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

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

FOREWORD

These guidelines present the basic concepts involved in the development 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 management of animal genetic resources and any other stakeholders with a leading role in designing and implementing *in vivo* conservation programmes for 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 conservation programmes.

The genetic diversity of the world's livestock species is in a state of continual decline, and the animal genetic resources that remain are often not used as efficiently as they could be. 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 implementing 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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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).

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

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 or other of the workshops or expert meetings. The electronic conference provided more than 1 600 subscribers to DAD-Net with access to the draft guidelines. The following persons contributed 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 Köhler-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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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

Glossary of selected terms[2]

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*.

[2] Within the definitions, other terms that are listed in the glossary are italicized.

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 $N_e = 1/2\Delta F$.

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)[3].

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 diversity: the range of genetic differences among organisms, which is typically evaluated at the within-species or within-breed levels for livestock populations. Criteria for measurement of genetic diversity include numbers of breeds within-species or levels of *heterozygosity* within breeds.

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[3] Millennium Ecosystem Assessment. 2005. *Ecosystems and human well-being: synthesis*. Washington D.C., Island Press (available at http://millenniumassessment.org/en/index.aspx).

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 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.

In vivo conservation: conservation of a breed through maintenance of live animal populations, which encompasses both *in situ* conservation and *ex situ in vivo* conservation.

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.

Locally adapted breed: a *breed* that has been in the country for a sufficient time to be genetically adapted to one or more of traditional production systems or environments in the country. The phrase "sufficient time" refers to time present in one or more of the country's traditional production systems or environments. Taking cultural, social and genetic aspects into account, a period of 40 years and six generations of the respective species might be considered as a guiding value for "sufficient time", subject to specific national circumstances.

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*.

Nucleus (or nucleus herd): a subpopulation of a breed under strict management within which *selection* can be applied with greater intensity than in the rest of population. Genetic response in the general population results from the subsequent use of the nucleus members as breeding animals.

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.

Polymorphism: the presence of multiple *alleles* at a given *locus* in the genome.

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.

USER GUIDANCE

Introduction

In vivo conservation is the conservation of a breed through maintenance of live animal populations, which encompasses both *in situ* conservation of the breed within its typical production system and *ex situ in vivo* conservation in a controlled environment. *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."

In situ and *ex situ* conservation methods are complementary. Combining the two approaches can provide a powerful conservation strategy. The most common form of *ex situ* conservation is *in vitro* cryoconservation of gametes or embryos in a gene bank. Cryoconservation can be supported by *ex situ in vivo* conservation. The latter approach implies the conservation of a limited number of live animals in a small breeding herd or a zoo; the animals are kept outside their original production environment and therefore adaptation to changing conditions is impaired.

The goal and structure of the guidelines

The objective of these guidelines is to provide technical guidance on the various conservation methods available and to serve as a decision aid in the development of conservation strategies. The guidelines describe concepts important in the design and establishment of animal breeding programmes that conserve genetic diversity and stimulate sustainable use, usually by generating increased income for the keepers of the livestock involved. The material presented is intended to be relevant to all species of livestock used in agriculture and food production. Where appropriate, species-specific guidance is given.

The guidelines aim to provide the technical background needed by organizations or individuals who want to set up, implement and monitor *in vivo* conservation programmes in a rational manner. They describe the tasks and actions that should be undertaken. Emphasis is placed on *in situ* programmes, because such programmes are likely to be the most relevant for long-term *in vivo* conservation objectives. The order of the sections generally follows the chronological order of establishing a conservation programme. The subsections have a fixed format: each consists of a rationale, an objective, required inputs and the expected outputs, followed by a set of tasks and actions that need to be undertaken in order to meet the desired objective. In some cases, the tasks and actions form a more or less chronological sequence. In others, they represent activities that may run concurrently or a set of options that can be drawn upon depending on the circumstances.

Most countries have nominated a National Coordinator for the Management of Animal Genetic Resources (National Coordinator)[4] 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 that can be consulted during the process. Many groups of stakeholders are involved in the conservation of animal genetic resources (FAO, 2007b; Oldenbroek, 2007),

[4] http://dad.fao.org/cgi-bin/EfabisWeb.cgi?sid=-1,contacts

including 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.

Many countries have developed national strategies and action plans for animal genetic resources (FAO, 2009) for the purpose of implementing the *Global Plan of Action* at national level, or are planning to do so. 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 countries that do not yet have a national strategy and action plan, the development of this broader strategy 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 a country has followed the advice offered in the guidelines on *Surveying and monitoring animal genetic resources* (FAO, 2011b), it will have taken the need to obtain data to plan a conservation strategy into account in developing its strategy for surveying and monitoring, and the planners of a conservation strategy will not be starting from scratch. The activities described in the FAO guidelines on breeding strategies, phenotypic characterization and molecular genetic characterization (FAO, 2010; 2011c; 2012) are also intended to be complementary, and all should be approached, as far as possible, in a coordinated manner.

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 limited availability of financial resources for conservation precludes 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 how to organize the institutions required for implementing programmes for *in vivo* conservation.

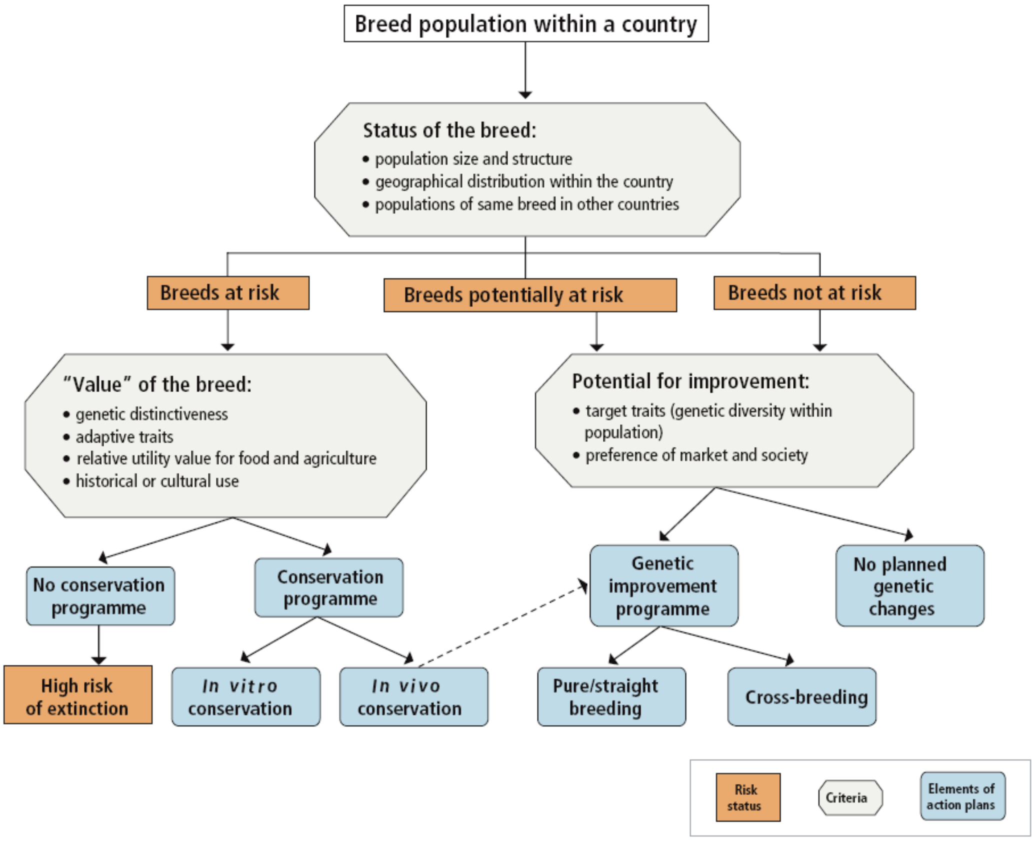
Section 6 deals with the design of effective conservation and sustainable use programmes, with special emphasis on the maintenance of genetic diversity within breeding populations.

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

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

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.

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



Source: FAO (2007b).

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 suited to their particular circumstances. Some countries may need outside assistance and advice if they plan to apply the more complex approaches described.

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1 Reviewing the roles of animal genetic resources and options for their conservation

Inventorizing species, breeds and their functions

RATIONALE

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) concluded 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 variety 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, 1999, 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. This led to the development of more specialized breeds and breeding lines. Performance and pedigree recording and human-controlled artificial selection of livestock has led, during the past 250 years, 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 within 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 meet the challenges posed by changing in production environments (e.g. due to climate change) and changing 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*, i.e. 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 a well-defined registered standardized breed or a specialized breeding line. 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.

Within a country, the livestock sector has to balance a range of policy objectives. Among the most urgent of these will generally be 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. 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, concentrating attention on a limited range of animal genetic resources to meet specific development goals may threaten the continued existence of some breeds. The loss of such breeds would result in genetic erosion: a decrease in the within-species genetic variability 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 to put in place adequate measures to promote conservation and sustainable use, and to ensure 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. Livestock products such as meat, milk, eggs, fibre and hides account for 40 percent of the value of world agricultural output. One-third of humanity's protein intake comes from animal products. Livestock also provide draught power and fertilizer for crop production. Livestock are thus are essential to the achievement of sustainable food security. In some developing countries, particularly those where pastoral systems predominate, the contribution of livestock production is even more important than global averages would suggest. 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 development of a national conservation programme for animal genetic resources should start with an overview of the country's livestock production systems, including the species and breeds involved in providing different livestock functions. A starting point might be the country report[5] 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)[6].

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

Inputs:

1. The country report submitted to FAO during the preparation of *The State of the World's Animal Genetic Resources for Food and Agriculture*.
2. Any relevant information about national animal genetic resources that has been produced since the preparation of the country report; in particular, the country's national strategy and action plan for animal genetic resources, if available.
3. The FAO guidelines *Preparation of national strategies and action plans for animal genetic resources* (FAO, 2009a), assuming no such strategy and plan have yet been developed.
4. The FAO guidelines *Breeding strategies for sustainable management of animal genetic resources* (FAO, 2010).
5. The FAO guidelines *Surveying and monitoring of animal genetic resources* (FAO, 2011).
6. The FAO guidelines *Phenotypic characterization of animal genetic resources* (FAO, 2012a).
7. 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 found in the country or the region

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

As described above (Box 1), the term "breed" has many possible definitions. Although the breed concept is often associated with industrialized countries and related production systems, it is imperative that each country has 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*

[5] ftp://ftp.fao.org/docrep/fao/010/a1250e/annexes/CountryReports/CountryReports.pdf.
[6] https://www.fao.org/dad-is.

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 an interbreeding population of animals whose members will be treated in the same way under national programmes developed for the 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 cross-breeding is practised, the resulting population of animals should no longer be recognized as part of the original breed, and ideally a new breed should be established if these crossbred animals are used to produce subsequent offspring.

Some countries have a formal protocol for the recognition of breeds, with certain standards that must be met before a population can be registered as a distinct breed. In India, for example, 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 in India 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 populations 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 proposed breed using a standard set of species-specific descriptors, a detailed history of the population and a list of characteristics that distinguish it 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 to the "breed" standards. In addition, the applicant must submit letters from at least three different breeders or owners, indicating:

- why they believe the population should become a recognized breed;
- how long they have been breeding the candidate population;
- the reasons for recognizing the proposed breed as a separate entity;
- activities undertaken to establish the distinct population (e.g. breeding strategies);
- any suggestions as to how to further improve the population in the long term; and
- characteristics that make the candidate breed clearly different and distinctive from all other breeds.

The application is then reviewed, and approved or rejected, by a breed registration committee of the 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. Where conservation is concerned, assigning animals to breeds will usually be important 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. Establish a baseline list of 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[7]. For many countries, these lists will be sufficiently up-to-date to accurately describe the current situation and provide a baseline for future comparison. Advice on breed surveys is provided in Section 2, and in more detail in the guidelines *Surveying and monitoring of animal genetic resources* (FAO, 2011).

Task 2. Describe the breeds and their functions

Action 1. Study relevant documentation

As described in the user guidance section, if the country has a national strategy and action plan (FAO, 2009a) this will probably provide the general 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 of national animal genetic resources.

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

If the country has not established a National Advisory Committee, 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 livestock 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 information on breeds and their functions

For each species, produce a table listing breeds and their functions. Include a short explanation of each. Submit the table to the National Advisory Committee for review. Livestock functions comprise a wide range of services to humankind. The functions of a given breed 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

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

financial services such as savings and insurance; provision of social status for its owners; or provision of nature-management services such as conservation grazing to promote wildlife habitats. It is also recommended that breeds that are "locally adapted" to their production systems be identified. Locally adapted breeds have been in the country for a sufficient time to be genetically adapted to one or more of traditional production systems or environments in the country and will often be the most relevant in terms of their genetic diversity.

Describing the dynamics of the livestock sector

RATIONALE

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

- population and/or economic growth and subsequent changes in demand for animal products;
- developments in trade and marketing, including increased regard for food quality and for safeguarding human health and animal welfare, and increased interest among consumers in niche products and sustainable use of resources;
- 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 in agriculture (FAO, 1996). Similarly, breeds developed for wool and fibre production may be threatened by the availability of synthetic fibres. The availability of alternative sources of fertilizer or financial services also shifts livestock keepers' objectives and may affect their breed choices. The emergence of new livestock functions and modification of existing roles challenge the existing 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 in 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 are 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 the need to adapt to global climate change underlines the importance of retaining a range 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 different animal species and breeds, along with threats to their survival and opportunities for their conservation and sustainable 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.
2. An update of the statistics in the report.

Output:

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

Task. Describe the dynamics of the livestock sector

Action 1. Describe the roles of different species and breeds

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

Action 2. Describe the dynamics of livestock systems and current and future drivers of change

The main drivers of change mentioned in the literature are listed above. 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 trends in the use of animal genetic resources

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.

Reviewing the status and trends of animal genetic resources

RATIONALE

As mentioned above, about 40 animal species have been domesticated for use in food production and agriculture. Five species – cattle, sheep, chickens, goats and pigs – dominate in terms of numbers and distribution. Cattle, sheep and chickens are widely found across all regions of the world, 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 20 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 22 percent of reported breeds are classified as being at risk (FAO, 2012), 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 used 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 the country or region.

Inputs:

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

Output:

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

Task: Produce estimates of past, present and future population sizes

Action 1. Obtain past and present population data 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 livestock 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, the country's national strategy and action plan will include plans to establish a programme of routine monitoring of breed population sizes (if such a programme does not already exist).

Action 2. Predict future population sizes

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 into the future 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. If breed population data are not available, consider general trends that may affect diversity

In many countries, reliable multi-year information on breed population sizes is not available. In such cases, considering the general characteristics and trends of the national livestock sector can provide an indication of the likely threat to the 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 locally adapted breeds of livestock? The answers to these questions may reveal whether livestock breeds are likely to be at risk, i.e. if the answer 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.

Identifying reasons for the loss of animal genetic diversity

There are several factors that place breeds at risk of loss and threaten livestock diversity (FAO, 2007b; FAO, 2009b). In developed countries, the greatest cause of genetic erosion is, by far, the growing trend towards 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, 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 locally adapted 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 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 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 threats to animal genetic resources are diverse and that there are a number of ways in which they 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 the country or region.

Input:

1. A description of the drivers of change in livestock systems.
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 the country or region.
- A general strategy for decreasing the impact of the various threats.

Task. Assess threats to genetic diversity

Action 1. Analyse the drivers of change in livestock systems

Assess the consequences of changes to livestock production systems for the breeds presently used in 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. Assess the probability 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 by such events. 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 (particularly any requirements for compulsory culling of animals). 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 localized disasters, it is important to determine the geographical distribution of breeds within the country or region.

Action 3. Summarize the risk factors and consider preventive measures

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

1. the risk of a breed being set aside because of economic drivers, resulting in a continual decline 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).

Identifying 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 requires substantial involvement of 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 locally adapted 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 breeds with particular 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[8].

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. This promotes the development of conservation measures for breeds at risk and promotes the emergence of niche markets for livestock products. In developing countries, the immediate concerns are more for food security and economic development.

Objectives for the 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. Livestock diversity also contributes to the 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 many ecosystems. The loss of this diversity would contribute to greater risk in these systems and reduce their ability to respond to trends and shocks. 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 removed from production and "given back to nature". Well-adapted grazing animals often 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 development 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 challenges. Relying on a small number of breeds is risky because it results in the loss of genes and gene combinations that, although they are not relevant at present, may become relevant in the future. For example, breeds may differ in their level of resistance and resilience to emerging diseases. 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 may be used in research into disease resistance and susceptibility, helping to achieve a better understanding of the underlying mechanisms and thus develop better 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.

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

Box 3

Colour sidedness: an example of genetic diversity conserved for 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 European 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 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 in terms of two main objectives:

1. conservation for sustainable utilization of rural areas, including economic activities, sociocultural roles and environmental services; and
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 are relevant to the breeds under consideration for inclusion in a conservation programme.

Objective: To determine national conservation objectives for each species.

Inputs:

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

Output:

1. Lists of conservation objectives at species and breed levels.

Task: Identify conservation objectives

Action 1. Consider potential objectives for conservation programmes

A conservation programme for a given species may have to take several objectives into account. For example, it is likely that ongoing provision of various economic, cultural and ecological functions will need to be ensured and that particular unique characteristics within the population will need to be maintained.

Action 2. Summarize the conservation objectives

Conservation objectives for each species can be summarized in two tables based on the two classification systems described above in the rationale (i.e. the five objectives and the two summarizing objectives).

