criteria related to breed survival. The following example is based on five factors:

1. population size
2. change in population size
3. geographic distribution
4. presence of formal breeding programmes
5. farmer satisfaction

Other criteria can be chosen, and the method can also be applied based on more or fewer than five factors. Potential additional or alternative criteria include the amount of cross-breeding, the ratio of breeding males to females, the presence or absence of marketing programmes and the level of civil unrest within the country or region.

For each criterion, a set of ordered categories should be established, with each successive category being associated with greater risk. A fractional value (i.e. <1.0) should be assigned to each category, with the value increasing in magnitude as risk increases. The size of the maximum value should correspond to the importance of the criterion. The sum of all maximum values should be <1.0. Adopting this approach, the following system could be used:

p is a parameter relating to estimated population size, as follows:

$p = 0.0$ if population size is $\geq$ 10 000 breeding females

p = 0.1 if population size is between 2 001 and 10 000

p = 0.2 if population size is between 1 001 and 2 000

p = 0.3 if population size is between 100 and 1 000

p = 0.4 if population size is < 100

c is a parameter relating to recent change in population size (e.g. previous 10 years), as follows:

c = 0.0 if population is relatively stable or increasing

c = 0.1 if population has decreased by 10 to 20 percent

c = 0.2 if population has decreased by >20 percent

g is a parameter relating to geographical distribution, as follows:

g = 0.0 if the breed is found in locations across the country

g = 0.1 if animals tend to be found one specific area of the country

b is a parameter relating to maintenance of pure-bred animals through formal programmes such as a breeding association or government nucleus, as follows:

b = 0.0 if a programme exists

b = 0.1 if no programme exists

f is a parameter relating to livestock keepers' opinions towards the economic or productive performance of their breed; it is based on a survey and scores are assigned on a 4-point scale where 1 = poor and 4 = excellent:

f = 0.0 if average farmer opinion ≥3

f = 0.1 if average farmer opinion <3

For breed i, extinction risk is equal to the sum of the values for the five parameters:

$$\text{risk}_i = p_i + c_i + g_i + b_i + f_i + 0.05 \text{ (Equation 6).}$$

The sum of all maximum values is 0.90 (0.3 + 0.2 + 0.1 + 0.1 + 0.1), whereas the minimum is zero, so the addition of 0.05 in Equation 6 above is to ensure a result between 0.05 and 0.95.

Step 2: Assign conservation values independent of genetic diversity.

The conservation value (CV) index procedure shown in Equation 1 and demonstrated in Box 11 should be applied to all breeds, except that factors associated with the genetic diversity of the breeds should be removed from the calculation, because these factors will be accounted for by the genetic markers. In order to use the approach of Gizaw *et al.* (2008) the CV resulting from Equation 1 should be standardized to fall within a range between 0.1 and 0.9.

To obtain standardized conservation values (SCV) from non-standardized (CV), the following procedure should be used:

- The breed with the greatest CV (CV_{max}) should be assigned an SCV of 0.9.
- The breed with the smallest CV (CV_{min}) should be assigned an SCV of 0.1.
- For a given breed *i* with CV between CV_{min} and CV_{max}, SCV can be determined by applying the following equation:

$$SCV_i = 0.1 + [0.8 * (CV_i - CV_{min}) / (CV_{max} - CV_{min})] \text{ (Equation 7)}$$

Application of this equation will result in a set of SCV that range between 0.1 and 0.9.

Step 3: Account for the genetic diversity of breeds on the basis of marker data.

To determine the relative importance of each breed with regard to its genetic diversity, the recommended strategy is to apply the approach of Bennewitz and Meuwissen (2005a) to determine the contribution of each breed to a "core set" of breeds that will capture the optimal amount of genetic diversity. The assistance of a statistician or mathematician will likely be necessary for this analysis.

The first step in the procedure is to calculate a matrix (M) of genetic relationships (marker-based kinships) according to alleles shared among the animals genotyped from each breed (see Box 17). Then a vector (**c**) of contributions of each breed to a "core set" of breeds that maximize genetic variability can be obtained by calculating the following matrix calculation:

$$\mathbf{c} = \frac{1}{4}\left[\mathbf{M}^{-1}\mathbf{F} - \frac{\mathbf{1}'_{\mathbf{N}}\mathbf{M}^{-1}\mathbf{F} - 4}{\mathbf{1}'_{\mathbf{N}}\mathbf{M}^{-1}\mathbf{1}_{\mathbf{N}}} \cdot \mathbf{M}^{-1}\mathbf{1}_{\mathbf{N}}\right] \quad \text{(Equation 8)}$$

where M^{-1} is the inverse of the kinship matrix among breeds, F is the diagonal of M (i.e. a vector of within-breed kinships) and $\mathbf{1}_N$ is a vector of ones of length equal to the number of breeds.

This calculation will yield for each breed a contribution parameter between 0.0 and 1.0. This parameter can be denoted D_i for a given breed *i*. Some breeds will likely contribute little diversity or distinctiveness and will have a contribution of zero.

Solving the above equation will require the use of software that performs linear and/or matrix algebra. Multifunctional mathematic and statistical packages can be used for matrix computations, such as the commercial MATLAB®, Mathematica® and "IML" module of SAS® and the freely available R package (http://www.r-project.org). Free and low-cost matrix algebra software are also available on the internet (see http://www.scicomp.uni-erlangen.de/archives/SW/linalg.html). Some web sites, such as http://people.hofstra.edu/Stefan_Waner/RealWorld/matrixalgebra/fancymatrixalg2.html and http://www.picalc.com/matrix-calculator.html perform calculations on line, although solving the above equation with these tools will require performing a series of successive single- or two-matrix operations.

Simple matrix computations can be also performed in Microsoft Excel®.

Step 4. Calculate total utility, which will be the basis for prioritization.

The breeds can then be prioritized based on total utility (U_i) according to the following formula:

$U_i = 4 \times (risk_i \times D_i) + SCV_i$ (Equation 9)

Where:

- U_i is the total utility for breed *i;*
- 4 is a constant value that determines the weight placed on the combination of risk and diversity (D) relative to conservation value (SCV) and can be changed according to national priorities; countries may consider comparing results using different values of this constant;
- $risk_i$ is the risk of extinction for breed *i*, as calculated in Step 1;
- D_i is the contribution of breed *i* to the overall genetic diversity of the collection of breeds, as determined in Step 3; and
- SCV_i is the standardized conservation value of breed *i*, from Step 2.

The breeds should then be ordered according to total utility (U) and the breed with the greatest total utility should be considered to have the greatest priority for conservation, the second greatest should be considered the second most important for conservation, etc.

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IV. CHOOSING THE APPROPRIATE CONSERVATION METHOD FOR EACH BREED

Once the breeds at risk have been identified and they have been prioritized for conservation, the next questions raised are: which conservation method should be used?" Is *ex situ* the appropriate method or is *in situ* conservation the method of choice? Or is a combination of approaches the best solution?

Rationale

As is explained in Section 1, *in situ*, *ex situ in vivo* and cryoconservation have different advantages and disadvantages.

The advantages of *in situ* conservation are that it:

- allows the breed to continue to develop in the context of changes in production conditions and offers greater opportunities for research;
- facilitates breed evolution and adaptation to the environment and gives insight into breed characteristics;
- helps maintain the indigenous knowledge of livestock keepers;
- creates possibilities for sustainable utilization in rural areas;
- allows the breed to maintain its cultural role and its contribution to nature management; and
- can be financially self-sustainable.

The disadvantages of *in situ* conservation are that it:

- exposes the breed to risks associated with catastrophic disasters and disease outbreaks; and
- does not protect (founder) alleles from genetic drift when the population is small (alleles with a low frequency in the population can easily disappear because of low numbers of breeding animals).

The advantages of *ex situ in vivo* conservation are that it:

- offers insurance against changes in production conditions and offers opportunities for research (but these advantages are much less marked than in the case of in situ conservation);
- allows for strict control of selection and mating decisions; and
- offers an opportunity to regenerate a breed quickly from the limited number of females available (with ex situ conserved semen) without applying a cross-breeding strategy.

The disadvantages of *ex situ in vivo* conservation are that it:

- inhibits breed evolution and adaptation to the contemporary production environment;
- contributes only minimally to objectives related to the sustainable utilization of rural areas;
- does not safeguard the breed against disasters and diseases;
- does not protect (founder) alleles from genetic drift; and
- can be costly in the long term, especially if the breed's productivity is low.

The advantages of cryoconservation (FAO, 2012) are that it:

- safeguards the flexibility of the genetic system;
- protects the genetic information of a breed against catastrophic events such as disasters and disease outbreaks;
- protects (founder) alleles from genetic drift (founder animals that are no longer in the recent generations of the pedigrees of living animals can be re-used for breeding); and
- requires relatively little cost for the maintenance of stored germplasm.

The disadvantages of cryoconservation are that it:

- inhibits breed evolution and adaptation to the environment;
- does not contribute to objectives related to sustainable utilization of rural areas; and
- implementation requires particular technical skills and the costs of establishing a cryoconservation programme can be high.

Objective: To choose the appropriate conservation strategy.

Inputs:

1. awareness of the advantages and disadvantages of the various conservation options available for the species and breeds to be conserved; and
2. national resources available for use in management of animal genetic resources, including infrastructure, facilities, financing, technical capacity and stakeholders.

Output:

- decisions on the conservation methods to be applied for the different species and breeds.

Task 1. Assess the applicability of the various conservation methods in your country

Some conservation methods (cryoconservation in particular) will require special equipment and expertise. Lack of these resources will limit the options available. For example, liquid nitrogen can be a limiting resource for cryoconservation in many countries. Techniques for cryoconservation of germplasm also differ in their practicality across species and according to the type of germplasm to be conserved. Capacity to collect and freeze semen is available in many countries, whereas cryopreservation of pig embryos requires a high level of technical capacity. *Ex situ in vivo* conservation requires access to animal housing facilities and possibly land for grazing or crop production. An inventory of stakeholders and the available expertise, technology and facilities should be taken. All types of conservation require a long-term investment by stakeholders if they are to be successful. Commitment by stakeholders to cooperate with the government and with other stakeholders should be secured before embarking on a programme for which such cooperation will be fundamental.

Task 2. Match breeds to the most appropriate conservation methods

1. Identify the conservation objectives relevant for each breed.

For each breed, consider the question: why is this breed on the priority list for conservation? The answer may influence the choice of conservation method. For example, if the main reason is the breed’s contribution to the future genetic diversity of the species and to the genetic flexibility, then cryoconservation is the primary method of choice. If the main reason is to ensure the continuation of the breed’s present functions in rural areas, then *in situ* conservation is the preferable method.

Action 2. Rank potential conservation methods according to their efficacy

Not all conservation methods will have the same efficacy with respect to the conservation objective. To accommodate cross-breeding (e.g. to introgress some unique alleles), *ex situ in vivo* conservation is very efficient. A relatively small number of pure-bred animals are maintained at a central facility, while the breed’s genes are transmitted more widely in the commercial population. If a breed is to be cryoconserved for the purposes of regeneration at a later date, then collection and storage of the breed’s germplasm in the form of semen will, in most species, be less expensive than the collection and storage of embryos. However, in the long term, breed regeneration using semen will be more time-consuming than regeneration using embryos, because in the former case, several generations of backcrossing are needed in order to obtain the conserved breed in a nearly pure state. When a breed is conserved *in situ*, farmers’ enthusiasm for keeping the breed (and thus the success of the programme) will depend strongly on the breed’s productivity and market prices for its products. Improving these aspects will likely increase efficacy of *in situ* conservation (see Sections 7 and 8).

Action 3. Consider the possible pitfalls and risk of failure of each conservation method and discard approaches with unacceptably high risk

When a breed is conserved *in situ,* risk factors include:

- disasters and infectious diseases, which may destroy the population, especially if the breed is concentrated within a small geographical area;
- disconnection between the management and the operation of a conservation programme; farmers have the right to operate their farms according to their own prerogatives and may even decide to abandon the breed if maintaining it is not financially attractive;
- genetic bottlenecks and high relationships between animals; small populations are at greater risk of inbreeding and loss of alleles by random drift if the population is not maintained correctly; and

- changes in government programmes; when a breed is used for purposes such as landscape management (see Section 8), subsidies may contribute a substantial amount of the breeders' income, and termination of the subsidy may induce breeders to forsake the conservation of the breed.

When a breed is conserved *ex situ in vivo,* risk factors include the following:

- high relationships between animals may cause inbreeding and loss of alleles by random drift, leading to decreased genetic variability, and perhaps poor fertility, fecundity and viability;
- opportunities for improving the population through a breeding programme are limited, so farmers participating in the conservation scheme often have to be subsidized; if the subsidy stops, the risk for loss of the breed increases; and
- populations conserved *in vivo* on government farms are vulnerable to changes in the financial priorities of the central government or the respective ministry.

When a breed is cryoconserved risk factors include the following:

- material for cryoconservation (gametes, embryos) must usually meet high sanitary requirements and animal disease may disturb or inhibit the collection of this material;
- freezing, maintenance and thawing of frozen material require special skills and reliable equipment and infrastructure; lack of plans to maintain these supporting resources will put the stored germplasm at risk; and
- electrical blackouts and ruptures of storage vessels can result in loss of viability in the stored materials.

Action 4. Rank techniques for costs

Once a decision has been taken as to which conservation methods have an acceptable level of risk, the costs of implementing these methods should be calculated. In the case of cryoconservation, the major cost consists of two parts: first, the collection and freezing of the material; and second, the use of the material to meet the conservation objective (e.g. introgression of alleles or regeneration of the breed). The maintenance costs of an animal gene bank are relatively low. The costs of *in situ* conservation may consist of subsidies provided to the keepers of the target breeds and the costs of realizing a breeding programme with special emphasis on the maintenance of the genetic variation. As noted above, many of these costs will recur for many years, and this must be accounted for.

Action 5. Choose the conservation method

Finally, the rankings for efficacy, risk of failure and costs should be considered together. The weight given to each factor will depend on the country's priorities and strategic preferences and the availability of resources, capacities and institutions. When artificial reproduction methods are well developed and widely applied, cryoconservation may be preferred. When only natural mating can be used to maintain the breed, *in situ* conservation is the first choice.

Task 3. Apply the chosen methods to reach the conservation objectives

The remainder of these guidelines provides advice on establishing and operating *in vivo* conservation programmes. For cryoconservation, see *Cryoconservation of animal genetic resources* (FAO, 2012).

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V. ORGANIZING THE INSTITUTIONS FOR *IN VIVO* CONSERVATION

The context in which an *in vivo* conservation programme is undertaken will vary greatly from country to country and from one species to another. Nevertheless, there are aspects that will be common among all programmes. Among the most important of these commonalities is the need for organization and for a plan for the sustainability of the programme. Organization is critical, because in most cases, many stakeholders will be involved in the programme. Although these stakeholders will have objectives of their own, they should all share the common goal of maintaining the breed in sufficient numbers to avoid its extinction or genetic erosion.

A wide array of stakeholders can contribute to breed conservation. For any individual breed, some types of stakeholders will be more important others, but the involvement of a range of stakeholders is usually critical to the long-term success of a conservation programme. Common stakeholders in the management of animal genetic resources include breeders (farmers and pastoralists), owners (farmers and pastoralists), users (e.g. of draught animals and breeding bulls), government institutions, breeders' associations, breeding companies, research organizations, NGOs and animal genetic resource societies, consumers of livestock products and marketers (Oldenbroek, 2007; EURECA, 2010).

Breeders usually own a significant proportion of the genetic resource, and are the most essential stakeholders. Most of the breeders will also be producers and they are of primary importance if the goal is to maintain the breed without economic subsidies (EURECA, 2010). "Buy in" by breeders is an absolutely essential component of any *in vivo* conservation programme. Success depends on the breeders having an understanding of and commitment to the conservation of pure-bred, viable populations. Successful conservation efforts generally involve multiple owners, working together for the survival of the breed. The pattern of ownership of animal genetic resources is distinct in important ways from that of plant genetic resources.

Breeders' associations contribute in several ways to the conservation of animal genetic resources, including through participation in and communication with the National Advisory Committee (FAO, 2009 – see Section 1), serving as a source of information on the breed and its roles, product development and promotion, marketing and providing technical support for breeders. Associations manage herdbooks and performance recording and are centres of organization and support. They may, however, be a biased sample of owners, with a disproportionate share of larger herds and of herds with high levels of management and innovation.

Stakeholders that are not private owners can have important roles in conservation, but it is always important for them to work closely with private breeders. Generally, the non-private institutions (governmental bodies and NGOs) should support private efforts and the involvement of private breeders.

Especially in several Asian, South American and African countries, governmental breeding farms are important reservoirs of animal genetic resources, and make breeding animals and semen available to private farmers in situations where they would otherwise be unable to access selected breeding material. Such institutions also contribute to breed characterization and other research. They have a very real responsibility to ensure that their programmes lead both to short-term and long-term benefits for farmers. Where appropriate, such institutions should be strengthened or established.

Governmental organizations can be effective in promoting and rewarding cultural and social benefits provided by breeds. European countries increasingly recognize the value of locally adapted breeds of grazing animals in the management of natural areas and the maintenance of historically and culturally significant countryside. These values are difficult to recognize and reward via the private sector alone. Many hobbyists keep and breed locally adapted breeds as a leisure activity. These non-production activities offer a great opportunity for breed conservation, but need institutional support to ensure proper conservation and management of genetic diversity.

Educational (university) and private research institutes also play roles in conserving breeds. These organizations can be especially important in providing the technical support needed to ensure that the genetic viability of small populations is maintained through proper attention to population structure and mating strategies. Private breeding companies likewise manage important breed populations in various species, although these resources may not be widely available for distribution. Many breeds or lines no longer developed for immediate commercial goals are set aside without long-term conservation plans.

This section gives the rationale, the tasks and the actions required by the different stakeholders with special emphasis for the breeding organizations.

Involving livestock keepers in community-based *in situ* conservation

Rationale

The conservation of animal genetic resources under sustainable management by farmers is one of the most effective and practical ways of conserving these resources with a minimum of inputs. This approach does not involve large financial expense and is feasible under field conditions. However, major attention should be paid to the economics of the targeted breeds. Breed conservation with the participation of farmers will be successful only if it is economically viable and if sufficient technical support is provided. Hence conservation projects aimed at the improvement and utilization of breeds should define their objectives clearly, especially with respect to the characteristics for which the breed has traditionally been valued. Conservation efforts should begin with characterization and evaluation of the breeds and identification of characteristics of economic, social and cultural value specific to each breed. Further advice on organizing such studies is provided in *Phenotypic characterization of animal genetic resources* (FAO, 2012b). A participatory approach, involving the farmers, breeders and other livestock keepers as much as possible is important, both to increase the accuracy of the information upon which the conservation programme will be based and to ensure interest and ownership of the programme on the part of the livestock keepers and thereby increase its sustainability. The livestock keepers and breeders will rarely accept a programme that deviates from their preferences (see Box 21). The role of an outside entity will primarily be to provide the inputs to improve the long-term survival of the target community and to provide technical support. FAO has produced a publication on community-based programmes for management of animal genetic resources that includes a number of practical examples (FAO, 2003a).

Box 21

Conservation of Hallikar cattle in India

The Timbaktu Collective is an NGO working in the Anantpur area in the State of Andhra Pradesh, India. Initially, their activities primarily dealt with improving the land and plant biodiversity in the drought-prone rainfed area. However, in 2005 they decided to expand their activities to cattle production because water availability had recently improved in the area and local farmers had begun cultivation. The Timbaktu team took the farmers to dairy centres in nearby towns and showed them the high milk producing Holstein-Friesian crosses. The farmers were not impressed, however. They opined that such animals would not suit the village production environment, and expressed their preference for the local breed – Hallikar – which used to be common in the area. The farmers knew that their main need was for draught power, with milk production as a secondary bonus. This opinion surprised the Timbaktu management, which had expected the farmers to want the higher-producing cross-breeds, but they accepted the farmers’ opinion. In 2007 and 2008, about 950 Hallikar cattle were purchased from the adjoining state and re-introduced to the Anantpur area. Now, five years later, the whole experiment can be deemed a success. All animals are used for draught purposes in crop cultivation and the cows produce 1 to 2 kg of milk per day, which meets the needs and expectations of the farmers. The number of Hallikar cattle has increased significantly in the village since their reintroduction.

Provided by Devinder K. Sadana.

Objective: To design, with livestock keepers, an *in situ* conservation programme that they will implement with the assistance of outside agencies; this ensures maintenance of the respective animal genetic resource because it promotes the autonomy of the community and the sustainability of the livelihoods of community members.

Inputs:

1. A breed at risk of extinction, but deemed of high value for conservation;
2. Basic knowledge of the location where the breed is raised and the lifestyle of the respective community of livestock keepers, their production system, their animals and their facilities;
3. An indication from the livestock keepers that they are interested in breeding and conservation; and
4. Earmarked technical and financial resources.

Output:

- A sustainable *in situ* conservation programme based on the active participation of livestock keepers.

Task 1. Identify the specific location and collaborators for conservation activities

Action 1. Pinpoint and study the geographic area where the breed is kept

Using the background information on the targeted breed and results from breed surveys (FAO, 2011b), the core of the breed's home region should be identified.

Action 2. Choose the communities with which conservation work will be undertaken

Several villages distributed in different parts of the breed's home region should be identified as candidates for participation in the conservation programme. The precise number of villages will depend on the population size of the breed to be conserved, its distribution across the area and across farms, and the resources available. If knowledge about the extent of livestock keepers' interest in participating in a conservation programme is already available, this may facilitate the selection process. Clearly, a programme is more likely to be successful if livestock keepers and other stakeholders are keen to participate The livestock keepers who own the animals that are truest to the ideal type targeted for conservation (e.g. free from cross-breeding or having superior phenotypic traits) should be encouraged to participate.

Task 2. Undertake a detailed participatory study of the targeted communities

Once the candidate communities have been chosen, the next step is to engage with them. In most cases, completing the activities described in Sections 1 to 3 will only have yielded the information needed to identify which breeds should be conserved and why. Much more information will be needed to develop a sustainable community-based programme for the conservation of these breeds. Community-based programmes will likely have to identify how breed conservation measures can complement the broader objective of improving the likelihoods of the community members. This will require multidisciplinary studies based on participatory approaches. Properly implemented, such approaches will not only offer an effective means of gathering information from the community, but also help to establish lines of communication that will facilitate collaboration during the subsequent implementation of the programme (Franzel and Crawford, 1987). General advice on participatory approaches in agriculture and rural development can be found in FAO (2003b). Their role in surveying and monitoring animal genetic resources is introduced in the respective guidelines in this series (FAO, 2011b). Specific examples of their use in animal genetic resource management include the work of Duguma *et al.* (2010).

Action 1. Undertake preparatory work including making initial contact with community leaders and agencies that may act as a liaison with the community

A top-down approach in which a study team simply visits the community unannounced and undertakes the study will often not work well and is not recommended. A step-by-step process of engagement that informs the members of the community about the intentions and goals of conservation work and any complementary activities will usually be necessary. The first contact should be with the leaders of the village or with prominent farmers (also referred to in this context as "role model breeders" – see Section 8). It may be helpful to work with the assistance of an organization that already has experience working with the community, such as an NGO or government extension service.

Action 2. Enlist the research team and perform the studies

At the community level, the problem of conserving animal genetic resources will likely be multi-faceted, due to the large number of possible threats to breed sustainability (see Section 1). Thus the research team will need to address not only genetic factors, but also economic and social factors. It should therefore be multidisciplinary.

The study should collect information on a wide number of topics, including standard production and breeding practices, perceptions of the breeders on the strengths and weaknesses of the targeted animal genetic resource, outputs obtained from the animals and their use or marketing, sources of agricultural inputs and marketing opportunities. Constraints affecting the production system should be identified. Much of this information should already be available if the activities described in Sections 1 to 3 have been undertaken. However, details particular to the communities targeted by the conservation programme will need to be obtained. In particular, the specific threats to the sustainability of the targeted breed should be identified in detail. Finally, an assessment of the willingness and capacity of community members to participate in conservation activities should be included.

Action 3. Evaluate the results

The results of the participatory surveys should be evaluated in a comprehensive manner in order to determine the most practical and efficient means of conserving the targeted animal genetic resource. A follow-up meeting with the community members is recommended.

Task 3. Facilitate the implementation of an *in situ* conservation programme based on the participation of the community

Figure 2 shows the possible interactions among stakeholders in a community-based programme for management and *in vivo* conservation of animal genetic resources. The ellipses indicate the major stakeholders (groups of livestock-keeping communities, the government, and breeders’ associations and other NGOs). Rectangular text boxes indicate the “goods” exchanged by each pair of stakeholders, with solid arrows showing the flow of these goods. Other stakeholders that may be involved in a community-based conservation programme include the private sector (marketing of products and provision of inputs) and the general public (consumption of products). Box 22 explains how farmers, the government and a breeders’ association have worked together to conserve of an important breed in Argentina.

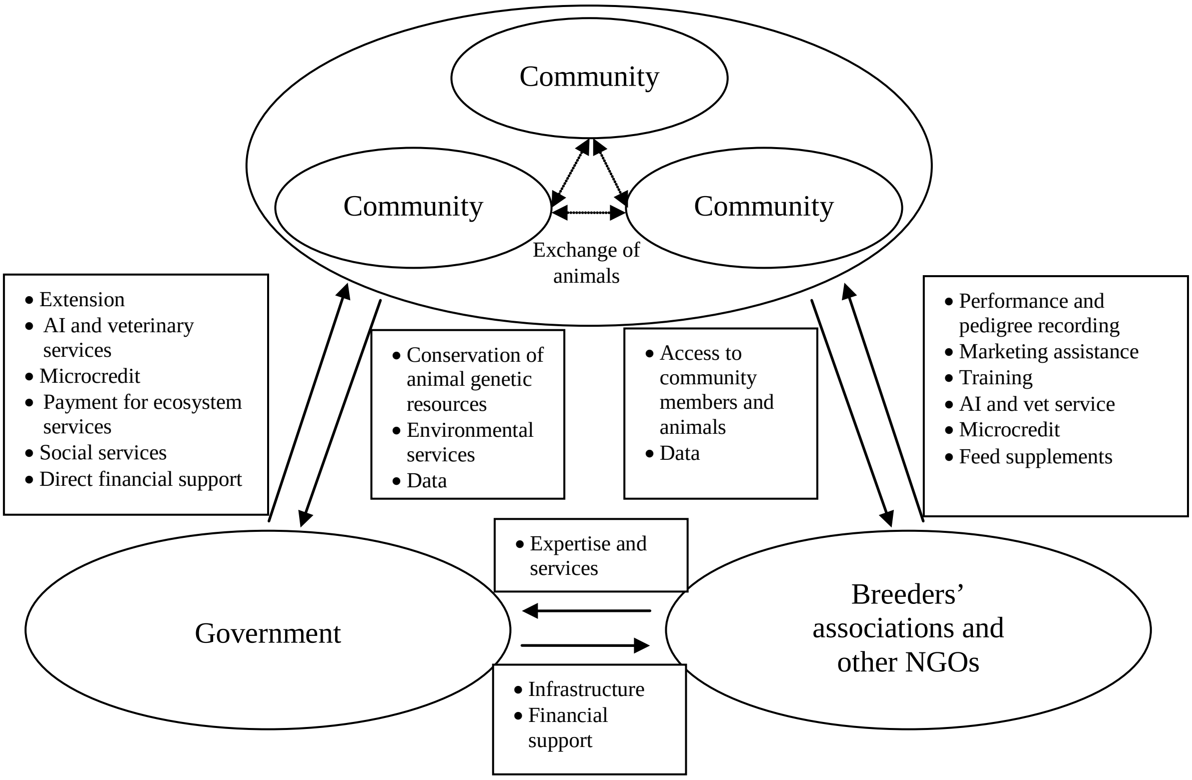
Box 22

Public-private partnerships for conservation of Criollo Argentino cattle

The Criollo Argentino is a local breed of cattle that evolved from a mix of the cattle breeds brought by the Spaniards to Argentina in the fifteenth century. Over time, the Criollo Argentino has co-evolved with the local environment and its adaptation to a variety of conditions is remarkable. However, the introduction of British breeds at the end of the nineteenth century confined the Criollo to the marginal regions of the country. This led to a reduction in the size of the breed’s population and drove it almost to extinction. In the 1960s, the National Institute of Agricultural Technology (INTA), a national research-extension organization, took on the task of rescuing and conserving the Criollo Argentino and promoted the creation of a breeders’ association, the Asociación Argentina de Criadores de Ganado Bovino Criollo, which in a joint effort with INTA established a programme for the promotion of the breed. Subsequently, INTA and several universities have taken responsibility for conservation and characterization activities. In particular, INTA maintains a network of 12 active animal germplasm banks, five of which are devoted to the Criollo Argentino. The primary method of choice for the banks is *in vivo* conservation, although one bank also employs cryoconservation. The institutional herds vary in size from 50 to 150 cows and are located in different agro-ecological regions across the country. INTA is planning to cooperate with the breeders’ association in genetic evaluation and characterization. The breeders’ association assists breeders in promotion and marketing.

Provided by Carlos Mezzadra.

Figure 2. Interactions among the possible stakeholders in a community-based breeding programme



As Figure 2 indicates, sometimes outside investment and assistance from the government or an NGO may be necessary in order to implement activities that help to ensure the sustainability of the targeted breed, especially in the initial phases of the programme. For example, construction of abattoirs or milk collection and processing facilities may increase livestock keepers' access to markets and thereby increase their incomes and the economic sustainability their livestock-keeping activities. Outside assistance may be necessary to promote such opportunities among potential investors. Livestock keepers may also be willing to invest in technologies that improve productivity, such as AI, veterinary services or supplemental feeding, or in training to improve marketing (e.g. in cheese or yoghurt production), but may not have access to credit services through which to obtain investment funds. Provision of such services may be a way of indirectly supporting *in vivo* conservation.

Action 1. Assist farmers in organizing a breeders' association

The animals belonging to breed population targeted for conservation will almost always be owned by a number of different people. Individual owners generally have the right to manage their animals as they see fit. However, breeders share some interests and some goals can be accomplished more easily as a group than by individuals. Therefore, formally organizing owners into a breeders' association can yield benefits both for the individual owners and for the sustainability of the breed (see Box 23 for an example of the many possible benefits of a breeders' association). It also creates a single entity with which the government or an NGO can work, which is likely to increase the efficiency of the conservation efforts. For long-term sustainability, it is imperative that breeders receive tangible benefits from being members of the association and that they drive the process. Detailed advice on establishing and monitoring breeders' associations is presented later in this section.

Box 23

The Banni Breeders' Association – a case study from India

The Banni Grassland in the Kachchh (Kutch) District of Gujarat in western India is the home of the Banni buffalo. The breed was developed by local pastoral communities, who employed their indigenous knowledge of breeding and the local ecosystem to create an animal genetic resource that is perfectly adapted to its unique environment. The Banni Grassland was once considered to be the finest and largest grassland in India, covering 2 400 km^2. However, in the mid-1970s the Banni Grassland started to suffer degradation. First, salinity of the soil increased as rivers flowing through the grassland were dammed, restricting water flow and inhibiting the ability of the waters to flush salts away from the soil surface. Second, the alien plant *Prosopis julifera* was introduced in the area and became a highly invasive species.

In 2008, with support from Sahjeevan, an NGO working on environmental conservation and revival of traditional livelihoods, the pastoral communities of the Banni formed an organization called Banni Pashu Uchherak Maldhari Sangathan (Banni Breeders' Association). The objectives of the association were to revive the livestock economy of the region, register the Banni Buffalo as a recognized breed, conserve the Banni Grassland and protect their customary grazing rights.

The breeders' association, in collaboration with State Department of Animal Husbandry, Government of Gujarat, the NGO Sahjeevan and Sardarkrushinagar Dantiwada Agricultural University, carried out data recording, prepared a description of the breed, and sent a registration application to the National Bureau of Animal Genetic Resources, the body responsible for recognition of breeds in India. In 2010, the Banni Buffalo was successfully registered as the eleventh Buffalo breed of India. This was the first case in India in which a community that developed and conserved a breed was able to gain official recognition for what they have been doing for centuries.

In addition to preparing for the breed registration, in 2008, the breeders' association started organizing an animal fair called “Banni Pashu Mela”, not only to promote the Banni breed, and its high profitability in the grassland ecosystem, but also to promote their unique pastoral way of life.

