Part 4

State of the art in the management of animal genetic resources

Introduction

This part of the Report gives an overview of the state of the art in methodologies and techniques for the management of animal genetic resources for food and agriculture (AnGR). As AnGR management is not an established scientific discipline, Section A outlines basic concepts that underlie FAO's understanding of the term. These concepts are the outcome of a series of expert meetings. Methodological developments in relevant fields of research are then highlighted, and important findings are illustrated through case studies. Finally, gaps in current knowledge are identified, and priorities for future research are proposed.

SECTION A: BASIC CONCEPTS

1 Animal genetic resources and breeds

AnGR are here defined as those animal species that are used, or may be used, for food production and agriculture,[1] and the populations within each. Distinct populations within species are usually referred to as breeds. The broad definition of the term "breed" used by FAO (Box 67) is a reflection of the difficulties involved in establishing a strict definition of the term.

Box 67
Definition of breed adopted by FAO

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 similar groups has led to acceptance of its separate identity.

Source: FAO (1999)

In developed countries, breeds are relatively clearly delineated. The role of breed societies, normally voluntary organizations, which supervise breeding standards, provide for the registration of animals, and promote the utilization of the breed, is important in this respect. A pattern of breed development based on recorded breeding and shared pedigrees emerged in western Europe during the late eighteenth century, with the first breed societies being established in England during the nineteenth century. Under the auspices of such organizations, a breed has come to be distinguished as a population sharing common ancestry, which has been subjected to similar selection objectives, and which conforms to certain established "breed standards".

Breeds are generally not completely isolated in genetic terms. They are constantly required to change in response to changes in market demand, and will at times be supplemented with bloodlines from other breeds (FAO, 2003). Moreover, despite the existence of societies ostensibly associated with specific breeds, the precepts to be followed when establishing criteria for the delineation of a breed remain vague. Definitions of breeds within a developed-country context have included "animals which share a common pattern of use in agriculture, a degree of uniformity of phenotype, and a common gene pool" (FAO, 1995) and "distinct intraspecific groups, the members of which share particular characteristics that distinguish them from other such groups" (FAO, 2003). Discussing the situation in the United States of America, Hammak (2003) notes that all that is required to start a breed registry is "to adopt specific requirements for eligibility and start to record ancestry." Similarly, under European Union (EU) legislation, there is no definition of a "breed" beyond the requirement that in order to be registered as a pure-bred animal, an animal's pedigree should be traceable to "parents and grandparents ... which are entered or registered in a herd-book of the same breed ... [and the animal itself should be] ... either entered or registered and eligible for entry in such a herd-book" (the

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[1] Fish are excluded as management requirements and breeding techniques are very different. The term "farm animal genetic resources", which had been used by FAO in relation to the Global Strategy for the Management of Farm Animal Genetic Resources, has been criticized on the grounds that it appeared to exclude animals not kept on farms, but in mobile systems.

quotation, from Council Directive 77/504/EEC, relates to bovine animals, but similar rules apply to other species).

There may, indeed, be little benefit in seeking a perfect definition. In the words of Jay Lush, a prominent figure in the field of animal breeding and genetics, “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” (Lush, 1994).

In the developing regions of the world, the situation is even more complex, and the term “breed” often has little meaning. Populations that are isolated from others, whether on geographical, ecological or cultural grounds, will tend to become distinct as a result of natural and artificial selection, and genetic drift (FAO, 2003). However, the names used to distinguish livestock populations do not necessarily correspond to the underlying genetic diversity. In many cases, animals will not correspond to any recognized breed, although there may be local terms referring to different populations.

Where distinguishing genetically diverse populations is difficult, molecular studies may contribute to the delineation of separate breeds and breed groups. Studying the cultural and ecological aspects of livestock keeping also serves as a means of identifying populations that merit being treated as separate breeds. The following definition is an example of such an approach: “A domestic animal population may be regarded as a breed, if the animals fulfil the criteria of (i) being subjected to a common utilization pattern, (ii) sharing a common habitat/distribution area, (iii) representing largely a closed gene pool, and (iv) being regarded as distinct by their breeders” (Köhler-Rollefson, 1997). Thus, in the absence of breed association records or molecular studies, the views of the livestock keepers themselves perhaps provide the best indicator of breed identity. It may be possible to identify groups of farmers who claim to be raising an animal of a distinct type; can reliably recognize the type; exchange germplasm only with other breeders dedicated to holding the same type; and indicate that such breeding practices have been ongoing for many generations (FAO, 2003).