Reviewing the status of each breed and developing management strategies

RATIONALE

As described above, as livestock production systems develop, many breeds are set aside from (or fail to become established in) commercial production. This creates the risk that the number of breeding animals within these 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 its future management can be determined by performing a SWOT (strengths, weaknesses, opportunities, threats) analysis (EURECA, 2010).

A SWOT analysis is a method used to evaluate 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 evaluating 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 stakeholders, along with the prospects 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 within which the breed is typically found. Based on this information, the stakeholders and entities to involve in the process can be identified.
- Identification by stakeholders of the strengths, weaknesses, opportunities and threats.
    - *Strengths* are positive characteristics of the 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 the 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.
    - *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 and 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).

The objectives of a SWOT analysis involve not only determining the current status of a breed, but also considering 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 the breed.

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

a. using the strengths to take advantage of the opportunities (SO-strategy);
b. using the strengths to reduce the likelihood and impacts of the threats (ST-strategy);
c. overcoming the weaknesses by using the opportunities (WO-strategy); or

d. reducing the likelihood of disastrous outcomes that may arise because of the combination of the weaknesses and the threats (WT-strategy).

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

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

Output:
- Alternative strategies for the conservation and use of the breed.

Task: Evaluate potential strategies for the future conservation and use of the breed

Action 1. Undertake a SWOT analysis of the breed and its stakeholders

The strengths 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 that has sound programmes for registering the 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 being kept by owners with a high average age. Another weakness might be that the population-genetic knowledge required for conservation activities is not available. Opportunities might 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 used to develop strategies based on them. One option is to translate the most important strengths and the most important opportunities into a strategy. Another approach is to confront the weaknesses of the breed with the opportunities and devise a strategy that aims to overcome the weaknesses by taking advantage of the opportunities.

Action 3. Formulate alternative conservation and use strategies and assess their 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 resources such as feed and housing.

Box 4

SWOT analysis of Eastern Finncattle

History

Eastern Finncattle (Finland) 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 the basis of 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 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).

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. Targeted conservation programmes were needed if the breed was going to survive, especially with any of its productive potential intact. A SWOT analysis revealed potential strategies.

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. 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 resulting birds 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 contributed to meeting 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 seeking alternatives to industrial production, which reversed the steady decline of the breed in both numbers and vitality.

Provided by Phil Sponenberg.

Comparing conservation strategies

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).

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.

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 the 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 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

This type of conservation 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 with regard to cryoconservation is whether 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 methods and conservation objectives. This information can be used to find the appropriate conservation method for meeting the conservation objectives for a given breed. From the table it can be concluded that *in situ* conservation is the method of choice in 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 conservation objective. *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 using 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. *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 both these cases, 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 advisable to complement *in vivo* conservation, whether *in situ* or *ex situ,* with cryoconservation of germplasm (see also Section 4).

Table 1. Conservation methods and objectives

	Method		
Objective	*In situ*	*Ex situ in vivo*	Cryoconservation
Flexibility of the genetic systems			
• 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 measures for the breeds of a given species.

Input:
1. List of breeds and species to be conserved.
2. List of potential conservation measures.

Output:
- A description of the conservation measures applicable for each species in the country.

Task. Evaluate potential conservation measures

Action 1. Assess the feasibility of implementing various conservation measures

The feasibility of implementing a given conservation measure will depend on the available infrastructure and technical capacity within the country. An *in vivo* programme can often only be organized effectively when an association of breeders exists or can be established, 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. Determine which conservation measures are relevant for which species

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

Action 3. Determine the prerequisites for implementing the conservation measures

Action 1 identifies feasible conservation measures, but some of these options may not be immediately accessible. For example, breeders interesting in conservation may be present, but it may be necessary to first organize them and provide training before an *in situ* conservation programme can be implemented. By evaluating 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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2 Identifying breeds at risk

Determining risk status

RATIONALE

Completing the actions described in Section 1 will provide an overview of the country's livestock breeds and their functions, within the broader framework of trends in the livestock sector and opportunities for conservation. The next objective should be to identify the breeds that are at risk of extinction, i.e. the breeds that need to be targeted by conservation programmes. Breeds' risk of extinction can be assessed using 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 breeds that are at risk. Determining conservation value and prioritizing breeds for conservation are dealt with in Section 3.

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 adopting the *Global Plan of Action*, countries agreed to establish or strengthen country-based early warning and response systems for their animal genetic resources. Assessing the risk status of the country's breeds is an essential element of such systems. Monitoring the risk status of transboundary breeds requires cooperation among countries.

We can define a breed's degree of risk 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 change in population size (for declining population sizes in particular) are the most important factors influencing a breed's risk of extinction. Obviously, the smaller a breed's 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 the 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.

Box 6

Growth rate and 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 $r = 1$, the 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 five-year population size estimates for different values of N_0 and r.

Example of growth dynamics over five years with different initial population sizes (number of breeding females) 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 sizes 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. In reality, small populations are more likely than larger ones to be affected by random variation in survival and reproductive rates. Nevertheless, this simple model provides important information for planning conservation actions. For example, it provides an estimate of the time period within which we have to act if population extinction is to be avoided.

Applying this framework is complicated by the difficulties involved in accurately predicting the population growth rate over several years. Few countries have 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 general trends are likely to be imprecise, so breed-based surveys should be given high priority.

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 chosen as the parents of the next generation. When populations are smaller, the fluctuations tend to be larger. This process of fluctuation tends to reduce genetic variation, because it increases the probability that alleles will be lost from the population. 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. a breed) is the most appropriate measure of its genetic variation. However, 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 that has equal numbers of males and females that have a uniform probability of contributing progeny and is 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 in the case of livestock. In livestock populations, N_e is usually smaller than the actual (*census*) population size because of a smaller number of breeding males than breeding 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: $\Delta F = 1/(2 \times N_e)$. A larger N_e is therefore considered advantageous because it is associated with more genetic variation and less inbreeding.

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 may 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 = the number of males and N_F = the number of females, provides a simple estimate of N_e and gives a useful general idea of the dynamics of genetic variability within a given population. For 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. If Wright's formula is used, simple adjustments can be applied to account for effects of selection (see Box 7). When pedigree information is available, more complex and precise methods for estimation of N_e can and should be used. These approaches have been reviewed by Leroy et al. (2012).

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. Real livestock populations obviously differ from such idealized populations, which have 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 idealized populations.

The simplest model (Wright, 1931), takes into account the fact that the number of breeding males and the number of breeding females are usually not equal: $N_e = (4*N_M*N_F)/(N_M+N_F)$, 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-described 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 using the model proposed by Santiago and Caballero (1995). Their method 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 known as best linear unbiased prediction – usually abbreviated "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 targeted by conservation programmes (see Section 7).

Even if there is 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 6.

In summary, 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).

When 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 and thus should allow most countries to assign their breeds to risk-status categories (see Task 2, Action 1 of this section). In countries where more information is available, additional, more accurate estimates of risk status 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 present in the country (from the tasks of Section 1).
2. Existing information about the size, composition, trends and geographical distribution of breed populations.
3. Existing information on the same or similar breeds in other countries.
4. FAO guidelines *Surveying and monitoring of animal genetic resources* (FAO, 2011).

Outputs:

1. New information about population size and trends and geographical distribution.
2. List of breeds with their respective risk statuses.
3. Methodology with which to update the risk statuses regularly.

Task 1. Determine the population size, trends and distribution, and cross-breeding activities

Action 1. Review available population data

Many countries lack formal systems for surveying 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's guidelines on *Surveying and monitoring of animal genetic resources* (FAO, 2011) provide advice on how to establish such systems.

Action 2. Assign responsibility for determining risk status

Responsibility for determining the level of risk of national animal genetic resources should be assigned to a specific entity. This entity might be the National Advisory Committee for Animal Genetic Resources or an equivalent body, a specialized task force established by the National Advisory Committee, or any other body that has sufficient knowledge of animal genetic resources and their management. The guidelines *Surveying and monitoring of animal genetic resources* (FAO, 2011) suggest 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 out surveys. The National Coordinator for Management of Animal Genetic Resources should participate in 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 is vital to the success of animal genetic resources surveys and in ensuring the quality of the results obtained (FAO, 2011). 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 on 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 the 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 the 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 radius of the largest circular area within which approximately 75 percent of the population lies (Alderson, 2009) and (b) number of herds and trends in these figures; and
- 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 and 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 artificial insemination (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 (e.g. mass selection, index selection, BLUP, optimum contributions selection, etc.): selection will usually accelerate the inbreeding rate if methods to control inbreeding are not implemented effectively (see Sections 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 (this serves 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 other 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, droughts, floods, and contingency plans for dealing with them; and
- presence and status of 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 the 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 should be put in place for all breeds within the country, 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".

Systems should, as far as possible, be harmonized across countries that may be collaborating in conservation activities. Communication and collaboration among National Advisory Committees for Animal Genetic Resources from neighbouring countries is therefore advisable.

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

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 population 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 the 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 = 2000 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 the 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.

Action 4. Analyse and interpret the 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 to identify and understand the factors influencing the degree of risk.

Data analysis should be preceded by accurate editing of the data 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 the guidelines *Surveying and monitoring of animal genetic resources* (FAO, 2011). 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 risk-status categories

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, 2012). As noted above, 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 of the most important parameters discussed in the previous subsections:

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, if implemented effectively, should increase breeds' chances of survival (i.e. decrease their risk of extinction). The risk-categorization system recognizes this by including subcategories for breeds that are included in conservation programmes (critical-maintained and endangered-maintained). These subcategories are particularly important for precise monitoring the diversity of animal genetic resources at global level.

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

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

In addition, a seventh category, unknown, is used to describe breeds for which population data have not been reported to DAD-IS. Breeds that are categorized as critical, endangered or vulnerable are considered to be at risk for extinction and thus are candidates for conservation activities.

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 population size is equal, populations belonging to species with low reproductive capacity, such as the horse, are at relatively greater risk than those 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 requires 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 reproductive 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	Ñandù	Guanaco	Horse
Ostrich	Partridge	Llama	Sheep
Peacock	Pheasant	Vicuña	Yak
Pig	Pigeon		
Quail	Rabbit		
Swallow	Turkey		

* Includes both domestic (*Anas platyrhynchos*) and Muscovy (*Cairina moschata*) ducks.

Risk status classification

Extinct: A breed is categorized as extinct when there are no breeding males or breeding females remaining and any cryoconserved genetic material that may be available is insufficient for breed reconstitution.

Cryoconserved only: Breeds that have no living male or female animals remaining, but for which there is sufficient cryopreserved material to allow for reconstitution of the breed, are assigned to the category cryoconserved only. The ability to reconstitute an otherwise-extinct breed depends on the amount of and type of stored germplasm. Requirements differ greatly according to species. Guidance on what constitutes "sufficient cryopreserved material" is provided in the FAO guidelines *Cryoconservation of animal genetic resources* (FAO, 2012).

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); or
- the overall population size is less than or equal to 120 (360) and the population trend is stable or decreasing; 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 stable.

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 the trend is stable or decreasing; 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 stable.

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; or
- the overall population size is greater than 1 200 (3 600) and less than or equal to 2 400 (7 200) but stable or decreasing; or
- the total number of breeding males is between 20 and 35 (i.e. the ΔF is between 0.5 and 1 percent).

Unreported population trends are assumed to be stable.

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. To allow more such breeds to be correctly assigned to the not at risk category (i.e. rather than classified as unknown), countries are encouraged to insert estimated population sizes into DAD-IS if data from a formal census are not available. 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 action. A population survey is needed; the breed could be critical, endangered or vulnerable.

Table 3. Risk categories according to 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 figures for populations with high reproductive capacity and Table 5 presents figures for species with low reproductive capacity.

Table 4. Risk categories for species with high reproductive capacity*

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	critical	critical	critical	critical	critical	critical	critical
	6 - 20	critical	endangered	endangered	endangered	endangered	endangered	endangered
	21 - 35	critical	endangered	endangered	vulnerable	vulnerable	vulnerable	vulnerable
	>35	critical	endangered	endangered	vulnerable	vulnerable	not at risk	not at risk
Stable or decreasing trend or ≤80% pure-breeding	≤5	critical	critical	critical	critical	critical	critical	critical
	6 - 20	critical	critical	endangered	endangered	endangered	endangered	endangered
	21 - 35	critical	critical	endangered	endangered	vulnerable	vulnerable	vulnerable
	>35	critical	critical	endangered	endangered	vulnerable	vulnerable	not at risk

= critical, = endangered, = vulnerable and = not at risk.

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

Table 5. Risk categories for species with low reproductive capacity*

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	critical	critical	critical	critical	critical	critical	critical
	6 - 20	critical	endangered	endangered	endangered	endangered	endangered	endangered
	21 - 35	critical	endangered	endangered	vulnerable	vulnerable	vulnerable	vulnerable
	>35	critical	endangered	endangered	vulnerable	vulnerable	not at risk	not at risk
Stable or decreasing trend or ≤80% pure-breeding	≤5	critical	critical	critical	critical	critical	critical	critical
	6 - 20	critical	critical	endangered	endangered	endangered	endangered	endangered
	21 - 35	critical	critical	endangered	endangered	vulnerable	vulnerable	vulnerable
	>35	critical	critical	endangered	endangered	vulnerable	vulnerable	not at risk

= critical, = endangered, = vulnerable and = not at risk.

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

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 affecting the degree of risk of animal genetic resources, now and in the future. However, the thresholds should not be applied uncritically. 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 the population having an average relationship and ΔF that are much greater than would be expected based on numbers of breeding males and females. In such cases, the need for action is as urgent as it is for 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 classify the breed according to the *ΔF* criteria of the DAD-IS risk-classification system rather than according to the number 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 radius of the largest circular area in which 75 percent of the population of a breed can be 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 the 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 percent, 7.5 percent 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 1 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 as when an *in vivo ex situ* programme has limited animal-housing facilities).

Breeding approaches that 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, the 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, males used in AI and herds. 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. Consider, for example, 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 the results of the risk categorization and consider 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 consequences
Risk category	Loss of diversity	Genetic defects	Susceptibility to random events
Critical	++++	++++	+++
Endangered	+++	++	+
Vulnerable	++	+	
Not at Risk	+	+	

Note: the number of plus 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)[9], others, such as the method proposed by the European Federation of Animal Science (EAAP), emphasize genetic erosion based on estimates of N_e. 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 and seek, as far as possible, to use

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

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 where 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 at global level. If national populations are at risk due to their small sizes, it is essential that countries collaborate and manage their national populations jointly as a 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 the provision of cultural, environmental or social services, or to develop niche products (see Section 8). In addition, larger 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 breeds' risk status to stakeholders

The degree of risk provides an indication of the amount of time that is available in which 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. The guidelines *Surveying and monitoring of animal genetic resources* (FAO, 2011) provide detailed information on how to report and communicate the results of surveys, and describe the importance of providing stakeholder groups with information that is tailored to their needs. They also provide 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 fund raising 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 are entered into DAD-IS or (for European countries) EFABIS. It is also important to communicate both to national authorities and to international collaborators the difficulties encountered in population monitoring and information dissemination, so that they can be taken into account in the planning of subsequent activities.

Task 3. Design and implement interventions

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 broadly similar for all categories, but the stress and urgency put on each will vary from one risk category to another. In planning interventions, consideration must also be given to 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 appropriate conservation measures

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 – in each risk category.

Table 7. Relative importance of population management objectives according to risk status

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

Note: the larger the number of plus (+) signs, the more important the respective objective. Minus (-) signs indicate that the activity should be avoided. Absence of a sign means that the activity can be practiced, but should be balanced with other factors, such as cost.

Populations categorized as critical will have already lost a major part of their original genetic variation. They 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 census population size of the breed while controlling inbreeding through judicious mating. In such populations, enlargement of the census 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 population 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 the management of genetic variation in the long term. Selection for productivity will often not be possible and will be antagonistic with increasing the population size and genetic variability.

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 population 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). Selection for productivity is less important than increasing genetic variability and population size, but may be implemented among males as the population approaches the vulnerable category. 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 response to selection 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 (see 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 population 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 AI 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 census population size is usually desirable, even for not-at-risk breeds. However, this will not be a priority in management plans for such breeds and should avoid creating competition for resources with breeds at risk. 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 require analysis to determine their risk status. Breed surveys should be undertaken as soon as possible.

Action 2. Implement the conservation measures

Whichever interventions are proposed, they should be undertaken in a timely and efficient manner. Detailed advice on specific interventions is presented in Sections 4 to 8.

Task 4. Monitor risk status

Livestock production systems in many parts of the world are being transformed rapidly. These changes can affect breeds’ demographic trends and genetic status within short periods of time. It is therefore advisable that countries should establish methodologies for regularly updating the risk status of their breeds, as well as early warning and information systems capable of monitoring changes in the nature and intensity of the major threats to the diversity of animal genetic resources. For example, cross-breeding activities should be strictly monitored, as should the number of males and their use in breeding, especially in populations where AI is widely practised. Efficient monitoring and analysis of population data are prerequisites for timely implementation of conservation measures.

The methods used for surveying 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 (2011).

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3 Determining the conservation value of a breed

Overview

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. 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 divided into two subsections, the first describing simpler approaches and the second more complex approaches. Specifically, the second subsection describes methods that use genetic markers for evaluating genetic variability, whereas the first subsection describes 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 their capacity to implement the 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

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, maintaining genetic diversity is a critical objective in 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 are 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, a breed of chicken is able to provide coloured eggs year-round, by a totally natural process.