The association also successfully negotiated with two dairy processors to start an organized milk collection system in the Banni region, which now collects more than 100 000 litres of milk every day. More dairies are now showing willingness to start operations in the Banni region.

With more than 900 members from all 19 village governments in the Banni Grassland, the Banni Breeders' Association is currently developing a participatory grassland conservation plan that draws on their traditional knowledge of grazing resources and understanding of sustainable resource utilization. The plan is designed to counter a standard fencing-based plan that was prepared by the governmental Forest Department without consulting the pastoral communities, despite the fact that these communities have been present in the Banni for more than 500 years and that they generate in excess of one billion rupees per year through the livestock production.

Provided by Devinder K. Sadana.

Action 2. Work with the community to establish a breeding programme

The community may be willing to work with the government or other stakeholders to develop and adopt a breeding programme to improve the productivity and maintenance of genetic variability (see Section 7), but may require assistance in organizational and technical matters. Outside assistance can facilitate the adoption of breeding goals and the development, implementation and maintenance of breeding programmes. Box 24 summarizes the establishment of a community-based breeding programme for sheep in Ethiopia, where a government research institute provided technical assistance in developing a breeding programme.

Box 24

A community-based breeding programme in Menz, Ethiopia

Menz is an area of north-central Ethiopia where sheep farming is a primary economic activity. In an effort to improve the livelihoods of the local people, the national government targeted improvement of sheep productivity, including the adoption of community-based breeding programmes. The local sheep had several positive characteristics, including adaptation to the local feed sources, parasite resistance and tasty meat, but opportunities for genetic improvement were limited by a lack of organization among the farmers, poor knowledge of breeding programmes, the absence of data recording and negative selection through the slaughter of the fastest-growing males.

The project started in 20007 and was undertaken by researchers at the Debre Berhan Agricultural Research Center. A planning workshop determined the precise project sites. A questionnaire was used to gather information about ongoing breeding and husbandry practices and to characterize the breed and the production system. Follow-up studies addressed selection procedures and marketing and social aspects. In May 2009, the researchers proposed a new selection programme, based on selection of the top 10 percent of rams for live weight, lamb survival and fleece weight and the use of the selected rams for up to two years. The farmers agreed to the new system and the system, which was launched in June 2009 by recording data on the animals in the various flocks. Training was provided to the farmers and each was provided with a record book. Since then, data have been recorded on all newly born animals. Selection of rams is done twice a year – in February and June. Rams are then distributed to breeding groups consisting of ewes managed together in communal grazing (eight rams per group). A farmer is nominated as the leader of each group and is responsible for rotating rams among the ewes and reporting on progress and any problems.

In addition to the breeding programme, several complementary initiatives were launched. To help generate interest among participants, at the time of selection, prizes are awarded to the owners of the best lambs in the programme and to the best farmers. In addition, technical assistance is provided on animal nutrition, diet formulation and disease control. Individual farmers are also selected and trained to provide basic community veterinary services. A cooperative is being developed for marketing and ongoing management of breeding activities.

The project is still in its initial stages and challenges remain, but many positive results are visible. Because of their role in designing the programme, farmers are keenly interested in the project and regard it as a way to improve their livelihoods.

Source: Getachew and Gizaw (2010).

Working together as a breeders' association, the community may, for example, identify the target traits in a selection objective within the breed. This is generally considered the most important issue in the genetic improvement of animals in a conservation programme. The objective should be clear enough to exploit the genetic potential existing in the population to the maximum extent possible. Genetic improvement will gradually increase the average genetic merit of the breed with respect to the chosen objective. The community may then participate in creating and promoting a brand for products derived from the breed. Such measures will strengthen the economic value of the animals and may ultimately lead to the breed becoming self-sustainable. In such cases, external support from the government can gradually be withdrawn and the breeders' association can take over the running of the programme. Details on establishing selection objectives are provided in the guidelines *Breeding strategies for sustainable management of animal genetic resources* in this series (FAO, 2010).

A breeders' association can take responsibility for aspects of operating a breeding programme, such as animal identification, performance recording and genetic evaluation, with or without financial and technical assistance from the government. Capacity to undertake such activities is one of the major advantages of having a breeders' association, because individual breeders will typically lack the time and technical capacity to perform them and because of the efficiency of having these activities performed by a central agency. Collaboration among different breeders' associations may further increase the efficiency of these activities, as may the establishment of associations for transboundary breeds that are present in more than one country.

Action 3. Establish a nucleus herd for management of genetic improvement

A nucleus herd of up to several hundred superior females and sufficient numbers of superior fertile males (about 1 for every 10 to 20 females) in the breed’s local region may be a key tool in managing the population. Within a nucleus herd, selection and mating decisions can be controlled more strictly, allowing the implementation of more complex and effective management approaches (see Sections 6 and 7). An “open” nucleus design, in which relationships are established between private livestock keepers and institutional herds, with gene flow both directions and ongoing identification of superior animals in both populations, may be particularly attractive for local breeders. They gain a larger ownership stake in the programme and can benefit both by obtaining superior germplasm from the nucleus and by having the opportunity to sell their best animals to the nucleus at a premium price. Furthermore, when managed correctly, open nucleus systems tend to reduce inbreeding relative to closed schemes. However, establishing and operating a nucleus herd requires significant technical and financial resources. Determining cost and benefits will be a critical first step in such an endeavour and support from the government or an NGO or from commercial organizations may be necessary.

Action 4. Provide incentives, including capacity building, and complementary institutions

Providing specific incentives or other assistance may be a fundamental step in directing a breed at risk back on a sustainable course. For example, livestock keepers may be abandoning a given breed, or even animal production in general, because they cannot market the products at a price or quantity high enough to ensure a satisfactory livelihood. Assistance in improving productivity or in establishing a consistent market for the breed’s products may increase livestock keepers’ income, and thereby provide support to the livelihoods of the community and, help ensure the survival of the threatened breed. Livestock keepers have an exceptional amount of indigenous knowledge and may thus already be sufficiently skilled in managing their breed. However, the breed may be threatened by factors outside the control of the livestock keepers or by insufficiency in a particular capacity that can be overcome through training. Alternatively, livestock keepers may actually be providing a service that can be regarded as a common good that is not being properly valued by the market (e.g. maintenance of genetic diversity or ecosystem conservation). In such cases, providing payment for the services provided may be considered, as long as such payments are not market-distorting and respect international trade agreements. These options are discussed in more detail in Section 8.

The loss of a particular breed may also be related to wider-scale rural development problems that are causing breeders (and their children) to give up livestock production entirely and seek other livelihood opportunities. If this is the case, incentives such as those discussed above may not be sufficient. It is important to consider such wider-scale threats and how they might be addressed. Perhaps it may be necessary to establish non-agricultural services, such as improved educational opportunities for children, improved health care and local off-farm employment opportunities to help sustain the community in general.

Establishing a breeders’ association

Rationale

Breeders’ associations (also known as “breed societies” or “breed associations”) can be essential to the long-term success of conserving animal genetic resources, by playing many roles, including as serving as an effective monitor for threats to the breed. Most standardized and international transboundary breeds are well-served by breeders’ associations that have clearly-documented procedures and functions. In most cases the functions performed by the breed associations of standardized breeds have been assumed as a universal model for other classes of breeds. Many local breeds have less formal organization but have a very high priority for conservation. Accommodating the needs of such breeds will often mean that some details of the model for standardized breeds will often have to be adapted.

Organizing breeders presents numerous challenges. If herds have been isolated for long periods of time, each breeder is very likely to consider his or her own herd to be the only typical one, which may lead to fragmentation and difficulty in establishing common goals (see Box 25). The leading traditional breeders are often elderly, and may not have heirs interested in continuing to keep the family livestock. This threatens breed viability, as it can easily lead to the loss of the culture surrounding the breed. Getting beyond individual pride and self-interest is challenging, but is crucial for long-term success. Traditional breeders have assumptions and beliefs that vary, and that strongly shaped breed development and maintenance. Therefore, they may be reluctant to adopt substantial changes, even if they may seem to an outsider as necessary for the breed's future survival.

Box 25

Colonial Spanish Horse breeders' associations in the United States of America

Breeders of Colonial Spanish horses in the United States of America conserve a very fragmented and dispersed breed based on non-standardized populations and feral animals. The result of strong local attachment has left many breeders with a skewed appreciation of the overall breed, and an intense focus on the local resource. The result is 20 different breeders' associations for this breed, which numbers at most 3 000 animals. Fragmentation makes long-term management and survival precarious. As a reaction to this, a few associations with an inclusive philosophy now also promote the breed. The fragmentation among the breeders is the result of strongly held opinions on breed purity, but at some point this leads only to a smaller and smaller gene pool that cannot avoid high levels of inbreeding in the long term.

Provided by Phil Sponenberg.

Breeders' associations are generally democratic institutions. Members have to meet requirements for active membership and participation and to agree to a set of rules. They are able to participate in shared decision-making, are eligible to register livestock and can benefit from recording schemes and promotional efforts.

Objective: To create a well-functioning breeders' association.

Inputs:

1. Genetic and demographic data on the breed;
2. List of breeders who keep animals of the breed;
3. Some knowledge of the history of the breed and its present functions; and
4. Knowledge of the goals of the breeders and their history of cooperation.

Output:

- A well-functioning breeding organization with a description of:
  - requirements for membership
  - registry protocols
  - rules and by-laws
  - dues and fees for members
  - communication methods for education and training
  - mechanisms for conflict prevention and resolution
- Communication between the breeders' association and national entities responsible for management of animal genetic resources.

Task 1. Assess the willingness of members of the community to establish a breeders' association

Action 1. Discuss the possibility of a breeders' association during the initial participatory studies

The success of a breeders' association will largely depend upon the number of breeders participating and their willingness and enthusiasm. The level of interest should be evaluated as soon as possible, so as to avoid futile investment of time establishing an organization that is not sustainable. The community members should be made aware of the benefits of breeders' associations and of the inputs required.

Action 2. Identify specific members of the community that may have a particular interest in joining a breeders' association and serving in leadership roles

A breeders’ association is a NGO and will only be successful if its leaders are well-respected in the community and committed to the association and to maintaining the breed. To ensure that breeders’ associations have sufficient grassroots support to ensure sustainability, some countries only provide governmental assistance after the associations are established and viable (see Box 26).

Box 26

A two-step approach to supporting breeders’ associations in Latin America

Some Latin American countries, such as Brazil and Colombia, have an interesting two-step approach to creating breeders’ associations. At the beginning, a group of breeders of a specific breed get together to create an organization that is considered a promotional association. The breeders then develop a set of breed descriptors and the by-laws, and invite new members to join the association to try to increase its membership. Once these phases are completed, the Ministry of Agriculture is contacted to examine the documents of the promotional association and to determine whether the population of animals referred to by the association warrants being considered as a distinct breed and whether the number of breeders is sufficient (e.g. in Colombia, there is a minimum requirement of ten breeders). If the Ministry of Agriculture considers that the promotional association adheres to all these requirements, it can be recognized, and becomes an official breeders’ association, with a mandate to operate the genealogical registration programme for the animals of that specific breed. Once the association is officially recognized, it is obliged to send an annual report of activities to the Ministry of Agriculture with copies of all registrations made during the year. The Ministry of Agriculture is then responsible for auditing the official associations. This procedure has proven to be successful and serves as an example that can be followed by countries that do not have a procedure for creating breeders’ associations.

Provided by German Martinez Correal and Arthur Mariante.

In some cases, the interest and dedication of a single person may be nearly sufficient to drive a breed’s conservation and development (see Box 27). However, even if a single individual is willing to sustain a breed, he or she may gladly accept outside assistance. This outside assistance may also decrease risks associated with having a single major breeder and stakeholder.

Box 27

Conservation of Tharparkar cattle in India

Conservation of a breed can be accomplished by the sheer vision, will and dedication of a highly motivated individual, as exemplified by the work undertaken by Mr Magraj Jain of Rajasthan in India. It was during 1990s that he recognized that the productivity of the livestock in the region was deteriorating, and that the primary reason for this was the diminishing numbers of the local Tharparkar breed of cattle, which by the late 1990s was at risk of extinction. Through his NGO, named SURE (Society to Uplift Rural Economy, Barmer, Rajasthan) Mr Jain undertook the task of raising young pure-bred Tharparkar bulls and distributed them one-by-one in 34 villages. Villages were selected based on discussions with stakeholders and the interest expressed by the local people. Each bull was given to a family in the village who agreed to maintain it in exchange for earnings obtained through the use of the bull by other farmers for natural-service mating of their cows. The services were recorded. When the progeny became mature, their milk yield was also recorded. By 2007, more than 2 100 pure Tharparkar cows had been born to these bulls and the project continues to this day.

Provided by Devinder K. Sadana.

Task 2. Develop and implement a process, involving the relevant stakeholders, through which a breeding organization is described and established

Action 1. Determine requirements for membership of the association

Most breeders’ associations have different classes of membership. Full membership in many associations is limited to people that actively own and breed animals. Breeder-members have voting rights, which ensure that control of the breed's future is determined by those most affected by decisions and who contribute to the conservation of the breed.

An important first step is to determine which animals and breeders are to be considered as representative of the traditional type of the breed. This process determines the foundation and forever shapes the descendant breed. The decisions regarding which breeders and animals to include within the breed usually occur simultaneously, because each affects the other. Outside entities, such as governmental organizations or NGOs, can help guide associations through this step. It is best to include animals that are pure-bred to the local population and to avoid any animals with known influence from outside breeds. However, if the number of verified pure-bred animals is too small to obtain a viable breeding population, standards may have to be relaxed somewhat to allow animals that are not pure-bred but have a high proportion of the desired breed to be included in the foundation stock (see Box 28). In this way a larger amount of genetic variation will be available immediately, which is likely to be useful for the future development of the breed.

Box 28

Incorporating non-pure-bred animals into a breed founder population

The concept of resemblance through common hereditary descent is a useful addition to any definition of a breed (see Box 1). Resemblance through common hereditary implies that, ideally, a breed has no exchange of genes with other breeds, i.e. that no introgression of genes from other populations takes place. A rule of thumb in practical breeding is that no more than 12.5 percent of outside (exogenous) genes (i.e. one of the eight great-parents is from another breed) should be accepted within a breed. Following this rule of thumb means that if an animal's proportion of exogenous-breed genes is greater than 12.5 percent, it is considered a member of a different "breed" and not allowed to be a member of a foundation population. Standardized herdbooks usually do not consider individuals with more than 12.5 percent exogenous genes to be pure-bred and most have much stricter rules for this percentage.

Provided by Phil Sponenberg.

In addition to a full regular membership category for active breeders, associations may consider also having other types of membership that may help to expand interest in the breed (and perhaps revenue for the association) but have limited influence over breeding policy. Such additional classes of membership may include associate membership for non-breeders or "junior" membership for non-adults. Members belonging to such categories typically do not vote, but are entitled to all other benefits of membership. In breeds that don't produce widely marketable products, such as many horse breeds, it may be necessary to include non-breeders as full members. In such breeds, non-breeders contribute to the breed through promotion and use, and their voices must be heard in decision-making.

Including new breeders in the association is essential, including breeders that are not members of the cultural group that originally kept the breed. Efforts to include new breeders can sometimes threaten traditional breeders, because some control over the future of the breed is usually surrendered. Expanding the group of breeders involves cultural change that affects how the breed is selected and valued. Managing these tensions is challenging.

Where possible, an association should have special designations for long-term traditional breeders that help to ensure their continued participation. Special allowances for such breeders may include discounted costs in registration procedures or waiving or reducing membership dues.

Action 2. Establish registry protocols

Most associations register animals and validate pedigrees. Procedures must be consistent and uniformly applied. A variety of software programs, each with strengths and weaknesses, are available. The pursuit of complete accuracy comes at an economic cost. For example, DNA validation of pedigrees can provide high accuracy, but is unrealistic both for animals that are of low individual economic value and for animals raised in extensive situations.

The registry function of a breeders' association for a non-standardized breed can often be similar to that for standardized breeds. For breeds raised in extensive production systems, especially in multi-sire herds and for species in which the animals have relatively low individual value (e.g. poultry, goats and sheep) other procedures are needed. One strategy is to register and monitor entire herds or flocks rather than individual animals. It is very important to ensure pure breeding. Procedures and validation must be tailored to fit each individual case, as they must reflect the realities of the local culture and local husbandry practices.

New and expanding breeders' associations must develop methods for including candidate animals in the registered population. Some approaches can be applied on an animal-by-animal basis (see Box 29), whereas others apply to whole herds. Box 30 presents an example of an animal-by-animal procedure and Box 31 gives an example of herd-based registry. In economically developed countries, it is common for new breeders' associations to have a short period in which foundation animals are registered, after which the registry is restricted to animals with registered parents and grandparents. This is a typical strategy for standardized breeds, but works poorly for non-standardized breeds because isolated pockets of pure-bred animals are likely to continue to be discovered for a long time. Procedures for inclusion of newly encountered animals must be developed, and must be applied uniformly and fairly.

Box 29

Incorporating non-registered animals in a herdbook

Inclusion of candidate animals should follow documentation of their origin and type. The history of the population (geography, foundation stock, length of genetic isolation, and the source and frequency of any additions of animals from other breeds) should be evaluated, as should the phenotypes of individual animals. Where possible, DNA analysis should be used to detect introgression from other breeds, but results must be interpreted carefully, as *bona fide* pure-bred animals from a long-isolated pocket of the breed will often have novel DNA variants with respect to the rest of the breed. These animals could be particularly valuable to the breed for their genetic distinctiveness, adding to genetic diversity. If desired, a progeny test can be done to validate animals' ability to reproduce the traditional type. This latter step is less important if DNA validation is possible, but is useful in cases where candidates have novel phenotypic variants (e.g. coat colour, horns). Inclusion of newly discovered animals may also be important for some standardized breeds with long-established herdbooks. For example, registering new animals can be essential to long-term conservation success of breeds with very small population sizes. Newly discovered animals must, however, enter the breed on equal footing with existing animals or their genetic contribution will be diluted out and any potential benefit from their inclusion in the herdbook will be forsaken.

Provided by Phil Sponenberg.

Performance and type classification recording schemes are important in many breeders' associations, especially where breeders want to implement selection programmes. These data are useful for breed improvement schemes, and breeders' associations are the logical place to maintain them.

Box 30

Protocol for addition of non-registered animals in the herdbook of Huacaya alpacas in Peru

Alpacas and llamas are among Peru’s most important animal genetic resources. To help improve their management, the Official Genealogical Registry for Alpacas and Llamas (OGRAL) was created in 1997 and a herdbook was established. One objective of OGRAL is to recognize and record the alpacas that conform to a desired phenotype, based on characteristics of their fleece and conformation, so that these animals can be added to the registry.

A committee composed of representatives of breeders’ associations, research institutions, NGOs and national universities established rules for registering alpacas of the Huacaya breed in a national herdbook. A visual scoring system was established with the following 100-point scale:

Fleece		
Fineness	40	70
Length	10	
Density	10	
Crimp	3	
Uniformity	7	
Conformation		
Head	10	30
Height	10	
Fibre coverage of rear legs	5	
General appearance	5	

Assessments are undertaken by official technicians that have been trained by the Ministry of Agriculture. Alpacas that obtain at least 75 points are allowed to be registered in the OGRAL herdbook Only about 1 percent of the population achieves registration and such animals have high value as breeding stock.

Provided by Gustavo Gutierrez.

Box 31

The protocols of the Coastal South Native Sheep Alliance in the United States of America

The Coastal South Native Sheep Alliance in the United States of America has developed new protocols for dealing with landrace conservation. Organization and rules are minimal, but a commitment to pure-bred breeding is the main objective underpinning the group. The basic rules include:

- Sheep of other breeds are not to be kept on the same property as a Gulf Coast flock recognized by the Alliance. This prevents introgression from other breeds, especially where animals are not individually identified and multi-sire mating systems are used.
- Each flock submits a brief flock history, including original sources and foundation year.
- Additions to the flock are documented by source, date and sex. Ideally, additions only come from other flocks recognized as pure-bred by the Alliance.
- Each flock participant reports census figures annually, including the sources of any additions.
- If breeders maintain different family groups, each is tracked as a separate flock.

These rules protect the genetic integrity of the breed, while allowing it to persist as a traditional local resource. However, they require commitment on the part of the breeders, and even the low level of breed-specific activity involved (documentation of flocks, documentation of additions, annual census) can be enough of a change from tradition to result in non-compliance.

Provided by Phil Sponenberg.

Action 3. Establish by-laws

Election procedures

Well-defined procedures for decision-making can help prevent confusion and controversy. By-laws determine members' eligibility, the mode of voting and the role of members in various sorts of decision. One extreme is a completely democratic form of organization in which members vote on every decision. This is generally limited to small associations. Larger associations usually have officers and/or a board of directors that makes decisions, with periodic elections to renew the board and ensure that it reflects the will of the membership.

It is important to establish election procedures, including the frequency of elections. Such rules encourage participation and develop loyalty and a sense of ownership of the association among the members. Participation of original breeders must be ensured and may require that their status is recognized in some way.

Board of directors

In most associations, the members elect a board of directors, which enacts specific procedures and policies. The number of directors can vary, but to ensure continuity it is best to have staggered terms. For example, if a board has six members with three-year terms, then elections for two of the positions on the board could be held each year. This would allow the two new members to serve with two members that have served for four years and two that have served for two years. This ensures continuity, but also refreshes the leadership with new ideas and enthusiasm. To ensure this end, many associations limit the number of consecutive terms that any individual board member can serve. Most boards include a convening president, a vice president, a secretary, a treasurer and, in smaller associations, a registrar.

Action 4. Determine membership dues and fees

Dues for membership and fees for services provided by the association, such as registration, are an important source of revenue that helps to meet the costs incurred by the association. In most situations, dues and fees are set by the membership or board of directors. Dues and fees must be set fairly and uniformly, and should have few changes over time. Dues and fees reinforce the message that registration and participation are valuable. Depending on the goals of the association and the variability in herd sizes, some breeders' associations may charge only membership dues with no additional fees for registration of animals. This encourages the registration of all animals and promotes the participation of breeders with large herds.

Box 32

Promotion of the Leicester Longwool sheep in the United States of America

The Leicester Longwool Breeders' Association in the United States of America has come to play an important role as the guardian of the largest national flock of this breed. The breeders' association discourages the usual competitive showing in favour of "card-grading" in which each sheep is individually evaluated by three judges for compliance with the breed standard. Following evaluation, each sheep is awarded a "card" determined by their relative quality: blue cards for superior breeding stock, red cards for good breeding stock, yellow cards for acceptable breeding stock, and white cards for those unacceptable as breeding stock. This process is educational because one of the judges speaks to the observers following the evaluation of each sheep, explaining the process and the results. This ensures effective education on breed type for both breeders and the general public.

Source: Sponenberg *et al.* (2009).

Action 5. Establish communication methods for educational and training programmes.

Communication within a breed association serves several different purposes, each of which will require specific mechanisms. Communication between breeders establishes a community among them. The goal should be to foster a feeling of belonging and participation so that breeders feel involved in, and essential to, the future of the breed. Newsletters, meetings, field days, shows and fairs, web sites and electronic chat groups can all foster this.

Associations also need to educate breeders on effective breed maintenance. The goal should be to have an informed and committed membership that is knowledgeable about population dynamics and their importance to conservation. Breeders must also understand breed type as it relates to traditional use and value. Educational methods include field days or workshops, traditional newsletters and electronic forms of communication.

Breeders' associations have an important role in promoting the breed and its products to an audience beyond the membership. Marketing and other promotional activities are essential for the long-term sustainability of an association (see Box 32).

Box 33

Accounting for cultural differences among members of breeders' associations

Breeders' associations must always reflect underlying cultural norms. This is especially challenging if a single breed is held by more than one cultural community. In the United States of America, the Navajo-Churro sheep has centuries-long connections with both Diné Navajo (indigenous) and Hispanic communities in New Mexico and Arizona, and more recently with Anglo breeders and enthusiasts.

Throughout its history, the Navajo-Churro population has oscillated widely, due in large part to various government interventions, including population displacement, subsidized cross-breeding and restrictions on grazing on public lands. Most recently, a large-scale culling programme in the mid-to-late 1900s pushed breed numbers to fewer than 500 head. In response, breeders and breeding programmes organized themselves to ensure that the breed did not drift to extinction. Breeders were fortunate in having key individuals in all three cultures that reached out to the other communities. These leaders built the Navajo-Churro Sheep Association with an organizational norm of cross-cultural appreciation and inclusion. Cultural diversity in the group is not ignored, but embraced and celebrated as an important aspect of breed conservation. This ensures that cultural diversity serves effective conservation rather than defeating it, by ensuring a strong commitment to the breed and its future.

Developing an inclusive association can be daunting, and although the Navajo-Churro Sheep Association has not yet fully integrated all breeders, especially among the indigenous communities, it applies an approach that considers the needs of the various ethnic groups. The Navajo-Churro registry depends on the inspection of each candidate sheep presented for inclusion in the flock book, even if both parents are registered. This model works best among the Anglo-American communities that are familiar with such procedures. These procedures are foreign to many of the Diné and Hispanic breeders, whose families have been raising the breed for centuries. To improve integration, the organization has Navajo-speaking and Hispanic inspectors dispersed throughout the traditional range of the breed so that traditional breeders have relatively easy access to inspection of their sheep. Having inspections done by members of the same cultural group facilitates communication, encouragement, and participation.

Breed-specific promotions for Navajo-Churro wool and meat have linked participation in the breeders' association with increased economic returns for these products. The Black Mesa Weavers for Life and Land, a non-profit enterprise assisting the Diné community in particular, has provided services for marketing wool and woollen products on a "Fair Trade" basis. Linking participation, breed recognition and enhanced commercial opportunities has ensured a viable association. Participation in the association has become an important way for each of the various communities to emphasize its individual culture and its contribution to the breed, which has increased a sense of ownership of the breed. Although obstacles for both the breed and its communities of livestock keepers remain, cooperation among the communities has improved the outlook for the future of the breed.

Source: Sponenberg and Taylor (2009).

Action 6. Develop and adopt a procedure for conflict resolution

Because breeders' associations comprise individual breeders, conflicts among members are certain to arise. Most conflicts are between individual members or breeders, but some arise from fundamental differences in basic philosophy of animal breeding (e.g. the breeding goal), production and sustainable use. It is important to have mechanisms in place to spot conflict early and to resolve it fairly and quickly. The goal of conflict resolution must always take into account the breed and its need for engaged and involved breeders that communicate and share. Conflict resolution is especially important for new associations of local breeds because they may have more traditional and isolated breeders. These conflicts must be judiciously solved if the breed is to expand rather than contract to the point of extinction. In some cases, conflicts can be foreseen and prevented or at least minimized. See Box 33 for a specific example where a breeders' association developed certain policies and practices accounting for cultural differences among members.

Ideally, it will be possible to reach a consensus and all members of the association will agree on a common strategy for breed conservation and development. However, in some cases the conflict may not be resolvable and the breeding association may split into factions, each of which having its own goals (see Box 34). In such cases population management is particularly important, because splitting the population will result in subgroups with smaller N_e and fewer resources for association activities.

Box 34

Introgression poorly accepted by some breeders of the Texas Longhorn in the United States of America

In some instances, conflicts among breeders may not be easily resolved and drastic action must be taken. Such a circumstance confronted breeders of the Texas Longhorn cattle breed in the United States of America. Different groups of breeders had opposing opinions regarding the philosophical choice between selecting for improved production and strictly maintaining a traditional phenotype. In particular, some of the breeders favoured using cross-breeding to improve production. Traditionally minded breeders were apprehensive about possible changes in type that may result from cross-breeding. These breeders felt that it was safest to select for traditional type within the breed so as to avoid losing unique aspects of the breed, particularly its adaptation to hot, dry environments. This difference in opinion has split the breed into two groups, with the more traditionally minded breeders' committed to pure breeding and resistant to changes in type and conformation. This effectively conserves the breed, but fixes conformation and production near current levels with little room for improvement. The long-term consequences of this decision are yet to be seen, although the chances of success are boosted by the fact that the traditional breed continues to excel in environmental adaptation and is sought as a maternal base in terminal cross-breeding programmes.

Provided by Phil Sponenberg.

Auditing the breeders' association and its activities

Rationale

Many breeders' associations need support from either governments or from NGOs in order for them to function well in conserving animal genetic resources. This support may be justified by the fact that activities of the association contribute to public benefits such as maintenance of biodiversity, rural development and increased food security. Support may be financial or logistical. The provision of support justifies periodic assessment of the associations' activities. Such evaluations help to ensure that the resources provided are being used effectively in conservation work.

Whether or not out outside support is being provided, a breeders' association should still undertake periodic auto-evaluations, to ensure that its members are being properly served and its goals with respect to animal genetic resources management are being effectively achieved.

Breeders' associations should actively monitor and appraise the role of the breed as a valued natural resource for the country. This task should include assessments of demand for the breed and its products and threats to its long term viability (FAO, 2010). Assessing and promotion of a breed's value usually requires a strong breeders' association, as weak or inactive associations may be overlooked by national efforts (FAO, 2009).

In some instances, particularly with rare breeds, the number of breeders is not large enough to perform all of the functions generally required from a breeders' association. Even when associations are large enough to perform the tasks needed for their breed, maintaining separate sets of infrastructure for each breed may not be financially efficient. In such instances, a wise alternative may be to create an umbrella organization that performs various administrative functions for a number of otherwise independent breeders' associations. An example of such a system is presented in Box 35.

Box 35

Combined Flock Book – a multibreed society in the United Kingdom

Small breeders' associations frequently have limited resources. This shortage of resources may cause inefficient administration, and is likely to prevent the provision of comprehensive breeding and support services to breeders and members. The creation of a central facility by a larger organization covering several breeds can overcome these problems.

In the United Kingdom, the Combined Flock Book was established by Countrywide Livestock Ltd in 1974 as the breed society for breeds that were unable to maintain their own administrative offices, and it currently provides services for eight breeds of sheep. The primary objectives of the Combined Flock Book are to protect the genetic integrity (pure-breeding) of each breed and to promote the value the breeds.

The Combined Flock Book originally operated within the structure Countrywide Livestock Ltd and was administered by a committee comprising one representative from each breed under the chairmanship of the President of Countrywide Livestock Ltd. Each breed also was supported by its own group of breeders who were concerned primarily with promoting their breed. The Combined Flock Book was later transferred to the NGO Rare Breeds Survival Trust under a similar arrangement.

The services provided by Countrywide Livestock Ltd included:

- registration of all pure-bred animals with details of individual identity, sire, dam, date of birth and sex, plus information on colour and horns where appropriate;
- calculation of inbreeding, kinship, and individual founder contributions for each breed;
- realization of DNA profiles for parentage verification, product provenance and assignment to breed;
- provision of advice on breeding policy and individual mating plans;
- promotion of member breeds through a web site, literature, exhibitions, and livestock shows; and
- conflict resolution.

Provided by Lawrence Alderson.

Objective: Develop an auditing process for a breeders' association and its breeding and conservation plan.

Inputs:

1. Laws and by-laws of the breeders' association; and
2. A description of the association's activities including the breeding and conservation plan.

Output:

- Description of an auditing procedure for a breeders' association and its activities.

Task 1. Evaluate participation and decision-making procedures

Action 1. Describe and evaluate the mechanisms for participation

Strong breeders' associations encourage broad participation from their members and producers (FAO, 2010). All members should feel welcome to participate and to contribute. Major decisions should be taken in a democratic manner, avoiding domination by one or a few persons. Some associations get dragged into various controversies arising from the dissension of a single or small number of people and while some individuals may hold very strong opinions, in most cases the breed itself loses support and members. Ensuring that an association functions in a way that ensures a sense of community and benefits all members to a fair degree is an important objective.

Action 2. Assess the decision-making processes

Breeders' associations need shared and open decision-making procedures to foster broad ownership of the association and high levels of participation. The actual keepers and breeders must be consulted and considered if the association's programmes are to be successful (FAO, 2010). Breeders and livestock keepers have intimate knowledge of the breed's production system. Their participation must be ensured by respecting their opinions and attitudes.

Action 3. Evaluate the provision of benefits to association members

Breeders' associations should provide expert or technical support to their breeder members (FAO, 2010), including husbandry, health care, animal selection and animal breeding techniques, when appropriate, and strategies for the long-term viability of the breed.