Within a breed there may be “stocks”, “strains”, “varieties”, or “lines”; these terms which are often used interchangeably describe populations within breeds that are phenotypically distinct as a result of human selection. The term “ecotype” refers to a population within a breed that is genetically adapted to a specific habitat.

2 Management of animal genetic resources

Management of AnGR focuses on maintaining genetic diversity. However, most scientific methods and techniques within the animal sciences (e.g. animal husbandry, animal breeding or genetics) have not been developed with this focus. Thus, there is no well-defined set of methodologies encompassed by the phrase “management of AnGR”. The overview presented here, therefore, selects the methodologies most relevant to the topic, guided by FAO’s definition:

> “AnGR management encompasses all technical, policy, and logistical operations involved in understanding (characterization), using and developing (utilization), maintaining (conservation), accessing, and sharing the benefits of animal genetic resources” (FAO, 2001).

As such, this part of the Report includes descriptions of methodologies for characterization and conservation (Sections B and F); because of their increasing importance, methods for molecular characterization are presented separately from other aspects of characterization (Section C). However, when it comes to utilization – using and developing AnGR for agriculture and food production – no clear concept has emerged. It is, therefore, not possible to present a comprehensive description of the state of the art in utilization. Nonetheless, FAO has started to identify key elements of such a concept, using as a starting point the definition of sustainable use proposed by the Convention on Biological Diversity (CBD):

> "Sustainable use is the use of components of biological diversity in a way and at a rate that does not lead to the long-term decline of biological diversity, thereby maintaining its potential to meet the needs and aspirations of present and future generations" (Article 2 of the CBD).

To meet this objective FAO has proposed that:

- wise use of AnGR is possible without depleting domestic animal diversity;
- AnGR with high levels of adaptive fitness to the environment concerned should be used, and sound genetic principles deployed; and
- development of AnGR includes a broad mix of ongoing activities that must be well planned and executed for success, and compounded over time.

Thus, an important element of (sustainable) use of AnGR is to ensure that locally adapted breeds remain a functional part of production systems. Adaptive fitness traits, some of which may not yet have been discovered, are of particular importance, as they are genetically complex and cannot easily be achieved by selection over a short period of time. Use of AnGR inevitably includes development – AnGR are dynamic resources, changing with each generation in interaction with the physical environment and according to the selection criteria of their keepers. The proposed approach for genetic improvement is to base breeding efforts on locally adapted genetic resources. This will help to avoid the loss of breeds with unique attributes. Existing genetic variation in animals' ability to use locally available resources, survive, produce and reproduce under the conditions of medium-to-low input farming should be exploited by well-designed breeding programmes. Complementary measures such as improvement in the provision of feed and water, treatment of diseases and parasites, and the management of reproduction will also need to be considered in strategies to improve the performance of these breeds.

Thus, genetic improvement methods are central to the development of breeds. Scientific methods for breeding programmes have, however, been developed mainly in higher-input production systems, and under favourable infrastructural conditions. Breeding programmes do not usually include maintaining genetic diversity within and between breeds as an explicit goal. The state of knowledge in the field of genetic improvement is described in Section D.

Ideally, breeding programmes should be part of a holistic strategy with the goal of sustainably intensifying production systems to improve the livelihoods of the producers. Sustainable intensification has been put forward as the ideal way of improving production systems, and is defined as follows:

> "Sustainable intensification of production systems is the manipulation of inputs to, and outputs from, livestock production systems aimed at increasing production and/or productivity and/or changing product quality, while maintaining the long-term integrity of the systems and their surrounding environment, so as to meet the needs of both present and future human generations. Sustainable agricultural intensification respects the needs and aspirations of local and indigenous people, takes into account the roles and values of their locally adapted genetic resources, and considers the need to achieve long-term environmental sustainability within and beyond the agro-ecosystem" (FAO, 2001).

Addressing these general principles for the use and development of AnGR is not merely a matter of scientific methodology, but requires an effective combination of methodologies and techniques with appropriate development policies. To support policy development, economic analyses are needed to describe the economic importance of locally adapted breeds, in particular from the perspective of the smallholder; to define the value of livestock genetic diversity; and to compare different management strategies. An overview of economic valuation methods is presented in Section E.