The Araucana hen is a chicken breed from Chile. It is recognized for its particular phenotypic characteristics, the presence of “earrings” (straight feathers extending from the neck, down past the ears) 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 be as much as 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 for describing the values of animal genetic resources that mirrors approaches used to describe other types of resource (see

Box 12). The system makes it easier to compare attributes that can be immediately marketed (such as milk or meat production) 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 the lesions produced when the larvae penetrate the skin at the start and the end of their life cycles. At El Nus Research Station, located in Antioquia, Colombia, many studies on the interactions between cattle and botflies have been carried out since 1948. Studies have shown that the progeny of animals that are not parasitized (i.e. that show resistance) are also resistant. This has 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). It may therefore be appropriate to give higher conservation priority to breeds that have greater cultural importance. In many areas of the world, traditional grazing over many centuries has contributed to the creation and maintenance of agro-ecosystems that have 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 farming systems and the natural environment retain their character and richness as long as the breeds and production systems 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 have 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 of the 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 of each breed based on non-demographic factors.

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

Outputs:
1. Information about factors affecting the conservation value of each breed.
2. Ranking of breeds on the basis of conservation value.

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

Action 1. Assign responsibilities for prioritizing breeds for conservation

To ensure clear and unambiguous decisions, the responsibility for determining the conservation value of breeds must be assigned to a specific entity. This 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 groups of stakeholders should be consulted.

Action 2. Determine the factors upon which the prioritization will be based

The first activity of the National Advisory Committee will be to evaluate the conservation objectives for each species (see Section 1). Based upon these objectives, it must then agree upon the factors to be considered in determining the conservation value of the breeds, as well as the relative importance of these factors.

The process of drawing up a list of specific factors for use in assessing conservation value may be facilitated by considering the country's overall strategy for the conservation of animal genetic resources. Bennewitz *et al.* (2007) outlined three strategies to consider.

1. Maximum risk strategy. This strategy considers only the degree of risk, and can be justified if the main objective of the country is 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 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 extinction 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 self-sustainable economically.

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 according to 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 successfully implementing a conservation programme is often lowest for the breeds at 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 the presence of a special trait. In such cases, considering all these factors may result in their over-emphasis in determining conservation priority.

If quantitative methods are to be used (see below in this section), the National Advisory Committee should assign to each of the factors influencing conservation value a numerical weight proportional to its the relative importance. Various approaches to the process of assigning weights have been proposed. One simple participatory and visual approach is known as “participatory piling” – 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 a framework 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 value for conservation. These values can be categorized as follows (Drucker *et al.*, 2001; FAO 2007a):

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 (e.g. cycling of soil nutrient, seed dispersal, fire control).

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 – results 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 for successful 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 the breeds). A statistical model is then used to determine the importance of a given attribute based on the frequency with which the profiles excelling in that attribute 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 depends greatly on the appropriateness of the design of the survey and the statistical analysis. Therefore, this approach will generally require consultation with a statistician or other scientist who has the relevant experience.

Box 13

Using choice models to value and rank breeds for conservation

Choice models can be used to understand the full range of values that livestock can have for people and to express them as a Total Economic Value. The values held by breeds range 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 on the basis of market transactions and are often undervalued if not assessed properly. In choice models, people are asked to state their preferences for hypothetical profiles describing the traits of a set of breeds. People choose their preferred profile, which allows estimation and comparison of how much they might be willing to pay for particular traits. Analysis of choice data reveals the values of traits relative to each other and allows the traits to be ranked. 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 livestock keepers already get paid to keep at-risk breeds, choice model results can help maximize the efficiency of such conservation programmes, by matching conservation payments to the value of each breed to the public.

Provided by Kerstin Zander.

Action 3. Gather the information needed for the prioritization

Once the factors influencing conservation priority have been identified, 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. If the presence of unique traits or of adaptation to a particular environment is regarded as important in assigning conservation priority, any such qualities should be noted. Likewise, any historical or cultural significance of the breeds should be noted. Pedigrees or genetic markers can provide insight into genetic variation (this topic is discussed in more detail in Section 5).

Ideally, countries will have already characterized their breeds phenotypically and genetically prior to undertaking a conservation priority-setting exercise (see *Phenotypic characterization of animal genetic resources* – FAO, 2012 and *Molecular genetic characterization of animal genetic resources* – FAO, 2011). If breeds have been fully and properly characterized, then the information required will have been gathered. 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 may need to consult a number of sources. Ideally, the persons chosen to collect the information will have some existing familiarity with the respective 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 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) is 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 are knowledgeable about the history of the 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 the 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. Evaluate the advantages and disadvantages of each breed

Section 1 describes the use of a SWOT analysis to assess the roles, functions and dynamics of livestock species and 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. 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 the 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 rather than a National Advisory Committee, 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 1 and absence 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, if a group of three breeds is being assessed for cultural significance, the breed with the most significance 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, committee members 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:

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

(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 are 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	1000	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 cow and cultural importance. It is an example of 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 of the hypothetical country 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.

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.

Action 1. Prepare a report on the 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. Meet 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.

Using information from genetic markers

RATIONALE

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

The previous subsection 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 subsection 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 the prioritization of breeds for conservation activities.

Inputs:

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

Outputs:

1. Quantified analysis of the genetic diversity of breeds in each species under consideration.
2. List of breeds prioritized for conservation.

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

Action 1. Obtain molecular genetic data

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.

Box 15

Genetic markers

Molecular genetic markers are observable sites of variability in the sequence of DNA that are associated with a characteristic of interest 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 for calculating 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 (SNPs) have recently been identified in several livestock species. For some of these species (e.g. cattle, goats, sheep, chickens and pigs) panels including tens of thousands of validated SNPs are already available to the scientific community, permitting genome-wide scans at a very low cost per data point. For others (e.g. buffalo), they will likely be available in the near future. 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 the conservation value of an animal genetic resource.

Given the rapid advance of DNA sequencing technology, whole-genome data will be 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 adaptive 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.

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 relevant FAO guidelines (FAO, 2011), but newer genotyping platforms such as SNP chips may be considered (depending 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 present 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 chicken populations in Southern Africa.

Box 16

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

Southern Africa is home to 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 populations are well-represented in the conservation flocks. A research project was therefore undertaken to answer these and other questions regarding the chicken populations of 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; 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 chickens (from South Africa) 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 colour and in some cases production performance), whereas few differences could be detected based on the DNA markers. 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; Southern African chicken populations shared three major haplotypes, which were concluded 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 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 and 2011b).

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

The appropriate approach to the assessment of genetic diversity will depend on the specific objective of the conservation strategy in terms of the type of genetic diversity to be conserved. For example, the objective 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 considered 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 (see Actions 3 to 7) is preferable.

Box 17

Estimating within-breed molecular genetic diversity

The simplest measure of within-breed genetic diversity is heterozygosity. Increased heterozygosity corresponds to greater genetic diversity. An animal is heterozygous at a given locus if its two alleles differ. Two measures of heterozygosity exist: observed heterozygozity (H_o) and expected heterozygosity (H_e). Observed heterozygosity at a given locus is calculated simply by observing the genotype of each animal sampled, counting the number of heterozygous animals and dividing this number by the total number of animals. Expected heterozygosity 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 alleles 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 (assortative mating) decreases H_o, whereas mating of non-similar animals (disassortative mating) increases H_o.

Molecular markers can 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 disequilibrium. 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 (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.

Action 3. Choose which objective method to apply

The use of objective approaches to account for molecular genetic diversity in the prioritization of breeds for conservation has been reviewed by Boettcher *et al.* (2010). The choice of which approach to apply in a given prioritization exercise will depend on the definition of genetic diversity that is being used. The Weitzman (1992) approach measures genetic diversity in terms of 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 breeds’ uniqueness is the only factor considered important and it is expected that breeds will not be crossed 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 options (Meuwissen, 2009).

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 in terms of the changes that have occurred through allelic substitution and have resulted in different allelic frequencies in the breeds.

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

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

where, for j different loci and k 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, respectively. Various software are available free of charge for estimating genetic distances from genetic-marker data. These include 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; 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 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 the case in which breeds x and y are the same) and averaged across loci. The following example is based on three breeds:

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

where m_{11} is the average simple kinship across all loci between 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 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 that can be used 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 the 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 should be prioritized within each risk category and that breeds within the higher-risk category should be given greatest priority. The objective methods of prioritization involving 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. 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. All breeds, regardless of risk category, can be assigned an equal risk of extinction (0.25, for example).
- Second, if the committee is willing to assume extinction probability is equal within each risk category, but would like to allow for prioritization across 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 the critical, endangered and vulnerable categories, respectively.
- Third, the committee may wish to estimate a specific extinction probability for each breed (in which case risk category will not be considered directly). Three general approaches can be used to estimate extinction probability. The first approach is to identify factors assumed to influence the probability of breed extinction and use them as parameters to define categories to which breeds can be 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 probability (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 which non-genetic factors to include in the 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 objective prioritization methods allow for the consideration of such factors. The information collected in Actions 3 and 4 of 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. Comprehensive approaches of this type have been proposed 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 approach based on the methods proposed by Reist-Marti *et al.* (2003) and Gizaw *et al.* (2008) is summarized step-by-step in Box 20.

Box 20

A step-by-step example of an objective method for 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 magnitude 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:

p = 0.0 if population size is ≥ 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 ten years):

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:

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:

b = 0.0 if a programme exists

b = 0.1 if no programme exists

f is a parameter relating to livestock keepers' opinions of 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 (in Section 3) 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 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 the core set can be obtained by performing the following matrix calculation:

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

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 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; these include 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-matrix 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:

$$U_i = 4 \times (\text{risk}_\text{i} \times D_i) + SCV_i \text{ (Equation 9)}$$

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 calculated in Step 3; and
- SCV_i is the standardized conservation value of breed *i*, as calculated in Step 2.

The breeds should then be ranked 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.

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.

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4 Choosing the appropriate conservation methods

Matching breeds and conservation methods

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

RATIONALE

As 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 roles and its contributions to nature management; and
- can be financially self-sustainable.

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

- leaves the breed exposed 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;
- 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, unless multiple conservation sites are available;
- 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 are that it:

- safeguards the flexibility of the genetic system through conservation of genetic variation;
- protects the breed’s genetic information 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 ongoing maintenance of stored germplasm.

The disadvantages of cryoconservation are that it:

- does not allow 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.
2. National resources available for use in the management of animal genetic resources, including infrastructure, facilities, financing, technical capacity and stakeholders.

Output:

1. Decisions on the conservation methods to be applied for the different species and breeds.

Task 1. Assess the applicability of the available conservation methods

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 may 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 feed 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 on the part of stakeholders to cooperate with the government and with other stakeholders should therefore be secured before embarking on a conservation programme.

Task 2. Match breeds to conservation methods

Action 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 its flexibility to adapt to changes in production conditions, 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. Identify conservation methods that will meet the objectives effectively

Some conservation methods will be more effective than others with respect to a given conservation objective. For example, 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 can be 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, breed regeneration using semen will be more time-consuming than regeneration using embryos, because if semen is used, several generations of backcrossing are needed in order to regenerate the breed in a nearly pure state. When a breed is maintained *in situ*, livestock keepers' enthusiasm for keeping it (and thus its prospects for survival) will depend strongly on the breed's productivity and market prices for its products. In such circumstances, measures that address production and market-related issues (see Sections 7 and 8) are likely to be important.

Action 3. Consider the possible pitfalls of each conservation method

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

- disasters and infectious diseases – these may destroy the population, especially if the breed is concentrated within a small geographical area;
- disconnection between the objectives of the livestock keepers and the objectives of the conservation programme – livestock keepers have the right to manage their herds or flocks according to their own prerogatives and may decide to abandon a breed if maintaining it is not financially attractive;
- genetic bottlenecks and a high degree of relatedness between animals – small populations in particular are at 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 livestock keepers' incomes, and termination of the subsidy may induce them to stop keeping the breed.

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

- (if animals are closely related) inbreeding and loss of alleles by random drift – leading to decreased genetic variability, and perhaps poor fertility, fecundity and viability;
- (if the breed is primarily maintained by livestock keepers) a lack of opportunities for improving the population through a breeding programme – this means that those participating in such conservation schemes often have to be subsidized; if these subsidies stop, the risk that the breed will be lost increases; and
- (if the breed is maintained on government farms) changes in the financial priorities of the central government or the respective ministry.

When a breed is cryoconserved, risk factors include:

- zoosanitary problems – material for cryoconservation (gametes, embryos) must usually meet high sanitary requirements; the presence of animal diseases may disrupt or inhibit the collection of this material;
- lack of resources – the availability of the skilled personnel and reliable equipment and infrastructure needed for a cryoconservation programme may be threatened by a lack of adequate planning;
- infrastructure failure, such as electrical blackouts and ruptures of storage vessels, which can result in loss of viability in the stored material;
- damage to storage facilities – natural disasters or civil unrest can result in the destruction or abandonment of the gene bank and consequent loss of the stored material. The risk associated with this factor can be alleviated by the establishment of multiple storage sites.

Action 4. Consider the costs of each conservation method

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 targeted breeds and the costs of realizing a breeding programme with special emphasis on the maintenance of 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 methods

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

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

Reference

FAO. 2012. *Cryoconservation of animal genetic resources.* FAO Animal Production and Health Guidelines. No. 12. Rome (available at http://www.fao.org/docrep/016/i3017e/i3017e00.htm).

5 Organizing the institutions for *in vivo* conservation

Overview

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 addressing 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 resources societies, consumers of livestock products and marketers (Oldenbroek, 2007; EURECA, 2010).

Breeders will usually own a significant proportion of the population targeted for conservation, and will therefore be the most essential stakeholders. Most of the breeders will also be producers (i.e. will raise livestock in order to obtain products or services for sale or use). Producers are of particular 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 also Section 1), serving as a source of information on breeds and their roles, product development and promotion, marketing and providing technical support for breeders. 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 breeders 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 breeders. Where appropriate, such institutions should be established or strengthened.

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 and research institutes also play roles in conservation. 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 describes the roles of various stakeholders in *in vivo* conservation, with special emphasis on the roles of breeders' associations.

Involving livestock keepers in community-based conservation

RATIONALE

The maintenance of animal genetic resources under sustainable management by livestock keepers is one of the most effective and practical ways of conserving these resources with a minimum of financial expense. However, such an approach will be successful only if it is economically viable and if sufficient technical support is provided. Hence the objectives of community-based conservation projects should defined clearly, especially with respect to the characteristics for which the targeted breeds have traditionally been valued. Conservation efforts should begin with characterization and evaluation of the targeted breeds and identification of characteristics of economic, social and cultural value specific to each breed. Further advice on organizing such studies is provided in the guidelines *Phenotypic characterization of animal genetic resources* (FAO, 2012b). A participatory approach that involves livestock keepers is important, both to increase the accuracy of the information upon which the conservation activities will be based and to ensure interest and ownership of the project or programme on the part of the livestock keepers and thereby increase its sustainability. Livestock keepers will rarely accept a programme that deviates from their preferences (see Box 21). The role of an outside entity in a community-based conservation scheme will primarily be to provide the inputs needed to promote the long-term survival of livestock-keeping livelihoods in the targeted community and to provide technical support. FAO has produced a publication on community-based programmes for the 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 restoring wetlands and forests, improving the land and plant biodiversity and undertaking small-scale organic farming 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 larger-scale 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 re-introduction.

Provided by Devinder K. Sadana.

Objective: To design, with the participation of livestock keepers, an *in situ* conservation programme that they will implement with the assistance of outside agencies and that ensures maintenance of the targeted breed by promoting the autonomy of the community and the sustainability of the livelihoods of community members.

Inputs:

1. A breed that is at risk of extinction and deemed to be of high conservation value.
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.
4. Earmarked technical and financial resources.

Output:

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

Task 1. Choose the location and collaborators for the conservation activities

Action 1. Identify and study the 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 holdings, 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. It will probably be necessary to identify how breed conservation measures can complement the broader objective of improving the livelihoods of 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 will 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

A top-down approach in which a study team simply visits the community unannounced and undertakes the study will rarely work well. A step-by-step process of engagement that informs the members of the community about the intentions and goals of the conservation work and any complementary activities will usually be necessary. The first contact should be with the leaders of the village or with prominent livestock keepers (sometimes 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 of working with the community, such as an NGO or government extension service.

Action 2. Enlist the research team and carry out the study

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 the livestock production and breeding practices of the community, perceptions of the livestock keepers on the strengths and weaknesses of the targeted animal genetic resources, outputs obtained from the animals and the use or marketing of these outputs, 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 the conservation activities should be included.