Action 4. Evaluate the procedure for inclusion of new members

The evaluation of mechanisms for including new breeders in the organization should include assessments of membership protocols and of the extent of participation by old and new breeders in the association and the registry. Breeders' associations should be inclusive and welcome new breeders. This is especially important when new associations are being formed for non-standardized breeds. It is essential that the community of breeders for each breed is growing rather than shrinking. Strengthening cooperation among breeders is an important role for breeders' associations (FAO, 2010).

Task 2. Appraise the genetic purity of the population

As noted above, public support to a breeders' association may be justified if the association is actively maintaining biodiversity by promoting maintenance of a valuable genetic resource. If this objective is not being reached, then continued support may not be warranted.

Action 1. Evaluate the level of pure-bred breeding as opposed to deliberate or casual introgression

This evaluation needs to include detection of overt and fraudulent introgression by breeders, as well as avoiding the inclusion of cross-breeds through inattention. Breeders' associations must insist on pure-breeding and emphasize this to members. Commitment to pure-breeding should be openly stated as a core value of the association. Competitive activities such as animal shows or production award contests are a way to promote interest in the breed and reward active participation, but they can also provide an incentive for fraudulent cross-breeding. In some cases, awards in the show ring or production contest can go to animals with obvious introgression from other breeds if not prevented by the breeders' association. This can send a very damaging signal to the breeder membership. In general, the association should insist that breeders recognize and appreciate the breed for what it is rather than trying to change it through crossing.

Action 2. Check accuracy of parental information

Correctness in animal identification is important in order to ensure freedom from undesired cross-breeding and precise evaluation of breeding values. As mentioned above, routine DNA tests will not be practical in many situations, but breeders' associations may care to adopt a programme that randomly checks the parentage of a proportion of animals by using DNA from the individual and its putative parents. The government may wish to audit such a programme, especially if support is being provided for identification and performance recording.

Task 3. Evaluate the status of the animal genetic resources under management

The breeders' association needs to maintain its identity and its sense of ownership of the breed. These aspects will be largely influenced by the autonomy of the association with respect to the breeding programme, with more autonomy leading to a greater sense of ownership. However, if outside financial support is being provided, then some reasonable conditions may be applied to this autonomy. Occasional auditing by the funding agency of the population and breeding programme may help to evaluate the breed's prospects for sustainability and identify threats to its viability.

Action 1. Analyse the population structure and its use in the breeding programme

Procedures for designating strains or families within the overall breed, mechanisms for census of the breed, and evaluations of population structure should be appraised. Effective breeders' associations periodically monitor the population structure of the breed. Breeders should be educated against temporary fads in breeding so as to ensure a broad representation in the next generation. The overuse a few well-known animals will result in a bottleneck. This is damaging in common breeds and disastrous in breeds that are at risk of extinction. Breeders' associations should educate breeders on healthy population structure. Recognition of the value of different strains or sire families within the breed can be very helpful, especially in non-standardized breeds where variation in different families can be relatively large. Breeders' associations should monitor the breed's population size, including the details of animals with large average genetic relationship with the rest of the breed.

Action 2. Evaluate the breeding and conservation programme

The plans for the management of the genetic variability of the population should be appraised, including periodic exchanges of breeding animals among breeding herds, and any cryoconservation activities, such as targeted freezing of gametes from under-represented animals. If the breeding and conservation plan involves genetic improvement, then the genetic and phenotypic trends of the population should be checked to gauge the effectiveness of these activities. Breeders' associations should be alert to herds and individual animals that are of high genetic diversity and importance to the future of the breed (FAO, 2005). Breeders' associations can actively promote rules and protocols that serve to prevent genetic erosion by encouraging genetic exchanges among member herds (FAO, 2010). However, such efforts need to be broadly based so as to ensure that no single herd swamps the breed by providing a disproportionate share of breeding animals.

Centralized *ex situ* conservation on institutional farms

Rationale

In situ conservation is usually the preferred option for *in vivo* conservation of animal genetic resources, due to the advantages discussed in Section 3. However, in some situations, *ex situ* conservation of live animals is a more practical option. For example, a breed may have reached a population size that is too small to be raised by a group of farmers. Alternatively, a breed may be valued primarily for its option and existence values (see Box 12), and therefore not profitable enough to be maintained by livestock keepers, but may still need to be immediately accessible in its live-animal form. Perhaps tight central control of breeding is required and such control can only be achieved via *ex situ* conservation on a single farm. Such programmes are typically operated by the government or NGOs rather than by the commercial sector.

In many countries, institutional farms are owned by government and NGOs that are dedicated to research, teaching and development. Most of these farms maintain economically important breeds of various animal species, and are used as demonstration centres as well as for the production and dissemination of superior germplasm. For example, India has a well-developed system of institutional farms. Establishing organized breeding farms is important, especially for genetically eroded breeds that have very small populations and are sparsely scattered in their home regions.

Ex situ conservation of livestock breeds by establishing breed-specific farms involves a substantial investment in infrastructure and other resources. For these reasons, *ex situ* conservation programmes are usually limited to a few very unique breeds and maintain relatively small populations. As explained in Section 2, the genetic constitution of a small population can change rapidly through genetic drift, possibly resulting in the loss of genetic peculiarities and reduction in genetic variability, so the most important challenge in managing the population in *ex situ* conservation is to sustain genetic variability.

Objective: Establish and maintain populations of important animal genetic resources in centralized breeding herds.

Inputs:

1. Lists and of local breeds that are candidates for *ex situ* conservation and descriptions of their characteristics; and
2. Knowledge of the location of individual animals from these breeds including those kept by

private breeders and on existing institutional farms.

Output:

- Institutional herds for at-risk breeds, with active programmes for maintaining their genetic variability.

Task 1. Undertake the necessary preliminary planning, including feasibility studies, and secure access to facilities and funding

Action 1. Assess the available institutional breeding farms

An *ex situ in vivo* conservation programme will be more financially feasible if existing facilities and personnel can be used. These facilities may include governmental or non-governmental farms.

Action 2. Determine the breeds to be targeted by the conservation programme

Following the procedures set out in Section 3, establish the targets regarding which breeds to include in breeding farms, paying close attention to breeds that have not already been targeted by existing programmes.

Action 3. Perform a feasibility study

As noted above, *ex situ* conservation of animal genetic resources *in vivo* is an expensive undertaking and requires substantial planning. The population is unlikely to be financially self-sufficient, so the agencies (public or private) supporting the conservation activities have to be convinced of their value. A feasibility study must be undertaken to determine the costs of establishing and maintaining the conservation programme. The assessment of costs must consider the initial acquisition of the animals, their maintenance, the acquisition or refurbishing of facilities, the maintenance of the facilities and personnel costs. Any revenues expected to be generated by the herd should also be accounted for.

Action 4. Identify possible donors

In addition to the government, NGOs with an interest in conserving the diversity of agricultural genetic resources should be considered.

Action 5. Prepare and present proposals for the conservation plan to government officials and/or donor agencies

A strong argument will be needed to convince donors to provide support for the conservation activities. The value of the animal genetic resources to be conserved must be stressed, including the opportunity costs of its loss. A well-done feasibility study (*Action 3*) will aid in preparing the proposal.

Task 2. Establish and operate the conservation programme

Assuming Task 1 has been completed successfully, the real work of establishing and operating the *ex situ* conservation programme can get underway.

Action 1. Establish the herds at the institutional farm

A general consensus suggests that an N_e of 50 is a reasonable goal for conserved populations of animal genetic resources (FAO, 1984; FAO, 1998). This need not be an immediate goal to be achieved at the start, but rather a goal to be aimed for over time through breeding management and continual acquisitions. In addition to stock that may already be available in institutional herds, animals can be purchased from livestock keepers in the breed's breeding tract. Although reducing the size of the base population for a conservation programme will save money, it may introduce a *founder effect* (a type of genetic drift resulting in loss of genetic variability when a new population is established by a very small number of individuals selected from a larger population). The allelic frequencies of the small sample of animals may differ from that of the larger population and some alleles may be lost completely.

Animals purchased from outside should be free from disease or any noticeable defects, conform closely to the desired breed characteristics and be as unrelated as possible. If possible, they should have above-average performance for traits of economic importance (production and adaptive traits) so as to promote the economic self-sustainability of the farm. The best available breeding males (at least one for every ten females) should be procured.

Action 2. Develop breeding and husbandry strategies for the institutional herd

Given that keeping the animals in an institutional situation allows for central control over breeding decisions, the most advanced systems for controlling genetic variability (i.e. minimal coancestry or optimal contribution theory – see Section 6) should be applied. Given the value of the animal genetic resources and substantial investment that the government or private donors will have made in establishing the conservation farm, exceptional effort must be taken to minimize the risk of diseases, accidents, genetic drift, inbreeding and contamination from other breeds. If artificial selection is being practised (or if natural selection may occur due to environmental differences between the natural and controlled environments), and because of the potential for genetic drift, it is possible that a genetic gap will develop between the conservation herd and the original breed in its native region and the population in the conservation programme. The potential for effects of this kind should be assessed and monitored. This "adaptation to captivity" is generally considered more important for wild animal species (e.g. Frankham, 2008), but may be relevant for livestock, especially those that come from a particularly harsh production environment.

Action 3. Establish a gene bank (i.e. in vitro cryobank) for periodic storage of germplasm from animals in the ex situ in vivo programme

Maintaining genetic material from animals in the original population will allow recovery of the genetic variability if the population drifts from its original base and will facilitate reconstitution of the breed if a catastrophic event (e.g. disease, fire or natural disaster) wipes out a significant portion of the live population. As noted in Section 4, *ex situ in vivo* conservation (especially on a single farm) carries risks, as all the live animals may be threatened if a catastrophe occurs.

Action 4. Organize participation by livestock keepers and institutions in the production and use of male animals

Ideally, it will be possible to use the *ex situ* population as a resource in the active management and improvement of the *in situ* population, for example, by making superior young males from the herd available for use in the general population.

Additional advice on *ex situ in vivo* management of animal genetic resources with very small populations can be found in guidelines produced by the European Livestock Breeds Ark and Rescue Net (ELBARN, 2009).

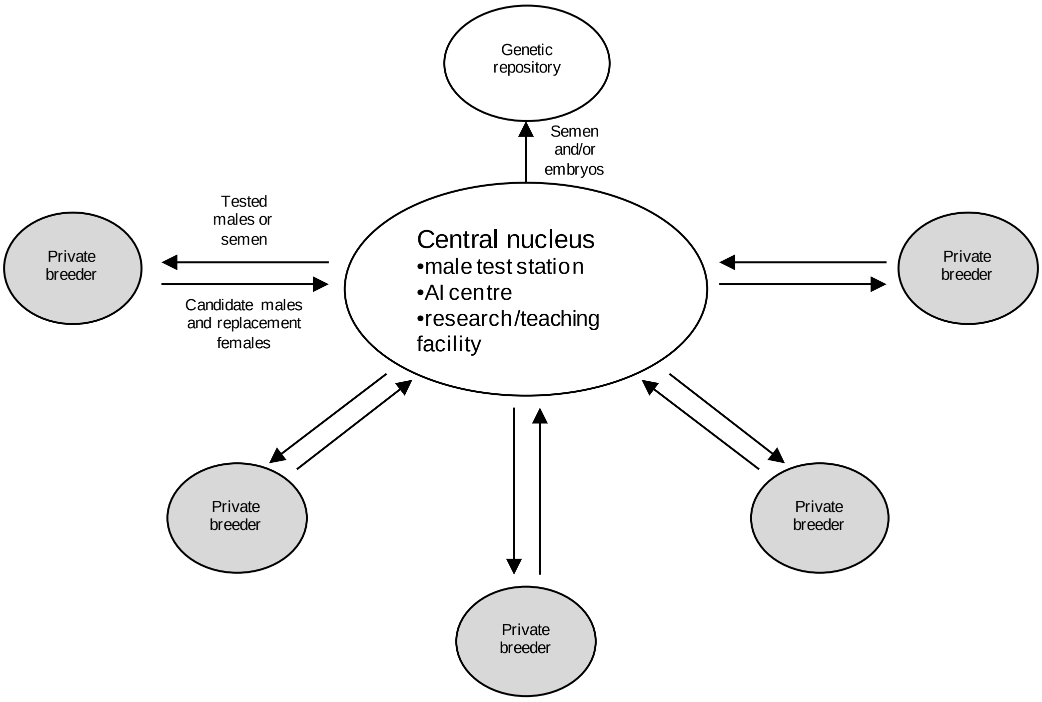
Dispersed *ex situ* conservation involving institutional herds and livestock keepers' herds

As noted above, the establishment and operation of an institutional farm for *ex situ in vivo* conservation of animal genetic resources can require a significant investment. One feasible means of overcoming this constraint is to expand the population through the use of a dispersed or decentralized model in which animals already available at established government farms are combined with those kept by NGOs and by private individuals who are willing to keep the animals on a commercial or hobby basis.

Many existing institutional facilities are already involved in important conservation activities. Nearly all could easily play a more significant role in conservation with little or no adverse effect on their other roles in development and animal breeding. The institutional farms could be associated with AI centres, nucleus herds and/or *in vivo* germplasm repositories. Livestock keepers would be both users and suppliers of germplasm. Facilities for producing frozen semen can be developed on such farms in order to disseminate the germplasm from pure-bred males typical of the breed to collaborating farmers. A network of several breed-specific herds can provide a basis for integrated breed conservation and systematic genetic improvement. The basic design of the model is shown in Figure 3.

An example of how certain institutional farms in India could be used for conservation is presented in Box 36.

Figure 3. An example of a decentralized programme for *ex situ* conservation of a breed by employing institutional herds belonging to private breeders and farmers



Objective: Establish and maintain populations of important genetic resources in one or more institutional nucleus and decentralized breeding herds.

Inputs:

1. Lists of breeds that are candidates for *ex situ* conservation and descriptions of their characteristics;
2. Knowledge of the location of individual animals from these breeds including those belonging to private breeders and existing institutional farms; and
3. Secured support from the government or a development agency.

Output:

- A network of institutional and local livestock keepers' herds with an active programme for sustainable management of an at-risk breed of livestock.

Task 1. Establish the conserved population

Action. Identify the base animals

At least 25, and preferably more than 50, female animals should be identified from among the institutional herd and livestock keepers' herds on the basis of breed characteristics and performance traits (production and adaptation). The animals should be tagged and recorded. Male animals (preferably at least one for every ten females) should also be identified and tagged and raised by their owners and made available to other livestock keepers for breeding purposes. The owners of candidate males may be provided with an incentive per female per year for rearing the animals and retaining pure-bred offspring.

Box 36

The role of Gaushalas in conservation in India

The Gaushalas of India are institutional self-contained cow shelters with their own land and housing facilities. They are usually supported by a combination of donations and government assistance. There are currently more than 4 000 Gaushalas across India. Most of these Gaushalas primarily cater to the needs of non-lactating, weak, unproductive and stray cattle, but it is estimated that more than a quarter of them have the potential to be used for *in vivo* conservation (Sadana, 2007). Many Gaushalas in India maintain pure-bred animals of different local breeds, often in greater concentrations than can be found in surrounding herds belonging to local livestock keepers.

A few progressive Gaushalas are repositories of well-described local cattle breeds and produce quality males. They thereby contribute directly to the conservation and improvement of these breeds. However, they do not have sufficient resources and technical support to conserve and improve these breeds in the most effective manner. Undertaking the following actions could allow these progressive Gaushalas to be utilized more effectively for *in vivo* conservation:

- Identify the Gaushalas with a large number of pure-bred animals belonging to breeds at risk.
- Support the development of the infrastructure necessary to transform these Gaushalas from rehabilitation centres into genetic resource centres.
- Within each Gaushala, group the pure-bred and non-pure-bred animals and house them separately – choose the pure-bred animals selectively if population sizes permit.
- Implement identification, performance recording and breeding programmes to improve the pure-bred stock through selective breeding.
- Distribute excess pure-bred stock to the local community, targeting farmers that are willing to continue pure-breeding of the animals.

An agreement should be made with the participating Gaushalas not to resort to cross-breeding or other such practices that may dilute the genetic purity of the breed. In return, the Gaushalas could be provided with scientific and technical support and, if necessary, with financial assistance. The Gaushalas should be encouraged and supported in identifying unique and value-added products of the local breeds so as to increase their economic value.

Provided by Devinder K. Sadana.

Task 2. Manage the conserved population

Various approaches can be used to manage the conserved population. Described below is a programme that is based on the distribution of male animals and/or semen.

Action 1. Mating of base animals to produce new males

The base females should be mated or inseminated with a male or semen of the same breed. The livestock keepers can be contracted to rear the resulting male progeny for up to six months. A large number unrelated young males should be selected for inclusion in the conserved population (around one for every ten to twenty females). Hereafter, there are two approaches that can be followed, depending upon whether the animals are to be raised by livestock keepers or by a development agency or institutional farm.

Action 2. Manage the selection and distribution of males

Option 1: Development agency or institutional farm

If AI technology is available, the selected young males are purchased by the development agency or institutional farm. The agency rears the males until maturity and then trains them for semen production. At maturity, a total of at least 25 males are selected on the basis of growth, semen quality and freezability. As many as 3 000 doses of semen from each male may be collected, cryopreserved and used in for breed improvement and conservation (more prolific species will requires fewer doses). The surplus breeding males are distributed to the farmers for natural mating in the breeding tract.

Option 2: Private livestock keepers

Individual livestock keepers rear the selected males and receive an incentive payment for maintenance costs. When the males reach breeding age, the livestock keepers maintain them and provide breeding services to the female animals in the local area through natural mating. The farmers charge a fee for the breeding services in order meet the expenses of further maintaining the breeding males. At this point the incentive payments stop and the livestock keepers are expected to maintain the males solely on the basis of the breeding fees.

Action 3. Design breeding and mating strategies

Selection of males and distribution of semen and males for mating should be implemented with the objective of maximizing genetic diversity according to the general theories described in Section 6 and in line with the conditions and technical capacity of the country. When technical capacity for applying complex breeding programmes is low, sire use should be uniform as much as possible (i.e. to achieve approximately equal numbers of offspring per sire). When technical capacity is greater, optimum contribution theory can be used in bull selection.

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VI. DESIGNING THE CONSERVATION PROGRAMME – MAINTAINING GENETIC VARIABILITY

As described in the preceding sections, a population's degree of risk and consequently its probability of survival are greatly dependent on the level of genetic diversity it harbours. High levels of genetic variability allow the population to adapt to changes in the environment or the production system and will prevent the rise of inbreeding and its deleterious consequences. Small populations, such as those that are likely to be targeted by conservation programmes, are more prone to lose genetic information. Therefore, implementing management strategies that maintain genetic diversity is crucial to the success of conservation programmes.

Two strategies can be used to manage the genetic diversity of small populations. The first of these is to maintain or increase the genetic variability within the population (this section):

1. adopt a general breeding strategy to maintain the conserved breed, based on a clear understanding of options for maintenance of the genetic variability;
2. consider adopting a mating strategy to decrease inbreeding; and
3. incorporate cryoconservation in the management of genetic variation in the *in vivo* programme.

The second potential strategy is to optimize selection response and genetic variability within the populations (Section 7)

1. adopt a general breeding strategy to maintain the conserved breed; and
2. design a breeding programme that generates genetic improvement while maintaining genetic variability.

In most cases, the choice between the two strategies will depend upon the population size – either census size or N_e. Genetic improvement runs counter to the objective of maintaining of genetic variability, so maintenance of variability will take precedence in small populations. As described in Section 2 (Task 3), maintaining variability should usually be emphasized for breeds with critical or endangered risk status, especially for the former. For vulnerable populations, the genetic improvement strategy becomes more realistic. However, the maintenance of genetic variation should always be an essential part of a breeding programme.

Maintaining genetic variability within small populations

Rationale

Loss of genetic information

In livestock populations of a stable size, the loss of genetic information (alternative alleles contributing to the genetic variability in the population) is usually caused by selection and genetic drift. In a very general sense, natural selection acts to eliminate deleterious alleles, while artificial selection tends to fix alleles that improve the phenotype of carriers. In small populations not subject to an explicit process of artificial selection, the impact of selection (either natural or artificial) is small (most of the genetic variants are neutral with respect to phenotype) and the fate of an allele (i.e. its eventual loss or fixation) is mainly driven by genetic drift, which is a random process. Genetic drift is the fluctuation of the frequencies of alleles (i.e. the number of copies of them in the population) due to the finite and random sampling of gametes to generate offspring (Falconer and Mackay, 1996). This random sampling operates at two levels. First, if the number of offspring is small and reproduction is not controlled (i.e. mating is random, resulting in variable numbers of offspring per individual) some members of the population may not contribute offspring to the next generation. The unique genetic information of these animals will be lost, while other animals will contribute multiple copies of their genetic information to the next generation. Second, to generate an offspring, each individual contributes a gamete carrying just one of the two alleles at each position in its genome. If the parent is heterozygous (i.e. it carries two different alleles at a given locus) only one of the two variants will be transmitted to a given offspring. This may result in the loss of genetic information even if all individuals leave offspring.

Consequences of the loss of genetic information

The consequences of the genetic drift process for small populations are:

- the probability increases that none of the copies of a particular allele will be transmitted to the next generation (i.e. genetic information will be lost); and
- the probability of mating between relatives (i.e. inbreeding) increases, and so does the probability that animals will inherit identical copies of an allele in any gene.

An increased proportion of mating between relatives occurs in small populations even when mating is random, and the probability of intra-family mating increases as the size of the population decreases. Of course, inbreeding arises in populations of any size if relatives are mated deliberately. The probability of homozygosity by descent is greater the higher the average degree of relationship between individuals in the population. Increased homozygosity reduces the expression of fitness-related or productive traits, compromising the survival of the population, a phenomenon known as "inbreeding depression" (see Box 37).

Box 37

Inbreeding depression

Livestock species are diploid, which means that each individual carries two copies of the genetic information (two alleles) at each position (locus) in its genome. At a particular locus, the two alleles can be the same (homozygous) or different (heterozygous). The performance of an individual for a given trait will depend on the type of alleles it carries. Sometimes an allele gives a visible effect only if it is in homozygosity (i.e. when both alleles are the same). Such alleles are called *recessive*. If the allele has deleterious effects (confers inferior expression of the trait) heterozygous individuals will have a normal performance, but they will be carriers of the deleterious allele. Genetic drift promotes an increase in the number of homozygotes. The deleterious alleles that were undetected because of the compensatory effects of heterozygosity become more frequently exposed and the mean value for the trait decreases. This decline in mean performance of the population is called inbreeding depression. If the allele has effects on fitness-related traits, the consequence is lower probability of survival. If the trait controlled by the locus involves productivity, the mean performance of the population will decrease and the profitability of the breed will be compromised. In either of these situations (decreased fitness or decreased profitability), the risk of extinction will be increased. Thus, small population sizes lead to both genetic and demographic consequences (see Table 6).

Inbreeding coefficient

The inbreeding coefficient (F) is a measure of diversity that ranges from 0 (non-inbred) to 1 (a completely inbred and homozygous individual, with two exact copies of all chromosomes). Inbreeding is unavoidable in small populations and if the pedigree can be traced far enough back, common ancestors will invariably be found, demonstrating that all animals are related. Therefore, the average F of a population is dependent on the definition of a reference/base population in which all individuals are assumed to be non-inbred and unrelated (e.g. founder individuals when pedigree recording started). Consequently, populations with many generations of genealogy will tend to have high average F, whereas populations with shallow pedigrees will have low F.

Because of this bias caused by differences in the depth of pedigree data, a more informative parameter is the rate of inbreeding (ΔF), defined as the change of inbreeding per generation relative to the amount of inbreeding that can still occur (i.e. $1 - F$). The advantage of this concept is that it is independent of a reference population, allowing comparison between populations whose histories are known to different degrees. Under several assumptions, ΔF can be calculated using simple formulae. Calculating ΔF helps in predicting the future performance of a population, determining the minimum composition of a viable population or designing management strategies. Further details of these methods are provided later in this section.

Rate of inbreeding

ΔF is also a useful parameter for describing the present situation of a population. It allows detection of events that occurred in the history of the population (e.g. bottlenecks, or periods when the population consisted of a reduced number of individuals) and also helps to determine the risk status of the breed (see Section 2). Additional genealogical analyses can also be undertaken to study the history of a population from the genetic perspective. These analyses yield parameters such as effective number of founders, founder genome equivalents and founder representation (Caballero and Toro, 2000) that help to determine how much variation the population had at its origin and how well the population has been managed in the past.

Effective population size

As explained in Section 2, effective population size (N_e) is a parameter that is commonly used to evaluate the genetic variability of a population, based on the assumption that larger populations will be less subject to random drift and will thus have more genetic variability. To review, N_e is the size of an idealized population that has the same rate of inbreeding (ΔF) as the real population. This idealized population has equal number of males and females, all of which have an equal opportunity to produce offspring. It is a theoretical concept – such a population would never really exist in a livestock breed. However, it serves as a basis for comparison. Various types of departure from the characteristics of the idealized population will affect the calculation of N_e. This increases the difference between the number of animals in the population (the census size) and the N_e (see Box 7 for a discussion of factors that affect the determination of N_e). There is a close relationship between ΔF and N_e ($\Delta F = 1/2N_e$) and, consequently, both parameters describe the same concept. For most situations, the loss of genetic variability (as measured by the parameter genetic variance) is also proportional to ΔF, which indicates that this parameter is a useful measure of the ability of a conservation programme to maintain genetic variability.

Relationship and coancestry coefficient

The relationship between individuals (measured using the coancestry coefficient, f, i.e. the probability of sampling alleles identical by descent from two individuals) is another helpful parameter because of its connection with classical measures of diversity. The global coancestry of a population reflects the extent to which the genetic information found in the different individuals is redundant. Mathematically, the average population coancestry is = $(1 - H_e)$ where H_e is the expected heterozygosity. As described in Section 3, H_e is a common measure of genetic diversity. When the numbers of males and females in the population are different, the global coancestry must be calculated as ¼ of the mean coancestry between pairs of males, plus ¼ of mean coancestry between females, plus ½ of the mean coancestry between every possible pair of sire and dam. The coancestry coefficient is also related to inbreeding because the F of the offspring is the f of the parents; an individual cannot carry alleles that are identical by descent if its parents did not share the allele, as each of the alleles at a locus comes from a different parent.

Rate of inbreeding and rate of coancestry

Rate of inbreeding (ΔF) is related to the probability of homozygosity by descent, and rate of coancestry (Δf) is related to loss of diversity. Under random mating, both parameters equalize in a few generations. However, if the population is subdivided or if assortative mating is practised (i.e. if mating of relatives is promoted or avoided), ΔF and Δf can diverge (Falconer and Mackay, 1996). Consequently, to determine the genetic endangerment of a population, N_e should be calculated from both ΔF and Δf. A population subdivided into several genetically isolated lines (e.g. through geographic isolation or deliberate breeding within families) may harbour high levels of population-wide diversity (low levels of global f), but will suffer from the harmful effects of large ΔF within in each subpopulation.

Both F and f can be easily calculated from genealogies. Consequently, it is highly recommended that, when the production system and physiology of the species allow, the pedigree of the population be traced through the generations by recording the sire and the dam of every individual. Pedigree recording will allow for the implementation of very effective management strategies (see later in this section and in Section 7) and will avoid the need to resort to more expensive methodologies such as molecular marker genotyping. Several computational methods have been developed to calculate F and f in any pedigree, including some that can deal efficiently with large genealogies. Free software is also available to perform such calculations. Two examples are ENDOG[8] (Gutiérrez and Goyache, 2005) and POPREP[9] (Groeneveld *et al.*, 2009), but many others have been developed (some of which are listed in Boettcher *et al*., 2009). Such programs tend to provide more informative and reliable results (and greater estimates of F) when pedigrees include more generations of data.

Minimum effective population size

The minimum acceptable N_e has been defined as the N_e of a population that is safeguarded from becoming extinct because of the effects of inbreeding depression (or other threats related to reduced genetic variability). In general, 50 has been established as an acceptable N_e, at least to guarantee the survival of the population in the short and medium term. Consequently, the desired ΔF per generation should not exceed 1 percent ($\Delta F = 1/[2\times50]$). This can be achieved with different population structures in terms of combinations of males and females. For example, with no selection (i.e. random number of offspring per parent) 25 breeding males and 25 females yield the desired value, but a decrease in the number of males has to be compensated for by increasing the number of females. For example, 20 males and 34 females, and 14 males and 116 females, also yield an N_e of 50 (for information on the computation of N_e see Box 7). The management procedures implemented in the population will affect the numbers of breeding animals needed for an N_e of 50. The required numbers will be lower when only conservation strategies are applied and higher when selection for a particular trait is applied (see Section 7). Of course, the population sizes described here are minimum sizes. Larger numbers of animals are always to be preferred for long-term survival of a population.

Direction of management strategies

From the above discussion it can be concluded that management strategies should aim to minimize genetic drift effects by minimizing ΔF (Δf) or maximizing N_e. The knowledge of the factors affecting N_e will aid in the design of effective conservation strategies. When the N_e of a population drops significantly lower than 50, it may reach a level where it cannot be sustained because of the negative effects of a lack of genetic diversity on fitness and fecundity and the accumulation of genetic defects. Such a situation is referred to as an extinction vortex, because population numbers are expected to decrease uncontrollably in each successive generation (like water draining from a sink or bathtub). For such populations, a more radical strategy of “genetic rescue” must be applied (see Box 38).

Objective: Understand the factors associated with genetic drift and develop strategies to minimize its occurrence.

Inputs:

Knowledge of the following characteristics of the breed to be conserved:

1. Size of the population;
2. Reproductive capacity of the species; and
3. Possibilities for exchange of genetic material between herds or flocks belonging to different stakeholders.

Output:

1. A general breeding plan that will minimize genetic drift and maintain genetic diversity.

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[8] http://www.ucm.es/info/prodanim/html/JP_Web.htm

[9] http://popreport.tzv.fal.de

Box 38

Genetic rescue

When a population is not fit enough to reproduce itself and, thus, the number of breeding animals is irrevocably decreasing in every generation, the population has become trapped in an extinction vortex. Such a situation often arises because of excessive inbreeding in the past (a bottleneck), a great drop in genetic variability levels and the accumulation of genetic defects. If a breed enters extinction vortex, two strategies can be implemented.

One option is to change the environment of the population (e.g. by establishing an *in vivo ex situ* programme) to a more favourable one where the animals can receive greater veterinary care and the fitness of individuals is high enough to survive and reproduce. Attention must be paid to ensuring that the population does not become adapted to the new, more favourable, conditions, as this may preclude the reintroduction of the population to its former production environment.

A second alternative is limited crossing with another breed that is adapted to a similar environment and ideally has specific adaptive traits that are similar to those of the at-risk breed. This process is known as genetic rescue. The number of introduced individuals should be kept to a minimum, but even a small amount of foreign (i.e. from a different breed, not necessarily from a different country) genetic material can have a large positive effect. For example, if a proportion p of foreign alleles is introduced, the proportional reduction in inbreeding is $1 - (1 - p)^2$. With the introduction of 10 percent foreign alleles, the inbreeding in the population is reduced by nearly 20 percent, depending on the initial F. For example, if $F = 0.30$, an introduction of 10 percent of outside alleles leads to a population with $F = 0.24$. The whole process has to be very carefully controlled so as to avoid excessive introgression of foreign genetic information. Among the cross-bred offspring, those showing the original phenotype should be selected to create the next generation by backcrossing with pure-bred individuals from the at-risk breed, until most of the foreign genetic information has been removed. Molecular markers can be used to increase the accuracy of selection decisions aimed at purging foreign alleles.

Task 1. Adopt a general breeding strategy to maintain the conserved breed, based on a clear understanding of options for maintaining the genetic variability of the population

Logistic and financial capabilities vary from one herds or population to another. Therefore, not all the strategies presented in the following pages will be feasible in every situation. The simplest actions are generally presented first, followed by more technical and sophisticated options. Breeders and other managers of animal genetic resources should decide which options are most appropriate for their particular situations. The first three *actions* are likely to be applicable in most conservation programmes.

Action 1. Include as many animals as possible from the start, as the extent of genetic drift depends on the number of individuals available

Animals should be healthy and, as far as possible, non-inbred and unrelated. However, related animals should not be eliminated if the capacity and financial resources of the programme allow them to be maintained. Efforts should be made to involve all the herds of the breed in the programme. Doing so will enable the programme to begin by exploiting the maximum possible variability and opportunities to diminish the action of genetic drift. In addition, females that have previously or routinely been crossed to males of other breeds should be recovered and used exclusively for within-breed matings. Clearly, if conditions permit, the real population size should be increased as quickly as possible to reduce the risk of extinction due to demographic stochasticity and to increase the N_e.