Another difficulty related to the concept of utilization, is that of clearly distinguishing it from *in vivo* conservation. This problem arises due to the fact that sustainable use is considered the preferred method of maintaining AnGR. Thus, when conservation is defined in the broad sense of ensuring maintenance of all relevant AnGR, it includes sustainable use. However, a more operational definition, which allows a clearer delineation of the subject, and which is used in Section F on methods for conservation, is that conservation comprises actions that are required because the continued use of a particular genetic resource is threatened. The role of conservation is to ensure that unique genetic resources are available to farmers and breeders in the future, and consequently, conservation can be considered as part of an overall strategy to use AnGR in a sustainable manner to meet current and future human needs. To inform decisions regarding conservation strategies, it is important to have an estimate of current risk status (see below), and also to identify threats likely to affect the breed in the near future. The latter allows interventions, such as any breed development necessary to maintain the breed, to take place at a sufficiently early stage.

Accessing and sharing the benefits of AnGR (also components of FAO's definition of AnGR management) are key areas for policy development. Interdependencies among regions in terms of their access to AnGR, and past and present patterns of exchange are described in Part 1 – Section C. Developments in biotechnology (described in Sections C and F) have facilitated exchange and use of genetic resources, have begun to detect genes regulating functional traits, and present new opportunities for the use of genetic material. Thus, they will play an important role in future patterns of access and benefit sharing (ABS). The contribution that methodologies developed in the social and political sciences can make to the formulation of adequate policies for ABS is, however, beyond the scope of this discussion.

3 Risk status classification

An assessment of the risk status of livestock breeds or populations is an important element in national planning of AnGR management. The risk status of a breed informs stakeholders whether, and how urgently, actions need to be taken. Gandini *et al.* (2004) define "degree of endangerment" as "a measure of the likelihood that, under current circumstances and expectations, the breed will become extinct." Accurately estimating degrees of risk is a difficult undertaking and incorporates both demographic and genetic factors.

Clearly, current population size is an important factor in determining risk status. A small population is at greater risk of being wiped out by natural disasters, disease or inappropriate management. However, a mere headcount of animals, or even of animals of breeding age, does not give the whole picture with regard to risk status.

Breeding between individuals sharing common ancestors tends to reduce the rate of allelic variation in the next generation. The genetic diversity of the population is, thus, reduced. The accumulation of deleterious recessive alleles may threaten the fitness of the population and negatively affect reproductive rates, thereby increasing the risk of extinction (Gandini *et al*., 2004; Woolliams, 2004). The extent of the risk is commonly expressed in terms of the rate of inbreeding (ΔF) in the population, which is a measure of the expected changes in gene frequencies in the population due to genetic drift (Woolliams, 2004). The rate of inbreeding is often inferred from the effective population size (N_e). As N_e goes up ΔF decreases, or more formally, $N_e = 1/(2\ \Delta F)$.

The value of N_e in a population is often approximated on the basis of the equation $N_e = 4MF/(M+F)$ where M and F are number of reproducing males and females. The method is based on the assumption that matings between these breeding animals are random. However, this assumption is rarely applicable in livestock populations, as some individuals contribute disproportionate numbers of progeny to the next generation. The way in which breeding is managed, for example the implementation of selective breeding programmes, influences the effective population size. Various techniques for adjusting the calculation to account for such factors have been developed, but require further data inputs (Gandini *et al*., 2004). Collecting the demographic data needed to calculate N_e is often problematic: there may be inconsistencies in census data and registration of females and offspring, some females may be used in crossing programmes, and not all females may be bred each year (Alderson, 2003). Another element that can influence the outcome of risk status estimations is the time interval over which risk is calculated. Because of the different generation intervals in different livestock species, calculations performed on the basis of the number of generations will produce different priorities from those calculated on the basis of years (ibid.).

Some implications of changes to the effective population size are important to note. At low levels of N_e, particularly below 100, the rate of loss of genetic diversity increases dramatically (FAO, 1992a).

For example, approximately 18, 10, 4, 1.6 and 0.8 percent of genetic diversity is lost in ten generations, when N_e is equal to 25, 50, 125, 250 and 500, respectively (ibid.). Additionally, it can be seen from the above equation that the value of N_e is far more readily influenced by changes affecting the male (smaller) breeding population than the female. This underlines the importance of considering the number of breeding males in any assessment of risk status.