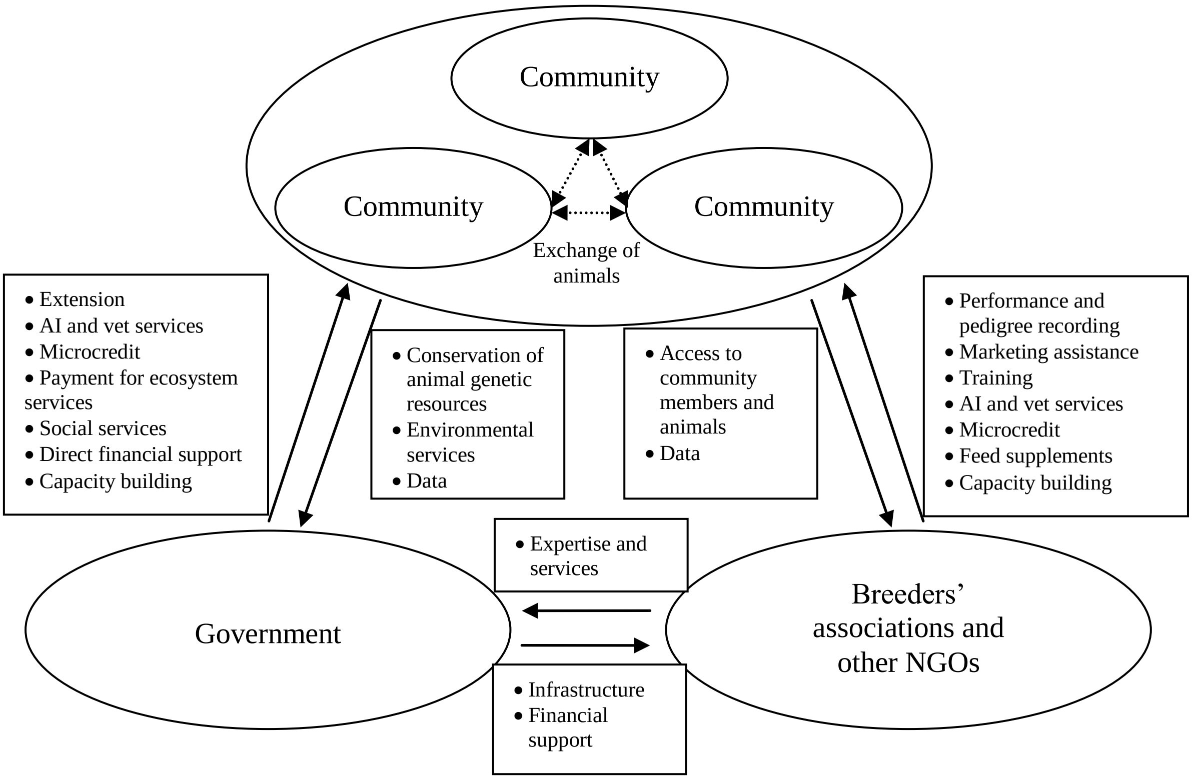
Action 3. Evaluate the results

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

Task 3. Facilitate the implementation of the community-based programme

Figure 2 illustrates 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 between 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 an important breed in Argentina.

Figure 2. Interactions among the possible stakeholders of a community-based conservation programme



Box 22

Public–private partnerships for the conservation of Criollo Argentino cattle

The Criollo Argentino is cattle breed that descends from various cattle breeds brought by the Spaniards to Argentina in the sixteenth 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 banks' primary method of choice 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.

As Figure 2 indicates, sometimes outside investment and assistance from the government or an NGO may be necessary in order to implement activities that promote 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. 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.

Finally, capacity building has been shown to be a key component of successful community-based conservation programmes (Brooks *et al.*, 2012). Although livestock keeping communities have a tremendous amount of traditional knowledge that must be incorporated in conservation activities, they will likely be poorly versed in specific approaches for management of genetic diversity, genetic improvement and novel husbandry approaches for increasing animal productivity. Therefore, capacity building is another service to be provided to the community.

Action 1. Assist livestock keepers to organize a breeders' association

The animals belonging to a 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 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. Depending on the geographical dispersion of the breed, eventual expansion of the association beyond the initial communities may be warranted. 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 to 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 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 the 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, the breeders' association, in 2008, 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 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 livestock production.

Provided by Sabyasachi Das.

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 implement a breeding programme to improve productivity and maintain 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 describes the role of a government research institute in the establishment of a community-based sheep-breeding programme in Ethiopia.

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 2007 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, 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 within a selection objective for the breed. This is generally considered the most important issue in the genetic improvement of animals in a conservation programme. The objective should be as simple and direct as possible to allow the genetic potential existing in the population to be exploited to the maximum extent. Genetic improvement will gradually increase the average genetic merit of the breed with respect to the chosen objective. Detailed advice on establishing selection objectives is 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 various 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 them performed by a central body. Collaboration among different breeders' associations may further increase the efficiency of these activities, as may the establishment of multicountry associations for transboundary breeds.

Action 3. Consider establishing a nucleus herd

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 in 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 establish complementary institutions

Providing specific incentives or other assistance may help direct an at-risk breed back onto a sustainable course. For example, livestock keepers may be abandoning a breed, or even animal production in general, because they cannot market the products at a price or in a 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 help ensure the breed's survival. Many 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 be providing a service that can be regarded as a common good, but 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 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 conservation efforts. They can play many roles, including serving as monitors of threats to breeds. Most standardized international transboundary breeds are well served by breeders' associations that have clearly documented procedures and functions. The functions performed by the breed associations of standardized breeds have been considered a universal model for other classes of breeds. Relative to standardized international transboundary breeds, the keepers of many locally adapted breeds have less formal organization. Accommodating the needs of these livestock keepers and meeting the conservation goals of the breeds will often mean that some aspects of the model for standardized breeds will have to be adapted.

Organizing breeders presents many challenges. If herds have long been isolated, each breeder is very likely to consider his or her own herd to be the only typical herd, 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 crucial for long-term success. Traditional breeders have assumptions and beliefs that have strongly shaped the development and maintenance of their breed. They may be reluctant to adopt substantial changes, even if to an outsider the changes seem necessary for the breed's 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. Strong local attachment has left many breeders with a skewed appreciation of the overall breed, and an intense focus on their local resources. The result is 20 different breeders' associations for this breed, which numbers at most 3 000 animals. Fragmentation makes the breed's 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 a certain point such divisions lead 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 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. A list of breeders who keep animals of the breed.
3. Some knowledge of the history of the breed and its present functions.
4. Knowledge of the goals of the breeders and their history of cooperation.

Outputs:

1. A well-functioning breeding organization, with documentation of:
    - requirements for membership;
    - registry protocols;
    - rules and by-laws;

- dues and fees for members;
- communication methods for education and training; and
- mechanisms for conflict prevention and resolution.

2. Communication between the breeders' association and national entities responsible for management of animal genetic resources.

Task 1. Assess the degree of support for establishing a breeders' association

Action 1. Discuss the possibility of establishing 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 in 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 members of the community that may be interested in joining or leading a breeders' association

A breeders' association is an 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 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 and asked to examine the documents of the promotional association and to determine whether the respective animal population warrants being regarded 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 officially recognized and become 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 its activities to the Ministry of Agriculture, with copies of all registrations made during the year. The Ministry of Agriculture is 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 yet 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 nearly be 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 the risks associated with having only one 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. Mr Magraj Jain of Rajasthan in India is one such example. It was during 1990s that he recognized that the productivity of the livestock in his local 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 – SURE (Society to Uplift Rural Economy; Barmer, Rajasthan) – Mr Jain took on 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. Plan and implement the establishment of the breeders' association

Action 1. Determine requirements for membership of the association

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

An important first step is to determine which animals and breeders are to be considered 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 which animals to include 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). This approach will mean that more 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). It 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 animal with 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 genes are more than 12.5 percent exogenous, 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 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 the other benefits of membership. In breeds that don't produce widely marketable food and fibre products, such as many horse breeds, it may be necessary to include non-breeder users of the breed 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.

Bringing new breeders into 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 breeders' associations register animals and validate pedigrees. Procedures must be consistent and applied uniformly. A variety of software programs, each with strengths and weaknesses, are available for this purpose. 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 of an association for a standardized breed. However, for breeds raised in extensive production systems, especially in multisire 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. Box 31 presents an example of a herd-based registry. In economically developed countries, it is common for new breeders' associations to have a short period during which foundation animals are registered and 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.

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 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 because of their genetic distinctiveness, which adds 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 the long-term success of conservation in breeds with very small population sizes. In such a situation, the newly discovered animals must, however, enter the breed on equal footing with existing animals. If not, their genetic contribution will be diluted out and any potential benefit from their inclusion in the herdbook will be forsaken. Well-established and sustainable breeds may wish to impose stricter standards entry of new animals, such as requiring a few (usually one to five) generations of documented pure-breeding before achieving entry in the official herdbook.

Provided by Phil Sponenberg.

Box 30

Protocol for adding non-registered animals to 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 comprising 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
Length	10
Density	10
Crimp	3
Uniformity	7
Subtotal	70
Conformation	
Head	10
Height	10
Fibre coverage of rear legs	5
General appearance	5
Subtotal	30
Total	100

Animals are assessed 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 multisire 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 to formally contribute, voting procedures and the role of members in various sorts of decision-making. 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 make 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 rules on the frequency of elections. Such procedures encourage participation and promote loyalty and a sense of ownership among the members. Participation of original breeders must be ensured and may require giving them some kind of special recognition.

Board of directors

In most associations, the members elect a board of directors that 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. Set membership dues and fees

Dues for membership and fees for services such as registration, are important sources of revenue that help to meet the costs incurred by the association. In most cases, dues and fees are set by the membership or board of directors. Dues and fees must be set fairly and uniformly, and should not be changed frequently. 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 decide to 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.

Action 5. Establish communication methods for educational and training programmes

Communication within a breeders' 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. Potential 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 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 world's largest national Leicester Longwool population. 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 its relative quality: blue cards for superior breeding stock, red cards for good breeding stock, yellow cards for acceptable breeding stock and white cards for animals that are 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, both for breeders and for the general public.

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

Action 6. Develop and adopt a procedure for conflict resolution

Because breeders' associations comprise individual breeders, conflicts among members are certain to arise. If not resolved judiciously, conflicts within the association can prevent the expansion of the breed population and may cause it to contract to the point of extinction. Most conflicts arise for specific disagreements between individual members or breeders, but some involve fundamental differences in the 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 resolve it fairly and quickly. Procedures for conflict resolution must always focus on the needs of the breed, including the need for engaged and involved breeders that communicate and share. Conflict resolution is especially important when establishing new associations for locally adapted breeds, because in these circumstances the breeders may be particularly traditional and isolated. In some cases, conflicts can be foreseen and prevented, or at least minimized. Box 33 presents a specific example in which a breeders' association developed policies and practices that account for cultural differences among members.

Box 33

Accounting for cultural differences among members of a breeders' association

Breeders' associations must always reflect underlying cultural norms. This is especially challenging if a single breed is kept 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, as well as more recently established connections with Anglo breeders and enthusiasts.

Throughout its history, the size of 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, and strengthens 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, who 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 for 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 from 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).

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 breeders' association may split into factions, each 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

Differing views on introgression among Texas Longhorn breeders in the United States of America

In some instances, conflicts among breeders may not be easily resolved, and drastic action may have to be taken. Such a conflict occurred among breeders of Texas Longhorn cattle 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 ensures the breed's for the short-to-medium term, but fixes conformation and production near current levels with little room for improvement. The long-term consequences of this decision are yet clear, 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 a breeders' association and its activities

RATIONALE

Many breeders' associations need support from governments or cooperating NGOs in order for them to function well in conserving animal genetic resources. This support may be justified by the fact that the activities of the association contribute to public benefits such as maintenance of biodiversity, development of rural areas or increasing 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 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 achieved effectively.

Breeders' associations should actively monitor and appraise the role of the breed as a valued natural resource for the country within the national livestock sector. This task should include assessments of demand for the breed and its products and of threats to its long-term viability (FAO, 2010). Assessing and promoting a breed's value usually requires a strong breeders' association, as weak or inactive associations may be overlooked by national policy makers and other stakeholders (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 to manage their respective breeds, maintaining separate sets of infrastructure for each breed may not be financially efficient. In such cases, 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 may lead to inefficient administration and is likely to mean that the association is unable to provide 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. 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 of the breeds.

The Combined Flock Book originally operated within the structure of Countrywide Livestock Ltd. It was administered by a committee comprising one representative from each breed, under the chairmanship of the President of Countrywide Livestock Ltd. Each breed was also 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 the Combined Flock Book include:

- 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.
2. A description of the association's activities, including the breeding and conservation plan.

Output:

- An auditing procedure for the breeders' association and its activities.

Task 1. Evaluate participation and decision-making procedures

Action 1. Evaluate the mechanisms for member participation

Strong breeders' associations encourage broad participation from their membership (FAO, 2010). All members should feel welcome to participate and contribute. Major decisions should be taken in a democratic manner, avoiding domination by one or a few persons. Some associations get dragged into controversies by a single person or a small group of dissenters. While such individuals may feel very strongly that their opinions are valid, in extreme cases the controversy leads to loss of support for the breed and loss of members from the association. Ensuring that an association functions in a way that promotes 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 that foster broad ownership of the association and high levels of participation. If an association's programmes are to be successful, the livestock keepers and breeders themselves – who will have intimate knowledge of the breed's production system – must participate in decision-making, and their opinions and attitudes must be respected (FAO, 2010).

Action 3. Evaluate the provision of benefits to association members

Breeders' associations should provide technical support to their breeder-members (FAO, 2010), covering (as appropriate to the circumstances) husbandry, health care, animal selection, animal breeding techniques, etc. They should also develop 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.

Task 2. Appraise the genetic purity of the population managed by the association

As noted above, public support for a breeders' association may be justified if the association is actively maintaining 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 (covert) 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. If awards in the show ring or production contest go to animals with obvious introgression from other breeds, 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 the accuracy of parental information

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

Task 3. Evaluate the management of the breed as a genetic resource

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

Action 1. Analyse the association's management of the population structure

Procedures for designating strains or families within the overall breed should be appraised, as should mechanisms for censusing the breed and evaluation of its population structure. Effective breeders' associations periodically monitor the population structure of the breed. Breeders should be educated against temporary fads in breeding, so as to ensure 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 how to maintain a 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 among 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 association's plans for managing the genetic variability of the population should be appraised. 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 of high importance to the future of the breed (FAO, 2005). 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. Procedures for genetic exchanges among herds should be covered by the appraisal, as should any cryoconservation activities, such as targeted freezing of gametes from under-represented animals.

Establishing a centralized *ex situ* conservation programme

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's population may have declined to such an extent that is too small to be raised by a group of livestock keepers. Alternatively, a breed that is valued primarily for its option and existence values (i.e. not for current use – see Box 12) and therefore not profitable enough to be maintained by livestock keepers, may still need to be immediately accessible in its live-animal form (as opposed to cryoconserved material). Perhaps tight central control of breeding is required and such control can only be achieved via *ex situ* conservation on a single farm. *Ex situ in vivo* programmes are typically operated by the government or by non-profit NGOs rather than by the commercial sector.

In many countries, the government and NGOs own institutional farms that are used for research, teaching and development. Most of these farms raise economically important breeds of various animal species, and are used as demonstration centres as well as for production and dissemination of superior germplasm. India, for example, has a well-developed system of institutional farms.

Conserving breeds by establishing dedicated 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 a reduction in genetic variability. The most important challenge in managing a population conserved *ex situ* is, therefore, to sustain genetic variability.

Objective: Establish and maintain populations of important animal genetic resources in centralized 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 kept by private breeders and on existing institutional farms.

Output:

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

Task 1. Plan the conservation programme and secure access to facilities and funding

Given the high costs of establishing and operating *in vivo ex situ* programmes, forward planning is critical both from the financial point of view and the perspective of maintaining sufficient genetic variability on both species and breed levels.

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. Decide which breeds will be targeted by the programme

Following the procedures set out in Sections 3 and 4, decide which breeds to include in the programme, paying close attention to breeds that have not already been targeted by other conservation programmes.

Action 3. Perform a feasibility study

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 programme. The assessment of costs must consider the initial acquisition of the animals, their maintenance, the acquisition or refurbishment of facilities, the maintenance of the facilities, and personnel costs. Any revenues expected to be generated by the conserved 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 as potential donors.

Action 5. Prepare and present conservation plans to government officials and/or donor agencies

A strong argument will be needed to convince donors to support the conservation activities. The value of the animal genetic resources targeted for conservation 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 programme

Assuming Task 1 has been completed successfully, the real work of establishing and operating 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 achieved 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 using 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 the conservation farm should be free from disease or any noticeable defects, conform closely to the desired breed characteristics and be as unrelated as possible. Ideally, 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 the 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 because of natural selection in a controlled environment that differs from the breed's "natural" environment), and because of the potential for genetic drift, it is possible that a genetic gap will develop between the conservation herd and the original population in the breed's native region. The potential for effects of this kind should be assessed and monitored. This "adaptation to captivity" is generally considered more important in 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 for storing germplasm from animals in the programme

Maintaining genetic material from animals belonging to the original population will allow genetic variability to be recovered 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 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).

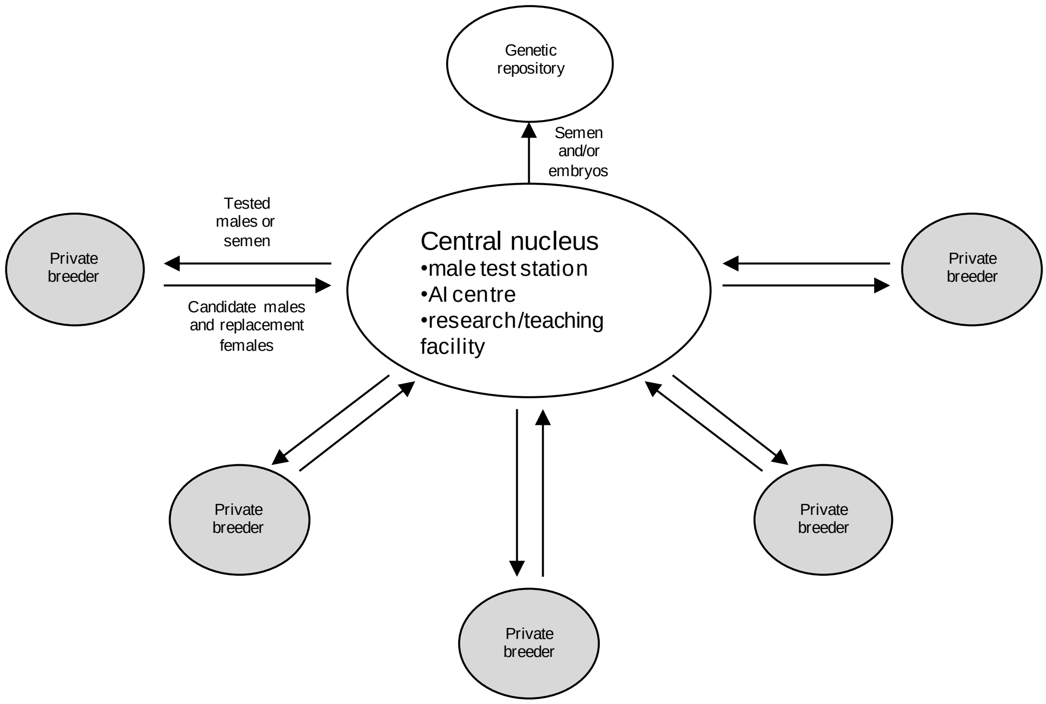
Establishing a dispersed *ex situ* conservation programme

RATIONALE

As described 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 herds already available at established government farms are combined with those kept by NGOs and by private individuals who are willing to keep animals on a commercial or hobby basis. Many existing institutional farms 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.