Action 2. Increase the number of breeding males

Half of the genetic information is transmitted by each sex. Therefore, the less-represented sex (usually the males) will be the deciding factor in decreasing N_e, irrespective of the number of individuals of the other sex that there are in the population. For example, assuming random numbers of offspring across males and females, a population with 2 males and 1 000 females has the same N_e as a population with 4 males and 4 females. With just one male, all the descendants will be at least half-sibs and average F will increase from zero to more than 0.125 in just one generation.

Action 3. Prolong the generation interval

The ΔF is defined per generation, as genetic drift occurs due to the random sampling of alleles when gametes are produced. However, if the *generation interval* (i.e. how long it takes to replenish a set of parents – see Box 39) is longer, the same ΔF per generation has to be divided among more years, diminishing the loss of genetic diversity per year. Generation interval can be increased by keeping individuals as long as they are able to reproduce and by extending their period of use by using their cryopreserved genetic material. As long as an individual or its genetic material is available for breeding, its genetic information is not lost and can contribute to enhancing the genetic variability in the breed.

Box 39

Generation interval

The generation interval (L) is the genetic unit of time for a population. It is defined as the average age of parents at the time of the birth of their straight-bred replacement. In many cases this parameter will be approximated by the average age of the parents at the birth of all the offspring, but this need not to be so. Due to differences in reproductive life spans, the generation interval may be different for males and females, and should be calculated separately. Because half of the alleles are contributed to the population by males and half by females, the generation interval is the average generation interval of the breeding males and the breeding females. For example, if offspring are born when the sires are one year old, and 60 percent and 40 percent of the offspring are born when dams are one and two years old respectively, $L_s = 1$ and $L_d = 0.6*1 + 0.4*2 = 1.4$ years (s = sire and d = dam*)*. Calculating the average gives a figure of 1.2 years for the L of the population. The longer individuals are used as breeding animals the greater L will be.

However, it is important to note that when a programme of selection and genetic improvement is implemented, an increased generation interval will reduce the response to selection per year. Thus, once a breed's population has increased to a size that is sufficiently large to allow selection (e.g. 500 females and $N_e > 50$), generation interval has to be balanced against the other factors influencing genetic gain and maintenance of variability. This topic is addressed in Section 7.

Action 4. Balance the contribution of each individual

The rationale of this action is to provide the same opportunity to all animals to transmit their genetic information to the next generation. In a simple situation where the numbers of males and females are equal and no selection is practised, the effective population size is approximately $N_e = 4N / (2 + S^2{}_k)$, where N is the census size and $S^2{}_k$ is the variance in the number of offspring contributed by each individual. If individuals' contributions are equalized, $S^2{}_k$ becomes zero and the N_e is twice the population census size (the largest possible N_e). In simple terms, equalizing contributions can be realized by obtaining one son from each male and one daughter from each female. However, such planning can be realized only under highly controlled conditions.

Regular selection and mating systems

When conditions permit, *Action 4* can be applied in a "regular" hierarchical system. In such a system, an equal number of females are mated to each male in every generation. The general idea is still to equalize contributions to the next generation and maximize the probability that every individual transmits its genetic information. The strategy works by performing a type of within-family selection (i.e. selecting the best of the sibs from each family) so that one male is obtained from each male family and one female from each female family (Gowe *et al.*, 1959). Under this procedure, the formula for the rate of inbreeding is $\Delta F = 3/(32N_M) + 1/(32\ N_F)$ (where N_M and N_F are the numbers of breeding males and females respectively) which is less than the ΔF obtained with random contributions:

$$\Delta F = 1/(8\ N_M) + 1/(8\ N_F).$$

This strategy can be refined so as to get an even smaller ΔF by controlling not only the numbers of offspring per parent but also the contribution of each individual to its descendants across generations (Sánchez-Rodríguez *et al.*, 2003 – see Table 8).

Table 8. Rate of inbreeding (percentage) and effective population size (in parenthesis) predicted under different management regimes

Number of males and females	Random selection	Within-family selection	
		Gowe	Sánchez-Rodríguez
3 ♂ 9 ♀	5.6 (8.9)	3.5 (14.3)	2.9 (17.2)
5 ♂ 25 ♀	3.0 (16.7)	2.0 (25)	1.7 (29.4)
6 ♂ 18 ♀	2.8 (17.9)	1.7 (29.4)	1.4 (35.7)
10 ♂ 50 ♀	1.5 (33.3)	1.0 (50)	0.8 (62.5)

Note that the formula for random contributions shown above only holds in the absence of selection on a trait, which is highly unrealistic for domestic animal populations. There is almost always some mass selection, because owners keep the individuals with high performance and thus co-select relatives more often than would occur by chance. Thus, this selection should be accounted using the method proposed by Santiago and Caballero (1995) (see Section 2). This simple approach involves dividing the ΔF arising from the formula by a factor of 0.7. However, under the above-described regular system methodology, within-family selection can be applied without increasing the rate of inbreeding (see Section 7 for further details).

Simple strategies

Sufficient control of contributions from individuals can be achieved with rather simple strategies. Where AI is practised, an approximately equal number of semen doses from each sire should be collected and distributed in order to minimize the variance in the number of offspring sired by the males. Recalling that the less-represented sex has the greatest influence on ΔF, a simple strategy might be to limit the percentage of offspring each sire contributes to the next generation. Implicitly this means that the largest number of sires possible is involved in the breeding programme. In the most extreme circumstances, each sire should leave only one son to the subsequent generation (if the population is growing the number of sons per sire should still be equal, but will be greater than one). In this way the variance in the number of sons sired by the males is reduced to zero. In highly prolific species, some attention should be also given to equalizing contributions from females, i.e. to avoid a situation in which a limited number of breeding females contribute progeny to the next generation, and in particular to ensure that the subsequent generation of sires comprises the offspring of different females.

Minimum coancestry contributions methodology using pedigrees

When pedigree data are available, the minimum coancestry contributions methodology, a more sophisticated strategy, can be applied. As explained above, the coancestry coefficient (f) is a measure of the probability that animals share identical alleles by descent. Relatives have common ancestors and are thus likely to carry identical copies of alleles. Some of the genetic information in relatives is redundant, and it does not matter which relative transmits it as long as the shared alleles pass to the next generation. Consequently, the individuals effectively contributing to the future population and the number of offspring from each individual can be derived on the basis of their coancestry with the rest of the population. In this process, animals that are closely related to the general population will be penalized (and only allowed to produce a few or no offspring), whereas relatively unrelated individuals will be chosen to produce more offspring. These latter animals are assumed to carry unique genetic information that would be lost if they did not produce offspring. This strategy minimizes ΔF, at least in the short and medium terms.

The minimum coancestry contributions methodology is robust against deviations from ideal conditions (accounts for related founders, does not need regular schemes with equal numbers of offspring per parent, can cope with mating failures). It also allows for the imposition of restrictions that correspond to the physiology of the particular species (e.g. maximum number of offspring from any individual). However, the methodology has some practical disadvantages. First, it requires tight control of the reproductive process and thus may only be applicable in particular populations, such as nucleus herds.

Second, the calculations are computationally complex. The aim of the methodology is to find the set of contributions c_i (i.e. number of offspring per individual *i*) that minimizes the function $\Sigma\,\Sigma\, c_i\, c_j\, f_{ij}$, where f_{ij} is the coancestry between every possible couple of individuals *i* and *j*. Even for small populations, the number of feasible solutions is huge, and finding the optimal solution requires the use of complex algorithms and the aid of computers. Therefore, expertise is required to implement the methodology. The free software METAPOP[10] (Pérez-Figueroa *et al.*, 2009) facilitates its implementation in a conservation programme without artificial selection.

The minimum coancestry contributions methodology was originally developed to work with coancestries calculated from pedigree data. It is thus strongly recommended that the pedigree of the animals be recorded in any *in vivo* conservation programme, so the coancestry can be calculated for the management of the population and the ΔF can be used for monitoring the success of the programme. The benefits obtained from the recording of the pedigree (just the sire and dam of every animal) generally exceed the extra cost the procedure involves.

Minimum coancestry contributions methodology using molecular information

In addition to measurement of genetic variability and prioritization of breeds (Section 3), molecular markers can be a powerful tool in the management of populations. When pedigree data are not available, molecular information can be used in the management of populations to decrease genetic drift. The possibilities for using molecular data in the management of animal genetic resource diversity include the following:

1. recovery, reconstruction or correction of partial genealogies (e.g. through paternity analysis for solving uncertain parentage – Jones *et al.*, 2010);
2. estimation of pedigree coancestry from molecular measures of similarity (Ritland, 1996); and
3. replacement of coancestry matrices based on pedigrees with the corresponding molecular coancestry matrices (Fernández *et al.*, 2005).

The outcomes of these three alternatives can be used as input for the implementation of the minimum coancestry mating strategy. Several computer tools exist for the estimation of pedigree relationships from molecular markers: for example, SPAGEDI[11] (Hardy and Vekemans, 2002) and COLONY[12] (Jones and Wang, 2009). A review of free software available for paternity analysis and for coancestry estimation can be found in Martínez and Fernández (2008).

Technological advances are continually decreasing the costs of molecular analyses, thus increasing the feasibility of their use in population management. In particular, the development and commercialization of panels of single nucleotide polymorphisms (SNP) has greatly expanded the precision with which molecular information can be used to manage genetic diversity (see Box 40). Further developments in genome sequencing will only expand the opportunities.

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[10] http://webs.uvigo.es/anpefi/metapop/
[11] http://ebe.ulb.ac.be/ebe/Software.html
[12] http://www.zsl.org/science/research/software/colony,1154,AR.html

Box 40

Population management using genomic information

The utility of marker genotypes for the management of populations depends on the amount of information they can provide about the diversity at the rest of the loci (i.e. the unmarked loci) in the genome. The information content is connected to the degree of correlation between genotypes at marker loci and the rest of the genome (this correlation is referred to as linkage disequilibrium), which is inversely related to the physical distance between loci in the genome and to the N_e.

When the number of markers is low (e.g. usual panels of microsatellites), the amount of information provided for genomic regions between markers is limited and genealogical coancestry (i.e. calculated from pedigrees) is preferred for the management of diversity (Fernández *et al.*, 2005). Nowadays, however, SNP chips containing a very large number of markers are available for many livestock species (up to 800 000 for *Bos taurus*). This high density ensures that every locus in the genome is in linkage disequilibrium with at least one SNP. Consequently, molecular coancestry is a more precise measure of genetic relationships between individuals than pedigree data, and greater diversity can be maintained when management is based on molecular genotypes (De Cara *et al.*, 2011).

Genome-wide information also allows for the measurement and maintenance not only of neutral genetic variability, but also of selective genetic diversity important for the productivity and evolution of the population. Therefore, SNP analysis of the genomes has become the method of choice for research and population management when DNA of individual animals is available or can be obtained, because the costs of SNP analysis are decreasing to an acceptable level.

Molecular information to clarify relationships between individuals

Even when a conservation programme includes pedigree recording, it is advisable to use molecular information to check the correctness of the pedigrees (e.g. to resolve paternity uncertainties) and to determine the genetic relationships among the founders of the programme (the term “founders” here refers to the base population of animals with which the conservation programme begins and after which pedigrees are routinely recorded). The ancestors of these animals are unrecorded and their pedigrees are thus uncertain. Traditionally, individuals at the base population are assumed non-inbreed ($F = 0$) and non-related ($f = 0$ for all pairs of individuals and $f = 0.5$ for self-coancestries). Most populations under conservation have been maintained with a limited number of individuals (parents) for one or more generations. Thus, assuming non-related founders is highly unrealistic and can lead to incorrect management.

A rough idea of relationship between founders can also be deduced from historical information obtained from their place of origin (e.g. the farm or geographic area from which they came). However, a more accurate approach is to construct a matrix of estimated coancestries based on molecular information on the founders (i.e. by using any of the methods and software described above). The coancestry of animals in subsequent generations is then calculated following the classical rules of pedigree analysis. Minimum coancestry contributions methodology will integrate the information about the relationships between founders, correcting for the disequilibria generated during the unmanaged generations that elapsed before the programme started.

The need to properly characterize relationships between founders is especially important for pedigrees with few recorded generations. In these situations genealogical parameters (e.g. F or ΔF) are poorly informative in the first generations of management, and decisions made at this point can have a huge impact on the probability of long-term success in maintaining variability. When little or no information about founders is available, extra effort should be made to ensure that all animals in the population produce offspring.

Action 5. Consider the use of embryo transfer in species with low reproductive rates

As noted in Section 1, reproductive biotechnologies such as AI and embryo transfer are occasionally cited as factors contributing to breed risk, as they facilitate the spread of germplasm across long distances and can contribute to shrinking N_e by decreasing the number of different parents required. However, the real reasons for breeds being at risk are factors such as their relatively low productivity and the lack of policies for their maintenance. In fact, when used strategically, reproductive biotechnologies can enhance conservation programmes.

For example, embryo transfer can increase the number of offspring per female. Increasing the number of offspring per female can have two positive effects. First, assuming that recipient females are of another breed, embryo transfer can be used to increase the census size of the population more quickly. Second, increasing the number of offspring per female is a very efficient way to equilibrate the ratio between male and female parents, especially if each female embryo donor is mated to multiple males. Sexed semen can provide similar (but smaller) benefits, at least in populations where (when unsexed semen is used) only a portion of the males born are needed for breeding.

Embryo transfer can also extend the generation interval, if used to obtain offspring from females that are no longer able to maintain pregnancies of their own. This benefit can be augmented further when combined with cryoconservation (see Task 3). This is a strong argument for cryoconserving embryos from populations that have a critical or endangered risk status in a gene bank.

One constraint to this approach is that embryo transfer can be technically demanding and requires considerable training to yield good results. Embryo transfer is also costly, so a financial feasibility study should be undertaken beforehand to evaluate the costs and benefits. Finally, the status of development of embryo transfer protocols is not equal across species and breeds within species. Most of the standard protocols have been developed for widely used commercial breeds of the major livestock species and some trial and error must be expected to adapt the standard protocols to less-common breeds and species.

Task 2. Adopt a mating strategy to decrease inbreeding

In the long term, the number of parents chosen and the number of offspring they produce are the main factors affecting genetic variability. However, after the selection of the parents, inbreeding and its detrimental effects can be further controlled by managing how the selected parents are mated with each other.

At least for one generation, the amount of genetic variability transmitted to or lost from the population is not dependent on the mating scheme but only on the number of offspring each individual contributes. However, the level of inbreeding (mean F) is highly dependent on which animals are mated to each other. The F of an individual is simply equal to the coancestry between its parents (f). The greater the relationship between sire and dam, the higher is the F of their progeny. Therefore, mating between relatives should be actively avoided. Several approaches (see *Actions* that follow) can be taken to avoid mating of relatives.

Action 1. Set a limit on the level of relationship between mates

The simplest way to decrease inbreeding to avoid mating between individuals that exceed a certain threshold of coancestry – for example half-sibs (e.g. $f = 0.125$). If potential mates are already inbred on the same ancestor, then this factor should also be accounted for, when possible. When several generations of the pedigree are known, the types of relationships that can be identified are more complex. In these cases, each livestock keeper could be provide (e.g. by the breeders' association) information on specific matings that should be avoided (or alternatively that are recommended).

Action 2. Establish the ideal set of matings for the entire population

A mathematically optimized approach to avoid mating of relatives has been developed and can be applied across a population. This approach is called the minimum coancestry mating design, and consists of finding the set of potential mates of selected parents that has the minimum average coancestry between partners (sires and dams). The methodology delays the rise of inbreeding, although does not reduce ΔF in the long term (Woolliams and Bijma, 2000). As is the case with the above-described optimal method of fixed contributions, the number of possible combinations is huge and the use of mathematical and computational techniques is required to solve the problem. Minimum coancestry mating design can be performed with the aid software, such as METAPOP[13] (Pérez-Figueroa *et al.*, 2009). Obviously this methodology can only be implemented in situations where mating is under central control. This rarely occurs in field conditions, but may be encountered in *ex situ* populations.

Action 3. Apply simple methods that do not require pedigree information

Circular mating systems

In the absence of genealogies, another mating strategy can be used. The idea is to arrange *n* families of individuals in a virtual circle. Male offspring from family 1 are always mated to females from family 2; males from family 2 are mated to females from family 3; and so on. Males from family *n* are mated to females from family 1. This strategy is known as the circular mating design (Kimura and Crow, 1963). An example of the implementation of such a programme is presented in Box 41. The methodology is easy to implement and ensures low ΔF in the long term, although it may increase ΔF in the short-term, due to partial subdivision of the population. When the population is maintained in several herds, and each herd is considered as a "family", the procedure converges with the so-called rotational system of breeding management. In this system some individuals are regularly (e.g. every year or every generation) exchanged between neighbouring herds and random mating is performed in the herds. This obviously implies some degree of organization and acceptance on the part of all participating livestock keepers. Past experience has shown that such a programme can be a great success or colossal failure, depending on the level of organization and cooperation among the livestock keepers. When starting from scratch (i.e. no previous subdivision of the population) one option could be to establish homogeneous groups by using cluster analysis methodologies to separate the population into as many lines as desired based on the genetic structure. When pedigree data are available, standard statistical software, such as SAS®, SPSS® or R, can be used to cluster animals according to their genealogical relationships. Various software are available for clustering based on molecular data, among which STRUCTURE[14] (Pritchard *et al.*, 2000) is one of the most commonly used.

Box 41

Mating systems to control inbreeding in Colombia

The Ministry of Agriculture of Colombia has maintained several nucleus farms for *in vivo* conservation of Criollo cattle breeds since 1936. During the initial decades of the breeding programmes, inbreeding was controlled by avoiding the mating of close relatives such as sire and daughter, son and dam, full and half sibs and cousins.

However, since 1991, the breeding programme of four breeds (Romosinuano, Blanco Orejinegro, Costeño con cuernos and Sanmartinero) was changed to the circular mating design. In each of the four breeds, all the animals were grouped into one of eight families according to their genetic relationships (i.e. eight families per breed). Then, the circular mating design was followed in each breed. Males of family 1 were mated to females of family 2, and so forth: 1→2→3→4→5→6→7→8→1. Several years later, the system was slightly modified – every three years the pattern is adjusted by skipping one family ahead: 1→3; 2→4; 3→5; 4→6; 5→7; 6→8; 7→1 and 8→2. This change was necessary because after a few breeding cycles, the females from family 2 were related to most of the males from family 1, females from family 3 to males from family 2, and so forth. To help facilitate the process and ensure proper matings, the offspring produced always receive the name or denomination of the dam's family.

Provided by German Martinez Correal.

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[13] http://webs.uvigo.es/anpefi/metapop/

[14] http://pritch.bsd.uchicago.edu/structure.html

Factorial matings

When females give birth multiple times during their lifetimes (which is the ideal scenario, as it increases the generation interval), factorial matings should be used. This means that each female should be given the opportunity to mate to different males. In this way, the number of possible mating combinations is larger and outcomes are better in terms of the amount of diversity maintained and the levels of inbreeding. In contract, hierarchical mating (mating each female to a single male), can result in the production of large full-sib families. When hierarchical mating is combined with selection (natural or artificial) the probability of selecting relatives is high. Moreover, if a male carries a dominant deleterious allele, the female genetic information has a high risk of being lost because all of its descendants may carry the deleterious allele. But if the female is mated to several males, its contribution will be safely transmitted through her offspring with other male partners.

Mate selection

Managing a population in two steps (i.e. first select individuals and determine their contributions, and then choose the mating design) is an option, but it may lead to complicated and less practical situations. For example, it may require the mating of a female with two males, which for many species is impossible in the same oestrous period without the use of reproductive techniques like MOET (multiple ovulation and embryo transfer). Therefore, it may be advisable to undertake both processes in a single step via a procedure called mate selection. The basis of this approach is determining the number of offspring to be born from each possible set of mates instead of from each individual. In this way, all physiological or logistical restrictions (e.g. limits on the number of mates per male or female, limits on the number of offspring per couple) can be accounted for.

Task 3. Incorporate cryoconservation in the management of genetic variation in the *in vivo* programme

Cryoconservation (for more information, see *Cryoconservation of animal genetic resources* – FAO, 2012*)* is another useful tool in a conservation programme (Meuwissen, 2007). It provides a manifold benefit to the programme, as it extends the reproductive lifespan of individuals (i.e. increases the generation interval) and increases the both the real population size and the N_e, as more individuals (which are less likely to be closely related) are available for mating at the same time. The storage of semen or embryos can address different objectives.

Action 1. Store genetic material from all animals at the start of the conservation programme

A first objective may be to use the collected material to create a “backup” of the breed, i.e. to store all the genetic diversity present at the beginning of the programme (one generation in case of embryos or somatic cells; two or more generations in case of semen). In the event of population extinction in the future, it will be possible to recover the breed using the stored material. The creation of such a bank is advisable for not-at-risk and vulnerable breeds and is strongly recommended for endangered and critical breeds that are likely to disappear in the near future. Obviously, storing material from all individual males and females would be feasible and logical only for a population at a critical level of risk.

In most situations, the germplasm is primarily stored for “insurance” purposes, and the probability that it will be needed is (hopefully) small. Therefore, approaches such as the storage of somatic cells that have low collection costs but high utilization costs (i.e. for cloning) may be logical options.

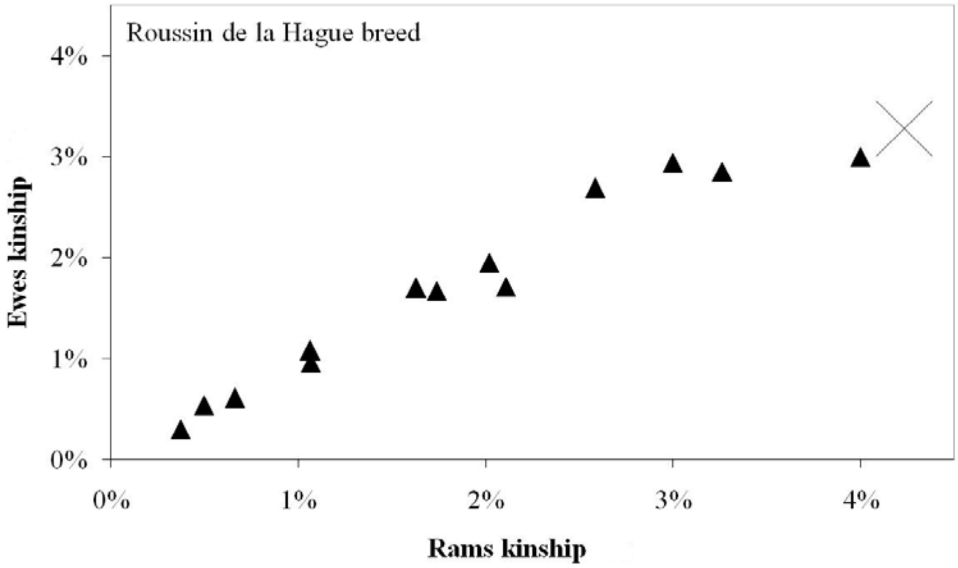
Action 2. Use cryoconserved material continually for management of the genetic diversity

A second objective of cryoconservation is to reinforce the *in vivo* programme. Cryoconserved germplasm can serve various purposes in a conservation programme. It may be used in a discrete way to help the population recover from a critical state (e.g. following a catastrophe that has reduced the population size). The cryopreserved material may also be used continually as part of the normal management procedure in a critical or endangered breed (Sonnesson *et al*., 2002). For example, cryoconserved semen, the number of sires can be increased, thus increasing N_e and decreasing costs (relative to keeping live males). In this scenario, collection of material for the gene bank should be a continual and permanent process that replenishes the doses used. Box 42 describes how the use of cryoconserved semen has helped increase genetic variability within a breed of sheep in France.

Box 42

Cryoconservation to increase the genetic diversity of a population *in vivo* – an example from France

The Roussin de la Hague is a French sheep breed that was considered to be at-risk during the 1990s. However, its status has improved considerably since then. The total number of ewes is now estimated to be more than 3 000. As part of the breed's recovery programme, semen from 13 rams was collected at the beginning of the 1990s and the stock was eventually moved to the French National Cryobank. An analysis was performed in 2010 to evaluate the genetic diversity of the rams in the *ex situ* collection relative to the active populations (i.e. the rams and ewes that are presently used by the breeders). Results are shown in the figure below. Based on pedigrees, individual kinship (▲) with the active rams (x-axis) and the active ewes (y-axis) was calculated for each cryoconserved ram and compared with the average kinship of the active rams with themselves and the active ewes (×).



Clearly, most of the cryoconserved rams are weakly related to the active population. Most of the rams have kinships of less than 2 percent with both current males and females and all have less relationship than the average of the *in vivo* population. The cryoconserved rams represent genetic diversity that no longer exists *in situ*. Other studies (Danchin-Burge *et al.*, 2009) have shown that the Roussin breed went through a bottleneck in the 1990s, when only three farmers were providing a large majority of the rams. Now that the breed's demography has improved, it is time to think about improving also its genetic diversity; some farmers have decided to use the semen from the cryoconserved rams to produce their replacement animals.

Provided by Coralie Danchin-Burge.

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VII. OPTIONS FOR BREEDING PROGRAMMES COMBINING CONSERVATION AND SUSTAINABLE USE

Breeds often face the risk of extinction because they provide inadequate economic returns to livestock keepers, who need to be compensated for the costs of inputs and labour and to sustain their livelihoods. The availability of highly specialized international transboundary commercial breeds with greater production potential speeds up this process. Many countries have chosen to import germplasm from such breeds in an effort to quickly increase productivity. However, the commercial breeds are often not suited to local conditions and require significant financial investment to exploit their genetic advantage in production potential. In many cases, the costs of these investments are not fully compensated by the additional production obtained. An alternative option is to take advantage of local breeds' advantage in adaptation to the prevailing environmental conditions and to implement breeding programmes to increase their productivity.

Importance of adaptation

Mirkena *et al.* (2010) summarized the genetics and adaptation in farm animals:

> *"Adaptive fitness is characterized by survival, health and reproductive related traits. The wealth of knowledge generated so far indicates that genetic variation for adaptive performance particularly disease resistance is ubiquitous both within and among breeds of livestock indicating that genetic studies on adaptation of farm animals can be determined at three genetic levels: species, breed and unique genetic variation among individual animals within a breed. In the warmer tropical areas, where pathogens and epidemic diseases are widespread, climatic conditions are stressful, and feed and water are scarce, locally adapted autochthonous breeds display far greater level of resistance and adaptation due to their evolutionary roots as compared to imported breeds. There are three pathways of genetic improvement: improvement of local breeds through pure-bred selection, breed substitution (by other local breeds or, more frequently, by exotic breeds), and systems of crossbreeding (terminal crosses, rotations, formation of synthetic lines). Whichever pathway to follow, choice of the most appropriate breed or breeds to use in a given environment or production system should be the first step when initiating a breeding programme and due attention must be given to the adaptive performance. A major limitation is that selection for less heritable traits such as fitness-related traits results in low selection response due to measurement problems and the underlying antagonistic biological relationships between productive performance and adaptive traits. The appropriate strategy for any breeding programme would therefore be to set suitable selection goals, which match the production system rather than ambitious performance objectives that cannot be reached under the prevailing environment. An area-specific approach utilizing the existing resources and taking into account the prevailing constraints appears to be the only reasonable sustainable solution. Such an approach would also enable in situ conservation of animal genetic resources, the only viable and practical conservation method in less developed countries compared to ex situ or cryoconservation approaches. Therefore, the importance of identifying the most adapted genotype capable of coping with the environmental challenges posed by any particular production system has been indicated."*

The production potential of breeds at risk is usually poorly documented due to the high cost of performance recording. Evidence for adaptive and fitness traits is often anecdotal. Knowledge gaps can be addressed by implementing or supporting characterization studies, but low economic returns will continue to threaten the survival of the breed(s) in the short term. Potential for long-term survival is meaningless if short-term survival is not ensured. Various measures can be taken to improve a breed's economic performance and provide livestock keepers with returns to justify maintaining the breed. Governmental support or incentive payments can help to rescue a breed in the short term, but are unlikely to be sustainable in the long term (EURECA, 2010).

Breeding for economic performance

Two main breeding strategies for enhancing economic performance are:

1. to increase production through within-breed selection; and
2. to implement cross-breeding between locally adapted breeds (with their unique adaptive and fitness traits) or between locally adapted breeds and transboundary commercial breeds (with greater genetic potential for production).

When the population size is small, it is of critical importance to optimize the selection response and the genetic variability within the population.

As in all conservation programmes (i.e. regardless of whether genetic improvement or maintenance of genetic diversity is the main goal), any proposed breeding programme must be must be thoroughly evaluated in advance, taking into account the expected benefits and costs and possible pitfalls. A wrong decision may drive the whole programme to complete disaster and the population to extinction. It is highly recommended that anyone planning to develop a breeding programme should contact people who have been involved in past attempts to develop such programmes in the same or similar populations and environments and learn from their successes and failures. Kosgey *et al.* (2006) point out some of the factors influencing the probability of success in the establishment of breeding programmes in local breeds. These factors include:

1. the ability of the programme to address the needs of local livestock keepers;
2. the compatibility of proposed changes and innovations with the existing production system;
3. the availability and appropriateness of incentives (economic and other) for the livestock keepers to participate in the programme; and
4. the extent of support services (e.g. veterinarians) available in the area.

Several promising options are outlined by Wurzinger *et al.* (2011).

Improvements through breeding

Rationale

Selection for production traits

The most obvious route to enhancing economic performance is to increase the production of commodities for the mainstream market, such as meat, milk and eggs. Success is most likely where the production potential of the local breed is already high but has not been sufficiently documented and appreciated (see Box 43). In such situations, interventions such as improvements in management and marketing may be sufficient to significantly increase economic return to the livestock keepers and improve the risk status of the breed (see Section 8). However, such situations may not be common. Almost any livestock breed will benefit directly from attention to classic animal breeding and improvement schemes. The potential of these breeding programmes to achieve greater productivity than obtained by transboundary commercial breeds will vary from place to place, and is likely to be greatest in challenging environments where breeds that are not locally adapted face major hurdles to survival and production due to problems with adaptation and fitness. However, implementation of breeding programmes may be more difficult in these areas as well.

Selecting for enhanced production in a pure-bred local breed is an attractive option. However, selection implies changing the breed, so consideration must be given to the possibility that some changes may not serve the long-term interests of the breed or its breeders. If a selection programme is planned carefully and if the breed’s adaptations to local conditions are maintained, then the result can be a well-adapted, productive breed. There are many examples that illustrate the success of such an approach: Nguni cattle in South Africa, Spanish goats in the United States of America (Box 44), Mertolengo cattle in Portugal, and Colonial Spanish Horses in the Americas. Establishing a pure-bred nucleus herd where emphasis is given to recording traits and selection of breeding animals can not only enhance selection for increased production, but also enhance publicity for the productive potential of the breed (FAO, 2003).

Box 43

The importance of locally adapted breeds in the Plurinational State of Bolivia

The Ayapaya llama is a local strain with high production potential that had been overlooked by most development programmes. These llamas are kept by the Wallat'ani highland community in Plurinational State of Bolivia and have better fibre traits than lowland animals have. Selection of local animals has been established as a formal activity (in contrast to unorganized past efforts) and benefits the local community. Similarly, in this environment, some local Bolivian guinea pig strains are superior to imported ones for litter size, number of young weaned and total weight produced. Identifying these local animal genetic resources of high production potential is important for achieving the dual goals of improving the livelihoods of livestock keepers while sustaining national animal genetic resources.

Source: Valle Zárate (1999).

Box 44

Optimum body weight for Spanish goats guarantees adaptation to the climate in Texas, United States of America

In the 1960s, West Texas ranchers began selecting local Spanish goats for production characters. Selection alone, with no cross-breeding, increased mature size of females from 35 kg to 70 kg. Breeders then discovered that females over 60 kg were less well adapted to the challenging semi-arid West Texas environment. Once they relaxed their perception of the ideal weight down to 60 kg, the breeders were able to have the increased production they sought, as well as the environmental adaptation they needed. Larger and non-adapted specialized breeds had little opportunity to compete. In addition, relaxing selection pressure on size and growth rate allowed for more emphasis on meat conformation. The result has been a very productive animal genetic resource that is also exquisitely adapted to its environment.