In addition to the current effective population size, degree of risk is related to population growth trends. As noted above, where populations are small there is a greater likelihood that adverse events or trends will lead rapidly to extinction. Above a certain population size the risk of such an outcome can be regarded as small (see below for discussion of the thresholds used in various risk status classifications). The more rapidly a population builds up to reach the critical size, the less it is exposed to the risk of extinction. Obviously, if population figures are low and the growth trend is negative, the prospects for the breed are not good. A complicating factor is that breed population growth rates often show considerable fluctuations over time, particularly where production conditions cannot be strictly controlled (Gandini *et al.*, 2004). Factors which may influence the variance of the population growth rate include the variability of market demand, patterns of disease, the existence of programmes for and awareness of AnGR conservation, the general economic stability of the agricultural sector, and the spatial distribution and density of the population (ibid.). Calculating the probability that the population size will lie within a given range at a given time in the future is, thus, fraught with theoretical and data-related difficulties. Despite such problems, current population trends are clearly a factor to be considered in assessing risk status. In addition to overall population size and growth rates, the risk status of a population is affected by other factors such as the number of herds, and the geographical concentration of the population, which influence exposure to threats such as disease epidemics; and by sociological factors such as the age of the farmers keeping the breed (Woolliams, 2004).

In 1992, FAO convened an Expert Consultation to develop recommendations for the assessment of risk status. The preference was for a breed risk status classification based on the concept of N_e, adjusted by trends in population size, extent of cross-breeding, extent of cryoconservation, and variability of family size. It was also suggested that the number of herds and trends in the number of herds should be included (FAO, 1992a). However, data limitations and the necessity of a consistent approach on a global scale meant that a simpler approach was adopted, based on the number of breeding females and males, and trends in population size (see below for details). In the future, as more complete data become available it may be possible to refine the method of calculation to account for the above factors, and also to adapt it to account for the different generation intervals of different species.

For planning and prioritization purposes, it is useful to classify breeds into risk status categories. The numerical boundaries between the different risk status categories used by FAO are intended to be indicators of the need to take action. A paper presented at the Expert Consultation in 1992 argued that a population size between 100 and 1 000 breeding females "implies that the breed is in danger of extinction. Without action its effective population size is inadequate in most cases to prevent continuing genetic loss in future generations. An increase in the degree of inbreeding is unavoidable and threatens the vitality of animals. There is a real danger either of spontaneous loss for example by sudden disease, or due to neglect by man" (FAO 1992b). Further, a population size of less than 100 breeding females indicates that "The population is close to extinction. The first action must be to increase the population size. At this level of threat, the genetic variability is often already reduced so that the population cannot be considered the same as the ancient breed" (ibid.).

As such, the following classification is used by FAO to describe the degrees of risk faced by livestock breeds:

- Extinct breed: The case when it is no longer possible to recreate a population of the breed. Extinction is absolute when there are no breeding males (semen), breeding females (oocytes), nor embryos remaining.
- Critical breed: A breed where the total number of breeding females is less than 100 or the total number of breeding males is less than or equal to five; or the overall population size is close

to, but slightly above 100 and decreasing, and the percentage of pure-bred females is below 80 percent.

- Endangered breed: A breed where the total number of breeding females is between 100 and 1000 or the total number of breeding males is less than or equal to 20 and greater than five; or the overall population size is close to, but slightly above 100 and increasing and the percentage of pure-bred females is above 80 percent; or the overall population size is close to, but slightly above 1 000 and decreasing and the percentage of pure-bred females is below 80 percent.
- Critical–maintained breed and endangered–maintained breed: Critical or endangered breeds that are being maintained by an active public conservation programme or within a commercial or research facility.
- Breed not at risk: A breed where the total number of breeding females and males is greater than 1 000 and 20 respectively; or the population size approaches 1 000 and the percentage of pure-bred females is close to 100 percent, and the overall population size is increasing.