Farms associated with AI centres, nucleus herds and/or *in vivo* germplasm repositories can all potentially become involved in such programmes. Livestock keepers participate both as users and as suppliers of germplasm. Facilities for producing frozen semen can be established on the institutional farms in order to disseminate germplasm from pure-bred males typical of the breed to collaborating livestock keepers. 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. A description of how certain institutional farms in India could be used for conservation is presented in Box 36.

Figure 3. A decentralized *ex situ* conservation programme involving institutional herds and private breeders



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 primarily cater to the needs of non-lactating, weak, unproductive and stray cattle, but it is estimated that more than a quarter of Gaushalas have the potential to be used for *in vivo* conservation (Sadana, 2007). Many Gaushalas in India maintain pure-bred animals of different locally adapted 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 locally adapted 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 the breeds in the most effective manner. The following actions could allow these progressive Gaushalas to be utilized more effectively for *in vivo* conservation:

- Identify Gaushalas with a large number of pure-bred animals belonging to breeds at risk.
- Support the development of the infrastructure needed 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 livestock keepers that are willing to continue pure-breeding 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 that can help to increase their economic value of the breeds they keep.

Provided by Devinder K. Sadana.

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 *in vivo 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
3. Secured support from the government or a development agency

Output:

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

Task 1. Establish the conserved population

Action 1. Determine the size of the base population and the criteria for selection

To ensure sufficient genetic variability, the base population should consist of at least 25, and preferably more than 50, female animals. In addition, there should be at least one male for every ten females. The precise numbers of animals in the base population will depend on practical factors, including the breed's census population size, the holding capacity of the institutional farm and the resources available. Criteria for selection should include traditional breed characteristics and performance traits (production and adaptation), as well as low genetic relationship to other animals within the breed, especially those already selected for the base population.

Action 2. Identify the base animals from among collaborating herds

The base males and females should be identified from among the institutional herds and the livestock keepers' herds on the basis of the selection criteria established under *Action 1*. The animals should be tagged and recorded. Females may be brought to the central institutional herd, whereas most of the males should be identified and tagged but then left to be raised by their owners and made available to other livestock keepers for breeding purposes. The owners of the males may be provided with incentives for rearing the animals and retaining pure-bred offspring.

Task 2. Manage the conserved population

Various approaches can be used to manage the conserved population. The following description outlines a programme based on the distribution of male animals and/or semen.

Action 1. Manage the 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. Livestock keepers can be contracted to rear the resulting male progeny for up to six months. A large number of 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, with the choice 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, at least 25 males are selected on the basis of growth and semen quality and freezability. As many as 3 000 doses of semen from each male may be collected, cryopreserved and used for breed improvement and conservation (more prolific species will require fewer doses). The surplus breeding males are distributed to livestock keepers 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 livestock keepers 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 as uniform as possible (i.e. to achieve approximately equal numbers of offspring per sire). When technical capacity is greater, optimum contributions theory can be used in the selection of males.

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5 Designing the conservation programme

Maintaining genetic variability within small populations

RATIONALE

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, i.e. those that are likely to be candidates for inclusion in conservation programmes, are more prone to losing 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 (described in this section) is to focus on maintaining or increasing the genetic variability within the population. The key elements of this strategy are to:

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

The second potential strategy (described in Section 7) is to optimize selection response and genetic variability within the population. The key elements of this strategy are to:

1. adopt a general breeding strategy to maintain the 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 genetic variability, so maintenance of variability should take precedence in small populations. As described in Section 2 (Task 3), if the breed's risk status is critical or endangered, especially the former, management should usually focus on maintaining variability. In populations classified as vulnerable, genetic improvement becomes more realistic. However, maintaining genetic variation should be an essential part of any breeding programme.

Loss of genetic information

In livestock populations that have 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 intense artificial selection, the impact of selection (either natural or weak artificial selection) is small (most of the genetic variants are neutral with respect to phenotype) and the fate of any given 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 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 genetic drift for small populations are that:

- 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 intrafamily mating increases as the size of the population decreases. Of course, inbreeding occurs 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. This phenomenon is 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 affects 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. 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.

Rate of inbreeding

Because of the 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 and in designing management strategies. Further details of these methods are provided later in this section.

ΔF is also a useful parameter for describing the present situation of a population. It allows detection of events that occurred in the population's history (e.g. bottlenecks or periods when the population consisted of a reduced number of individuals) and also helps in determining the risk status of the breed (see Section 2). Additional genealogical analyses can also be used to study the history of a population from the genetic perspective. These analyses yield parameters such as the effective number of founders, founder genome equivalents and founder representation (Caballero and Toro, 2000), which can help in determining 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 numbers 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 ΔF 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 equal to (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 pairs of 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 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 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 for performing such calculations is also available. Two examples are ENDOG[10] (Gutiérrez and Goyache, 2005) and POPREP[11] (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 the 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. 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. This 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 known as "genetic rescue" must be applied (see Box 38).

Box 38

Genetic rescue

When a population is not fit enough to reproduce itself and, therefore, 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 an extinction vortex, two strategies can be implemented to remedy the situation.

One option is to change the environment of the population to a more favourable one (e.g. by establishing an *ex situ in vivo* programme). Better management and veterinary care may raise the fitness of individuals sufficiently to allow them to survive and reproduce. However, 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

[10] http://www.ucm.es/info/prodanim/html/JP_Web.htm
[11] http://popreport.tzv.fal.de

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 foreign 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.

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

Inputs:

Information on 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:

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

Task 1. Adopt a breeding strategy that maintains the breed's genetic variability

Logistic and financial capabilities vary from one herd 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. Actions 1, 2 and 3 are likely to be applicable in most conservation programmes.

Action 1. Include as many animals as possible from the start in order to minimize genetic drift

The animals included in a conservation programme 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. This 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 been crossed to males of other breeds should be recovered and used exclusively for within-breed matings. Clearly, if conditions permit, the real (census) 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 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 how many individuals of the other sex 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 breed's genetic variability.

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, increasing the 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 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 can be approximated as follows: $N_e = 4N / (2 + S^2_k)$, where N is the census size of the population 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 $\Delta F = 3/(32N_M) + 1/(32N_F)$ (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: $\Delta F = 1/(8N_M) + 1/(8N_F)$. 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* and effective population size** under different management regimes

		Within-family selection	
Number of males and	Random selection	Gowe	Sánchez-

females			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)

* Expressed as a percentage (predicted).

** In parenthesis (predicted).

Note that the formula for random contributions shown above only holds in the absence of selection on a trait, which is somewhat unrealistic for domestic animal populations kept by private individuals. 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. This selection should be accounted for 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 the contributions of 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 is made up of 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 (it accounts for related founders, does not need regular schemes with equal numbers of offspring per parent and 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, implementing the methodology requires expertise. The free software METAPOP[12] (Pérez-Figueroa *et al.*, 2009) facilitates its use 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 that 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 recording pedigrees (just the sire and dam of every animal) generally exceed the extra costs the procedure involves.

Minimum coancestry contributions methodology using molecular information

In addition to their use in measuring genetic variability and prioritizing 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 potential uses molecular data 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 inputs for implementing the minimum coancestry mating strategy. Several computer tools for estimating pedigree relationships from molecular markers are available: examples include SPAGEDI[13] (Hardy and Vekemans, 2002) and COLONY[14] (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.

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 use in 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

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

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 in the base population are assumed to be non-inbred ($F = 0$) 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 relationships 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 reducing N_e by decreasing the number of different parents required. However, the main reasons for breeds being at risk are usually 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. This 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 (if 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 pregnances 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 the use of embryo transfer is that it can be technically demanding. Obtaining good results requires considerable training. 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 is likely to be needed to adapt the standard protocols for use in less-common breeds and species.

Task 2. Adopt a mating strategy that decreases 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 the actions below) can be taken to avoid the mating of relatives.

Action 1. Set a limit to the degree of relationship between mates

The simplest way to decrease inbreeding is to avoid mating between individuals that exceed a certain threshold of coancestry. For example, one approach may be to avoid mating between half-sibs and pairs of animals with equal or greater coancestry (i.e. $f < 0.125$). If potential mates are already inbred on the same ancestor, then this factor should also be accounted for if 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 provided (e.g. by the breeders' association) with 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 for avoiding the 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 first establishing a list selected parents and then matching males and females to obtain the minimum average coancestry across all sets of 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 in the case of the above-described optimal method of fixed contributions, the number of possible combinations is huge and solving the problem requires the use of mathematical and computational techniques. Minimum coancestry mating design can be performed with the aid software such as METAPOP[15] (Pérez-Figueroa *et al.*, 2009). Obviously, this methodology can only be used in situations where mating is under central control. This rarely occurs in field conditions, but may occur 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,

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

1963). An example of a programme based on this strategy 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 requires 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. STRUCTURE[16] (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) has followed the circular mating design. In each of the four breeds, the animals were grouped into eight families, based on their genetic relationships (i.e. eight families per breed). The circular mating design was then 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.

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 contrast, 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 the male carries a dominant deleterious allele, the female genetic information has a high risk of being lost, because all the descendants may carry the deleterious allele. In contrast, 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 selecting individuals and determining their contributions, and then choosing the mating design) is an option, but it may lead to complicated and less practical

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

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 such as MOET (multiple ovulation and embryo transfer). Therefore, it may be advisable to take both decisions in a single step via a procedure called mate selection. This approach is based on 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 into the management of genetic variation

Cryoconservation (for more information, see *Cryoconservation of animal genetic resources* – FAO, 2012) is another useful tool in a conservation programme (Meuwissen, 2007). It both extends the reproductive lifespan of individual animals (i.e. increases the generation interval) and increases 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 be used to address different objectives.

Action 1. Store genetic material from animals at the start of the conservation programme

A first objective may be to use the collected genetic 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 the case of embryos or somatic cells; two or more generations in the case of semen). If at some point in the future the live population becomes extinct, it will be possible to recover the breed using the stored material. The creation of a bank of genetic material is advisable for not-at-risk and vulnerable breeds and is strongly recommended for endangered and critical breeds. Obviously, storing material from all individual males and females would be feasible and logical only for a population at a critical level of risk. Selection of individuals for cryoconservation is discussed in *Cryoconservation of animal genetic resources* (FAO, 2012).

In most situations, the germplasm is primarily stored for "insurance" purposes, and the probability that it will be needed is (hopefully) small. Approaches that have low collection costs but high utilization costs, such as the storage of somatic cells (the high costs are associated with the re-establishment of the population through cloning), may therefore be logical options.

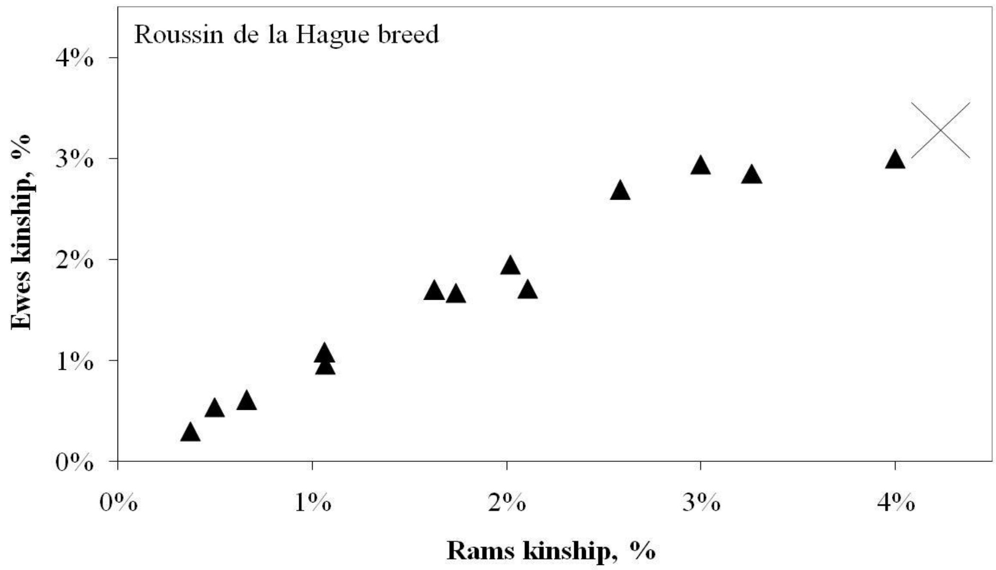
Action 2. Use cryoconserved material continually in the management of genetic diversity

Cryoconservation can also be a means of reinforcing the *in vivo* programme. In this context, cryoconserved germplasm can serve various purposes. 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). It may also be used continually as part of the normal procedures for managing a critical or endangered breed (Sonnesson *et al.*, 2002). For example, cryoconserved semen can be used to increase the number of sires and thereby increase the N_e and to decrease costs (relative to keeping live males). If cryoconserved material is used continually, collection of material for the gene bank should also be an ongoing process that continually 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 and 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 of extinction 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. In 2010, an analysis was performed 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 were being 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 not closely 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 a more distant 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 also improving 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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7 Establishing a breeding programme for conservation and sustainable use

Overview

Breeds often face the risk of extinction because they provide inadequate economic returns to livestock keepers, i.e. raising these breeds does not compensate the livestock keepers for the costs of inputs and labour or allow them to sustain their livelihoods. The availability of highly specialized international transboundary commercial breeds with greater production potential increases the likelihood that locally adapted breeds will be abandoned. Many countries have chosen to import germplasm from specialized international transboundary 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' adaptedness to the prevailing environmental conditions and to implement breeding programmes to increase their productivity.

The importance of adaptation

Mirkena *et al.* (2010) summarized the genetics of 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 that 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

The two main breeding strategies for enhancing economic performance are:

1. to increase production through within-breed selection; and
2. to implement cross-breeding between different locally adapted breeds (with their unique adaptive and fitness traits) or between locally adapted breeds and commercial transboundary 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 establishing breeding programmes in locally adapted 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. veterinary services) available in the area.

Several promising options are outlined by Wurzinger *et al.* (2011).

Choosing a breeding strategy

RATIONALE

Selection for production traits

The most obvious route to enhancing economic performance is to increase the production of commodities, such as meat, milk and eggs, for the mainstream market. Success is most likely where the production potential of the targeted 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 classic animal breeding and improvement schemes. The potential of breeding programmes to raise the productivity of locally adapted breeds beyond that of 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 because of problems with adaptation and fitness. However, implementation of breeding programmes may be more difficult in these areas.

Box 43

The importance of locally adapted breeds in the Plurinational State of Bolivia

The Ayopaya 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 the Plurinational State of Bolivia and have better fibre traits than lowland animals. A formal approach to the selection of local animals has been established (in contrast to unorganized past efforts) and is benefiting the local community.

In the same 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 and sustaining national animal genetic resources.

Source: Valle Zárate (1999).

Selecting for enhanced production in a pure-bred locally adapted 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 help to publicize the productive potential of the breed (FAO, 2003).

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 the 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.

Factors affecting opportunities for selection

A breed's census population size affects the potential usefulness of selection. In the case of breeds with small populations (i.e. critical or endangered status), it is difficult to implement 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 improving the incomes and livelihoods of people who depend on low external input production systems. These breeding programmes must have objectives that are consistent with the producers' objectives. The aim must be to meet some market demand and thereby provide a return on producers' investments 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 keepers 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 behaviours and values (Van Arendonk, 2010).

Sustainable breeding

In most locally adapted breeds, selection must focus on increasing performance and making the breeds more 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 evaluated while keeping in mind the technical, financial and infrastructural requirements for implementing the breeding programme and the need 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 the animals that are top performers in the local environment so that they can be selected for breeding and their contribution to the next generation 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 the individual growth rates of calves to putting more emphasis on female fertility and longevity as contributors to overall herd productivity. One easy way to monitor fertility is to brand an "X" on the back of any cow that fails 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 recording system 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. However, 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, potentially decreasing N_e with overuse. 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 the 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 the 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 because they were not sustainable for use in this remote region due to a 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 to increase production in locally adapted breeds.

Inputs:

1. Assessment of the productive potential of locally adapted breeds.

2. Evaluation of non-market traits (e.g. adaption and longevity).

Outputs:

1. Strategies for increasing performance in pure-bred animals and, where relevant, of cross-breeds.
2. 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.
3. Analysis of the costs of the breeding programme, which should be kept as low as possible for low input – low output breeds.

Task 1. Implement 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 which production and other traits should be improved

Decide which production traits will be measured. Clearly, a measurement of the yield of the targeted product (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 superior adaptation, as can rebreeding intervals or litter sizes. The cost of rearing replacements is important, as is the quality and quantity of feed required and 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 providing multiple products and services beyond the usual market commodities. Fertility and mortality are traits of major importance. 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

In the early 1970s, 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 and the crossbred animals were not well adapted to the production environment. These factors, as well as the declining quality of fleeces for use in producing local textiles, caused the incomes of the sheep producers to stagnate relative to those they obtained under the traditional systems. At this point, it was recognized that improving 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 have all benefited from a well-thought-out sustainable system.