Provided by Phil Sponenberg.

Attention to the long-term effects of selection

Cross-breeding with high-output international transboundary breeds has been promoted because gains in production can be often seen in a single generation. Response to within-breed selection is not as rapid. However, most locally adapted breeds have not undergone selection that specifically targets the production of commodities. In such cases, with a proper design, it is often possible to make reasonably rapid gains in production traits in the first few generations of a selection programme. Pure-bred selection programmes also usually provide more long-term security for the communities keeping the breeds than is provided by a cross-breeding scheme. However, this argument will not always be intuitively accepted, because the initial improvement in production in a pure-bred selection programme will usually lag behind the initial boost imparted by cross-breeding and the heterosis effects in the first cross. Part of the reason for the relatively large improvements that can be obtained by selecting within a locally adapted breed is the relatively high heritability of production characters, and the relatively low heritability of traits of adaptation and resistance. This means that more rapid and secure progress can be made by selecting a locally adapted breed for increased production than can be made by selecting for adaptation in a high-output international transboundary breed. Non-standardized locally adapted breeds are very likely to be more variable than high-output international transboundary breeds, and the highest performing animals can have great productive potential. Unfortunately, the mental image of a highly productive, temperate breed can sometimes overpower the long-term strategy of selection within a locally adapted breed, with breeders impatient for a quick response to high demand for livestock products.

Selection opportunities in relation to the state of the breed

Breed census size affects the potential usefulness of selection. In the case of breeds with small population (i.e. critical or endangered status), it is difficult to undertake selection without creating potentially dangerous bottlenecks. Therefore, although a achieving an N_e of 50 should be a short-term goal for an *in vivo* conservation programme, the long-term goal should be to exceed this threshold while making genetic improvement. Principles outlined in Section 6 should be carefully applied so as to maintain genetic variation in the long term. Mating decisions in more populous breeds should consider both population maintenance and selection for improved production. In developing countries, within-breed improvement programmes can contribute to improved income and livelihood of people who depend on low-input production systems. These breeding programmes must have outputs that are consistent with the producers' objectives and aim to meet some market demand and thereby provide a return on producers' investment in improving the breeding stock. The bottom line is that successful adoption of a technology (e.g. AI) depends on its feasibility and its compatibility with the needs of the livestock keeper and the production system. The technology has to be relatively simple, relatively cheap, and above all, involve relatively little risk. It is necessary to look at the production system holistically, and involve the livestock keepers at every stage in the planning and operation of the breeding programme, while integrating traditional behaviour and values (Van Arendonk, 2010).

Sustainable breeding

Most locally adapted breeds must be selected for increased performance so that they become competitive in the production of standard commodities. The immediate economic needs of the owners demand this. Any pure-bred selection programme should also conserve the breed as a genetically, historically and culturally distinct animal genetic resource. Options for increasing performance must be carefully evaluated for long-term effects on the evolution of the breed; the technical, financial and infrastructural requirements of implementing a breeding programme and the ability to maintain sufficient genetic diversity within the breed to ensure its sustainability. Effective ways to measure performance cheaply and accurately are important and often require creative strategies for animal identification and record keeping (see Boxes 45 and 46). However, systems that function in one production environment may not be feasible in another (see Box 47). The goal is a sustainable system that works to identify consistently those animals that are top performers in the local environment so that they can be selected for breeding and their contribution to the next generation can be ensured.

Box 45

A simple recording system improves cattle fertility in the Bolivarian Republic of Venezuela

Some large commercial beef ranches in the Bolivarian Republic of Venezuela have changed from measuring individual growth rates of calves to putting more emphasis on female fertility and longevity as greater contributors to overall herd productivity. One easy solution to monitoring fertility was to brand an "X" on the back of any cow failing to wean a calf in any year. No cow is allowed two "X" marks, as she is culled after failing a second time. With the record system being marked on each individual animal and easily readable in the field, the result has been increased fertility in commercial cow herds. Year of birth is also branded onto the animals, enabling easy evaluation of both longevity and fertility. Similar systems might include ear tags or ear notches for cattle and other species instead of branding.

Provided by Phil Sponenberg.

Box 46

Animal evaluation by card-grading – an example from the United Kingdom

Animal shows are a good way to promote a breed and to generate interest among breeders. The show ring has also provided the traditional visual inspection method for simple evaluation of breeding animals, but this system has some drawbacks. First, it focuses attention on a small number of animals that are placed first in their class, and gives “star” status to the champion. As a result, these few “fashionable” animals frequently attract undue patronage by breeders, which concentrates their influence in the breed. The outcome is loss of within-breed diversity. In addition, the show ring often emphasizes traits that have questionable value for productivity and survival.

Since the 1980s the use of card-grading (see also Box 32) has been promoted in the United Kingdom by the Rare Breeds Survival Trust (RBST) for the evaluation of livestock animals. The card-grading approach is fairly simple and straightforward, but avoids concentrating attention on a few animals for breeding.

Purpose

The purpose of card-grading is to classify a population into broad groups of potential genetic merit by visual inspection and thereby prevent domination by a single animal or small group of animals.

Procedure

Animals are classified into four groups by the award of a coloured card: red card for above average; blue card for average; yellow card for below average; and white card for disqualified animals.

Advantages

Card-grading can be applied to any species of livestock and standards can be adjusted to obtain a visual scoring system that most accurately evaluates productivity and fitness. The proportions of animals likely to receive each card can be set at levels that allow loss of genetic variability to be avoided, i.e. by ensuring that several animals are likely to receive red cards. However, the standards should be set against a theoretical ideal, meaning that at some events perhaps no animals will receive red cards.

Limitations

Card-grading is a visual inspection and therefore not a perfect guide to breeding ability, especially for traits that are strongly influenced by management and other environmental factors.

It is a subjective evaluation and relies on the expertise and conformity of graders.

Despite these limitations, selection based on card-grading has the potential to yield genetic improvement at a relatively low cost.

Provided by Lawrence Alderson.

Box 47

Molecular selection not feasible for alpacas in Peru

In Macusani, Puno, Peru the alpaca export market disrupted the local market for alpaca breeding stock and other products. This caused a change in breeding objectives. An attempt was made to change from traditional systems to more high-tech systems that used marker assisted selection and pedigree-based programmes. However, these approaches all failed in the local situation, because they were not sustainable in this remote region due to lack of infrastructure and lack of cultural familiarity with these techniques. Recapturing the previous traditions of visually classing males for breeding has helped to re-establish advances in the production of alpacas with high local value and appreciation.

Provided by Phil Sponenberg.

Objective: To develop a breeding programme for local breeds to increase production.

Input:

1. Assessment of the productive potential of local breeds; and
2. Evaluation of non-market traits (e.g. adaption and longevity).

Outputs:

- Strategies for increasing performance in pure-bred animals and, where relevant, of cross-breeds;
- A comparison of these strategies for their immediate effects on commodity production as well as their effects on long-term maintenance of adapted animal genetic resources for local food security; and
- Analysis of the costs of the breeding programme, which should be kept as low as possible for low input – low output breeds.

Task 1. Implementation of a pure-breeding programme with selection for production

Action 1. Analyse the history of selection within the breed

Information on the selection, exchange and use of sires, along with any records of gains from selection should be collected and analysed. Evaluate also the population structure and production potential of animals relative to the type of production system. Determine where the top-producing animals of the breed are located, and how they are being used.

Action 2. Decide on the production and other breeding goal traits that should be improved by breeding

Decide which production traits will be measured. Clearly, a measurement of the yield of the product to be sold (e.g. meat, milk, fibre or eggs) is essential. In species with multiple offspring, number of offspring per pregnancy is also an important trait. However, profitability is affected both by production and by the costs of production. Functional traits that affect the cost of production, such as longevity, fertility, environmental adaptation, and ability to withstand stressors such as walking long distances to graze, may be as important as production. Defining these latter traits carefully can benefit well-adapted breeds (see Box 48). The guidelines *Breeding strategies for sustainable management of animal genetic resources* (FAO, 2010) provide advice on identifying important traits and determining breeding goals. Replacement and mortality rates can be used to identify superiority in adaptation, as can rebreeding intervals or litter sizes. Cost of rearing replacements is important, as is the quality and quantity of feed required and any requirements for other special management measures. Labour and veterinary costs should be included in the assessment, as should the financial return from the sale of products and offspring. Lifetime profitability is a key component. Adapted livestock are likely to have long productive lives, as well as multiple outputs, products, and services beyond the usual market commodities. Fertility and mortality are major traits. Smaller animals will frequently exceed the performance of larger ones for these traits (FAO, 2010).

Box 48

Fleece quality as a sustainable breeding goal for sheep in Chiapas, Mexico

More than 20 years ago, sheep production among the Tzotzil people in Chiapas, Mexico, changed from pure-breeding of local breeds to cross-breeding to enhance the production of meat. However, the Tzotziles do not consume sheep meat. This factor, as well as declining quality of fleeces for local textile needs, caused the incomes of the sheep producers to stagnate compared to those obtained under the traditional systems. At this point, it was recognized that performance for culturally relevant traits is a sound breeding objective. This led to the development of an effective open nucleus breeding system, based on selection for fleece quality, visual inspection and organization of ram distribution controlled by the local community. Attention to local practices ensured greater participation as well as enhanced economic return. The producers, the environment and the local culture all became beneficiaries of a well-thought-out sustainable system.

Source: Perezgrovas *et al.* (1997).

Action 3. Implement identification, registration and performance recording

An appropriate system for identification and pedigree recording of individual animals must be developed and implemented, and important performance and functional traits should be measured. All traits must be evaluated in all populations to ensure that no important information is omitted from the final decision-making process. Deciding how to measure production is important, as different measures may yield different results and vary in efficiency. For example, measuring only first lactation records of milk production may select different animals from those selected by measuring lifetime production. Repeated measurements of the same trait will increase accuracy, but also costs. Production measures should maximize total economic return. Factors such as longevity and cost of inputs can demonstrate the advantages of local animal genetic resources over imported ones.

Action 4. Recording and selection for production, fitness and body conformation traits should be implemented in relevant environments

Improved commodity production can be antagonistic with respect to maintenance of traditional type in some breeds, especially when animals are adapted to difficult environments. Measures of productivity for such breeds should include productivity with low inputs in their natural production environments. Traits associated with functionality, reproduction, survival and fitness should be recorded as well. Lifetime productivity can indicate longevity and fitness, as a useful addition to measures such as growth rate or lactation yields per day. If survival in difficult environments is necessary, then adaptation to these environments must be taken into account in selection programmes. Unfortunately, recording and selection for traits associated with function and fitness is often more difficult than for production. Heritability tends to be smaller and traits are often more difficult to record. Innovative approaches may be needed for efficiency.

Action 5. Decide on the selection and breeding strategy that is most likely to succeed in improving production

For conservation, the most common approach will be to apply a pure-breeding strategy. However, sometimes the productivity of the animals that have low genetic ability for production can be enhanced by crossing them with a more productive breed (see below). In this respect, it may be worthwhile to capture the value that a pure-breed has in providing hybrid vigour to cross-bred offspring that can be marketed while the pure-breed is maintained (FAO, 2010).

Optimizing selection response and genetic variability within small populations

Rationale

Response to selection

As noted throughout this section, one of the options for increasing the probability of survival of an endangered or vulnerable breed is to improve its profitability. Increasing the productivity of a breed will usually make it more profitable and therefore increase its chances for self-sustainability. However, improving a population’s genetic ability for productivity and maintaining its genetic variability (i.e. high N_e) are antagonistic processes. Some compromise is required.

Classical theory on the response to artificial selection states that the “selection response” or gain (G) in the mean value of the trait per year can be calculated using the following equation:

$$G = i\rho\sigma/L,$$

where i *is* the selection intensity, ρ the correlation between the estimated and the real breeding value of the individuals (also known as the accuracy of selection and equal to the square root of heritability when selection is based on phenotypes), σ the additive genetic standard deviation for the trait (i.e. genetic variation) and L the generation interval. Consequently, to obtain greater responses, the values of i, ρ and σ should be increased and the value of L reduced.

Maintenance of genetic variation vs. response

Selection intensity is a measure of the pressure put on the population and is related to the ratio of selected animals to candidate animals in the population. Larger values are obtained by selecting fewer individuals as parents for the next generation. However, this practice will reduce N_e, an outcome that is in conflict with the main objective of a conservation programme, and will lead to higher levels of inbreeding and reduced genetic diversity. More accurate estimates of breeding values (i.e. increased ρ) are often obtained by using information about relatives in addition to the individual phenotypes. This strategy will lead to the co-selection of relatives, especially for traits with low heritability, contributing again to the loss of diversity and an increase in inbreeding. Short generation intervals will also increase the gain but, as described above, also increase the amount of genetic variability lost per year. Recall that in Section 6 (Task 1, Action 3) increasing the generation interval was suggested as a means of increasing genetic variability, highlighting the trade-off between genetic improvement and the maintenance of variation. The presence of σ in the numerator of the selection-response equation gives another reason for maintaining genetic diversity (i.e. high σ) in the breed, as response is greater when σ is larger and no response for a trait can be obtained if there is no genetic variation. In summary, all the actions that can be taken to improve the gain in response oppose the general objectives, from the genetic point of view, of a conservation programme. Consequently, some balance must be established between the various forces.

Objective: To improve the productivity of a breed while avoiding the loss of genetic variability as much as possible.

Inputs:

1. Knowledge of the following characteristics of the breed to be conserved:
    - size of the population
    - reproductive capacity of the species
    - characteristics of the production system
2. Awareness of country’s livestock development objectives and existing and potential markets for animal products.

Outputs:

- Agreement among stakeholders with regard to traits to be improved and relative importance of genetic gain and maintenance of diversity;
- Clearly defined selection goal in terms of the trait(s) to be improved; and
- A general breeding plan that will optimize genetic improvement and will maintain genetic diversity.

Task 1. Adopt a general breeding strategy to maintain the conserved breed

Action 1. Determine which trait or traits are to be improved in the conserved breed

The determination of the objective of selection (i.e. the breeding goal: the trait or traits we want to improve in the population) has to be done in consultation with stakeholders. This process is described in more detail in the guidelines *Breeding strategies for sustainable management of animal genetics resources* (FAO, 2010). This evaluation could be done in conjunction with the studies conducted to investigate the conservation values of the breed (Section 3). If the presence of a particular characteristic has been identified as an important justification for maintaining the breed, this characteristic should obviously be included in the breeding goal, because reducing performance for that trait would diminish or remove the justification for maintaining the breed. If this characteristic is a qualitative trait, it is important to ensure that selection to improve other productive traits does not cause the characteristic to disappear from the population.

The ability to provide products for a specific niche market can make animals more valuable (see Section 8). If a niche market is to be targeted, the trait(s) that will affect the breed’s competitiveness in this market should be identified. For example, if milk from a given breed is going to be used for the manufacture of a particular type of cheese, the traits selected for should include not only the amount of milk produced, but also the quality, in terms of milk protein and fat content, as well as (if possible) traits related to cheese production. To derive a breeding goal, it is necessary to determine for each trait the increase in profit that will be obtained when the trait is improved by one unit. This increase in profit indicates the relative value of each of the traits, which can be summed up to form the breeding goal. When feasible, a selection index should be created with traits that are measurable and that correlate as highly as possible with the breeding goal. Ideally, breeding goals should be kept as simple as possible so as to ensure that the really important traits are improved. Secondary traits can initially be accounted for simply by requiring that the breeding animals meet minimum acceptable levels for each trait. These traits can be formally incorporated into the selection index at a later point when the selection programme is well established and the population has increased its census size. Culling of affected animals for control or elimination of genetic defects may be an example of selection for a secondary trait (see Box 49).

Box 49

Selection to eliminate genetic defects

Genetic defects tend to be more common in populations with low genetic variability. Populations at the start of conservation programmes may show genetic defects at frequencies of greater than 10 percent. Consequently, in addition to developing a breeding programme for other traits, explicit actions have to be taken to remove the genetic information that provokes the disease, or at least to reduce the frequency of deleterious alleles to a reasonable level.

The effectiveness of strategies to remove genetic defects will be affected by the nature of the genetic determination of the particular defects. Genetic defects are often controlled by a single gene. In such cases, the inheritance of the disease and the detection of carriers of the deleterious alleles are simple. In many cases the deleterious allele is recessive and thus only expressed when in homozygous form (i.e. in a double copy). The manifestation of such defects is more common in small populations (particularly those with a small N_e) because homozygosity is increased when genetic variability is decreased. When the defect is recessive, many individuals (heterozygotes) will carry the allele but not show the defect. Genealogies may be used to identify individuals with a high probability of being carriers. To eliminate the defect, first animals showing the disease and then carriers should be avoided as parents of the next generation, as long as the programme is not compromised by a too large a reduction in the number of breeding individuals. If a DNA test exists for the gene responsible for the defect, individuals can be genotyped and carriers unambiguously detected and excluded from the breeding programme.

When the trait has a polygenic determination and behaves as a quantitative trait with different degrees of expression of the disease, a regular selection programme should be implemented to eradicate the defect from the population. In any case, it should be stressed that the measures taken to eliminate the defect should include restrictions on the loss of genetic diversity so that the breed avoids troubles brought about by a rise in inbreeding. For example, it may be necessary to slow down the eradication of a recessive allele (Sonesson *et al.*, 2003).

Obviously, not all defects are genetically determined and selection, and breeding will not influence the occurrence of such defects.

Action 2: Agree upon the acceptable rate of inbreeding in the conserved population

The acceptable rate of inbreeding per generation (ΔF) will depend on the status of the population and the characteristic of the species. For highly endangered breeds, the values proposed in Section 2 can be used for pure conservation programmes, i.e. $\Delta F \leq 1$ percent (assuming this is possible). As long as the population is not in the critical or endangered categories, restrictions can be relaxed and a larger ΔF can be chosen. In commercial breeds, there is a general consensus that the maximum acceptable ΔF is about 2 percent, but the figure may vary between species. Remember that the more emphasis given to the maintenance of diversity, the lower the response obtained on the selected trait, and vice versa. One option is to predict the expected gain for a range of ΔF and choose the compromise solution that best meets both objectives.

Task 2. Design a breeding programme that generates genetic improvement while maintaining genetic variability

Action 1. Evaluate the circumstances under which the breeding programme will be applied

Various actions can be taken to achieve some selection response while maintaining genetic variability at an acceptable level. The appropriate measures will depend on the species, the production system, the ownership of animals and level of central control of breeding decisions, the level of cooperation among breeders, the availability of technical capacity and infrastructure, and various other factors,

Action 2. Consider the various options for balancing genetic improvement and maintenance of genetic variability

Numerous options have been proposed for increasing genetic variability when applying selection. Five options are presented below, roughly in order of increasing complexity.

Option 1. Determine the ideal number of parents when applying selection

The first approach to the control of inbreeding during selection is to determine the number of males (N_M) and number of females (N_F) that would give the desired (acceptable) rate of inbreeding (ΔF) and then select the best N_M males and the best N_F females, according to the selection goal. Then each of the selected animals should contribute the equal number (i.e. equal within sex) of offspring to the next generation. The desired number of animals of each sex (according to the ΔF desired) can be obtained by using the formulae presented in previous sections, such as $\Delta F = 3/(32\ N_M) + 1/(32\ N_F)$ (Gowe *et al.*, 1959).

The process of selecting the best animals to be parents is called “mass selection”. This type of selection can also be called “truncation selection”, because it involves selecting all animals above a certain threshold or “truncation point”. In this case, the truncation point for males (females) is the selection criterion, such as phenotype or estimated breeding value, of the N_M^{th} highest male (N_F^{th} ranked female).

Option 2. Apply within-family selection

A simple and effective way to control the ΔF while improving the genetic potential of a breed for a productive trait is to implement within-family selection. As explained in Section 6, within-family selection consists of selecting one male from each sire family and one female from each dam family (i.e. each sire is replaced by one of his sons and each female by one of her daughters). Following this strategy, the population maintains a larger N_e than it would with random contributions (see Table 9), but there is still some room for selection. Instead of choosing a son or daughter at random from each family, the best animal(s) in each family for the traits of interest is(are) chosen, thereby obtaining some gain in the traits. The selection intensity will depend on the size of the families, and will thus vary by species. However, the rate of gain will not be exceptionally large in any species, because this approach exploits only the within-family variability and ignores the genetic differences between families. Nonetheless, within-family selection is a sensible and easy way to achieve low ΔF in selection programmes.

Option 3. Apply family selection

The opposite of within-family strategy is family selection, a method in which all selected individuals are taken from the family (or group of families) with the highest average trait value. This method provides greater response than within-family selection, but also leads to greater losses of diversity and higher ΔF, as all the selected animals are close relative.

In reality, a wide range of options ranging from complete within-family to complete family selection can be considered. For example, Table 9 illustrates a hypothetical situation in which a breed consists of eight families, each of which has four males and four females, from which a total of eight animals of each sex have to be selected based on individual genetic values and/or family means for the traits of interest in the breed. The two extreme options are:

1. selecting the best single individual of each sex from each family (represented by row 1 in Table 9), or,
2. selecting the best animals from the two families with the highest mean value (Option 2).

But there are several intermediate solutions that will differ in the response they yield and the N_e they imply. All solutions have to be tested to find the one that yields the desired ΔF.

Table 9. Different ways of selecting individuals from eight families and the expected responses to selection and inbreeding (in percentage) that they imply

	Distribution of family sizes									
Options	Male/female pairs taken from each family (n)								Response	F (%)
1	1	1	1	1	1	1	1	1	5.90	7.96
2	4	4	0	0	0	0	0	0	17.42	42.76
3	4	3	1	0	0	0	0	0	18.17	35.81
4	4	2	2	0	0	0	0	0	17.87	33.26
5	4	2	1	1	0	0	0	0	17.78	30.59
6	3	3	2	0	0	0	0	0	17.30	30.59
7	3	3	1	1	0	0	0	0	17.21	27.80
8	4	1	1	1	1	0	0	0	16.38	27.80
9	3	2	2	1	0	0	0	0	16.91	24.87
10	3	2	1	1	1	0	0	0	16.24	21.79
11	2	2	2	2	0	0	0	0	14.91	21.79
12	2	2	2	2	1	1	0	0	14.85	18.57
13	3	1	1	1	1	1	0	0	14.23	18.57
14	2	2	1	1	1	1	0	0	13.56	15.20
15	2	1	1	1	1	1	1	0	10.83	11.66

Source: Toro and Pérez-Enciso (1990).

It must be emphasized that the real number of animals that need to be kept to ensure the desired N_e is affected by a combination of factors that include selection model, mating ratio and the size of the families (see Table 10).

Table 10. The minimum number of sires to be used per generation to achieve an effective population size of 50 or more, for different mating ratios and expected family sizes, and assuming $h^2 = 0.4$

	Mass selection							Within-
Mating	Lifetime offspring						Random	family
ratio	4	8	12	16	20	36	selection	selection
≥5	21	23	25	27	28	30	15	10
4 to 5	21	25	27	28	29	32	16	11
3 to 4	23	26	28	30	31	35	17	11
2 to 3	25	29	32	34	36	40	19	11
1 to 2	31	38	43	46	48	55	25	13

Source: Woolliams (2007).

Option 4. Implement weighted selection

Notice that implementing Options 2 and 3 reduces ΔF at the cost of a lower response than is obtained through mass selection with a fixed number of males and females selected (Option 1). Ideally, it would be desirable to control ΔF without losing response. According to the rules of strict truncation selection, the selected individuals should contribute the same number of offspring to the next generation. However, if this condition is relaxed and differential contributions are allowed, more individuals can be selected without losing selection intensity, and a larger N_e obtained (see Box 50 for an example). This is possible because the best individuals are allowed to contribute relatively more, with their contribution proportional to their genetic value (phenotype or estimated breeding value). This methodology is called “weighted selection”, because more “weight” is given to the better individuals. The disadvantages of weighted selection are the need to keep more individuals as selection candidates, which implies increased costs for the maintenance of these extra animals, and somewhat greater complexity than strict truncation selection.

Box 50

Weighted selection – an example

A recent study by Moreno *et al.* (2011) used simulated data to compare weighted selection versus truncation selection in a small population (32 animals of each sex). Under truncation selection, the 32 individuals of each sex were evaluated per generation and 8 were selected as parents. Each selected individual contributed four sons and four daughters to maintain the census size of the population. This process resulted in a selection intensity of 1.235 and the N_e was 19.8. When weighted selection was implemented, the optimal scheme corresponded to selecting the best 12 individuals of each sex, but the number of offspring obtained from each of them was allowed to vary. Specifically, the 12 selected animals were allowed to produce 6, 4, 4, 3, 3, 3, 2, 2, 2, 1, 1, and 1 offspring each, respectively, ordered from highest to lowest in genetic value (i.e. the best animal of each sex produced six offspring, whereas the 12th best animal produced only a single offspring). In this scenario, the selection intensity was exactly the same as in the truncation selection scenario (1.235), but N_e was nearly doubled (31.5), as more individuals contributed offspring.

Source: Moreno *et al.* (2011).

Option 5. Apply optimum contribution strategy for selection

Weighted selection determines particular individuals' contributions to the next generation based exclusively on their genetic value for the selected trait(s). However, the simple approach described in Box 49 is only optimal if the genetic relationships between animals are equal for all pairs. This condition is not realistic in animal breeding, as differences in the relationships between pairs will almost certainly be present. When pedigree information is available, a superior solution, called the "optimum contribution strategy" is possible. The optimum contribution strategy accounts for the coancestry of candidates as part of the decision criteria and is thus a logical approach to minimizing inbreeding for a given level of genetic response. This methodology is recommended as the most powerful way of dealing with genetic gain and inbreeding at the same time (Meuwissen, 1997). The aim of this approach is to vary the numbers of offspring produced by selected individuals so that they are proportional not only to their genetic value for the selected trait (as with weighted selection), but also to their degree of relationship with the rest of the population.

In the animal breeding context, the degree of relatedness is usually expressed as the additive relationship, which is twice the coancestry between any couple of individuals. Following the optimum contribution strategy, if there is a group of relatives that have high values for the trait of interest, not all of them will be allowed to contribute offspring. Not surprisingly, however, as was the case with minimum coancestry contributions (Section 6), the implementation of optimum contributions requires a highly controlled production system, several generations (at least four) of complete pedigree information, and the use of complex mathematical procedures (see Box 51).

Action 3. Implement and monitor the chosen breeding programme

Once the desired programme is chosen, extensive cooperation with breeders and other stakeholders will be required for implementation. All of the options listed in Action 2 will require recording of performance information for the traits upon which selection will be based and all but Option 1 require some pedigree data (knowledge of parents as a minimum).

Box 51

Optimum contributions strategy of selection

To better account for the two opposing forces, genetic response and genetic variability (ΔF), both of them should be included in the objective function but with opposite sign (+response and $-\Delta F$). The expected mean value for the selected trait of the next generation components can be estimated as the product of the value of parents by the number of offspring they contribute. Expected inbreeding is calculated by multiplying contributions and coancestries. Therefore, the objective function to optimize is $\Sigma\, c_i\, v_i - \Sigma\Sigma\, c_i\, c_j\, f_{ij}$, where c_i is the contribution of individual i, v_i is its genetic value for the selected trait and f_{ij} is the coancestry between individuals i and j, which is considered for every possible pair of animals. In practice, the term regarding ΔF is treated as a restriction, and the algorithm searches for the solution (i.e. combination of offspring contributed by each individual) with the highest ΔG but not exceeding the desired value for ΔF. Several methods have been proposed to solve this optimization problem, all of which require the use of computer programs. The program EVA[15] (Berg *et al.*, 2006) is one of the software available to manage a selection programme with restriction on the inbreeding levels.

Cross-breeding for enhanced production

Rationale

The potential of cross-breeding

The use of cross-breeding as part of a conservation effort may seem counterintuitive, but it can be a valuable option in certain situations. The concept of using limited cross-breeding for genetic rescue of an extremely endangered population with small N_e is introduced in Box 38. There are, however, other instances where cross-breeding may be able to play a role in a conservation programme. Cross-breeding can be particularly beneficial when the objective of the conservation programme is to use the beneficial genes of a breed at risk without having to obtain high economic returns from the pure-bred population.

Cross-breeding provides the opportunity to combine the genetic characteristics of different breeds. It is recommended when there are multiple breeding-goal traits that have antagonistic genetic relationships, such as between production and fertility or between production and quality of the product. It can be difficult to improve such traits simultaneously in a single breed. For example, combining the adaptive traits of a locally adapted breed with the production traits of an introduced international transboundary breed might be attractive. However, cross-breeding is only effective and sustainable if the breeding system is carefully chosen and well planned. The breeds used should be available in the long term and the plans should be strictly followed by the livestock keepers. A section in the guidelines on *Breeding strategies for sustainable management of animal genetic resources* (FAO, 2010) is devoted to cross-breeding.

Cross-breeding strategies

One simple strategy for maintaining local animal genetic resources is to apply cross-breed to the non-recorded and low-producing surplus local females, while maintaining pure-breeding (and within-breed selection) among the best animals of the local breeds. This procedure of limited and targeted cross-breeding not only saves the more productive well-defined local breeds but also maximizes the contribution of the lower-producing animals to local commodity production and food security.

Breeds that have been characterized for production potential and determined to be economically sustainable should be managed through breeding systems with the purpose of enhancing their productivity, and their female animals should generally not be used for cross-breeding. These breeds should instead be improved through selective breeding within the pure breed. Breeds that have been characterized as low producing, or those that are already crosses of local breeds, are logical candidates to have their production improved by using genetically superior germplasm either from local well-

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[15] http://eva.agrsci.dk/index.html

defined improved breeds or from international transboundary breeds that are relevant for the local production systems. The decision to cross-breed should then be based on economic factors (costs versus expected returns) and degree of agreement by the keepers of the local animals.

Unregulated and unmonitored cross-breeding can rapidly erode the numbers and genetic integrity of any breed that is used widely for cross-breeding. The utility of many breeds comes specifically from their role in organized cross-breeding systems, so attention must be given to maintaining a sufficiently large and well-managed pure-bred population to ensure the continued availability of animals for the cross-breeding system.

Information required for planning cross-breeding systems

When a breed is used in a cross-breeding programme, specific information should be collected during breed surveys and characterization. Useful information about the breed's role in cross-breeding includes population numbers and the current proportion of pure-bred as opposed to cross-bred breeding. Recording the number of females mated pure quickly captures this aspect of the breed's dynamics. The data collected should also include the ultimate fate of cross-bred and pure-bred offspring, and whether these are terminal (i.e. marketed without producing offspring) or used for further reproduction. Assessments should include the relative quality (high, medium, low) of the animals used in pure-breeding and those used in cross-breeding. It is important to describe the role of each sex in the cross-breeding production system (e.g. are males used for cross-breeding with other breeds or are females used in this role?). Ideally, pure-bred populations will be undergoing selection for enhanced performance as measured in both pure-bred and cross-bred offspring.

Implementing cross-breeding systems

The planning and implementation of a cross-breeding programme should be based upon a clear understanding of what is wanted as an outcome of the programme. If the objective is to increase production in a local breed, cross-breeding with an introduced breed may be considered. A fairly common and simple approach used to improve production is to cross a local breed with a high-output international transboundary breed. This can be done with one of two goals in mind,

1. replacing the local genetics, i.e. by making continual successive crosses to the introduced breed, or
2. upgrading the local breed, i.e. by crossing to the introduced breed until the population contains a high proportion (usually >75 percent) of introduced-breed genetics.

The replacement strategy is clearly *not* conservation and frequently fails in tropical or other environmentally stressful regions because the resulting animals are less well adapted to the local conditions than the original population were. Thus, before embarking on a strategy that will lead to the elimination of local animal genetic resources through replacement breeding, the consequences of such a strategy must be thoroughly investigated. Local animal genetic resources can usually make a valuable contribution to the local production system in the long term, in which case their survival and availability must be ensured. At the very least, the local animal genetic resources to be replaced *in vivo* should be cryoconserved. Breed introduction should usually not even be considered unless the enhanced production (locally realized and not only potentially possible) can be expected to be at least 30 percent greater than that obtained from the pure local breed (FAO, 2010). When this is the case, a system that involves producing F1 animals and conserving the pure local population should receive primary consideration. As noted above, a sound strategy is to cross-breed the relatively lower-producing portion of the local population and to reserve the most productive local animals for pure-bred breeding.