The FAO system outlined above is not the only existing classification of risk status. Another classification was developed for the European Association of Animal Production–Animal Genetic Data Bank (EAAP–AGDB), and is now used by the European Farm Animal Biodiversity Information System (EFABIS) (http://efabis.tzv.fal.de/). It covers breeds of buffalo, cattle, goat, sheep, horse, donkey, pig and rabbit in 46 European countries, and is based on genetic risk – as represented by expected cumulative rates of inbreeding in 50 years (ΔF–50). Calculations are based on the familiar equation $N_e = 4MF/(M+F)$ (see above) with its inherent assumptions (EAAP–AGDB, 2005). Breeds are classified into one of five categories according to ΔF–50: not endangered, <5 percent; potentially endangered, 5–15 percent; minimally endangered, 16–25 percent; endangered, 26–40 percent; and critically endangered, >40 percent. Breeds may be shifted to a higher risk class based on a set of additional risk factors: a high rate of incrossing with other breeds; a downward trend in the number of breeding females; or a low number of breeding herds (ibid.).

The EU, under Commission Regulation (EC) No. 817/2004, sets out risk status thresholds for the purposes of providing incentive payments to farmers keeping threatened breeds. Calculations are based on the number of breeding females summed across all EU countries. Separate thresholds are established for each species: cattle – 7 500, sheep – 10 000, goats – 10 000, equidae – 5 000, pigs – 15 000 and avian species – 25 000. Some arguments can be put forward in support of these rather high thresholds. Gandini *et al.* (2004) note that while in the European context a breed with 1000 or more breeding females can generally be self-sustainable, this is not always the case, and that it is easier to prevent a population from losing self-sustainability than to restore it.

The NGO Rare Breeds International has also developed a system based on the number of registered pure-bred breeding females, which classifies priority breeds into four categories: critical, endangered, vulnerable and at risk (Alderson, 2003). Other factors (number of breeding units, number of unrelated sire lines, population trends, distance between major breeding units), which would ideally be included in an estimation of risk status, are disregarded in the interests of avoiding excessive complexity in the calculations (ibid.).

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SECTION B: METHODS FOR CHARACTERIZATION

1 Introduction

Characterization of AnGR encompasses all activities associated with the identification, quantitative and qualitative description, and documentation of breed populations and the natural habitats and production systems to which they are or are not adapted. The aim is to obtain better knowledge of AnGR, of their present and potential future uses for food and agriculture in defined environments, and their current state as distinct breed populations (FAO, 1984; Rege, 1992). National-level characterization comprises the identification of the country's AnGR and the surveying of these resources. The process also includes the systematic documentation of the information gathered so as to allow easy access. Characterization activities should contribute to objective and reliable prediction of animal performance in defined environments, so as to allow a comparison of potential performance within the various major production systems found in a country or region. It is, therefore, more than the mere accumulation of existing reports.

The information provided through the characterization process enables a range of interest groups, including farmers, national governments and regional as well as global bodies to make informed decisions on priorities for the management of AnGR (FAO, 1992; FAO/UNEP, 1998). Such policy decisions aim to promote further development of AnGR while ensuring that these resources are conserved for the needs of present and future generations.

2 Characterization – as the basis for decision-making

A key consideration for the management of AnGR at the national level is whether, at a given point in time, a particular breed population is self-sustainable or whether it is at risk. This primary assessment (baseline survey[2]) of breed/population status is based on information on:

- the population size and structure;
- geographical distribution;
- within-breed genetic diversity; and
- the genetic connectedness of breeds when populations are found in more than one country (e.g. the Djallonke sheep of West Africa).

If a breed/population is not as risk, no immediate steps to implement conservation measures are necessary. Nevertheless, as part of national livestock development plans, decisions have to be taken as to whether a genetic improvement programme is needed – in response, for example, to changing market conditions. Decisions regarding such improvement programmes are mainly guided by information on long-term benefits to livestock keepers and society.

When a breed/population is found to be at risk, active conservation strategies have to be implemented or the potential loss of the breed must be accepted. To allocate the limited resources that are available for conservation programmes, breeds need to be prioritized. These decisions may be based on the genetic distinctiveness, adaptive traits, relative value for food and agriculture or historical/cultural values of the breeds in question. This information is also needed to decide, whether *in vivo* or *in vitro* strategies or a combination of both appears to be the most promising approach. If the breeds to be conserved are found in more than one country, decisions should be taken at the regional level. Thus,