Source: Perezgrovas *et al.* (1997).

Action 3. Implement identification, registration and performance recording

An appropriate system for the identification and pedigree recording of individual animals must be developed and implemented. Important performance and functional traits should be measured. When possible, all traits should be evaluated in all populations to ensure that no important information is omitted from the final decision-making process. Costs and difficulty of measurement may preclude recording of some traits, however. When some information is missing, the ramifications must be considered. Deciding how to measure production is important, as different measures may yield different results and vary in efficiency. For example, measuring milk production only during the first lactation will decrease costs, but may lead to the selection of different animals from those that would be selected based on lifetime production. Repeated measurements of the same trait will increase accuracy, but will also increase costs. Production measures should be chosen with the objective of maximizing 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. Implement trait recording and selection in relevant production environments

Improving commodity production can be antagonistic to the maintenance of traditional type in some breeds, especially when animals are adapted to difficult environments. Measures of productivity for such breeds should include measures of their productivity when kept in their natural production environments with low levels of inputs. Lifetime productivity can indicate longevity and fitness, and serves as a useful complement 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. Traits associated with functionality, reproduction, survival and fitness should therefore be recorded. 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 that improve efficiency may be needed.

Action 5. Decide on the selection and breeding strategy that is most likely to improve productivity

For conservation, the most common approach will be to apply a pure-breeding strategy. However, sometimes the productivity of animals that have low genetic ability for productivity can be enhanced by crossing them with a more productive breed (see below). If crossbreeding is an acceptable option, it may be worthwhile to capture the value of the at-risk breed as a source of hybrid vigour in cross-bred offspring that can be marketed while the locally adapted population is maintained as a pure-breed for parental stock (FAO, 2010).

Optimizing selection response and genetic variability in 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 of being self-sustainable. 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 individual phenotypes. This strategy leads to the co-selection of relatives, especially for traits with low heritability, contributing again to a loss of diversity and an increase in inbreeding. Likewise, short generation intervals increase the gain, but 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, but also recall that the trade-off between genetic improvement and the maintenance of variation was also highlighted. The presence of σ in the numerator of the selection-response equation indicates 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, as far as possible, the loss of genetic variability.

Inputs:

1. Knowledge of the following characteristics of the breed to be conserved:
    - size of the population;
    - reproductive capacity of the species; and
    - characteristics of the production system.
2. Awareness of the country's livestock development objectives and existing and potential markets for animal products.

Outputs:

1. Agreement among stakeholders with regard to the traits to be improved and the relative importance of genetic gain and maintenance of diversity.
2. Clearly defined breeding goal in terms of the trait(s) to be improved.
3. 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. Decide which trait(s) to improve in the conserved breed

Determining 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 undertaken 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 of the milk in terms of protein and fat content, as well as (if possible) traits related more specifically 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 include 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 census size of population has increased. Culling affected animals to control or eliminate genetic defects is 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. At the start of conservation programmes, populations may show genetic defects at frequencies greater than 10 percent. Consequently, in addition to developing a breeding programme for other traits, action must be taken to remove the genetic information that provokes the defect, 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 defect and the detection of carriers of the deleterious alleles are, relatively simple. In many cases, the deleterious allele is recessive and thus only expressed when in homozygous form (i.e. in a double copy). Such defects are manifested more commonly 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 can be used to identify individuals with a high probability of being carriers. To eliminate the defect, first animals showing the defect, and then carriers, should be avoided as parents of the next generation (as long as the programme is not compromised by 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 defect has a polygenic determination and behaves as a quantitative trait with different degrees of expression, a regular selection programme should be implemented to eradicate the defect from the population. Whatever the circumstances, it is important that the measures taken to eliminate the defect 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 the eradication of a recessive allele (Sonesson *et al.*, 2003).

Obviously, not all defects are genetically determined. Selection and breeding will not influence the occurrence of such defects.

Action 2: Decide what rate of inbreeding is acceptable 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 breeds at high risk of extinction, $\Delta F \leq 1$ percent is recommended, assuming this is possible. In the case of populations that are not in the critical or endangered categories, restrictions can be relaxed and a larger ΔF can be justified if it occurs as a result of intense and accurate selection. 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 the breeding programme

Action 1. Evaluate the circumstances in which the breeding programme will be implemented

Various measures 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 the 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 options for balancing genetic improvement and maintaining genetic variability

Numerous options for increasing genetic variability when applying selection have been proposed. 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. Each of the selected animals should contribute the same number of offspring (i.e. equal within sex) 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 and females is the selection criterion (e.g. the phenotype or estimated breeding value) of, respectively, the N_M^{th} highest ranked male and the N_F^{th} highest 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 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 relatives.

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 having 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 Option 1 in Table 9); or
2. selecting the best animals from the two families with the highest mean value (Option 2).

However, 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. Expected inbreeding (*F*) and genetic response to various options of family selection

Options	Distribution of family sizes Male/female pairs taken from each family (n)								*F* (%)	Genetic response*
1	1	1	1	1	1	1	1	1	7.96	5.90
2	4	4	0	0	0	0	0	0	42.76	17.42
3	4	3	1	0	0	0	0	0	35.81	18.17
4	4	2	2	0	0	0	0	0	33.26	17.87
5	4	2	1	1	0	0	0	0	30.59	17.78
6	3	3	2	0	0	0	0	0	30.59	17.30
7	3	3	1	1	0	0	0	0	27.80	17.21
8	4	1	1	1	1	0	0	0	27.80	16.38
9	3	2	2	1	0	0	0	0	24.87	16.91
10	3	2	1	1	1	0	0	0	21.79	16.24
11	2	2	2	2	0	0	0	0	21.79	14.91
12	2	2	2	2	1	1	0	0	18.57	14.85
13	3	1	1	1	1	1	0	0	18.57	14.23
14	2	2	1	1	1	1	0	0	15.20	13.56
15	2	1	1	1	1	1	1	0	11.66	10.83

*Measured in units of genetic standard deviations.
Source: Toro and Pérez-Enciso (1990).

It must be emphasized that the real number of animals that need to be kept in order 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. Minimum number of sires per generation to achieve an effective population size $\geq$50*

Mating ratio**	Mass selection Lifetime offspring 4	8	12	16	20	36	Random selection	Within-family 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

*Heritability was assumed to be 0.4.
**Number of females per male.
Source: Woolliams (2007).

Option 4. Implement weighted selection

Within-family (Option 2) and family selection (Option 3) reduce 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 can be 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, ordered from highest to lowest in genetic value, were, respectively, allowed to produce 6, 4, 4, 3, 3, 3, 2, 2, 2, 1, 1 and 1 offspring each (i.e. the best animal of each sex produced six offspring, whereas the twelfth-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 contributions strategy

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 method – known as “optimum contributions strategy” – can be used. Optimum contributions 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 (Sánchez *et al.*, 2002). This method is recommended as the most powerful way of dealing with genetic gain and inbreeding at the same time (Meuwissen, 1997). The aim 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 in 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 contributions 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 is 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).

Box 51

Optimum contributions strategy of selection

To better account for the two opposing forces, genetic response and genetic variability (ΔF), both should be included in the objective function, but with opposite signs (+ for response and - for ΔF). The expected mean value for the selected trait of the next generation of offspring can be estimated as the product of the value of parents by the proportional 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 response to selection but not exceeding the desired value for ΔF. Several methods for solving this optimization problem have been proposed, all of which require the use of computer programs. The program EVA[17] (Berg *et al.*, 2006) is one of the software available to manage a selection programme with restriction on the inbreeding levels.

Action 3. Implement and monitor the breeding programme

Once the programme has been chosen, it will need to be implemented. This will require extensive cooperation with breeders and other stakeholders. All of the options listed in Action 2 will require recording performance information for the traits upon which selection will be based, and all but Option 1 will require some pedigree data (knowledge of parents as a minimum).

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 a small N_e is introduced in Box 38. There are, however, other instances where cross-breeding may play a role in a conservation programme. Cross-breeding can be particularly useful 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. Its use is recommended when there are multiple breeding-goal traits that have antagonistic genetic relationships, such as those between production and fertility or between the quantity produced and the quality of the product. It can be difficult to improve such traits simultaneously in a single breed. This may, for example, mean that combining the adaptive traits of a locally adapted breed with the production traits of an introduced international transboundary breed is an attractive option. However, cross-breeding is only effective and sustainable if the breeding system is carefully chosen and well planned. The breeds used need to be available over the long term and the cross-breeding plans need to be strictly followed by the participating livestock keepers. A section in the guidelines *Breeding strategies for sustainable management of animal genetic resources* (FAO, 2010) is devoted to cross-breeding.

Cross-breeding strategies

One simple strategy for maintaining locally adapted animal genetic resources is to cross-breed the non-recorded and low-producing surplus locally adapted females, while maintaining pure-breeding (and within-breed selection) among the best animals of the locally adapted breeds. This limited and targeted cross-breeding not only saves the locally adapted breeds while improving them genetically, 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 as a pure-breed should be managed through breeding systems that aim to enhance their productivity. Female animals belonging to these breeds should generally not be used for cross-breeding. These breeds should instead be improved through within-breed selection. Breeds that have been characterized as low producing, or those that are already crosses of various locally adapted

[17] http://eva.agrsci.dk/index.html.

breeds, are logical candidates to have their production improved by using genetically superior germplasm either from well-defined improved breeds from the local area or introduced 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 the extent of interest and agreement on the part of the local livestock keepers.

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.

When a breed is being used in a cross-breeding programme, specific information should be collected during breed surveys and characterization studies. Useful information about the breed's role in cross-breeding includes its population size 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 locally adapted breed, cross-breeding with an introduced breed may be considered. A fairly common and simple approach used to improve production is to cross a locally adapted breed with a high-output international transboundary breed. This can be done with one of three goals in mind:

1. replacing the local genetics, i.e. by making continual successive crosses to the introduced breed;
2. upgrading the locally adapted breed, i.e. by crossing to the introduced breed until the population contains a high proportion (usually >50 percent) of introduced-breed genetics; or
3. maintaining the locally adapted breed as a pure-breed, but using cross-breeding to produce a population of commercial animals that are used for production, but not for breeding.

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 was. 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. Locally adapted 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 should be ensured. At the very least, the local animal genetic resources that are 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 locally adapted 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 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-bred 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 good maternal traits are occasionally crossed and the 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 belonging to 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 of 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 to meet 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

Use of sexed semen in the production of 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 makes it possible to increase the numbers of offspring of one sex in a closed population and thereby to increase the intensity of selection in 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 population size, semen sexing could be used to breed replacement heifers from the cows with the highest genetic merit. This would provide a one-time boost to the genetic level of the herd. The largest economic benefit of using sexed semen in a pure-bred herd would come from the ability to use the remaining dairy cows to produce 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 to produce 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. In the Brazilian system, 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 locally adapted 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 may mean that the census size of the population is greatly reduced, which increases the risk of extinction.

Breaking the cycle in which a low census population size limits the potential for within-breed improvement is difficult. Small population size limits the selection intensity that can be applied and/or increases inbreeding. If a larger 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 census 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 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 that could be mated to the temperate cows to produce offspring that are 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 with 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 from one of the two breeds used to produce the original two-way cross, and their female offspring are mated to a sire from the other breed. This alternating pattern of sire-breed usage is then continued in subsequent generations.
- Three-way rotation: sires from three breeds are used in successive alternating generations on the cross-bred dams of the previous generation.
- Multibreed rotation: 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 the exchange of females between herds or villages, which decreases costs and disease transmission. Only the sires have to be purchased (individually or collectively) by the owners of the females. AI will eliminate even the need to purchase 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 may thus show high variation in phenotype. Also, if one of the breeds is an exotic breed, maintaining the rotation may require continual importation of new germplasm. Rotational schemes involving a large 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, one 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 belonging to 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 genes from and contributing genes to 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 a high-output 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 proportional contributions of the foundation breeds to achieve a combination that is well adapted to the local production environment. Although forming 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).

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 genetic proportions differ from 50 percent per breed.

Decreased uniformity.. With matings involving cross-bred parents, the proportions of the genes of the foundation breeds in the offspring can theoretically range from 0 to 100 percent, resulting in 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. This 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 most of 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. Establishment of a breeders' association (See Section 5) should be done in complement to development of a composite breed.

Cross-breeding and conservation

All three 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 effort if it is to achieve the desired results. Indiscriminate cross-breeding is a major threat to locally adapted breeds (Tisdell, 2003) and has often yielded unsatisfactory results in terms of increasing productivity.

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 conservation option..
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 the breed's production system(s), including markets for products.
4. Inventory and characteristics of other relevant locally adapted 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 that maintains 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 cross-breeding system that conserves an animal genetic resource

Cross-breeding programmes that are not well planned are likely to fail to reach the desired objectives. A comprehensive plan 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 an ad hoc committee for this purpose. The committee should include key stakeholders.

Action 1. Outline the objectives 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. Such secondary objectives may include improving the livelihoods of the livestock keepers and meeting local demand for animal products. In addition to considering outcomes in terms of the products that will be produced by the cross-bred animals, it is also important to consider how constraints associated with the local production system can be overcome. For example, the cross-bred animals will ideally have a greater genetic potential for production, but they may also require more inputs. Factors that restrict the 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 other breeds for possible inclusion in the cross-breeding system

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 of all potential complementary breeds should be drawn up. Both breeds available as live animals 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 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 populations are obviously preferable, 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 probably be less than that of cross-breeds.

Action 5. Describe the contributions of the different breeds to the cross-breeding system

Attributes of locally adapted 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 are often chosen to increase production. Also determine the sex of the animals to be contributed by each breed, as some breeds may excel in maternal traits (e.g. milk production and litter size), whereas others are superior for paternal traits (e.g. growth and meat quality).

Action 6. Choose the optimal cross-breeding system

Develop a cross-breeding system that enhances the performance of low-producing locally adapted animals, while ensuring that the genetics of the high-producing locally adapted animals are maintained in the breeding population. When population sizes allow, protocols that ensure the use of some high-producing females from the target breed for pure-bred breeding should be established. Select a group of breeding males that can be widely used locally.

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 the livestock keepers that will be implementing the programme and subject to its costs and benefits must be consulted.

Task 2. Implement and monitor the cross-breeding programme

Once the cross-breeding plan 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 the guidelines *Breeding strategies for sustainable management of animal genetic resources* (FAO, 2010). A summary is presented here.

Action 1. Prepare for the start of the cross-breeding programme

Before a cross-breeding programme can be launched, various prerequisites have to be accounted for. A feasibility study of the proposed programme should be undertaken. Financial analysis of the programme is usually warranted, especially if substantial investments are required. Specialized personnel may need to be appointed to manage the programme. Infrastructure for communication and transport of animals may be needed.

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 management required by cross-bred animals may differ from that required by the original pure-bred animals, so training activities for livestock keepers may be needed.

Action 3. Implement the cross-breeding programme

The cross-breeding programme will require continual attention and monitoring to detect and resolve unexpected problems. Regular communication and exchange with livestock keepers is critical. 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 (or equivalent body) 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 the development of synthetic breeds are likely to benefit from the establishment of a new breeders' association and AI services. Support for research on ways to improve the programme will also 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 genetic improvement and facilitate the general management of mating systems. They will also provide documentation that can be used in 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 whether its objectives are being met. In particular, programmes established with the aim of contributing 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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8 Increasing the value and sustainability of conserved breeds

Identifying sustainable use options for breeds under conservation

RATIONALE

Section 7 describes how selective breeding can be used to improve an at-risk breed's genetic merit for production and thereby improve its ability to compete financially with other breeds. It is generally recommended that conservation strategies for endangered and vulnerable breeds include such an approach, provided their N_e is sufficiently large. However, genetic improvement may not be enough to make a breed economically competitive. In most instances, the difference between the production levels of locally adapted 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 cases, 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 approaches aimed at increasing the value of the targeted breeds.

Depending on the circumstances, many different kinds of action can be taken to promote the sustainable use of breeds targeted for conservation. Examples include the following (Oldenbroek, 2007):

- Safeguarding the breed's production environment 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 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 terms of their production potential and 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 or 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. Appealing aspects of a breed's home production environment can be used to promote its products, for example through labelling schemes. Such an approach requires collaboration with breeders, producers, and marketers to develop a value chain, and with consumers to ensure that sufficient demand exists.
- Marketing products based on social concerns for improved animal welfare and food quality and safety. 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 in 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. A product may appeal to some consumers because buying it helps to ensure the future existence of an at-risk breed.
- Drawing on the ecological functions of livestock in nature management to provide an additional source of income. In many areas of the world, 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 sources, 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 appropriate incentive schemes. However, the potential touristic value of some breeds – linked to their appearance, farming systems or folklore traditions – could be exploited by the tourism industry with beneficial effects for livestock keepers.

Additional advice on these various options is provided in the subsequent subsections.

Objective: To document opportunities for promoting sustainable use.

Input:

- A list of breeds by species and a description of the characteristics of each breed.

Output:

- A list of realistic options for promoting sustainable use and plans for how to exploit them.

Task. Plan measures to promote sustainable use

Action 1. Identify opportunities and threats

As part of characterization efforts (see Sections 1 and 3), the importance of the breed to the local area should have been documented. This information may reveal opportunities for promoting the sustainable use of the breed. Threats should also be documented, including 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 the breed's weaknesses include low productivity, improving livestock management should be among the first opportunities considered. 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 breed's characteristics and match them to opportunities

Consider whether the breed has particular characteristics that can be used in exploiting specific opportunities. This can be done, for example, by creating a table in which the breed's characteristics (e.g. adaptability, unique products, grazing ability) are listed down the left margin and opportunities (e.g. improving management, specialized or niche production, hobby farming, use in nature conservation) are listed across the tops of the columns. Cells in the table can then be marked to show which opportunities are relevant to which characteristics.