According to Schmidt and Van Vleck (1975) two main classes of cross-breeding system can be distinguished:

1. systems that require maintenance of the pure-breeds (pure-bred and rotational crosses); and
2. development of a new (synthetic) breed by systematically mating cross-bred females and cross-bred males.

Pure-bred crosses

Pure-bred crosses involve the mating of pure-bred animals from different breeds for one or two generations so as to produce cross-bred animals that "terminate" the breeding system. Such strategies are generally defined by the number of breeds involved:

- Two-way crosses: individuals of two pure breeds are mated and the offspring are used only for production (i.e. not for breeding). For example, the dairy cows with the lowest breeding values for milk production in a herd are not selected as dams for producing replacement dairy animals, but are mated to a bull from a beef breed to produce offspring that have better capacity for beef production than pure dairy calves.
- Three-way crosses: two-way cross females are mated to a sire from a third breed to produce offspring used for the production goal. For example, in pork production, two breeds with high fertility and maternal traits are occasionally crossed and cross-bred sows then mated to a sire from an excellent meat-producing breed to obtain a large number of piglets with the characteristics desired for pork production. Sometimes the two-way cross females are mated back to a sire of one of the parent breeds – this is known as a backcross. Sexed semen can be used to enhance such a cross-breeding programme if animals from one sex are more desirable for production purposes (see Box 52).
- Four-way crosses or double two-way crosses: two-way cross females are mated to two-way cross males to produce the animals used for the production goal. For example, this type of cross-breeding is the preferred breeding method employed by multinational breeding companies for specialized egg and broiler production.

Box 52

Effect of sexed semen in producing a final cross in dairy cattle

The availability of sexed semen in dairy cattle has been eagerly anticipated for many years, and recent developments in fluorescence-activated cell sorting have brought this technology to commercial application. In recent years, a number of AI companies have started to offer sexed semen to their farmers. Semen sexing provides the potential to increase the numbers of offspring of one sex in a closed population, thereby increasing the intensity of selection for that sex. Semen sexing enhances the farmers' ability to obtain a larger number of replacement heifers from their own herds. In a herd with a stable herd size, semen sexing could be used to breed replacement heifers from the cows with the highest genetic merit. This will create a one-time lift of the genetic level of the herd. The largest economic benefit of using sexed semen in pure-bred herds would come from the ability to use the remaining dairy cows for the production of cross-bred animals for meat production Semen sexing can be used to increase the efficiency of producing F1 dairy hybrids. For an F1 scheme to be sustainable, part of the pure-bred population needs to be mated to bulls of the same breed to produce replacements. The number of cows that need to be mated for breeding replacements can be nearly halved by the use of sexed semen. In addition, the number of F1-females that are produced can be nearly doubled by using sexed semen. In other words, the number of pure-bred cows that need to be kept for the production of F1 hybrids can be reduced by 60 to 75 percent, depending on the sex ratio resulting from the use of sexed semen. The economic benefit of this reduction is largest when pure-bred cows and cross-bred cows are competing for the same resources. Benefits are smaller in a stratified cross-breeding system, such as that used in Brazil where dairy farms buy replacement F1 females, than in the poultry or pig industry. The replacement females are produced in areas where land is less expensive, using Holstein semen on Brazilian dairy zebu breeds.

Source: Van Arendonk (2010).

When implementing two-breed crosses involving the use of imported animal genetic resources, the use of the local breed as the source of pure females and the exotic breed as the source of sires is strongly recommended. Two-way crosses require only a limited number of sires, so maintaining a population solely for the production of males could result in a greatly reduced census size, which would increase the risk of extinction.

Breaking the cycle in which low census numbers limit the potential for within-breed improvement is difficult. Small population sizes limit the selection intensity that can be applied and/or increase inbreeding. If a higher census size can be coupled with good record keeping and selection, then progress can be made in increasing productivity, which will subsequently increase the breed's value and help secure its sustainability in commercial settings. If the only perceived value of a breed is as a component of a cross-bred population, then securing the breed in sufficient numbers for pure-bred selection will be difficult. Moreover, breeds with small population sizes are likely to be overlooked as resources for commercial purposes, and therefore remain in low numbers and at risk of extinction (see Box 53).

Box 53

Two-tiered demand for Criollo Saavedreño cattle in the Plurinational State of Bolivia

The use and conservation of Breeds that excel in cross-breeding involve complicated issues. Temperate breeds such as the Holstein and Brown Swiss have been imported into the Plurinational State of Bolivia in an effort to increase milk production, but pure-bred cows belonging to these breeds have had difficulty surviving in the environment of the Bolivian Tropical Lowlands. To address this problem, the Criollo Saavedreño cattle breed was created under the guidance of Dr John V. Wilkins from the British Tropical Mission in Bolivia with the purpose of providing bulls to be mated to the temperate cows to produce offspring better adapted to the local conditions. The Criollo Saavedreño was created by selecting bulls from Criollo breeds throughout Latin America that had already been selected for improved milk production.

While the development of this breed was successful and the Saavedreño bulls meet with a brisk demand for use in cross-breeding, the pure-bred cows are much less in demand than the cross-bred cows. This has meant that the number of pure-bred animals has remained relatively low (some few hundred head mostly at a single government installation). As a consequence, selection within the breed remains somewhat lower than that achieved in breeds that have larger population sizes. Production is unlikely to diminish, but selection differentials are unlikely to be high enough to quickly increase genetic merit for productivity. This situation gives rise to a cycle in which low population size prevents within-breed progress in selection for production, which in turn ensures that the population remains small.

Provided by German Martinez Correal.

Rotational crosses

There are three general types of rotational crosses:

- Crisscrosses: a two-way cross female is mated to a sire of one of the two breeds used to produce the original two-way cross and their female offspring are mated to a sire of the other breed. This alternating pattern of sire-breed usage is then continued in subsequent generations.
- Three-way rotation: Sires of three breeds are used in successive alternating generations on the cross-bred dams of the previous generation.
- Multibreed rotation: such rotation schemes can be extended to the use of four breeds (four-way rotation) or to the continued use of sires from new breeds (indeterminate rotation).

An advantage of rotational crosses is that they do not require exchange females between herds or villages, which decreases costs and reduces disease transmission. Only the sires of the breeds involved have to be purchased by the owners of the females. AI will eliminate even the need to purchase the sires. Another advantage is that the rotational systems maintain high heterosis, 67 percent with a two-breed rotation and even more when additional breeds are involved. A disadvantage is that the producing and reproducing offspring will eventually represent different generations and therefore different combinations of breeds and thus can show high variation in phenotype. Also, if one of the breeds is an international transboundary breed, maintaining the rotation may require continual importation of new germplasm. Rotational schemes involving a high number of breeds can be problematic in terms of monitoring and require the availability of a wide variety of germplasm. Three-way rotations may be the most efficient compromise.

Composite breeds

In some unfortunate cases, either the population size of a breed at risk will be too small to avoid an extinction vortex (see Section 6) or its production potential will be too low to justify the establishment of a breeding programme for its conservation. In such cases, an option that may be considered is to sacrifice the breed as an independent entity, but conserve its genes by crossing it with another breed (or breeds) to create a new "composite" breed (also known as a "synthetic" breed). If two or more breeds are at high risk of extinction, they can be combined together to form a composite breed. Box 54 describes how the genetics of now-extinct cattle breeds in Sweden have contributed to contemporary populations. Bennewitz *et al.* (2008) have proposed a method (based on genetic markers) for determining which breed to match with an at-risk breed so as to conserve the maximum diversity among all the breeds within a country. Complementarity of phenotypes may also be used as a basis for matching breeds, especially in situations where molecular information is not available.

Box 54

Genes of "extinct" Swedish cattle breeds conserved in today's populations

The data for Sweden in DAD-IS at the end of 2011 listed 22 cattle breeds, including four that are classified as extinct. Although animals of these four breeds can no longer be found, the history of the breeds suggests that many of their genes are conserved in current populations. During the late nineteenth and early twentieth centuries, the populations of three of these breeds, the Herrgård, Småland and Skåne, were grouped together and used to form the fourth breed, a composite called the Rödbrokig Svensk Boskap (RSB or Red-pied Swedish). The RSB continued to evolve as well and in 1928 this breed was merged with the Swedish Ayrshire to form yet another composite, the Svensk Röd och Vit Boskap (SRB). Since then, although its name has not changed, the SRB has remained dynamic, incorporating and contributing genes to and from similar breeds in other Scandinavian countries.

Source: Bett *et al.* (2010).

Many composite breeds have been developed in the past 50 to 100 years (e.g. Shrestha, 2005). One particularly common strategy for tropical environments has been to create composite breeds by *inter se* mating of cross-bred animals that have resulted from an initial cross of an international transboundary breed to a locally adapted breed (or more complex combinations of more than two breeds). Selection usually stabilizes the exotic inheritance at around 50 percent, because in most cases any exotic influence above this results in a decline in most important economic traits because of poor adaptation. The long-term objective of producing a composite breed should be to stabilize the proportions of the foundation breeds to achieve a combination that is well adapted to the local production environment. Although formation of a composite breed can effectively conserve the genes of a breed at risk and yield a new genetic resource of potentially higher value and sustainability, the process is not simple and has its disadvantages and potential pitfalls (see Box 55).

Cross-breeding and conservation

All three of the cross-breeding systems (pure-bred crosses, rotational crosses and development of a composite breed) may be considered when developing a cross-breeding programme for conservation, although the composite breed approach is likely to involve the loss of at least one breed during the creation of another. It must be stressed that any cross-breeding approach requires a great deal of management to achieve the desired results. Indiscriminate cross-breeding is a major threat to local breeds (Tisdell, 2003) and has often yielded unsatisfactory results in terms of increasing productivity.

Box 55

Potential difficulties and pitfalls in the development of composite breeds

Increased complexity – in the initial years of a composite breeding programme (i.e. before a stabilized population is reached), animals of different generations may be present within the same herd or other breeding group. Animal identification and pedigree recording are necessary in order to ensure that animals with the desired proportions of each breed are mated. This factor is especially important when more than two breeds are involved or if the desired final proportions differ from 50 percent per breed.

Decreased uniformity – with matings involving cross-bred parents, proportions of the genes of foundation breeds in the offspring can theoretically range from 0 to 100 percent, resulting in a wide variation in appearance and performance.

Decreased productivity – heterosis in matings of cross-bred parents will usually be less than in crosses of pure breeds. Thus, performance may appear to decrease in the generations between the F1 and the stabilized composite, which may disappoint and discourage breeders.

Need for pure-bred populations – ideally, the pure-bred foundation breeds should remain available for infusion of genetic diversity if needed. However, this will be impossible in situations where the breed at risk is entirely integrated into the composite breed. Cryoconservation may be an option that allows this problem to be overcome.

Loss of cultural value – although the genes of breeds that are exclusively conserved in a new composite breed will be maintained, the breed itself will cease to exist and, therefore, some of the cultural significance of the breed is likely to be lost.

Ambivalence of breeders – unless they are closely involved in the planning and enthused about the idea, breeders' loyalty to the breeding scheme may be lower than it would be to a scheme based on a breed that they have a long history of keeping. They may therefore be more inclined to abandon the programme if success is not readily apparent. Alternatively, if close involvement gives them a sense of ownership of the breeding scheme, they may be proud of it and regard themselves as pioneers and innovators.

Objective: To develop a stable cross-breeding system that conserves an animal genetic resource.

Inputs:

1. A breed at risk for which development of a cross-breeding programme is a viable option for conservation;
2. Information about the breed at risk, including its population size and risk status, its strengths and weakness, and the opportunities and threats that may affect its long-term sustainability;
3. A description of breed's production system(s) including markets for products; and
4. Inventory and characteristics of other relevant local breeds and exotic breeds. This should include the breeds' production characteristics as well as breeding programmes for their maintenance and improvement, and their roles in cross-breeding systems.

Output:

- A sustainable cross-breeding programme for maintenance of an animal genetic resource, either as a pure breed that contributes animals to a subsequent cross, or by incorporating beneficial genes into a synthetic breed.

Task 1. Develop a system for cross-breeding to conserve an animal genetic resource

Cross-breeding programmes that are not well planned are likely to fail, or at least not to reach their desired objectives. A comprehensive plan for should thus be devised before commencing any cross-breeding activities. The National Advisory Committee on Animal Genetic Resources may take responsibility for this plan, or may choose to form a special *ad hoc* committee. The committee should include key stakeholders.

Action 1. Outline the desired outcomes of the cross-breeding system

The primary goal of any conservation programme will be to maintain the targeted animal genetic resources (as pure breeds or in the form of their important genes). Secondary objectives that support this main goal should be formulated. Examples of such secondary objectives may include improving the livelihoods of the livestock keepers and meeting local demand for the products of the animals. The products to be produced should be considered and overcoming constraints of the production systems must be accounted for. For example, the cross-bred animals will ideally have a greater genetic potential for production, but they may also have a greater demand for inputs. Factors that may restrict availability of such inputs may limit the feasibility of the cross-breeding programme.

Action 2. Evaluate the status of the targeted breed

The activities described in Sections 1 to 3 will provide most if not all of the information needed to make informed decisions on the establishment of a cross-breeding programme for conservation. Among the most important pieces of information are the census size of the population and its N_e, the breed's strong and weak traits, and the particular threats to its survival. Awareness of the breed's main stakeholders and some indication of their willingness to participate in a cross-breeding programme are also crucial.

Action 3. Evaluate the other breeds that are potentially available for inclusion in the cross-breeding plan

Cross-breeding will only be viable if genetic material from the complementary breeds in the cross is readily available in sufficient and sustainable quantities. A list should be made of all such breeds. Both other breeds from which live animals are available, and breeds for which only semen is available should be considered. The adaptability and productivity of these breeds in the local production environment should be determined through literature review and/or studies that document their phenotypic characteristics and performance levels (FAO, 2010). Special attention should be given to unique genes or traits that affect the complementarity of these breeds with the breed targeted for conservation.

Action 4. List the cross-breeding systems that are relevant for the production system

A critical initial decision will be whether or not the breed targeted for conservation can realistically be maintained as a pure-bred population. All pure-bred crossing and rotational systems require the maintenance of a population of pure-bred animals. Pure-bred crossing systems will require the largest populations, because they require the availability of two groups of females: one to maintain the pure population and another to produce F1 animals. Rotational cross-breeding systems will generally only require the production of sires (or access to preserved semen) to provide germplasm for cross-breeding.

As described in previous sections, the N_e of the pure-bred population should be ≥50, excluding the pure-bred females that are crossed to produce F1 animals in pure-bred crossing systems. Larger population sizes are preferable, obviously, to allow for greater selection within the pure breed. When N_e is significantly less than 50, incorporating the population into a synthetic breed may be the most practical option.

Maintaining pure-bred populations will also require the availability of stakeholders (either livestock keepers or government institutions) that are willing to maintain the breed, even though its production potential will likely be less than that of cross-breeds.

Action 5. Describe the function of the target breed and complementary breeds in the cross-breeding system

Attributes of local breeds that can be exploited through cross-breeding usually include characteristics such as disease resistance and stress resistance, quality and composition of animal products, adaptation to particular environments or production systems, and the ability to utilize coarse roughage and crop residues. The complementary breeds often are chosen to increase production.

Action 6. Choose the optimal cross-breeding system

Develop cross-breeding to enhance the performance of low-producing local animals, and reserve high-producing local animals for use in pure-breeding systems. Establish protocols that ensure some use of high-producing females from the target breed for pure-bred breeding. Select a group of breeding males that can be widely used locally. Determine how many breeds (usually between two and four) are needed to attain the final mix of traits that will provide the desired economic performance. Also determine the gender of the animals to be contributed by each breed.

Action 7. Present the plan to a wider group of stakeholders for final approval

Although various stakeholders, including key livestock keepers, should be intimately involved in the planning of a cross-breeding programme, the final plan should be presented to a wider group of stakeholders for discussion, revision if necessary and final approval. In particular, large numbers of livestock keepers that will be implementing the programme and subject to its costs and benefits must be consulted.

Task 2. Organize the logistics, implement and monitor the cross-breeding plan

Once the genetic plan for cross-breeding has been developed and agreed upon by stakeholders, the next step is to organize, launch and operate the plan, including procedures for monitoring its success. These activities are described in detail in *Breeding strategies for sustainable management of animal genetic resources* (FAO, 2010). A summary is presented here.

Action 1. Prepare the plan for the start of the cross-breeding programme

Before a cross-breeding programme can be launched, various factors have to be accounted for. For example, specialized personnel may need to be appointed to manage the programme. Infrastructure for communication and transport of animals may be needed. A financial analysis of the programme may be warranted, especially if substantial investments are required.

Action 2. Establish the financial and organizational structures

If outside investment is needed, these funds will have to be secured – most likely from the government or a specialized NGO. The cross-bred animals may require management that is different from that used to raise the original pure-bred animals, so training activities for livestock keepers may be required.

Action 3. Implement the cross-breeding programme

The cross-breeding programme will require continual attention and monitoring to detect and resolve unexpected problems. The appointment of a committee of particularly competent livestock keepers to aid in providing advice to their contemporaries and feedback to the National Advisory Committee for Animal Genetic Resources is recommended. Extension services should be established or strengthened and used to disseminate solutions to problems encountered.

Action 4. Organize the delivery of cross-breeding services

Cross-breeding programmes may require systems for exchange of germplasm that are more complicated than those for pure-breeding programmes. For pure-bred crosses, F1 animals may be produced on one or more farms and distributed to others. For rotational systems, breeders will need to have access to males of a variety of breeds, either as live animals or through AI. Programmes for synthetic breeds will likely benefit from the establishment of a new breeders' association and AI services. Support for research on ways to improve the programme will likely be beneficial.

Action 5. Improve the cross-breeding services and promote uptake

Promotion of the cross-breeding programme will help increase the number of livestock keepers involved, which will likely improve its success through various economies of scale and thus improve the sustainability of the targeted animal genetic resources. Programmes for animal identification, performance and pedigree recording will also contribute to the genetic improvement of animals and aid in general management of mating systems, as well as providing documentation for the evaluation of the programme.

Action 6. Evaluate the cross-breeding programme for benefits obtained and sustainability

The programme will need to be evaluated periodically to determine if its objectives are being met. In particular, programmes established to contribute to conservation need to be evaluated in terms of their effects on the targeted breed. The results of these analyses should be reported to all stakeholders, including livestock keepers, policy makers and any funding agencies.

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VIII. OPPORTUNITIES TO INCREASE THE VALUE AND SUSTAINABILITY OF BREEDS IN *IN SITU* CONSERVATION PROGRAMMES

Section 7 describes how selective breeding can be used to improve an at-risk breed in terms of genetic merit for production, and thereby improve its abilities to compete financially with other breeds. Although selection for increased production is usually recommended (as part of a comprehensive breeding goal) for endangered and vulnerable breeds with sufficiently large N_e, genetic improvement may not be enough to make the breed economically competitive. In most instances, the difference between the production levels of local breeds and high-output transboundary breeds is large. As genetic improvement is a rather slow process, many years may be required before a low-output breed achieves a competitive level of production. In other instances, a breed may be uniquely adapted to its environment and selection may upset this balance, with detrimental effects on both the breed and its environment. Therefore, although genetic improvement is usually recommended, conservation programmes should include additional, short-term approaches aimed at increasing the value of the targeted breeds.

Opportunities for sustainable use of breeds targeted for conservation

Rationale

There are several measures that can, depending on the circumstances, be taken to promote the sustainable use of breeds targeted for conservation by stabilising or increasing the incomes of their owners (Oldenbroek, 2007):

- Safeguarding the production environment in which the breed is found or the traditional lifestyle of its keepers.
- Improving the management of the animals at farm level. The production level of animals is affected by their genetic ability and the by their management (e.g. quantity and quality of the feed provided, housing and disease control). Although improving management requires investment, it will usually provide greater economic returns.
- Developing high-quality products for niche markets. Breeds have genetic differences in production potential and in the quality of their products. In general, selection for high production has a negative effect on the quality of products. Breeds targeted for conservation may have lower production potential than other breeds, but they may be the source of high-quality products (e.g. cheese, cured meats and textiles) that can be sold in niche markets where per-unit prices are higher, and this can compensate for the lower amount of product obtained.
- Promoting high-quality products by highlighting their connectedness to their places of origin. Such factors can be used to promote the products, for example through labelling schemes. Such activities require collaboration with breeders, producers and marketers to realize the enhanced price for the high-quality products, as well as with consumers, to ensure that sufficient demand exists.
- Marketing products may be based on social concerns for improved animal welfare. Intense selection for high production has decreased fitness traits in many high-output international transboundary breeds. These weaknesses are typically magnified if the breeds are kept environments to which they are not adapted. Breeds raised in their traditional production systems are likely to be healthier than animals introduced to these production systems.
- Marketing products based on concerns about breed conservation, i.e. because buying them helps to ensure the future existence of an at-risk breed.
- Drawing on the ecological functions of species and breeds in nature management to obtain an additional source of income. In many areas of the world, natural grasslands, wetlands or heathlands would become forest or low-value scrub if the vegetation were not shortened regularly. Governments may be willing to pay for the service of maintaining these areas.

Grazing herbivores are already used to conserve such habitats in many countries. Well-adapted breeds of cattle, sheep, goats and horses can be conserved in large numbers to fulfil this task.

- Drawing on governmental support or incentive payments from other source to sustain the societal and cultural functions of livestock species and breeds, including their roles in promoting tourism. This opportunity is often discussed, but it seems to be very difficult to realize. However the potential touristic value of some breeds – linked to their appearance, farming systems or folklore traditions – could be rather easily exploited by the tourism industry with beneficial effects for livestock keepers.

Objective: To document opportunities for conserving breeds.

Input:

1. List of breeds by species and characteristics of each breed.

Output:

- A description of the opportunities to secure the position of breeds or to generate more income.

Task 1. Select the opportunities for utilizing the targeted breed

Action 1. Determine the relevant opportunities and threats affecting the species to which the breed belongs in the country as a whole or in the local area

As part of characterization efforts (see Sections 1 and 3), the importance of the breed to the local area should be documented, as it may reveal opportunities that can be exploited to promote its sustainable utilization. The analysis of threats should include not only the effects of low productivity, but also other factors such as loss of access to the animals' production environment or cultural factors taking the livestock keepers away from farming.

If low productivity is found to be a weakness of the breed, improving livestock management should be among the first opportunities considered, as this will usually yield the fastest results, can be applied in almost all situations, and can complement other approaches. Not all opportunities are relevant for all species. For example, organic farming is usually not a good option for horses, and management of natural areas provides limited opportunities for chickens. Cheese production is a real opportunity for milk-producing cattle, sheep and goat breeds.

Action 2. List the characteristics of the breed and combine them with different opportunities (improving management, specialized or niche production, hobby farming, use in nature conservation, etc.)

For example, a table can be created in which the breed's characteristics are listed down the left margin and opportunities listed across the tops of the columns. Cells in the table can then be marked to show which opportunities are relevant to which characteristics.

The matching of characteristics and opportunities can be done as part of the SWOT analysis of breeds described in Section 1, by identifying a strategy that combines Strengths and Opportunities (SO-Strategy). Box 56 shows a list of the strengths of the Nguni cattle breed of South Africa and opportunities to exploit these strengths.

Action 3. Describe the realistic opportunities for the breed and make a plan to exploit each of these opportunities

Based on the relevant combinations of characteristics and opportunities identified in Action 2, specific measures to take advantage of these opportunities can be proposed. The activities required should be outlined and relevant stakeholders identified. The strengths and weakness of the opportunities should be noted, along with any obstacles that need to be overcome. The chances of success of a programme to exploit the opportunity should be assessed.

Box 56

Strengths of the South African Nguni cattle breed and opportunities to increase its value

The Nguni is a local South African cattle breed that has been raised by indigenous communities for nearly 1500 years. Because of its relatively small size and prejudicial preference for their own breeds, the Nguni was regarded as inferior by the settlers that colonized the country in the latter part of the last millennium. At different stages throughout history, the government supported specific programmes that favoured exotic breeds, leading to the near annihilation of the Nguni through “grading up” and breed substitution. The negative perception of the breed persisted until about 25 years ago when local officials began to appreciate the positive aspects of the breed. Well-designed characterization studies demonstrated that the Nguni was quite competitive with exotic breeds when compared in the same production environment. Having evolved in the area, the Nguni is well adapted to the prevailing climatic conditions and endemic diseases and pests. The government has realized that the Nguni could be a valuable animal genetic resource, especially for resource poor farmers, and the Nguni breed is now making a comeback, based both on its value for meat production in harsh environments and by on other strengths. The table below outlines the breed’s strengths and the corresponding opportunities to add value.

Strength	Opportunity
adaptability	low-cost production in marginal areas
meat quality	branded products, cross-breeding
unique coat patterns	specialty leather products
tick resistance	higher-quality hides (no tick-bite damage)
sloping rump structure	easy calving, lower production costs

Source: Ramsay *et al.* (2000).

Preparing a Biocultural Community Protocol for documenting a breed’s characteristics and the indigenous knowledge of its keepers

Rationale

In many instances, particularly in developing countries, breeds at risk have been developed and are largely kept by members of a specific community. These communities will often have a very strong cultural tie to their breed and strong interactions are likely to exist among the community, the breed and the surrounding environment in which the community and its animals exist. The community will often hold a wealth of indigenous knowledge on how to sustainably co-manage the animals and the local environment. In such cases, the survival of the breed will depend not only on its characteristics, but also on the continued existence of the community and the ability of community members to maintain satisfactory livelihoods in the face of external forces. The endangerment of the breed may be an indirect result of threats to the existence of the community itself. For example, loss of access to grazing lands or sources of water may hinder the ability of pastoral communities to continue their traditional lifestyles, including raising their particularly adapted livestock. Documenting the functions of a breed and the cultural practices and indigenous knowledge of the community that keeps it can inform policy-makers about their importance to society in general, including their role in the conservation of biological diversity.

One approach to gathering, organizing and disseminating this information is to develop a Biocultural Community Protocol a concept originally developed by the NGO Natural Justice of Natural Justice, 2009; LPP and LIFE Network, 2010). BCP are formal documents prepared on the basis of consultations between members of livestock-keeping communities (or other types of communities) and lawyers and experts in indigenous knowledge. They record (among other things) information about communities’ breeds, their roles in the livelihood of the communities, the indigenous knowledge of the community and the role of the community in managing diversity. Community protocols are recognized by the CBD and referred to in the *Nagoya Protocol on Access and Benefit Sharing*

(Nagoya Protocol)[16]. Box 57 describes the development of a Biocultural Community Protocol for the Samburu community in Kenya.

Presenting a BCP to policy makers will raise awareness of the activities of the community with respect to preservation of agricultural biodiversity and may help encourage the development of policies that are favourable to the continued existence of the community keeping the breed at risk and thus favourable to the survival of the breed. In addition, the activities through which the BCP is developed are usually educational to the livestock keepers themselves, increasing their awareness of the value of their resources and of their rights and responsibilities. The process of developing the BCP generally serves to empower the livestock keepers and their community.

Objective: To develop a BCP for keepers of a breed at risk.

Inputs:

1. An indigenous community with a breed at risk;
2. Knowledge of the characteristics of the breed, traditional practices in its management, its cultural significance and its interaction with the environment; and
3. A facilitating organization and a team of legal and other experts.

Outputs:

- A BCP relating to the breed at risk and its community of livestock keepers; and
- Community members informed about their rights and the value of their breed.

Task 1. Gather stakeholders and discuss the concepts underlying the content of the proposed BCP

Action 1. Establish a working relationship between the facilitating organization and the local community

Ideally, BCP are initiated and developed by the communities themselves. This is not realistic, however, in most situations, as many communities will not even be aware of the existence of BCP and not have access to the precise legal expertise required. Thus, the process is usually facilitated by an NGO or other external organization, ideally with an ongoing relationship with the community. If no such organization exists, then time must be spent in achieving familiarity between the facilitators and the community. Background research on the community should be undertaken before the process is initiated. Even if an ongoing relationship with the community has been already established, the process should be done very deliberately, at a pace set by the community rather than the facilitators.

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[16] http://www.cbd.int/abs/

Box 57

The Samburu Biocultural Community Protocol and conservation of the Red Massai sheep in Kenya

Background

The Samburu are a part of Maa speaking pastoralists found in Kenya and The United Republic of Tanzania. In addition to the Samburu, the Maa community includes the Maasai of southern Kenya and northern United Republic of Tanzania and Likipia and Chemus of northern Kenya. The Samburu are found in the dry region of northern Kenya. They keep many indigenous livestock species and breeds, including the Red Maasai sheep. This fat-tailed hair sheep has been kept by the Maa community for centuries. It is renowned for its drought tolerance, general hardiness and disease resistance, especially against gastrointestinal parasites. More importantly, this sheep plays an important role in the livelihood and food security of the Samburu, as well as serving numerous social-cultural functions Kosgey, 2004). More recently, the breed's unique genetic characteristics have attracted the attention of scientists, keen to understand their possible commercial benefits.

Although the Red Massai has valuable adaptability traits, its meat production is relatively low and the survival of the breed is threatened by intensive and sustained promotion of cross-breeding programmes with Dorper sheep and high market demand for large-bodied crosses. As a result, many Red Maasai sheep keepers are abandoning the breed in favour of the crosses. This is despite the fact that the increased incidence of droughts observed recently in Kenya is decimating the less hardy Red Maasai-Dorper crosses. The development of a Samburu BCP was therefore proposed, with the objective of reversing this trend by reinforcing the importance of the Red Maasai sheep and encouraging the livestock keepers to continue maintaining the breed.

The process

Although outside experts usually play a major role, the development of BCP is based on a participatory process that ensures that the communities involved take the ownership of the process and the product. The Samburu BCP[17] was initiated by a team that was composed of lawyers from Natural Justice, staff from the League for Pastoral Peoples, a female Raika community leader (with experience developing a BCP for her own community in India), a member of LIFE Network Africa and one prominent member of the Samburu community. The team held a series of meetings with the Samburu to create awareness. Later, the team facilitated a representative group of the Red Maasai breeders to document their local knowledge. Based on these interactions, a draft BCP was developed and then translated into the Samburu language. The translated version was then presented to a representative group of the Samburu community at a workshop during which they critiqued, amended and endorsed the contents. In addition, the Samburu used this opportunity to suggest a way forward regarding the use of the BCP and conservation of their local livestock breeds. They agreed to use the BCP as learning tool for their young generation, to inform the world of their important contribution to global biodiversity, to initiate village-level conservation efforts and to promote the endorsement of the BCP by other Maa communities. The document was then edited, typeset and published. The published document was launched at a ceremony organized in the Samburu territory and attended by officials from the Kenyan Ministry of Livestock Development and LIFE Network.

The benefits

The process of developing the BCP offered Samburu livestock keepers an opportunity to reflect on the sociocultural dimension of their livestock and enabled them to document their role in maintaining the diversity of animal genetic resources and ecosystems. They also became more informed about national and international processes and frameworks that recognize their role, and how they can be used them to draw attention from the outside world. The interaction between the Samburu and government officials at the launch of the BCP document and the subsequent wider sharing has promoted the exchange of ideas on issues relating to the conservation of local breeds and highlighted the role of the livestock keeper at both the national and international levels. In fact, the process of developing a BCP was an empowering process for the Samburu, as it helped them to think through various opportunities that may be inherent in their animal genetic resources. It also allowed them to flag their local breeds as their property and put on record the role of their traditional knowledge in the development of these animal genetic resources. The publication of the BCP generated excitement and interest among the Samburu, who were very happy to see their information published, and this has kindled their interest in initiating community-based breed conservation activities.

Provided by Jacob Wanyama.

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[17] http://www.pastoralpeoples.org/docs/Samburu_Biocultural_Protocol_en.pdf

Action 2. Hold a series of meetings to collect and discuss information on the community's customs, practices, indigenous knowledge and long-term plans and their objectives in developing a BCP

Meetings with various community members should be held to gather information and discuss challenges facing the community. Ideally, attendance should be balanced for gender and other factors, so as to ensure comprehensive representation. Information collected should include the characteristics of the breed, especially those characteristics that are particularly special or unique; traditional practices, methods and technologies used to manage the breed and its genetic diversity; and any particular efforts taken to care for the natural biodiversity within the environment where the breed is kept. Public goods that the community produce by keeping their livestock should be noted. The breed's cultural and ceremonial importance should be noted. Problems faced by the community that threaten their continued existence and ability to maintain their animal genetic resources should be discussed. Problems that may have political solutions, such as more favourable regulation of access to grazing or payment for environmental services, should be particularly highlighted.