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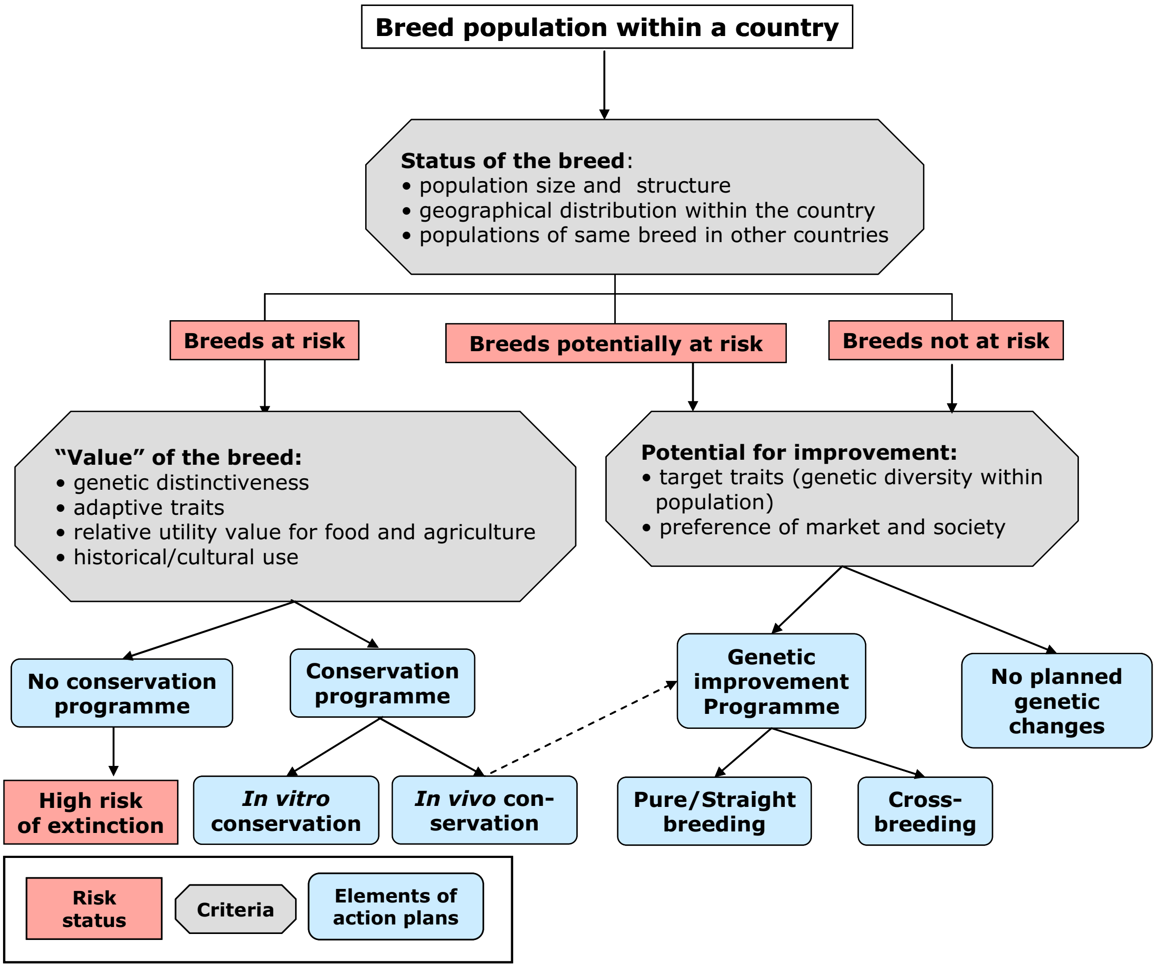
[2] Baseline information is related to a particular target animal population at a given time and within a given production environment. Depending on the degree of change, these descriptions may need to be updated about once a generation. The baseline study should characterize phenotypic and molecular attributes of the breeding females and males in the population. About 100 adult females and about 30 adult males are needed for phenotypic characterization, but about a third of this size may be sufficient for molecular diversity estimation.

regional coordinating institutions/organizations, and supporting national policies, are required to facilitate such decisions and to implement actions. To date, only a few examples of multi-country actions in AnGR management have been reported.