Matching the characteristics and opportunities can be done as part of the SWOT analysis of breeds described in Section 1, i.e. 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.

Box 56

Strengths of the Nguni cattle breed and opportunities to increase its value (South Africa)

The Nguni is a South African cattle breed that has been raised by indigenous communities for nearly 1 500 years. Because of its relatively small size, and because of 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 various stages in 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 breed is now making a comeback, based both on its value for meat production in harsh environments and 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).

Action 3. Determine which opportunities are realistic and make plans to exploit them

Based on the combinations of characteristics and opportunities identified in Action 2, specific measures can be proposed. The activities required should be outlined and relevant stakeholders identified. The strengths and weakness of the proposed measures should be noted, along with any obstacles that need to be overcome. The chances of successfully implementing the measures should be assessed.

Preparing a Biocultural Community Protocol

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 between the community, the breed and the surrounding environment. 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 locally 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 complementary biological diversity.

One approach to gathering, organizing and disseminating this information is to develop a Biocultural Community Protocol (BCP), a concept originally developed by the NGO Natural Justice (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. BCP record (among other things) information about communities' breeds, the roles of these breeds in the livelihoods of the communities, the indigenous knowledge of the communities and the roles the communities play in managing diversity. Community protocols are recognized by the CBD and referred to in the Nagoya Protocol on Access and Benefit Sharing[18]. Box 57 describes the development of a BCP for the Samburu community in Kenya.

Box 57

The Samburu Biocultural Community Protocol and conservation of the Red Massai sheep of Kenya

Background

The Samburu are a part of the Maa-speaking pastoralist community of 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 sociocultural 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 Biocultural Protocol (BCP) was 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 a BCP is based on a participatory process that ensures that the communities involved take ownership of the process and the product. The Samburu BCP[19] was initiated by a team 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 of the process. Later, the team facilitated a representative group of Red Massai 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 the conservation of their local livestock breeds. They agreed to use the BCP as learning tool for their younger 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 the 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

[18] http://www.cbd.int/abs/
[19] http://www.pastoralpeoples.org/docs/Samburu_Biocultural_Protocol_en.pdf

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 to draw attention from the outside world. The interaction between the Samburu and government officials at the launch of the BCP document and subsequent wider interactions have promoted the exchange of ideas on issues relating to the conservation of locally adapted breeds and highlighted the role of the livestock keeper at both 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.

Presenting a BCP to policy-makers will raise awareness of the community's activities with respect to the preservation of agricultural biodiversity and may encourage the development of policies that are favourable to the continued existence of the community and thus favourable to the survival of the breed(s) they keep. In addition, the activities through which a 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 a 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.
3. A facilitating organization and a team of legal and other experts.

Outputs:

1. A BCP relating to the breed at risk and its community of livestock keepers.
2. Community members informed about their rights and the value of their breed.

Task 1. Discuss the proposed Biocultural Community Protocol with stakeholders

Action 1. Establish a working relationship between the facilitating organization and the local community

Ideally, BCP are initiated and developed by the communities themselves. In most situations, however, this is not realistic, as many communities will not even be aware of the existence of BCP and do not have access to the precise legal expertise required. Thus, the process is usually facilitated by an NGO or other external organization, ideally one that has an ongoing relationship with the community. If no such organization exists, then time must be spent in building familiarity between the facilitators and the community. Background research on the community should be undertaken before the process is initiated. Even if a relationship with the community has been already established, the process of preparing the BCP should proceed very deliberately, at a pace set by the community rather than the facilitators.

Action 2. Hold a series of meetings to collect information and discuss options

Meetings should be held with various community members 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 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 recorded. The breed's cultural and ceremonial importance should also be noted. Problems that threaten the community's continued existence and its ability to maintain its animal genetic resources should be discussed. Problems that may have political solutions, such as the need for 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 provide valuable information.

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. 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(s) and as producers of public goods. Training and direct assistance on data collection and documentation, legal empowerment and facilitation of meetings with policy-makers should also be provided.

Task 2. Prepare the Biocultural Community Protocol

Action 1. Develop an outline of the Biocultural Community Protocol

There are no formal and rigid rules regarding the contents of a BCP, but it is important to ensure that all relevant information is presented in a logical and organized manner. The BCP that have been produced to date by livestock-keeping communities[20] have generally had the following format:

- Description of the community
    - location and environment
    - history
    - customs, values and laws
- Description of the animal genetic resources
    - special traits
    - cultural significance
- Description of the community's traditional knowledge
    - for management of animal genetic resources
    - for management of biodiversity in general
- Statement on access and benefit sharing
- Current and future threats and challenges
- Call for action by policy-makers
- Statement of commitment to protect biological diversity
- Statement of the community's rights according to international law

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 Biocultural Community Protocol in a format and language appropriate for policy-makers

The BCP is a legal document, so its language must reflect this. It is for this reason that the 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

[20] http://www.pastoralpeoples.org/biocultural protocols.htm

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. Consider potential problems in the development of the Biocultural Community Protocol

Although BCP are intended to benefit the community, there is potential for negative consequences, and care should be taken to ensure that problems do not occur.

Action 1. Facilitate rather than push the development of the Biocultural Community Protocol

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. Influence of the personal biases of the facilitators 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 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.

Task 4. Publicize and distribute the Biocultural Community Protocol

Action 1. Present the Biocultural Community Protocol to policy-makers

In order for the BCP to yield any effect, 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 Biocultural Community Protocol 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 and the challenges it faces – and about the BCP – may help to drive action by policy-makers. The facilitating organization may be expected to play a major role in this activity.

Implementing a “role model breeders” programme

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. Complementing genetic improvement by improving management will therefore help promote a breed’s economic sustainability. Improved management can contribute greatly to raising production levels and thereby provide owners with enhanced economic return in the near term. This helps them to maintain the breed until the effects of genetic improvement can be realized. Thus, improvements to management should go along with the breeding and genetic aspects of breed maintenance. However, it is important to ensure 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". 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). Note, however, that the particular name attached to such breeders varies across countries and regions. The term "master breeder", for example, is sometimes used. All breeds can benefit from programmes that identify role model breeders and disseminate their knowledge and techniques. 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

Role model breeders of "Heritage Turkeys" in the United States of America

The American Livestock Breeds Conservancy[21] 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 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, 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.

Role model breeders combine scientific knowledge and art. 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 breeder's years of experience.

Objective: To create strategies for benefiting from role model breeders and disseminating their knowledge.

Input:

- A list of potential role model breeders.

Outputs:

1. A compilation of role model breeders' knowledge.
2. A strategy for benefiting from role model breeders.
3. Learning materials for disseminating the role model breeders' knowledge.

Task 1. Prepare an inventory of role model breeders' knowledge

Action 1. Identify role model breeders

[21] www.albc-usa.org

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 a record-keeping system exists) and surveys of breeders.

Action 2. Interview role model breeders to discover the techniques and attitudes behind their success

Observe role model breeders at work. Face-to-face interviews with role model breeders are 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 to them. In the past, techniques were passed on directly as one generation of breeders worked with the next. However, transgenerational succession in livestock keeping is becoming increasingly uncommon and does not provide a basis 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. Such techniques should be documented for the benefit of present and future generations. Note what traits are being measured or noticed, and what consequences these have for production or viability.

Task 2. Disseminate role model breeders' knowledge and encourage its use

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. 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, 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 that recognize outstanding breeders. Certain countries offer similar awards to people that make particular contributions to breed conservation. 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. In 2007, to help aid the *in situ* conservation of livestock breeds, the LIFE Network (Local Livestock for Empowerment of Rural People), a group of NGOs, proposed the idea of introducing "Breed Saviour Awards" recognizing individual livestock keepers or whole communities that make notable efforts to conserve and improve 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 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 Devinder K. Sadana.

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.

Capitalizing on niche market production

RATIONALE

Worldwide there are several examples of breeds that produce high quality and distinctive products that contribute effectively to their conservation. Efforts to enhance the value of breed-specific products are as valid as efforts to enhance a breed’s levels of production, and may be a more realistic strategy for breeds belonging to species in which a few extremely productive breeds dominate the market. When breed-specific products command a premium in the marketplace, the producers obtain greater monetary returns and this increases the security of the breed. In some cases, the enhanced value derives from a unique characteristic of the product itself. In others, it derives from the appeal of buying a locally grown product. Niche marketing can be an ideal strategy in situations where products can be marketed in a way that emphasizes traditional techniques and local ties (LPP *et al.*, 2010). This kind of marketing can involve existing traditional products and or newly developed products with unique characteristics.

Niche marketing can help breeds that have somewhat less productive potential to compete with international transboundary breeds that have been intensely selected to generate high yields of mainstream commodities (see Box 60). Breed-specific products can appeal to consumers that are interested in regional products and can be especially important in safeguarding animal genetic resources that are firmly tied to, and readily identified with, a specific region.

Box 60

Heritage Turkeys span ethnic and religious boundaries in United States of America

A very successful example of niche-product 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 that of 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 successful practices of the early and mid 1900s have been recaptured from a very nearly complete loss.

Provided by Phil Sponenberg.

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 the fact that 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.

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. Cash-strapped societies are less likely than more affluent ones to be able to afford this relative luxury. However, while this is generally the case, it also remains true that traditional products can and do attract increased demand even in societies where disposable income is minimal. The price differential for the preferred local products can provide enough economic advantage to allow the breeders of the animals to continue to keep them. As incomes rise and disposable income becomes more available, traditional products can gain an increasingly large share of the total market.

Objective: To develop a business plan for marketing niche 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.
4. Awareness of constraints to developing and marketing niche products.

Outputs:

1. A list of potential niche products from the breed. This will usually include traditional products as well as more innovative and creative new products.
2. A plan for marketing the products.

Task 1. Identify potential niche products and services

Action 1: List breed characteristics that might be targeted for niche marketing

The 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. The 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 characteristics helps to safeguard sheep breeds in 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 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 presents 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 in the manufacture of distinctive ponchos and other textiles. A producers' cooperative has now targeted these distinctive products for promotion to the tourists that visit the picturesque region where 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 (e.g. in the production system 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.

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 realizing 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 appreciated 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 rare 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 through public auctions. These auctions cater to the mass market and are attended by buyers who purchase mainstream breeds. Rare breeds do not conform to standard requirements and attract a price below the standard market price.

Provided by Lawrence Alderson.

Action 3. Conduct a workshop to creatively formulate marketing plans

Workshops are an excellent way to bring together stakeholders from all stages of the production and marketing chain to brainstorm and propose ideas about how to market a special product and plan the interventions required to put such plans into place. Relevant stakeholders usually include producers (livestock keepers), nutritionists, retailers, butchers, food manufacturers, cooks, consumers, marketers and craftspeople. Inviting a wide range of stakeholders to the workshop should allow it to produce an extensive list of products and services that could potentially be marketed to niche consumers. Hiring outside facilitators may improve the efficiency with which such workshops generate and organize the new ideas.

Action 4. Prioritize the potential niche products and services

In general, because of limited resources, only the most promising ideas should be targeted for production and promotion. 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 to spread 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 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, the product is an extension of its traditional use. In addition to the ice cream initiative, creative efforts at new product development have led to the use of manure from the breed in paper making, which is then used to manufacture greeting cards. This unusual product has met with demand that has far exceeded expectations. Production tends always to lag behind demand. Both these products – one more traditional, one very novel – have increased economic returns 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. Plan and implement a niche marketing campaign

Action 1. Write a business plan

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 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 the market for 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 the potential market

Preparation of the business plan should be followed by a market survey and feasibility analysis. Establishing a niche market will require investment of both time and money. One-time costs will be incurred in preparing the marketing plan, and marketing will require ongoing 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 value 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

The term “qualification” is used to describe a process in which products are differentiated based on a specified set of production practices and an associated name or label (Tregear et al., 2007). Qualification labels serve as information signals that enable producers to stimulate favourable consumer responses, particularly when consumers are faced with choosing between products within the same category.

Qualification can be linked to the geographical origin of the product. For example, many rural areas of Europe produce regional foods with strong historical identities. Consumers are often willing to pay a higher price for these products because of their high quality or because of some other appealing characteristic associated with their production. A label that indicates the geographic origin of a product can therefore be a valuable marketing tool. In the European Union, labels of this type are regulated by law. Council Regulation (EC) No 510/2006 lays down rules on the protection of designations of origin and geographical indications of agricultural products via two labelling schemes: Protected Designation of Origin (PDO) and Protected Geographical Indication (PGI).

These protection tools help to improve the profitability of the breeds that produce the local products. For example, in the French Northern Alps, the milk of Abondance and Tarentaise cattle is used for the production of Reblochon and Beaufort cheeses, and in Italy the milk of Reggiana cattle is used to produce Parmigiano Reggiano cheese (Gandini and Oldenbroek, 2007).

Van der Meulen (2007) has developed a methodological tool for evaluating 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.

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.

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 who don’t rely on the breed for their livelihoods. 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.

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 may be a means of highlighting its uniqueness. Furthermore, such links often involve regions that have existing positive reputations for natural beauty or interesting cultural heritage. Many consumers like to buy products from local sources to support the local economy and reduce environmental impacts associated with transporting products. Van der Meulen (2007), describing the situation in the Netherlands, notes that products marketed on the basis of their places of origin 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 label. The raw materials may come from several farms in the area and products are usually made by single producers.

Regional-typical origin food products. These have multiple producers. They have a product-related geographical delimitation and are characterized by a long-lasting tradition spanning several 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. The product is named after the place of production 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.

Another way to improve the value of the products obtained from a breed is to adopt or promote a production system that differs clearly from mainstream production and is clearly defined. Organic production (see Box 68) is an example.

Box 68

Doubling the price of Drenthe Heath lambs in the Netherlands

The Drenthe Heath sheep arrived in the northeastern 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, the owners of three flocks have started to market their lambs as *Drènts Heidelaom*, an organic product. The lambs are produced in a well-defined market chain. This has doubled the price the shepherds get 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[22], 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 by the Slow Food organization as part of the Ark of Taste (a catalogue of heritage foods that are often at risk of extinction).. Fifth, arrangements were made for collaboration among flocks and this resulted in a "Presidium"[23] of the Slow Food organization: Drenthe Heath Lamb or in the language of the region *Drènts Heidelaom*.

Provided by Kor Oldenbroek.

Objective: To enhance the value of existing niche products through geographical or cultural ties.

Inputs:

1. Knowledge of a breed's distinctive products, production processes and roles.
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 breed's products.

Task. Develop a plan to enhance the value of a breed's products

Action 1. Evaluate products and potential markets

Prepare a detailed evaluation of the targeted breed's products and potential markets for them. The evaluation should include details of any particular traditions to which the breed is linked and any existing trademarks for its products. The exercise should not be limited to the targeted breed itself. It should also include products from other breeds that compete for market share. Where competing products exist, the relative 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.

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 its ability to adapt to harsh

[22] http://www.skal.nl/english/tabid/103/language/nl-nl/default.aspx

[23] 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.

nutritional and environmental conditions, are currently being developed by the Chilean Government.

Provided by Ignacio Garcia Leon and Pascalle Renee Ziomi Smith.

Each product should be evaluated objectively for factors, such as quality and distinctiveness, that will enhance demand. Capacity to supply the product should also be evaluated to ensure that any potential market demand can be met.

Action 2. Identify opportunities to improve the products and their marketing

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. Highlighting other roles of the breed, such as ecosystem services (see below), may improve the marketability of a food product. Promotion of the product's contribution to 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 quality of the product or give it a distinctive taste. Standards for animal husbandry may allow products to be promoted on the basis of good animal welfare.

Action 3. 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 that will ideally lead a customer to choose the product over a competing option.

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 in the 1950s tens of thousands of these sheep roamed the West Stara Planina mountainsides, their numbers have dwindled to fewer than 200 animals from each breed today. Conservation of these breeds safeguards a cultural monument that developed over hundreds of years and an 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 breeds has extraordinary thermo-isolation characteristics, as well as fibre firmness that differentiates it from the wool of other breeds. To take advantage of these factors as a basis for promoting 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 in shearing, washing, spinning and knitting the wool.

Provided by Sergej Ivanov.

An additional, more formal, option is to develop a trademark or use special label 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. 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 consumers' confidence in the validity of the process.

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 or 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[24], 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 locally adapted breeds and crop varieties (Box 72).

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. The extent of interest from consumers and producers/farmers had to be researched extensively. Moreover, 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 consumers 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 it.

The Arca-Deli® Awards are presented annually (starting in 2011) to products and services from locally adapted livestock breeds and cultivated plants. The award is presented to products and services that are considered recommendable as a model or example of good practice. The Arca-Deli Award® label can then be used on the labelling of the 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

[24] http://www.save-foundation.net

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.

Capitalizing on the roles of livestock in providing ecosystem services

RATIONALE

As noted in Sections 1 and 3, livestock often play an important role in maintaining landscapes that have a long history of traditional grazing. Removing grazing animals from such ecosystems may lead to the loss of habitats that are valued for their rich biological diversity. For a review of the effects of grazing on biodiversity, see Rook *et al.* (2004). Grazing animals can also be used for various other landscape-management activities such as preventing the encroachment of scrub or forest onto land set aside from agricultural production. Cattle, sheep, goats and horses are the species most commonly used for landscape and habitat management, but other species, including pigs (see Box 73), can also provide similar services.

Box 73

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 by the pigs 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.

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.

When livestock have grazed a given ecosystem for many generations, they 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 becomes 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 develop a plan to use locally adapted animal genetic resources in nature management.

Input:

- Requirements for species and breeds that are well adapted for use in nature management.