Action 3. Obtain solid and preferably quantitative data about the community and its management of resources

The BCP will be a much more powerful document if it is based on strong and tangible evidence, rather than subjective political commentary. For example, inventories of plant and wild animal biodiversity in lands traditionally used for grazing may demonstrate that livestock keeping should be promoted in that area rather than restricted. Mapping, photos and video recordings can support the information collection process.

Action 4. Provide relevant and appropriate training to community members

The process of preparing a BCP can be even more important to the community than the final document that results from the process. The community members should be informed about policy instruments such as the *Global Plan of Action* and the *Nagoya Protocol* and of their rights as developers of their breed or breeds and as producers of public goods. Training on data collection and documentation, legal empowerment and facilitation of meetings with policy-makers should also be provided.

Task 2. Prepare the BCP

Action 1. Develop an outline of the BCP to ensure that all relevant information is presented in a logical and organized manner

There are no formal and rigid rules regarding the contents of a BCP, but the BCP that have been produced to date by livestock keeping communities[18] have generally had the following format:

1. Description of the community
    - location and environment
    - history
    - customs, values and laws
2. Description of the animal genetic resources
    - special traits
    - cultural significance
3. Description of the community's traditional knowledge
    - for management of animal genetic resources
    - for management of biodiversity in general
4. Statement on access and benefit sharing
5. Current and future threats and challenges
6. Call for action by policy-makers
7. Statement of commitment to protect biological diversity
8. Statement of the community's rights according to international law

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[18] http://www.pastoralpeoples.org/bioculturalprotocols.htm

In addition, appendices with supporting information, such as detailed records of the biodiversity the community has developed, a bibliography and a description of the process used to prepare the BCP are often included.

Action 2. Write the BCP in a format and language appropriate for policy-makers, the primary target audience

The BCP is recognized as a legal document, so its language must reflect this fact. It is for this reason that involvement of lawyers is a key aspect of preparing a BCP. The BCP must also be understood and approved by the community, so particular effort must be taken to explain the precise meaning of the final text to representatives of the community. Multiple versions of the BCP may be necessary, as the language used by the community may not be the official national language of the country.

Task 3. Publicize the BCP and distribute it to policy makers and other relevant stakeholders

Action 1. Present the BCP to policy makers

In order for the BCP to yield any effects, policy-makers have to be made aware of its existence. As a minimum, the BCP must be distributed to the relevant policy-makers. If possible, a more dynamic approach should be adopted, whereby representatives of the community and the facilitating organization meet face-to-face with the policy-makers.

Action 2. Promote the BCP to the general public

In a democratic system, the government is supposed to act according to the will of the people. Therefore, informing the public about the community, its way of life, its contribution to the maintenance of biodiversity, the challenges it faces and the BCP, may help to drive action by policy-makers. The facilitating organization may be expected to play a major role in this activity.

Task 4. Foresee and make plans to avoid obstacles and problems in the development of the BCP

Although BCP are intended to produce a positive impact on the community, the potential for negative consequences exist and care should be taken to ensure that problems do not occur.

Action 1. Facilitate, rather than push or drive the process of BCP development

The facilitating organization must adhere to its role – facilitation. The process must be driven by the community, with guidance from outside when necessary. Some communities may be reluctant to publicize information about their customs and way of life. Biases must be avoided when writing the document.

Action 2. Guard against biopiracy

Some communities may fear that increasing awareness of their animal genetic resources and their special traits will increase the chances that transnational companies or other external entities will attempt to reap financial benefits from these resources without equitably sharing the benefits. Such biopiracy has occurred with plant genetic resources. However, there is some doubt as to whether the same level of opportunities and interest exists in the case of animal genetic resources (Hoffmann, 2010). To help prevent such problems, material transfer agreements should be used to establish the terms for the use of any genetic material from the local animal genetic resources or indigenous knowledge that is distributed outside of the community. The rights of the community with respect to the animal genetic resources and knowledge should also be outlined in the BCP.

Improving management through extension activities and "role model breeders" programmes

Rationale

As described in Section 7, genetic improvement can improve a breed's economic performance and thereby increase its competitiveness and its chances of survival. Genetic improvement is permanent and cumulative, but it is a multigenerational process and its benefits are felt only in the relatively long term. A complementary approach to help ensure the economic sustainability of a breed is to improve its management. Improved management can contribute greatly to improved production, and provides owners with enhanced economic return in the near term, helping them to maintain the breed until the effects of genetic improvement can be realized. Improvements to management should go along with breeding and genetic aspects of breed maintenance. However, it is important that any improvements introduced are appropriate to the economic, social, cultural and environmental constraints of the local situation. In most circumstances, duplicating a temperate-zone intensive-production model is either not possible or not sustainable. Extension activities are a very effective way to build livestock keepers' capacity to improve the management of their animals, and can be implemented in cooperation with breeders' associations.

Most breeds can benefit greatly from the contributions of a few "role model breeders". Note that the particular name attached to the concept of a role model breeder varies in different countries and regions; "master breeder", for example, is another term that is occasionally used. In these guidelines, the term "role model breeder" is used to describe livestock keepers that have a great deal of indigenous knowledge that allows them to manage their animals well and to operate efficient breeding systems (see Box 58 for an example). Programmes that identify such individuals and then disseminate their knowledge and techniques are useful for all breeds. Role model breeders have expertise in both livestock management and genetic selection. This is important knowledge for future generations. It should be made available in a form that can be widely disseminated for the benefit of current and future breeders and of the breed itself.

Box 58

The contribution of role model breeders to the revival of the "Heritage Turkey" in the United States of America

The American Livestock Breeds Conservancy[19] has countered the slow erosion of traditional breeding techniques with a role model breeders programme (called "Master Breeders") that captures the knowledge and experience of these breeders. The first effort involved the production of non-industrial "Heritage Turkeys". Heritage Turkeys comprise a variety of locally adapted breeds of domestic turkey in the United States of America that retain various traditional characteristics that are no longer present in the modern commercial strains. Among these characteristics are the abilities to survive under extensive management conditions and to reproduce without the aid of AI. Turkey production in extensive settings was once common, but it is now a hard-to-find alternative to industrial production. As extensive systems declined in number, so too did the techniques used to raise turkeys, select breeding birds and ensure that production characteristics remained at a high level within the constraints of an extensive system.

Key breeders were identified and interviewed, and their techniques were then disseminated to a broad audience through a series of workshops held in different geographic regions. The programme has increased the number of Heritage Turkey breeders using time-tested selection techniques in their flocks. This has put the future of the heritage breeds on a firm footing based on their productive potential. Role model breeders are often also experts in marketing their breeding stock and the unique products of their animals.

Provided by Phil Sponenberg.

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[19] www.albc-usa.org

Role model breeders combine both scientific knowledge and art, and their strategies come from years of careful observation and experience. Their techniques are often intuitive, so they can be difficult to quantify and document. A careful outside observer can help define a role model breeder’s practices so that others can benefit from the breeders’ years of experience.

Objective: To create strategies for benefiting from role model breeders and to disseminate their knowledge.

Input:

1. List of potential role model breeders.

Output:

- A compilation of role model breeders’ knowledge;
- A strategy for benefiting from role model breeders; and
- Learning materials for disseminating the role model breeders’ knowledge.

Task 1. Prepare an inventory of role model breeders’ knowledge and experience

Action 1. Identify role model breeders

Actively search for highly regarded breeders of each breed. Such breeders may be identifiable based on the performance of their animals or because of their reputation within the breeder community. Therefore, relevant sources of information include performance records (assuming such a record-keeping system exists) and surveys of breeders.

Action 2. Interview role model breeders carefully to fully discover the techniques and attitudes that lead to their success

Observe role model breeders at work. Use this as an opportunity to uncover details that are second nature to the breeder and are among the keys to their success. Careful observation can tease out small details of management and selection.

Action 3. Document and define the role model breeders’ intuitive management techniques

Role model breeders’ techniques will only benefit other breeders if they are communicated. In the past this was accomplished by one generation working closely with the previous generation. However, transgenerational succession in livestock keeping is becoming increasingly uncommon and is not applicable for broader extension activities that need to reach a large audience. Documenting role model breeders’ methods so that they can be communicated to others helps to bridge this gap. Special attention should be paid to facilities for keeping animals and animal-handling techniques.

Action 4. Document and define the role model breeders’ intuitive selection criteria

Selection decisions are usually based on techniques that have proven valuable over many years. Some techniques may appear illogical, but nonetheless produce valuable results in the population. Such techniques should be documented for present and future generations. Note what traits are being measured or noticed, and what consequences these have for production or viability.

Task 2. Disseminate the role model breeders’ knowledge and encourage its application

Action 1. Make the information obtained from the role model breeders widely available

Tools for disseminating role model breeders’ knowledge can include handbooks, educational books, brochures, web sites, seminars and workshops. Workshops and field days can be particularly helpful as they can bring people into direct contact with role model breeders, thus creating opportunities for future networking, and can reinforce the transmission of ideas and techniques on animal improvement. In many instances, knowledge that is transferred first-hand through visual means and hands-on experience will be retained more readily than knowledge gained from reading or attending a lecture or presentation.

Action 2. Reward or otherwise recognize role model breeders for their contributions

Most role model breeders do what they do through their own initiative, either for personal satisfaction and/or to make their animals more productive and profitable, and thus do not necessarily expect to be rewarded for their actions. Nevertheless, they may appreciate formal acknowledgement of their activities and contributions to breed conservation. Many breeders’ associations have annual award programmes to recognize outstanding breeders. Certain countries offer similar awards to people that make particular contributions to the conservation of local breeds. An example from India is given in Box 59.

Box 59

The Breed Saviour Award in India

India is the putative centre of domestication for various livestock species and home to many animal and plant genetic resources for food and agriculture. Therefore, conservation of these resources is a national priority. To help aid the *in situ* conservation of livestock breeds, in 2007 the LIFE Network (Local Livestock for Empowerment of Rural People), a group of NGOs, proposed the idea of introducing "Breed Saviour Awards" to recognize individual livestock keepers or whole communities that make notable efforts to conserve and improve local livestock breeds. In 2010, this concept was endorsed by world-renowned plant breeder Dr M.S. Swaminathan. The Breed Saviour Awards programme is now being implemented annually by SEVA (Sustainable-agriculture and Environmental Voluntary Action) in collaboration with the LIFE Network, and it is supported by the National Biodiversity Authority. The award comprises a prize of 10 000 rupees and a special certificate. It is given annually to at least 20 honourees. Profiles of past winners can be viewed at http://www.sevango.in/breedkeepers.php. The profiles present examples of role model breeders who initiated their breed conservation efforts on their own, often improving their livelihoods as well.

Provided by Sabyasachi Das.

Award programmes can be beneficial not only in rewarding existing role model breeders for their contributions to breed sustainability, but also in encouraging novice breeders to apply their techniques and become role model breeders of the future.

Opportunities for conserving breeds through niche market production

Rationale

Worldwide there are several examples of breeds that produce high quality and distinctive products with the products contributing to effective breed conservation. Efforts to enhance the value of breed-specific products are as valid as efforts to enhance levels of production in a breed and may be a more realistic scenario for breeds of species where a few extremely productive breeds dominate the market. When breed-specific products obtain a premium in the marketplace the result is increased monetary return to producers, with an associated increase in breed security. In some cases, enhanced value is due to a unique product, in others it is due to increased appeal from to being able to buy a locally-grown product. Niche marketing can be ideal for certain situations if the products are marketed in a way that emphasizes traditional techniques and local ties (LPP *et al.*, 2010). Such efforts can involve existing traditional products and can also include newly developed products with unique characteristics.

These efforts can help local breeds that have somewhat less productive potential to compete with common international transboundary breeds that have been intensely selected to generate high yields of mainstream commodities (see Box 60). Promotion comes from consideration and attention to the uniqueness of breed-specific products. Breed-specific products can have broad appeal to consumers that are interested in regional products and can be especially important in safeguarding local animal genetic resources that are firmly tied and readily identified with a specific region.

Breed-specific promotions present a host of challenges as well as opportunities (LPP *et al.*, 2010). Challenges include the fact that the targeted breeds may lack recognition, and their products may be available in such low quantities that marketing is difficult because of uneven or sporadic availability. Organizing local producers can be a hurdle that is difficult to overcome, and making links to a stable ongoing market can be problematic. In most situations, the process will be most successful if led by a “champion”, a person or organization with a special interest in promoting the niche-marketing enterprise and making sure it works. On the positive side, local products often have some unique quality that can provide the basis for a marketing campaign. Highlighting the local character of such products and their producers can have a very beneficial effect in the local area. It focuses attention on local genetic resources and local traditions and thereby works to save both. Benefits accrue locally, and increase overall local economic capacity.

Box 60

Heritage Turkeys cut across ethnic and religious boundaries in United States of America

A very successful example of promotion in the United States of America has involved several traditional turkey varieties raised in traditional systems. This promotional effort contrasts these "Heritage Turkeys" with the more common (and inexpensive) industrially produced birds. One of the more important unifying cultural events in the United States of America is Thanksgiving Day, a celebration held in late November that involves a celebratory meal. This meal has traditionally involved consumption of turkey and associated side dishes, and is a celebration that cuts across ethnic and religious boundaries in the United States of America. Nearly everyone participates, and it is, in a very real sense, the one focused celebration that is common to nearly the entire country.

The significance of turkey as part of the celebratory Thanksgiving Day meal has made it possible to promote traditionally raised, Heritage Turkey varieties for consumption at this one feast. Though the cost of the heritage birds may outstrip commercially produced birds by up to ten times, the demand for the heritage birds is currently so high that it goes unmet. The demand for adult birds has also dramatically increased the demand for poults of these varieties, which has in turn allowed hatcheries greatly to increase the size of their breeding flocks. The increased demand has reversed the trend that seemed to be leading to the certain extinction of many of these varieties. This reversal has been directly related to the promotion of a specific product, raised in a specific way, for a specific feast. This is all the more remarkable because the demand for the Heritage Turkeys is miniscule when compared to the millions of industrially produced birds consumed on Thanksgiving Day. Increasing the size of breeding flocks has also increased the interest of breeders in traditional techniques of bird evaluation and selection. Through this, the previously successful practices of the early and mid 1900s have been recaptured from a very nearly complete loss.

Provided by Phil Sponenberg.

Focusing on breed-specific products has the advantage of providing a reasonably secure market niche for a breed's unique capabilities. In many situations this requires a market with the potential to value uniqueness over more standardized commodities, and cash-strapped societies are less likely than more affluent ones to be able to afford this relative luxury. While this is generally the case, it also remains true that traditional products can and do find increased demand even in societies in which disposable income is minimal. The price differential for the preferred local products can often provide enough economic advantage to help the breeders of the animals that produce them. As incomes rise and disposable income becomes more available, these traditional products can gain an increasingly large share of the total market.

Objective: To develop a business plan for marketing high-quality products from a breed targeted for conservation.

Inputs:

1. A "champion" who will lead the niche-marketing process;
2. A list of the unique characteristics of the breed to be conserved;
3. Knowledge of the potential interest of consumers in buying niche products; and
4. Awareness of constraints to developing and marketing niche products.

Outputs:

- A list of potential niche products from the breed. This will usually include traditional products as well as more innovative and creative new products; and
- A plan for marketing the products.

Task 1. Create a list of potential products and services obtainable from the breed, and prioritize these for feasibility in under the constraints of the production and marketing environment

Action 1. List the characteristics of the breed that could possibly be exploited by marketing

Activities described in Sections 1 to 3 will provide the basis for identifying and developing niche products. The special traits of the breed and its products will have been identified through this characterization process. This information may be augmented by conducting additional surveys of key breeders and other livestock keepers, potential customers and other members of the value chain such as processors, manufacturers and marketers. Box 61 explains how keepers of a Mexican sheep breed capitalized on the special characteristics of its wool.

Box 61

Exploiting fleece helps to safeguard sheep breeds – Chiapas, Mexico

Shepherdesses in Chiapas, Mexico, raise sheep that have specific fleece characteristics that have traditionally been important in the production of local textiles. Thanks to programmes that drew on the input and participation of the shepherdesses, these fleece characteristics have been incorporated into breeding programmes. The result has been that the sheep have become more appreciated, their populations have risen and their owners have become more dedicated to their conservation.

Source: Perezgrovas (1999).

Action 2. Identify markets for the breed-specific products

A complement to *Action 1* is to identify potential markets. Market identification can also be done prior to identifying the particular products. Box 62 shows an example of how a new market was found for an existing product.

Box 62

Marketing handicrafts made from Linca sheep wool in Patagonia, Argentina

The Linca sheep of the Patagonia region of Argentina is an endangered breed of coarse-wool sheep that has traditionally been used for the manufacture of distinctive ponchos and other textiles. A producers’ cooperative has now targeted these distinctive products for promotion to the tourists that come to the picturesque region in which the breed is found. This has greatly increased the value of the raw wool. It has also provided work in the local community for the shearers, spinners and weavers needed to ensure a supply of the distinctive textiles.

Source: LPP *et al.* (2010).

Although preparing a product for a single marketing outlet may be a logical first-step, sales may be more robust and resistant to variability if multiple markets are found. Multiple marketing outlets can also account for variability, for example, in the production systems of the various breeders or in the quality of the product. Box 63 describes the multi-outlet system used for marketing meat from the White Park breed of cattle in the United Kingdom.

Action 3. Conduct a workshop at which stakeholders from all stages of the production and marketing chain come together to creatively formulate potential plans

Relevant stakeholders usually include producers (farmers and pastoralists), nutritionists, retailers, butchers, food manufacturers, cooks, consumers, marketers and craftspeople. Inviting a wide range of stakeholders to the workshop should it to produce an extensive list of products and services that could potentially be marketed to niche consumers.

Action 4. Prioritize the products and services that can be obtained from the breed, targeting a few of the best ones for production and promotions

Various factors may influence the potential of a niche product to support breed conservation. Highest priority should be given to any products that already have a recognized place in the market that can realistically be expanded (either more sales or higher prices or both) through more promotion. This approach is called “market penetration” and is usually the simplest and most successful strategy.

Another relatively safe strategy is to seek the spread of an existing product into new markets, thus increasing total revenues. The most risky strategy is to develop entirely new products. This approach requires both product and market development. Box 64 shows how this somewhat risky strategy can produce high rewards for breed conservation.

Box 63

White Park cattle – a case study in meat marketing in the United Kingdom

White Park cattle are a native British breed classified as being at risk of extinction. The population comprises 900 breeding cows, 73 breeding bulls (65 natural service and 8 AI) plus young stock. They are kept in 81 herds, which are widespread throughout the United Kingdom. They are adapted to extensive grazing systems and have special value for use in conservation grazing projects.

Non-breeding stock are reared in non-intensive systems, ideally finished off grass, and are usually slaughtered at 30 to 36 months of age at about 580 kg to yield a carcase of about 325 kg. Breeders have two main options for marketing and to realize a better price:

1. Direct sale from the breeder or owner to a premium market. White Park beef is noted for its high-quality (especially flavour and marbling) which has been noted since at least the early seventeenth century when King James I of England renamed the loin “Sir Loin”. White Park beef enjoys strong demand from the gourmet market of hotels, restaurants and specialist retailers (often in London, but also elsewhere) and can command a premium price of more than twice the standard market price.
2. Marketing through the Traditional Breeds Meat Marketing Scheme, which was created in the United Kingdom, in 1994, by the Rare Breeds Survival Trust. Traditional Breeds Meat Marketing is a multibreed organization that accepts only animals belonging to endangered breeds. It enables breeders and owners who do not have the confidence or ability to supply the gourmet market to obtain a premium price (25 percent above standard market price) by taking advantage of a structure of finishing units, local abattoirs and specialist retail butchers, all approved by the Rare Breeds Survival Trust.

Breeders without access to either of these two special markets are forced to sell to the standard commodity market, with sale through public auction. Public auctions cater to the mass market and are attended by buyers who purchase mainstream breeds of livestock. Endangered breeds do not conform to standard requirements and attract a price below the standard market price.

Provided by Lawrence Alderson.

Box 64

Desert Dessert ice cream helps to conserve Raika camels in India

The conservation of Raika camels in India has involved production and marketing of one fairly obvious commodity, ice cream made from their milk. Creative marketing came up with the name “Desert Dessert” for this distinctive product. As the breed has always been used for milk production, this product is an extension of its traditional use. In addition, creative efforts at new product development have used manure from the breed in paper making, which is then used to manufacture greeting cards. This unusual product has met with demand that far exceeded expectations. Production tends always to lag behind demand. Both of these products – one more traditional, one very novel – have increased the economic return to the pastoralists stewarding the breed. This has made the breed and traditional systems in which it is kept much more secure.

Source: www.lpps.org

Task 2. Evaluate the feasibility of using niche products to support the conservation of a breed

Action 1. Write a business plan and organize a short production and marketing chain for each product

Consult an economics or business expert who can help formulate a business plan and map out the market chain. This will also require collaboration with other stakeholders along the proposed market chain. To be successful in marketing a specialized product from a specific breed, it will be necessary to distinguish it from the standard products in the marketplace that can be produced by mainstream breeds. This requirement must be considered in the business planning. Distinguishing a product can be approached in four ways: product, price, place and promotion, also known as the “four Ps” or the “market mix”. A common strategy is to market a breed-based product by focusing on its higher quality (or at least the perception that it has higher quality) or its distinctive taste or appearance. An example is presented in Box 65. Direct marketing can yield multiple benefits. It can “cut out the middleman”, increasing the margin of the sale returned to the livestock keeper and perhaps increasing the loyalty of customers who want to be sure about the source of their food. Promotion is an essential part of niche marketing. The entire business plan will likely be based on reaching new customers that may not be aware of the positive characteristics of the breed-based product.

Box 65

Marketing rose veal from Randall Lineback cattle in the United States of America

Randall Lineback cattle in the United States of America are an old, triple-purpose (milk, meat, draught) breed that came to be at risk of extinction because of its inability to compete with specialist dairy and beef breeds. Its meat and milk production levels are such that competition in mainstream commodities is unlikely to succeed as a strategy for ensuring the security of the breed. Therefore, Randall Lineback breeders sought to establish and market a distinct, higher-value product. Creative promotion of “rose veal” (meat from yearling animals) has established a ready market for this product in restaurants. The premium that is obtained contributes to the economic return obtained by the producers.

Provided by Phil Sponenberg.

Action 2. Undertake a formal analysis of the business plan and potential market

Formulation of the business and marketing plan should be followed by a market survey and feasibility analysis. Establishing a niche market will require investment in both time and money. One-time costs will be incurred in preparation of the marketing plan and marketing will require continuing expenditures. Market research will provide some insight into whether customer demand will be sufficient to enable the investments to be recouped.

Action 3. Produce a relatively small amount of the product and market it on an experimental basis

Even if the business plan and market analysis suggest that the planned niche marketing scheme is highly likely to be profitable, it may be prudent to start cautiously. For breeds with a low population size, starting on a small scale may be necessary. If the marketing programme is supported by outside investors, these investors may want to see some return on their investment before supporting scaling up.

Action 4. Evaluate sales and increase production according to market demand

An objective of almost any *in vivo* conservation programme will be to increase both the real and the effective population sizes so that the breed is no longer at risk of extinction. Niche marketing plans will have to evolve and grow in concert with the size of the breed population. This may involve simply selling more product in the same market, expanding into new markets, creating new products or any combination of these options. Care must be taken, however, to ensure that expanding the market does not affect the factors that made the product attractive in the first place (e.g. quality and distinctiveness) and that the market can handle any increased demand without negative effects on the price.

Enhancing the value of existing niche products through ties to geographical origin or cultural significance

Rationale

In many cases it may not be immediately obvious which specific characteristics of the breed have the potential to be used in the development of high-quality products for niche markets. In such cases, a study should be carried out to determine which characteristics are relevant. In other instances, breed-related products may already exist, but not yet be exploited fully. One factor that can be important for marketing is the uniqueness of the product, particularly with respect to its place of origin (see Box 66).

Box 66

The role of qualification labels for regional products

Tregear *et al.* (2007) concluded that qualification processes may bring socio-economic benefits to rural areas. These may play a role in linking local and non-local actors and the non-local actors can bring extra revenues in the local area. Qualification labels, like Protected Designation of Origin (PDOs) and Protected Geographical Indications (PGIs) are market mechanisms, information signals used by producers to stimulate favourable consumer responses, particularly when consumers are faced with choosing between products within the same category. Tregear *et al.* (2007) further argue that specification and labelling of a product raises its market profile and distinguishes it from competing items. Qualified producers of the regional product distinguish themselves from others by following a defined code of practice that attains certain standards or quality levels, for which consumers are willing to pay a premium. An example of existing qualification labelling is the labelling of organic products based on the control of the organic production methods and principles. In many rural areas of Europe regional foods with a strong historic background are produced and marketed in niche markets. To safeguard production in rural areas and to protect the products of rural producers the European Economic Community made regulation 2081/92. The focus is in regulation 2081/92 offering PDOs and PGIs. For PDOs, products must have quality characteristics from the local area, while for PGIs products have a specific quality attributable to the local area (Tregear *et al.*, 2007). These protection tools are already in place to improve the profitability of local breeds. For example, in the French Northern Alps the milk of Abondance and Tarentaise cattle breeds is used for the production of Reblochon and Beaufort cheeses and in Italy the Reggiana cattle breed produces the milk for the processing of Parmigiano Reggiano cheese (Gandini & Oldenbroek, 2007). The interest in Europe (and overseas) for regional products has fostered the success of organizations such as Slow Food[20] that help promote the potential benefits of their consumption.

Van der Meulen (2007) developed a methodological tool to evaluate the contribution of various factors to the connectedness of food products to their places of origin. Four factors can be distinguished:

Territoriality refers to “the degree of physical connection between a product and its region of origin”. All the phases in the supply chain – production, processing, distribution, etc. – are taken into account, i.e. if all these take place in the region of origin, the territoriality is considered to be particularly high.

Typicity refers to “place-specific peculiarities of the production process and the final product”. Put another way, these are “the physical aspects that distinguish the production process and the final product *in as far as* they are unique or logically linked to the place of origin”

Traditionality refers to the “rootedness of ... [a product’s] ... history in its place of origin”. The most concrete aspect of traditionality is the length of time that has elapsed since the product first appeared in the region. Other elements include links to local culture and history.

Communality refers to “shared experience and practices, reflected in the presence of multiple producers (farmers, processors) and their collaboration”. It is considered that such links strengthen the impression that the product is part of a shared local culture.

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[20] http://www.slowfood.com

The market value of products that target niche markets based on geographical origin, are affected by all four factors. Labelling schemes (see Box 67) can help ensure that the producers of unique products are able to benefit from the premium prices that niche-market customers are willing to pay.

Box 67

Marketing products on the basis of their place of origin

Many consumers value information about the place of origin of their food. Certain products are perceived favourably by consumers because of the products' places of origin. This favourable perception can arise for a number of reasons. For example, linking a product to a region renders it unique. Furthermore, the link often involves a region with an existing positive reputation for its natural beauty or interesting cultural heritage. Many consumers also like to buy products from local sources, to support the local economy and reduce environmental impacts associated with transport. Van der Meulen (2007), describing the situation in the Netherlands, notes that such products fall within a number of different categories:

Farmhouse origin food products. These are offered in farm shops, gift baskets, box schemes and specialized food stores.

Farmers-group origin food products. These come from a group of farmers producing and selling food, working with codes of practice and with registered geographical names and logos as collective trademarks.

Region-label origin food products. Several products may be sold under the same single label. The raw materials may come from several farms in that area, and products are usually made by single producers.

Regional-typical origin food products. For these there are multiple producers, with a product-related geographical delimitation, a long lasting tradition over generations and a distinctive production process and final product. The raw material does not always come from the traditional production area.

Artisanal origin food products. These are produced by small-scale individual food producers and the product is named after the place where they are located or the producer involved. The emphasis is on the processing techniques and not on the origin of the raw material.

Appropriated origin food products. These are former regional-typical origin food products that have become appropriated by a single company either because other producers have gone out of business or because of mergers.

The distance between the farm of origin and the consumer varies greatly. The methods of processing likewise vary from simple to complicated. These differences give rise to the need for qualification labels that guarantee the origin of the food and the location and methods of production and processing.

In some regions, mostly in developed countries, rarity in and of itself can give a breed a value in the eyes of some breeders or potential breeders. If a breed that has a strong regional identity faces the risk of extinction, both local residents and outside visitors may be attracted to the idea of keeping and conserving it. This can greatly facilitate the maintenance of the breed. However, developments of this kind can create challenges. For example, the selection environment of the breed may change, especially if keeping it becomes merely a hobby activity for relatively wealthy people that don't rely on the breed for their livelihood. Changes in the selection environment can be especially important if dictated by competitive showing or exhibitions. Animal selection by breeder groups with an eye for traditional type can be an effective countermeasure against the tendency for type to shift over time.

Another way to improve the value of the products obtained from a breed is to adopt or promote a production system that deviates clearly from mainstream production and is clearly defined: for example, organic production (see Box 68).

Box 68

Doubling the price of Drenthe Heath lambs in the Netherlands

The Drenthe Heath sheep arrived in the northeast part of the Netherlands 6 000 years ago. They were kept and survived on this region's infertile sandy heathlands. Through adaptation and natural selection the Drenthe Heath sheep became a rather small animal with sturdy legs and low fleshiness. As a result, the carcass weight and the meat-to-bone ratio are low relative to standard meat-sheep breeds. It is the only Dutch sheep breed with horns. Nowadays the flocks are primarily used for nature management. They are guided by shepherds, a sight that tourists visiting the area find very appealing. Approximately 2 000 ewes are registered in the Drenthe Heath Sheep Herdbook. Recently a group of three flocks has started to market their lambs as *Drènts Heidelaom,* an organic product. The lambs are produced in a well-defined market chain. This doubled the price the shepherd got for lambs, relative to the anonymous lamb market.

The production chain was set up as follows: First, the organic management of the flock and the organic growing of the lambs until slaughter were organized. These management practices are controlled and verified by Skal[21], the Netherland's official certification and inspection body for organic production. Second, a small local abattoir was contracted to slaughter the lambs in the most humane manner possible. Third, arrangements were made for the carcasses to be transported and sold to a specialized butcher producing organic lamb chops, ham of lamb and lamb sausages. These products are sold by the butcher at organic farmers' markets in cities in the western part of the Netherlands. Fourth, together with the Foundation for Conservation of the Drenthe Heath Sheep, the Slow Food organization in the Netherlands was consulted. Because of the special natural management and nutrition of the sheep and lambs, Drenthe Heath lamb has a special "wild" taste. Because of this and the cultural–historic significance of the sheep and the product, Drenthe Heath lamb was recognized in the Ark of Taste by the Slow Food organization. Fifth, arrangements were made for collaboration among flocks and this resulted in a "Presidium" of the Slow Food organization: Drenthe Heath Lamb or in the language of the region *Drènts Heidelaom.* A "Presidium" is a small project to support groups that champion the production and marketing of an artisan food that addresses economic, environmental, cultural and/or social objectives that are considered favourable by the Slow Food organization.

Provided by Kor Oldenbroek.

Inputs:

1. Knowledge of a breed's distinctive products, production process and roles; and
2. Awareness of current marketing systems and their potential to enhance the value of breed-specific products.

Output: A plan to enhance the value of the high-quality products of a breed.

Task. Formulate opportunities to enhance the value of the high-quality products of a breed

Action 1. Describe the products of the breed, the markets available for them and any other relevant information, including special traditions or existing trademarks

A detailed evaluation of the products of the local breed(s) of interest must be undertaken. This activity should not be limited to the target breed itself. It should also include products from other breeds that compete for market share. Where competing products exist, the relative value and advantages and disadvantages of each must be considered. In some cases, the evaluation will have to consider several products from the same breed (see Box 69). In such cases, the appropriate strategy may be to concentrate on one of the products or to treat all the products as a single package of goods.

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[21] http://www.skal.nl/english/tabid/103/language/nl-nl/default.aspx

Box 69

Chilota sheep offer various marketing opportunities in Chile

The Chilota sheep descends from Iberian sheep breeds introduced into the Chiloé Archipelago of Chile by the Spanish conquerors. This animal is characterized by its multicoloured fleece and small body size. It can be found with or without horns. The breed has a high potential for dairy production, being genetically close to the Spanish Castellana and Churra breeds. The breed population is distributed throughout the 26 islands of the Archipelago. The coloured wool is used by local craftswomen and the lambs are a renowned gastronomic product of the islands. The Chilota has now been officially registered as a breed in Chile and a pedigree registration programme has recently been launched, with 1 200 animals registered in about 25 farms. Research programmes on the rusticity of this breed, particularly with regard to its ability to adapt to harsh nutritional and environmental conditions, are currently being developed by the Chilean Government.

Provided by Ignacio Garcia Leon and Pascalle Renee Ziomi Smith.

Action 2. Assign a score for each factor (quality, distinctiveness, access to markets) to each product

Each product must be evaluated objectively for issues of quality and distinctiveness that will lead to enhanced demand. In addition, the supply must be evaluated to ensure that any potential market demand can be met.

Action 3. Describe the opportunities to enhance the scores for the different factors

For each product, propose options that will enhance quality, distinctiveness, or market access. For example, collaboration with restaurants or speciality food stores can improve market access. Linking other roles of the breed, such as ecosystem services (see below), may improve the marketability of a food product. Promotion of gender equity may be possible if the value chain is structured in a way that is particularly beneficial to women. Use of voluntary private standards may be a valuable option. For example, establishing standards for animal feeding (e.g. emphasis on pasture rather than stored feeds) may improve the product quality or give it a distinctive taste. Standards for animal husbandry may allow for the promotion of products on the basis of good animal welfare.

Action 4. Develop plans to enhance the value of the products through manufacture, trademarking or marketing

This phase of the planning will probably involve interaction with people that have special expertise in production and marketing. Preferably they should have a particular appreciation of local and unique aspects of products and their manufacture. Many niche market animal products have a unique history or other feature of human interest. Promotion of the “story” behind the product is a way to distinguish it in the marketplace (see Box 70). In marketing terminology, these characteristic aspects of the product underlie its “unique selling position” (USP), the factors which will ideally lead a customer to choose the product over a competing option.

An additional, more formal option is to develop a trademark or use special labelling to differentiate the product in the market place and provide a level of assurance with regard to its quality. Developing a label or trademark can be time-consuming and costly and requires particular expertise. Therefore, collaboration with a third-party (such as a specialized NGO – see Box 71) that performs this task for multiple stakeholders can provide cost-savings and increase effectiveness. Consumer awareness of the label will also probably be greater if there are more products in the marketplace carrying the same label (at least up to a certain point, beyond which the distinctiveness will be lost). Labelling and certification by an independent third-party may increase the consumers’ confidence in the validity of the process.

Box 70

Marketing products from Serbian sheep based on links to traditional livelihoods

The Karakachan and Pirot are among the most endangered sheep breeds in Serbia and the Balkan region. Whereas tens of thousands of these sheep roamed the West Stara Planina mountainsides in the 1950s, their numbers have dwindled to fewer than 200 animals from each breed today. Conservation of these breeds is important to safeguard a cultural monument that developed over hundreds of years and animal genetic resource that has good resistance to harsh conditions and local diseases, an aesthetic shape and modest needs in terms of production inputs. The wool of these sheep breeds has extraordinary thermo-isolation characteristics, as well as fibre firmness that differentiates them from the other sheep breeds. To take advantage of these factors to promote the survival of the breeds, the breeders' association "STADO" developed a programme for processing the wool and marketing hand-knitted clothing (e.g. socks, jackets, cardigans, sweater vests and ponchos). These products are made using 100 percent wool in its natural colour (dark brown from the Karakachan breed and white from the Pirot breed). Marketing programmes inform potential customers that they are not only supporting the initiative to preserve these endangered sheep breeds but are also ensuring the livelihoods of the households engaged in breeding and maintaining the sheep flocks and shearing, washing, spinning and knitting the wool.

Provided by Sergej Ivanov.

The process of developing a label through a third party will typically include the following phases:

- The relevant product or service is identified and documented, and the information is provided to the certification service.
- The certification service tests the suitability of the product or service against the criteria established for the use of the label.
    - If some criteria are not fulfilled, a plan should be drawn up to ensure that they can be fulfilled.
- Once all criteria are fulfilled a contract is signed for the use to the label.
- The stakeholders (farmers, breeders' association, NGO, etc.) work with experts to develop the USP of the product/service, usually giving particular consideration to its history, culture and geographic origin. The risk status of the breed may also contribute to the USP, as customers may react positively to purchasing a product if it helps prevent a breed from becoming extinct.
- The product is launched, usually locally at targeted sites, such as farmers' markets and specialty stores, using promotional material, press releases, meet-the-farmer events, etc. Emphasis is given to the USP.
- A percentage of the profit obtained from selling the product is used to pay for the use of the label.

The SAVE Foundation[22], an international NGO that acts as an umbrella organization for European associations working for the conservation of agrobiodiversity, has recently developed both a label for products and an award system for producers that work with local breeds and crop varieties (Box 72).

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[22] http://www.save-foundation.net

Box 71

Heritaste® and Arca-Deli® - two options for adding value to agrobiodiversity

Heritaste® is a voluntary certification verified by a third party and awarded by SAVE Foundation to farmers and producers who wish to add value to their products through extra labelling. Heritaste® guarantees that the product comes from breeds and varieties considered to be a part of the local cultural heritage and in need of promotion in order to secure their conservation. Products range from meat and dairy products through to clothing and carpets. Services include extensive grazing of protected areas as well as therapies and tourist attractions. Producers pay for the right to display the Heritaste® label, to cover the costs of the development and certification activities.

The process of development from an initial idea to a usable label was long and complex. Not only was it necessary to establish and agree upon criteria and conditions for use, but also factors such as the cost of certification, and the extent of interest from consumers and producers/farmers had to be researched extensively. In addition, various definitions had to be established for terms and concepts that may seem obvious to people working in the field but are quite obscure to the laypersons that are the final consumer of the labelled products. This process took the form of many discussions with stakeholders and a public consultation. The resulting label reflects the needs and wishes of all the stakeholders wishing to make use of the label.

The **Arca-Deli®** Awards are presented annually (starting in 2011) to products and services of locally adapted livestock breeds and cultivated plants. The award is presented to products and services seen as being recommendable as a model or example of good practice. The Arca-Deli Award® label can then be used on the labelling of products and services as a means of adding value.

Arca-Deli® provides a good alternative for farmers and producers who cannot afford or do not require a Heritaste® certificate. The award can be valuable especially in local markets and encourages other farmers and producers to improve the quality of their own products and services. This means that the niche products associated with locally adapted breeds and varieties become, on a small scale, more competitive and more economically viable.

For more information see http://www.save-foundation.net/english/market.htm

Provided by SAVE Foundation.

Exploiting the roles of species and breeds in providing ecosystem services

Rationale

In many parts of the world, traditional grazing with herbivores created and maintained ecosystems with high biological value (for a review on effects of grazing on biodiversity see Rook *et al.*, 2004). Similarly, many landscapes have been shaped through time by traditional farming systems. The results of such co-evolution processes between local breeds, traditional framing systems and the natural environment retain their character and richness as long as grazing is maintained. In countries with intensive agricultural systems, some arable land is set aside and not used for agriculture. If no additional measures are taken, these lands will become forests within a foreseeable time span. If conversion to forest is not desirable, grazing by herbivores can maintain an open landscape. In many countries cattle, sheep, goats and horses are used to maintain grasslands, wetlands and heathlands. Even pigs can perform environmental services (see Box 73).

Livestock species differ in their grazing behaviour, and there are even differences between breeds within a species (Saether *et al.*, 2006). The choice of the species and the breeds for use in conservation grazing should be carefully adjusted to meet the required grazing effects. The animals should also have appropriate physiological characteristics (robustness), especially if they are to be used in harsh environments. Ecosystem services such as conservation grazing often involve large areas of land. This means that a large number of animals are required and offers great opportunities for conserving herbivore breeds.

Box 72

Macedonian autochthonous pigs help maintain biodiversity

Traditional pig husbandry in Bosnia-Herzegovina and The Former Yugoslav Republic of Macedonia is important for reasons beyond meat production. The traditional production system involves free-range grazing, and the local pigs are appreciated for their digging activities, which keep the ground open. When pigs root to find buried food they act like living ploughs. They are especially valuable for soil management in floodplains, where the soil can become hard and compacted once the floodwaters recede. The shallow digging aerates the soil and encourages the natural biodiversity. The hoof-imprints promote the germination of seeds. The microhabitats created encourage the growth of insects, which serve as a link in a food chain that includes a wide range of other fauna.

Provided by Elli Broxham.

When livestock have grazed a given ecosystem for many generations, the animal genetic resources and the other components of the ecosystem (i.e. plants, wild animals and micro-organisms) will have evolved together and have become dependent on one another. Loss of one component of the ecosystem, such as a breed that goes extinct for economic reasons, may upset the balance among the remaining components, leading to their loss or a decline in their abundance (Gregory *et al.*, 2010). Payments to livestock keepers to ensure that their animals continue to providing their unique ecosystem services may be justifiable from the perspective of biodiversity conservation.

Although ruminant livestock produce large quantities of methane, a greenhouse gas that contributes to climate change, grazing livestock also help sequester carbon by removing plant material and encouraging regrowth and thus the movement of carbon from the air into soil organic matter (Leibig *et al.*, 2010). Assuming that locally adapted animal genetic resources are more appropriate grazers than their non-adapted counterparts, payment for the carbon sequestered could be an additional justification for public support for their *in situ* conservation.

Objective: To determine the opportunities for using species and breeds in nature management.

Input:

1. Requirements for species and breeds in nature management and relevant characteristics in species and breeds.

Output:

- A list of species and breeds that may be used in nature management.

Task. Select species and breeds for nature management

Action 1. Interview the stakeholders involved in nature management and formulate a plan for nature management with herbivores

The livestock keepers may not be the owners of the land on which nature management is needed. Discussions should be held with all types of stakeholders to develop a feasible plan for nature management using controlled grazing.

Action 2. Describe the grazing behaviour of species (and breeds if relevant)

Collect information on relevant characteristics of species and breeds. Pay special attention to adaptive traits that enable the animals to flourish in harsh environments. Take particular note of documented evidence of specific breeds' adaptations to specific environments and of existing nature management roles for which livestock keepers are currently not being compensated. Box 74 provides an example of a special adaptation found in Criollo cattle in Colombia.

Box 73

Use of Criollo cattle for weed control in Colombia

Paspalum virgatum, commonly referred to as “maciega” in Colombia (known as “talzequal” and “paja cabezona” in other countries), is a grass that thrives in the humid tropics. Its nutritional value is low, as is its palatability. The mature grass is coarse and fibrous. It is abrasive to the mouths of most cattle and is therefore usually consumed only during the early stages of its growth. For these reasons, maciega is commonly considered a weed. Furthermore, its seeds are particularly viable, so it is highly invasive and difficult to eradicate via conventional means.

However, not all cattle refuse to consume maciega. The local Criollo cattle have adapted to grazing on lower-quality forages and will consume maciega throughout its life cycle. The best-documented example of this trait is in the Velasquez cattle, which is actually a synthetic Criollo breed developed at the Hacienda Africa in the central Magdalena Valley of Colombia. The ability of the Velasquez to consume maciega precludes the need for its control with expensive, and largely ineffective, herbicides. This saves money and avoids damage to the local plant and micro-organism biodiversity.

Source: Martinez Correal (2007).

In general, the possible benefits of grazing livestock on wild biodiversity and carbon sequestration have not been well-researched, especially with regard to variability in the benefits provided by different livestock breeds. Such research may be a priority for governments considering paying livestock keepers for ecosystem services or to establishing support for carbon sequestration and or penalties for greenhouse gas production.

Action 3. Match the requirements with the relevant information on the species and the breeds

Decide which species and breeds might be effective in nature management. A nature management plan should be drawn up, including stocking rates and seasonal variation in pasture production and the life cycles of the local wild plants and animals.

Action 4. Write an action plan on how to incorporate species and breeds into nature management and how to make this profitable

Income from nature management is often realized through government-sponsored conservation programmes. In some countries, such programmes already exist and the only need is to enrol in the programme. In other countries, such programmes would need to be created and adopted, which would require lobbying of policy-makers and subsequent development of a fair and effective system of payment for ecosystem service.

Private landowners may be willing to pay for weed control or pasture restoration or provide low-cost access to grazing land. Meat and milk produced from the animals may have a distinctive and favourable taste that results from the grazing of particular plants. These products may thus have an added value that could be exploited in niche markets.

It should be emphasized that population sizes larger than those described in Section 2 as being necessary to reduce genetic erosion and extinction risk may be needed to guarantee the provision of ecosystem services. For example, a few herds might not be sufficient to maintain agro-ecosystems such as the Dehesa in Spain (associated with farming of the Iberian pig) or summer Alpine pastures in Europe (associated with farming of some cattle breeds). This needs to be considered when developing a plan to exploit ecosystem services in breed conservation. Breeders’ associations or other groups negotiating terms for ecosystem services need to consider the capacity of the services that their breed can provide, both in the present and in the future, considering current population sizes and expected survival and reproductive rates. Unfortunately, information on the effects of number of herds, animals and their distribution on the maintenance of environmental values is not widely available, so a site specific investigation is likely to be needed. New research on this topic is therefore welcome.

Capitalizing on the potential societal and cultural functions of species and breeds in tourism and social events

Rationale

Some breeds in need of conservation fulfil several services that may be poorly recognized or formally valued by society. Most of these are related to broad benefits to society that do not involve the provision of a specific marketable product. Among these are the roles species and breeds play as attractive elements of rural areas or in creating traditional agricultural landscapes. In many societies, animals have cultural or religious functions. Some breeds may provide several services and functions (see Box 75 for an example). In the case of some of these non-commodity services, the general benefit to society and to the local economy can warrant governmental support or payment of incentives to owners and keepers for the social and cultural benefits that they provide but which are otherwise difficult to quantify and reward. In most countries, the provision of such payments to livestock owners remains difficult to achieve.

Box 74

The cultural value of Madura cattle in Indonesia

One of Indonesia’s important animal genetic resources is the Madura cattle breed (Barwegen, 2004). Phenotypic evidence suggests that Madura cattle could have been derived from three-way crosses, between *Bos* (*bibos*) spp., *Bos indicus* and *Bos taurus* types. Madura cows have a small head, while the head of the bull is bigger. They have a long body in relation to their legs. Their hoofs are strong. Their height varies between 1.16 m and 1.24 m. The Madura breed is reported to be one of the best draught animals in the world relative to its size. This breed is mainly confined to the island of Madura (Madura Island is a densely populated, small island, about 4 497 km^2 in size, located off the northeast coast of Java). Madura cattle are extremely well adapted to the climate of the island. The farmers use all crop residues and large quantities of browsed and fallen leaf material to feed their cattle. The climate is tropical with definite wet and dry periods. Madura cattle bring both economic and cultural benefits to the Maduranese people. They are used in the “Karapan”, a famous traditional bull race on Madura Island. The people have a strong cultural attachment to Madura cattle and to the Karapan racing. Another traditional activity, known as “Sonok”, is a contest in which pairs of cows or heifers walk harmoniously with accompanying traditional music. These cultural events attract many local people and tourists and help to safeguard the high value of the cattle and the existence of the breed.

Provided by Phil Sponenberg.

Objective: To incorporate the societal and cultural functions of a breed in a programme for its conservation.

Inputs:

1. List of breed characteristics;
2. Reports of any important cultural and social functions such as unique phenotypes that have become a part of the cultural landscape or participation of animals in cultural events; and
3. Names of important stakeholders.

Output:

- A proposal for governmental or private support or incentive payments or a business plan for obtaining market recognition and generating financial returns.

Task 1. Identify the most important social and cultural functions of a breed

Action 1. Determine the present and potential social or cultural functions of a breed

Phenotypic characterization will ideally identify breeds, most important characteristics, but particular social and cultural functions may not necessarily be noted. Key stakeholders should be consulted to obtain information on these functions and their history and significance. Box 76 describes the unique social and cultural functions of the Chilote horse from Chile.

Box 75

The Chilote horse and therapy programmes in Chile

This Chilote horse is a breed developed on Chiloé Island in the south of Chile. It descends from horses brought centuries ago by settlers from the Iberian Peninsula. It has remained genetically isolated from mainland populations and has adapted to the humid climate and wetlands that distinguish the island. The breed is characterized by a hard, resistant hoof, short stature and refined skeletal structure. The Chilote horse has also been selected over decades for a quiet temperament. These particular characteristics give the Chilote a unique value, as they are perfectly adapted for use in sports for children and therapy for disabled people.

The management and development of this rare breed has been possible because of long-term government support and partnership with the private sector. This cooperation has ensured that the breed has been conserved and that it has gained value in the marketplace. Plans are being made for an even brighter future. The breed's population is still small, but breeders would eventually like to expand their market beyond Chile, even to markets such as North America and Europe. These efforts will require continued public–private partnerships, both for the establishment of a breeders' association to record performance and pedigree records and for support to research on genetics and reproduction.

Provided by Ignacio Garcia Leòn and Pascalle Renee Ziomi Smith.

Action 2. Document the various societal groups using and benefiting from these functions

Beneficiaries of the social and cultural functions of livestock will usually be a wider group than the livestock keepers that use the animals for income generation. When the animals have a religious function, all persons following that particular religion may be beneficiaries. When a function is cultural, all persons within the geographical area of interest may derive some benefits. When the presence of the breed attracts tourists, operators of local hotels, restaurants and stores have a financial stake in the breed's maintenance. When a breed somehow contributes to rural development in a general sense, then the public at large benefits, perhaps even people living outside the local community where the breed is found.

Action 3. Valuate the functions and services either in terms of their contribution to the local economy or the potential loss that would be suffered if they were not fulfilled

As explained Section 3 (Box 10), there are many ways in which an animal genetic resource can contribute value to society. In most cases, the functions of animal genetic resources referred to in this section do not involve direct use, and thus their values cannot easily be measured. Marketing is also problematic, as the benefits are often dispersed across a wide range of stakeholders, each of whom derives a small amount of utility, which may be difficult to measure or estimate. In addition, the breeds will usually have been providing the services in question for many years. Therefore, determining the added value of these services may not be practical and it may be simpler to estimate the value of the breed's contribution in terms of the loss that would be incurred if the functions and services were no longer available. For example, the Valdostana cattle breed in Italy is associated with a special festival that draws many tourists to its local area (see Box 77). The loss of this breed could be valuated in terms of the expected decreases in hotel, restaurant and other revenues tied to the festival.

Action 4. Determine the best approach (public or private) to incorporate cultural and social functions into breed conservation

The stakeholder analysis described in Action 2 should ideally determine which stakeholders are benefiting the most from the maintenance of the breed at risk, and the economic study (Action 3) should help quantify the benefits reaped by each stakeholder group. This information will facilitate the process of determining whether public or private sources of support should be sought. Public sources of funding are more appropriate when benefits are spread evenly over a large group of stakeholders. Potential sources include community or regional governments, or other broadly-based social groups such as churches or charitable foundations with an interest in social and cultural maintenance.

Box 76

The cultural value of Valdostana cattle in Italy

The Valdostana Castana cattle are farmed in the Aosta Valley, in the northwestern Alps of Italy. Gandini and Villa (2003) showed that a considerable cultural value can be attributed to this breed, in that it has been a central element of life in rural Valdostana, and today acts as a custodian of local culture. These cattle have a considerable influence on the valley landscape, as they are taken up to alpine pastures in the summer. Fontina cheese and other gastronomic traditions are linked to the breed. Furthermore, the breed is used in the "Battle of the Queens", a tradition that developed from older "Queen of Horns" traditions and consists of a series of competitions between cows. All these aspects are currently exploited by summer tourism, but are only partially are recognized by the market: Fontina cheese is in high demand at the national level, and people pay to attend the final tournament of the Battle of the Queens in Aosta. However the breed’s important cultural role in maintaining the rural landscape is not captured by the market. Nevertheless, recent economic investigations among summer tourists and residents indicate a consistent willingness to pay for the breed’s role in maintaining the landscape. The challenge is to get the market to recognize and capture this consumer interest.

Provided by Gustavo Gandini.

Task 2. Prepare a proposal to solicit support from potential sources in local, regional or national governments or from private entrepreneurs

Action 1. Identify the relevant authority and seek an initial meeting at which plans for a project to capture the value of the breed’s contribution to society can be explained

The major contributions of the breed (and its production system) and the plans to capture the value of these contributions should be condensed and distilled into a brief and targeted pre-proposal or concept note. The most convincing and compelling arguments should be stressed, with realistic discretion regarding chances of success and potential pitfalls. The ways in which the financial support will be used must be summarized in clear terms, as well as the additional benefits that are foreseen as a result of the investment. The primary goals of this process will be to receive an invitation to prepare a full proposal and to force those making the proposal to crystallize their ideas into a tangible and realistic work plan.

Action 2. Prepare and submit a full proposal

If the funding organization finds the pre-proposal to be of interest, it will likely invite the submission of a full proposal. The full proposal will generally be much more detailed and will require a greater level of planning. The format of the full proposal will vary widely depending on the organization and it will provide instruction and guidance regarding the information that is needed. However, a justification, an overview of the state of the art or of previous projects with similar objectives, a description of beneficiaries, a work plan with milestones and delivery dates, and a detailed budget are aspects that will be required for nearly any grant proposal, regardless of the donor.

Task 3. When the market recognizes a cultural or social value write a business plan to capitalize on these values

Governments should not be the only option considered as sources of support, especially if relevant stakeholders among the public can be identified (or identify themselves). Crowd funding is a recently developed option that may be effective, especially if the need is for seed money to start a project. Crowd funding involves the solicitation (usually via the internet) of a relatively small amount of money from each of many different people.

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Appendix 1. Glossary of selected terms[23]

Allele: One of the alternative forms of DNA at a given *locus*. The relative frequencies of alleles at a locus are the basis for molecular-based measures of genetic diversity.

At-risk breed: a *breed* with demographic characteristics (primarily population *census size*) suggesting that it will fail to exist in the future unless a conservation programme is implemented.

Biocultural Community Protocol: a document that is developed after a community undertakes a consultative process to outline their core cultural and spiritual values and customary laws relating to their traditional knowledge and resources. In this they provide clear terms and conditions regulating access to their knowledge and resources (Natural Justice, 2009).

Bottleneck: a period during which the size of a given population (such as a breed of livestock) is reduced to a very small number, thus eliminating many *alleles* and hence a large proportion of the genetic variability.

Breed: either a subspecific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species, or a group for which geographical and/or cultural separation from phenotypically separate groups has led to acceptance of its separate identity and/or a group for which geographical and/or cultural separation from phenotypically similar groups has led to acceptance of its separate identity (this is the definition according to FAO, however, many definitions of the term breed can be found in the literature – see Box 1). For the purposes of the guidelines, a breed will be a sub-specific group of domestic livestock with a common history for which its members will be treated in a common manner with respect to genetic management.

Breed standard: a description of the characteristics of the “ideal” animal to be achieved through the breeding programme of a *standardized breed*.

Carrier: an animal that is heterozygous at a locus that has a deleterious recessive effect. The animal will appear normal, but can pass the defective allele to its offspring, which will express the negative effect if they receive the defective allele from the other parent.

Census size: (or simply “population size”) the number of living animals in a population at a given time. Census size is usually greater than *effective population size*, a measure that accounts for genetic relationships among animals.

Choice modelling: a statistical approach that involves collecting data regarding the choice of stakeholders among various options, followed by analysis of the factors influencing the choices made. Choice modelling can be used to establish relative weights among factors to consider when prioritizing breeds for conservation.

Circular mating: a design for the management of genetic diversity, whereby males of one (the first) family are always mated to females of a second family, males of the second family are mated to females the third family, and so on, with males of the last family closing the circle by being mated to the females of the first family. This design ensures that no mating occurs within families. Likewise, for population-level management, herds or villages can replace families in a design that is often called *rotational mating.*

Coancestry (coefficient): (abbreviated f and also known as the *kinship or kinship coefficient*) the probability that a randomly selected allele from two individuals (at the same locus) is identical by descent from a common ancestor.

Composite breed: a new *breed* developed from the systematic crossing of two or more *breeds*.

Cryoconservation: conservation by cryopreservation of a *breed’s* genetic material (usually semen, embryos or somatic cells) *in vitro*, in a non-living state, so that live animals can, if necessary, be regenerated in the future.

ΔF: the proportional change in the average *inbreeding* of a population in a generation. The *effective population size* (N_e) can be estimated as $N_e = 1/2\Delta F$.

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[23] Within the definitions, other terms that are listed in the glossary are italicized.

Ecosystem services: the benefits people obtain from ecosystems. These include provisioning services such as food, water, timber, and fibre; regulating services that affect climate, floods, disease, wastes, and water quality; cultural services that provide recreational, aesthetic, and spiritual benefits; and supporting services such as soil formation, photosynthesis, and nutrient cycling (Millennium Ecosystem Assessment, 2005)[24].

Ecotype: a subpopulation within a *breed* that is genetically adapted to a specific habitat.

Effective population size: (abbreviated N_e) the size of a hypothetical *idealized population* that would generate the values of diversity parameters observed for a given population of interest. The N_e corresponds to the number of breeding animals per generation and is usually smaller than the actual population count.

***Ex situ in vivo* conservation:** conservation of a *breed* through maintenance of live animal populations not kept under normal management conditions (e.g. zoological parks and in some cases governmental farms) and/or outside of the area in which they evolved or are now normally found. There is often no clear boundary between *in situ* and *ex situ in vivo* conservation and care must be taken to describe the conservation objectives and the nature of the conservation in each case.

Extinction vortex: the condition in which the *effective population size* of a *breed* is so small that the detrimental effects of *inbreeding depression* on fertility and survival prevent the population from propagating itself. A *breed* in this state is in need of *genetic rescue*.

Factorial mating: allowing a female to mate with multiple males in her lifetime, which increases genetic diversity (see *hierarchical mating*).

Founder: one of the animals that were used in the past to establish a current *breed.* Presumably, today's breeds were developed by selecting a group of similar animals from a large population and then interbreeding them for many generations. Genetic variability in a group of founders is lower than that in the larger population. The smaller the number of founders, the larger the decrease in variability.

Founder effect: a type of *genetic drift* resulting in a loss of genetic variability when a new population is established by a very small number of *founders* selected from a larger population.

Generation interval: (abbreviated L) the time between successive generations in a breeding population. It can be calculated as the difference between the average age of offspring and parents and may differ between male and female parents. Increasing the generation interval can increase *effective population size*.

Genetic defect: a heritable detrimental condition determined by the effects of one or a few genes. Inheritance of genetic defects is often *recessive* and thus they are more commonly observed in populations that have small *effective population size,* because the chance of *homozygosity* through descent of the deleterious *allele* from a common ancestor is greater.

Genetic distance: a measure of the genetic differences between two populations (or species) calculated on the basis of allelic frequencies in both populations.

Genetic drift: (or simply "drift") the change in the frequency of an *allele* due to random sampling. Genetic drift is greater in small populations and it usually decreases genetic diversity by decreasing *heterozygosity.* In the most extreme case it results in *monomorphic loci*.

Genetic marker: (or molecular marker) a sequence of DNA with observable variability (polymorphism) that provides information about variation that is not directly observable.

Genetic rescue: applying limited cross-breeding to save a population that is in an *extinction vortex* due to effects of *inbreeding depression*.

Heterosis: (or hybrid vigour) is the increase in performance (size, production, fitness) of cross-bred animals over the average of its parental *breeds,* which occurs due to increased *heterozygosity*.

Heterozygosity: the condition where both *alleles* at a given *locus* are different. Heterozygosity is generally advantageous, because a favourable *allele* can often compensate for the effects of an inferior

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[24] Millennium Ecosystem Assessment. 2005. *Ecosystems and human well-being: synthesis*. Washington D.C., Island Press (available at http://millenniumassessment.org/en/index.aspx).

or detrimental *allele* at the same *locus*. Mean heterozygosity is often used as a measure of genetic variability.

Hierarchical mating: mating a female to the same male throughout her lifetime (see *factorial mating*).

Homozygosity: the condition in which both alleles at a given locus are the same. Homozygosity is generally unfavourable.

Idealized population: a (hypothetical) randomly mated population with equal numbers of males and females, contributing uniform numbers of progeny, and not subject to other forces that change genetic variability, such as mutation, migration and selection. Idealized populations form the theoretical basis for computing *effective population size*.

***In situ* conservation:** conservation of a *breed* through continued use by livestock keepers in the production system in which the livestock evolved or are now normally found and bred. Successful *in situ* conservation usually requires changing the economic and market environment, allowing a breed to be financially sustainable.

Inbreeding: the mating of relatives. Inbreeding is generally detrimental because it increases *homozygosity*. Inbreeding is more common in small populations because a greater proportion of animals are related because of the decreased number of possible ancestors.

Inbreeding coefficient: (abbreviated F) a measure of the level of *inbreeding* equal to the probability that the *alleles* at any given *locus* are identical because they were each inherited from a common ancestor of the two parents.

Inbreeding depression: the reduction in performance for a given phenotypic trait due to negative effects of *inbreeding*.

Kinship (coefficient): see *coancestry*.

Landrace: (or Landrace breed) a *breed* that has largely developed through adaptation to the natural environment and traditional production system in which it has been raised.

Linkage disequilibrium: a non-random association between the *alleles* carried at different *loci* by an individual. This usually occurs because two loci are located closely together on the same chromosome.

Local breed: a *breed* that occurs in only one country.

Locus: a distinct region of DNA (often a gene) in the genome.

Marker assisted selection: (abbreviated MAS) the use of DNA markers to improve response to selection in a population.

Mate selection: an approach in which genetic variation in a *breed* is managed by selecting the sire/dam combinations that will result in the greatest genetic variability, rather than selecting the most genetically diverse parents in a first step and determining the mating in a second step.

Minimum coancestry contributions methodology: an approach to the selection of breeding animals that maximizes genetic diversity by emphasizing individuals that are relatively unrelated to the population in general.

Monomorphic locus: a *locus* that is fixed at a given allele in a population, so that all animals are *homozygous* and there is no genetic variability at the *locus*.

Optimum contributions strategy: a method of selection that chooses the best set of parents for increasing genetic gain while maintaining genetic variability. Genetic value of potential parents and their relationships with each other are considered simultaneously.

Panmictic population: a population within which all animals can mate with each other.

Productivity: a phenotypic trait that accounts not only for the quantity of a given output produced by an animal or *breed* (on the average), but also the inputs required to achieve those outputs.

Recessive inheritance: the phenomenon by which an *allele* must be in a *homozygous* state in order for its effects (usually negative) to be observed.

Role model breeders: livestock keepers that have a great deal of indigenous knowledge allowing them to manage their animals well and also to efficiently select animals to obtain their desired genetic goals. Such breeders can be a valuable resource for community-based breeding programmes, by sharing their knowledge with others.

Rotational mating system: see *circular mating*.

Selection: any process, natural or artificial, that results in different probabilities of survival (and particularly in numbers of offspring) among members of a population. Selection tends to decrease genetic variability because the genes of non-selected animals are not passed to the subsequent generation.

Selection intensity: a standardized measure of strength of selection, related to the superiority of chosen parents relative to the population average. Selection intensity increases as the proportion of animals chosen as parents decreases.

Standardized breed: a *breed* of livestock that was developed according to a strict programme of genetic isolation and formal artificial selection to achieve a particular phenotype.

SWOT analysis: a decision-making tool that (in the context of animal genetic resources management) consists of listing the strengths, weaknesses, opportunities and threats associated with a *breed* and using the results to develop a strategy for future management of the breed.

Transboundary breed: a *breed* that occurs in more than one country. **Regional** transboundary breeds are found only among countries in the same region, whereas **International** transboundary breeds exist in multiple regions.

Truncation selection: choosing as parents all animals with a phenotypic or genetic value exceeding a given threshold and obtaining equal numbers of offspring from each (as far as possible). See *weighted selection*.

Unit of conservation: the distinct population of animals to which a conservation programme is applied. For the purpose of these guidelines, a *breed* of animals within a given country is the unit of conservation.

Weighted selection: choosing as parents all animals with a phenotypic or genetic value exceeding a given threshold, but obtaining relatively more offspring from the superior animals. Emphasizing certain parents more than others allows for a greater selection response (or equal response with greater *effective population size*) than by simple *truncation selection*, but is more complex and costly.