Output:

- A list of species and breeds that may be used in nature management.

Task. Identify opportunities for using species and breeds in nature management

Action 1. Interview stakeholders and formulate a strategy for using livestock in nature management

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 scheme for nature management using controlled grazing. Such stakeholders may include the land owners, local government officials involved in nature conservation and possibly private individuals or societies with an interest in maintaining natural landscapes and biodiversity.

Action 2. Describe the grazing behaviour of potentially relevant species and breeds

Collect information on species and breed characteristics relevant to nature management in the local ecosystems. Take particular note of documented evidence of specific breeds' adaptations to specific environments or of any relevant breed-specific grazing behaviours. It is also important to note existing nature management roles for which livestock keepers are currently not being compensated. Box 74 describes a special adaptation found in Criollo cattle in Colombia that enables them to provide effective weed-control services.

Box 74

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 that grazing livestock may provide in terms of promoting 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 establishing support for carbon sequestration or penalties for greenhouse gas production.

Action 3. Match the demand for conservation services to the characteristics of the livestock

Decide which species and breeds might be effective in nature management in the local ecosystem. A nature management programme 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 for incorporating livestock into nature management

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 to 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. Marketing schemes may also be developed based on the ecological contributions of the breed[25].

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 across a large area of land. 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 societal and cultural functions of livestock

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 that species and breeds play as attractive features 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 livestock keepers for the provision of social and cultural benefits that are difficult to quantify and reward by other means. In most countries, the provision of such payments to livestock owners remains difficult to achieve.

Box 75

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.

[25] http://www.agap-ynysmon.co.uk/

The breed is mainly confined to the island of Madura (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. A list of breed characteristics.
2. Details 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.
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 future social or cultural functions of the breed

Phenotypic characterization studies will ideally identify breeds' most important characteristics. However, particular social and cultural functions may not necessarily be noted. Key stakeholders should be consulted to obtain information on such functions and their history and significance. Box 76 describes the unique social and cultural functions of the Chilote horse in Chile.

Box 76

The use of the Chilote horse in therapy programmes in Chile

The Chilote horse is a breed developed on Chiloé Island in the south of Chile. It descends from horses brought many centuries ago from the Iberian Peninsula. It has remained genetically isolated from mainland populations and has adapted to the humid climate and wetland ecosystems that distinguish the island. The breed is characterized by a hard resistant hoof, short stature and refined skeletal structure. It has also been selected over decades for a quiet temperament. These particular characteristics give Chilote horses a unique value, as they are perfectly adapted for use in sports for children and therapy for disabled people.

The management and development of the Chilote 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 like eventually 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 to support research on genetics and reproduction.

Provided by Ignacio Garcia Leòn and Pascalle Renee Ziomi Smith.

Action 2. Document the various societal groups benefiting from the social or cultural 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 social or cultural functions

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 that may be difficult to measure or estimate and, therefore, difficult to price and recover. 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 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.

Box 77

The cultural value of Valdostana cattle in Italy

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 acts as a custodian of local culture. These cattle have a considerable influence on the local landscape, as they are taken up to alpine pastures in the summer. Fontina cheese and other gastronomic traditions are linked to the breed. The breed is also 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 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. 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.

Action 4. Determine the best approach (public or private) for incorporating the social or cultural 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. 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 and other broadly-based social groups such as religious or charitable foundations with an interest in social and cultural issues.

Task 2. Prepare a proposal to solicit support from potential donors

Action 1. Identify potential donors and seek an initial meeting to explain plans to capture the value of the breed's contribution to society

The major contributions of the breed (and its production system) and the plans to capture the value of these contributions should be 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 must 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 particular funding organization, which will provide guidance regarding the information that is needed. However, any grant proposal, regardless of the donor, is likely to require the following elements: 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.

Action 3. Consider novel options to capitalize on the breed's cultural or social functions

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). Crowdfunding is a recently developed option that may be effective, especially if the need is for seed money to start a project. Crowdfunding involves the solicitation (usually via the internet) of a relatively small amount of money from each of many different people. The success of crowd funding depends on having a promotional idea that appeals to a wide audience, especially from an emotional perspective. In developing a crowdfunding plan, seeking expert assistance is highly recommended.

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Overview of Sections, Tasks and Actions

SECTION 1. REVIEWING THE ROLES OF ANIMAL GENETIC RESOURCES AND OPTIONS FOR THEIR CONSERVATION

Inventorizing species, breeds and their functions

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

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

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

Action 3. Establish a baseline list of breeds

Task 2. Describe the breeds and their functions

Action 1. Study relevant documentation

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

Action 3. Summarize information on breeds and their functions

Describing the dynamics of the livestock sector

Task. Describe the dynamics of the livestock sector

Action 1. Describe the roles of different species and breeds

Action 2. Describe the dynamics of livestock systems and current and future drivers of change

Action 3. Describe trends in the use of animal genetic resources

Reviewing the status and trends of animal genetic resources

Task: Produce estimates of past, present and future population sizes

Action 1. Obtain past and present population data and analyse trends

Action 2. Predict future population sizes

Action 3. If breed population data are not available, consider general trends that may affect diversity

Identifying reasons for the loss of animal genetic diversity

Task. Assess threats to genetic diversity

Action 1. Analyse the drivers of change in livestock systems

Action 2. Assess the probability of disasters and disease outbreaks

Action 3. Summarize the risk factors and consider preventive measures

Identifying objectives for conservation

Task: Identify conservation objectives

Action 1. Consider potential objectives for conservation programmes

Action 2. Summarize the conservation objectives

Reviewing the status of each breed and developing management strategies

Task: Evaluate potential strategies for the future conservation and use of the breed

Action 1. Undertake a SWOT analysis of the breed and its stakeholders

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

Action 3. Formulate alternative conservation and use strategies and assess their viability

Comparing conservation strategies

Task. Evaluate potential conservation measures

Action 1. Assess the feasibility of implementing various conservation measures

Action 2. Determine which conservation measures are relevant for which species

Action 3. Determine the prerequisites for implementing the conservation measures

SECTION 2. IDENTIFYING BREEDS AT RISK

Determining risk status

Task 1. Determine the population size, trends and distribution, and cross-breeding activities

Action 1. Review available population data

Action 2. Assign responsibility for determining risk status

Action 3. Gather information about each breed population
Action 4. Analyse and interpret the data
Task 2. Identify breeds eligible for conservation activities
Action 1. Assign breeds risk-status categories
Action 2. Refine the categorization of risk
Action 3. Interpret the results of the risk categorization and consider the consequences for each breed
Action 4. Disseminate information about breeds' risk status to stakeholders
Task 3. Design and implement interventions
Action 1. Identify appropriate conservation measures
Action 2. Implement the conservation measures
Task 4. Monitor risk status

SECTION 3. DETERMINING THE CONSERVATION VALUE OF A BREED

Accounting for factors other than risk status

Task 1. Assess conservation priority according to non-demographic factors
Action 1. Assign responsibilities for prioritizing breeds for conservation
Action 2. Determine the factors upon which the prioritization will be based
Action 3. Gather the information needed for the prioritization
Action 4. Evaluate the advantages and disadvantages of each breed
Action 5. Rank the breeds for conservation priority
Task 2. Disseminate information to stakeholders
Action 1. Prepare a report on the breed prioritization
Action 2. Meet with stakeholders to explain the results of the prioritization

Using information from genetic markers

Task 1. Gather the data needed to apply objective prioritization methods.
Action 1. Obtain molecular genetic data
Action 2. Agree upon specific genetic objectives for the maintenance of diversity
Action 3. Choose which objective method to apply
Action 4: Estimate extinction risk
Action 5: Determine which non-genetic factors to include in the prioritization
Action 6: Prioritize breeds for conservation
Task 2. Disseminate information to stakeholders

SECTION 4. CHOOSING THE APPROPRIATE CONSERVATION METHODS

Matching breeds and conservation methods

Task 1. Assess the applicability of the available conservation methods
Task 2. Match breeds to conservation methods
Action 1. Identify the conservation objectives relevant for each breed
Action 2. Identify conservation methods that will meet the objectives effectively
Action 3. Consider the possible pitfalls of each conservation method
Action 4. Consider the costs of each conservation method
Action 5. Choose the conservation methods
Task 3. Apply the chosen methods

SECTION 5. ORGANIZING THE INSTITUTIONS FOR IN VIVO CONSERVATION

Involving livestock keepers in community-based conservation

Task 1. Choose the location and collaborators for the conservation activities
Action 1. Identify and study the area where the breed is kept
Action 2. Choose the communities with which conservation work will be undertaken

- Task 2. Undertake a detailed participatory study of the targeted communities
  - Action 1. Undertake preparatory work
  - Action 2. Enlist the research team and carry out the study
  - Action 3. Evaluate the results
- Task 3. Facilitate the implementation of the community-based programme
  - Action 1. Assist livestock keepers to organize a breeders' association
  - Action 2. Work with the community to establish a breeding programme
  - Action 3. Consider establishing a nucleus herd
  - Action 4. Provide incentives, including capacity building, and establish complementary institutions

Establishing a breeders' association

- Task 1. Assess the degree of support for establishing a breeders' association
  - Action 1. Discuss the possibility of establishing a breeders' association during the initial participatory studies
  - Action 2. Identify members of the community that may be interested in joining or leading a breeders' association
- Task 2. Plan and implement the establishment of the breeders' association
  - Action 1. Determine requirements for membership of the association
  - Action 2. Establish registry protocols
  - Action 3. Establish by-laws
  - Action 4. Set membership dues and fees
  - Action 5. Establish communication methods for educational and training programmes
  - Action 6. Develop and adopt a procedure for conflict resolution

Auditing a breeders' association and its activities

- Task 1. Evaluate participation and decision-making procedures
  - Action 1. Evaluate the mechanisms for member participation
  - Action 2. Assess the decision-making processes
  - Action 3. Evaluate the provision of benefits to association members
  - Action 4. Evaluate the procedure for inclusion of new members
- Task 2. Appraise the genetic purity of the population managed by the association
  - Action 1. Evaluate the level of pure-bred breeding as opposed to deliberate or casual introgression
  - Action 2. Check the accuracy of parental information
- Task 3. Evaluate the management of the breed as a genetic resource
  - Action 1. Analyse the association's management of the population structure
  - Action 2. Evaluate the breeding and conservation programme

Establishing a centralized ex situ conservation programme

- Task 1. Plan the conservation programme and secure access to facilities and funding
  - Action 1. Assess the available institutional breeding farms
  - Action 2. Decide which breeds will be targeted by the programme
  - Action 3. Perform a feasibility study
  - Action 4. Identify possible donors
  - Action 5. Prepare and present conservation plans to government officials and/or donor agencies
- Task 2. Establish and operate the programme
  - Action 1. Establish the herds at the institutional farm
  - Action 2. Develop breeding and husbandry strategies for the institutional herd
  - Action 3. Establish a gene bank for storing germplasm from animals in the programme
  - Action 4. Organize the production and use of male animals

Establishing a dispersed ex situ conservation programme

- Task 1. Establish the conserved population
  - Action 1. Determine the size of the base population and the criteria for selection
  - Action 2. Identify the base animals from among collaborating herds
- Task 2. Manage the conserved population
  - Action 1. Manage the mating of base animals to produce new males

Action 2. Manage the selection and distribution of males
Action 3. Design breeding and mating strategies

SECTION 6. DESIGNING THE CONSERVATION PROGRAMME

Maintaining genetic variability within small populations

Task 1. Adopt a breeding strategy that maintains the breed's genetic variability
Action 1. Include as many animals as possible from the start in order to minimize genetic drift
Action 2. Increase the number of breeding males
Action 3. Prolong the generation interval
Action 4. Balance the contribution of each individual
Action 5. Consider the use of embryo transfer in species with low reproductive rates
Task 2. Adopt a mating strategy that decreases inbreeding
Action 1. Set a limit to the degree of relationship between mates
Action 2. Establish the ideal set of matings for the entire population
Action 3. Apply simple methods that do not require pedigree information
Task 3. Incorporate cryoconservation into the management of genetic variation
Action 1. Store genetic material from animals at the start of the conservation programme
Action 2. Use cryoconserved material continually in the management of genetic diversity

SECTION 7. ESTABLISHING A BREEDING PROGRAMME FOR CONSERVATION AND SUSTAINABLE USE

Choosing a breeding strategy

Task 1. Implement a pure-breeding programme with selection for production
Action 1. Analyse the history of selection within the breed
Action 2. Decide which production and other traits should be improved
Action 3. Implement identification, registration and performance recording
Action 4. Implement trait recording and selection in relevant production environments
Action 5. Decide on the selection and breeding strategy that is most likely to improve productivity

Optimizing selection response and genetic variability in small populations

Task 1. Adopt a general breeding strategy to maintain the conserved breed
Action 1. Decide which trait(s) to improve in the conserved breed
Action 2: Decide what rate of inbreeding is acceptable in the conserved population
Task 2. Design the breeding programme
Action 1. Evaluate the circumstances in which the breeding programme will be implemented
Action 2. Consider the options for balancing genetic improvement and maintaining genetic variability
Action 3. Implement and monitor the breeding programme

Cross-breeding for enhanced production

Task 1. Develop a cross-breeding system that conserves an animal genetic resource
Action 1. Outline the objectives of the cross-breeding system
Action 2. Evaluate the status of the targeted breed
Action 3. Evaluate other breeds for possible inclusion in the cross-breeding system
Action 4. List the cross-breeding systems that are relevant for the production system
Action 5. Describe the contributions of the different breeds to the cross-breeding system
Action 6. Choose the optimal cross-breeding system
Action 7. Present the plan to a wider group of stakeholders for final approval
Task 2. Implement and monitor the cross-breeding programme
Action 1. Prepare for the start of the cross-breeding programme
Action 2. Establish the financial and organizational structures
Action 3. Implement the cross-breeding programme
Action 4. Organize the delivery of cross-breeding services
Action 5. Improve the cross-breeding services and promote uptake

Action 6. Evaluate the cross-breeding programme for benefits obtained and sustainability

SECTION 8. INCREASING THE VALUE AND SUSTAINABILITY OF CONSERVED BREEDS

Identifying sustainable use options for breeds under conservation

Task. Plan measures to promote sustainable use

Action 1. Identify opportunities and threats

Action 2. List the breed's characteristics and match them to opportunities

Action 3. Determine which opportunities are realistic and make plans to exploit them

Preparing a Biocultural Community Protocol

Task 1. Discuss the proposed Biocultural Community Protocol with stakeholders

Action 1. Establish a working relationship between the facilitating organization and the local community

Action 2. Hold a series of meetings to collect information and discuss options

Action 3. Obtain solid, and preferably quantitative, data about the community and its management of resources

Action 4. Provide relevant and appropriate training to community members

Task 2. Prepare the Biocultural Community Protocol

Action 1. Develop an outline of the Biocultural Community Protocol

Action 2. Write the Biocultural Community Protocol in a format and language appropriate for policy-makers

Task 3. Consider potential problems in the development of the Biocultural Community Protocol

Action 1. Facilitate rather than push the development of the Biocultural Community Protocol

Action 2. Guard against biopiracy

Task 4. Publicize and distribute the Biocultural Community Protocol

Action 1. Present the Biocultural Community Protocol to policy-makers

Action 2. Promote the Biocultural Community Protocol to the general public

Implementing a "role model breeders" programme

Task 1. Prepare an inventory of role model breeders' knowledge

Action 1. Identify role model breeders

Action 2. Interview role model breeders to discover the techniques and attitudes behind their success

Action 3. Document and define the role model breeders' intuitive management techniques

Action 4. Document and define the role model breeders' intuitive selection criteria

Task 2. Disseminate role model breeders' knowledge and encourage its use

Action 1. Make the information obtained from the role model breeders widely available

Action 2. Reward or otherwise recognize role model breeders for their contributions

Capitalizing on niche market production

Task 1. Identify potential niche products and services

Action 1: List breed characteristics that might be targeted for niche marketing

Action 2. Identify markets for breed-specific products

Action 3. Conduct a workshop to creatively formulate marketing plans

Action 4. Prioritize the potential niche products and services

Task 2. Plan and implement a niche marketing campaign

Action 1. Write a business plan

Action 2. Undertake a formal analysis of the business plan and the potential market

Action 3. Produce a relatively small amount of the product and market it on an experimental basis

Action 4. Evaluate sales and increase production according to market demand

Enhancing value through ties to geographical origin or cultural significance

Task. Develop a plan to enhance the value of a breed's products

Action 1. Evaluate products and potential markets

Action 2. Identify opportunities to improve the products and their marketing

Action 3. Develop plans to enhance the value of the products through manufacture, trademarking or marketing

Capitalizing on the roles of livestock in providing ecosystem services

Task. Identify opportunities for using species and breeds in nature management

Action 1. Interview stakeholders and formulate a strategy for using livestock in nature management

Action 2. Describe the grazing behaviour of potentially relevant species and breeds

Action 3. Match the demand for conservation services to the characteristics of the livestock

Action 4. Write an action plan for incorporating livestock into nature management

Capitalizing on the societal and cultural functions of livestock

Task 1. Identify the most important social and cultural functions of a breed

Action 1. Determine the present and potential future social or cultural functions of the breed

Action 2. Document the various societal groups benefiting from the social or cultural functions

Action 3. Valuate the social or cultural functions

Action 4. Determine the best approach (public or private) for incorporating the social or cultural functions into breed conservation

Task 2. Prepare a proposal to solicit support from potential donors

Action 1. Identify potential donors and seek an initial meeting to explain plans to capture the value of the breed’s contribution to society

Action 2. Prepare and submit a full proposal

Action 3. Consider novel options to capitalize on the breed’s cultural or social functions