Figure 47
Information required to design management strategies



For decisions on conservation strategies and on development programmes for self-sustainable breeds, comprehensive characterization information is needed, and should include:

- description of the typical phenotypic characteristics of the breed population, including physical features and appearance, economic traits (e.g. growth, reproduction and product yield/quality) and some measures (e.g. range) of variation in these traits – the focus is generally on the productive and adaptive attributes of the breed;
- description of the production environments (Box 68), both the original habitat and the current production system in which the population is kept – some breeds are kept in more than one production environment, in a number of countries, and sometimes outside their original geographical area;
- documentation of any special characteristics (unique features) of the population in terms of adaptation and production – including responses to environmental stressors (disease and parasite challenge, extremes of climate, poor feed quality etc.);
- images of typical adult males and females in their typical production environment;
- relevant indigenous knowledge (including but not limited to gender-specific knowledge) of traditional management strategies used by communities to utilize the genetic diversity of their livestock;

- description of ongoing management (utilization and conservation) actions and the stakeholders involved; and
- description of any known genetic relationships between breeds within or outside the country.

In addition to the information listed for both pathways (conservation and development), the following supplementary information is useful to guide the choice of priority breeds and geographic areas for conservation programmes:

- genetic distinctiveness of the breeds and their significance with respect to the total genetic diversity among the breeds under consideration (in order to maximize the diversity conserved for the benefit of future human generations);
- origin and development of the breeds; and
- unique genetic (or phenotypic if genetic attributes are not known) characteristics and their significance in current or anticipated production settings.

National decision-makers need to identify the breeds in which genetic improvement programmes would be most beneficial. Such programmes could include breeds classified as at risk, and form part of a conservation programme. Investments in breed improvement should be justified by adequate returns to investment. These are determined by performance levels, special adaptive characteristics and/or specific uses and values of the breeds in a given production environment or in relation to anticipated changes in the production environment (including market conditions). Thus, performance data, description of particularly useful attributes and values, and a detailed description of the general production environment are essential to guide decisions on breed development programmes.

The set of information needed for the development of appropriate breeding programmes also allows the choice of breed to be reconsidered as the production environment evolves, whether through changes to husbandry practices, market conditions, cultural preferences, or biophysical (e.g. climatic stress or disease challenge) factors. Similarly, this information is needed in the design of AnGR restocking schemes undertaken following natural disasters (drought, floods etc.), disease outbreaks or civil unrest. Restocking may be based on AnGR available within the country, from other countries in the region, or from another region of the world. In all cases, restocking schemes should seek to obtain the animals that are best adapted to the production environment into which they will be introduced.

Management decisions may differ in type and scope at subnational, national, regional and international levels. It is, therefore, important that relevant information on breed characteristics is made accessible to decision-makers at all levels. For example, it may happen that a country decides not to invest in the conservation of a specific local breed, but a regional or international organization decides that the breed is a unique genetic resource, and that it is in the global interest to conserve it.

Box 68
Production environment descriptors for animal genetic resources

A comprehensive description of the production environment is essential to make use of performance data and to understand the special adaptations of breeds/populations. Adaptive fitness of breeds is complex and difficult to measure directly, but can be characterized indirectly by describing the primary variables (criteria) which have affected an animal gene pool (breed) over time, and have probably maximized its adaptive fitness for that environment. Thus, an (improved) description of production environments would be extremely valuable, in order to better understand the comparative adaptive fitness of specific AnGR.

In January 1998, an expert group met in Armidale, Australia, and devised a very detailed and well-structured approach, using five main criteria to characterize most, if not all, production environments, for all animal species used for food and agriculture. The five criteria were: climate; terrain; disease, disease complexes and parasites; resource availability; and management interventions (FAO, 1998). At a second level of hierarchy three to seven indicators for each criterion were formulated to characterize (i.e. describe and measure variables in) the production environments. For each indicator two or more verifiers were identified to specify or measure each indicator. The workshop noted that many developing countries had very little capacity to collect and analyse production environment variables, and that, a less complex descriptive system would, therefore, be preferable as it would be more likely to be used. Despite these concerns, the system proposed required very detailed information. A less detailed and more pragmatic approach to describing production systems would probably facilitate efforts to begin to fill the current large gaps in breed documentation. However, a detailed approach should be encouraged whenever this is possible.

The system devised at the meeting in Armidale appears to be the first attempt to develop a structured set of production environment descriptors (PEDs) for use in the characterization of livestock breeds. The Domestic Animal Genetic Resources Information System (DAGRIS) database, developed by the International Livestock Research Institute (ILRI) includes a field devoted to the “habitat” of each breed, but there is no set structure to the entries, and the information provided to date is quite limited. Oklahoma State University’s “Breeds of Livestock” database provides some information on production environments, but this is again not based on a systematic set of descriptors.

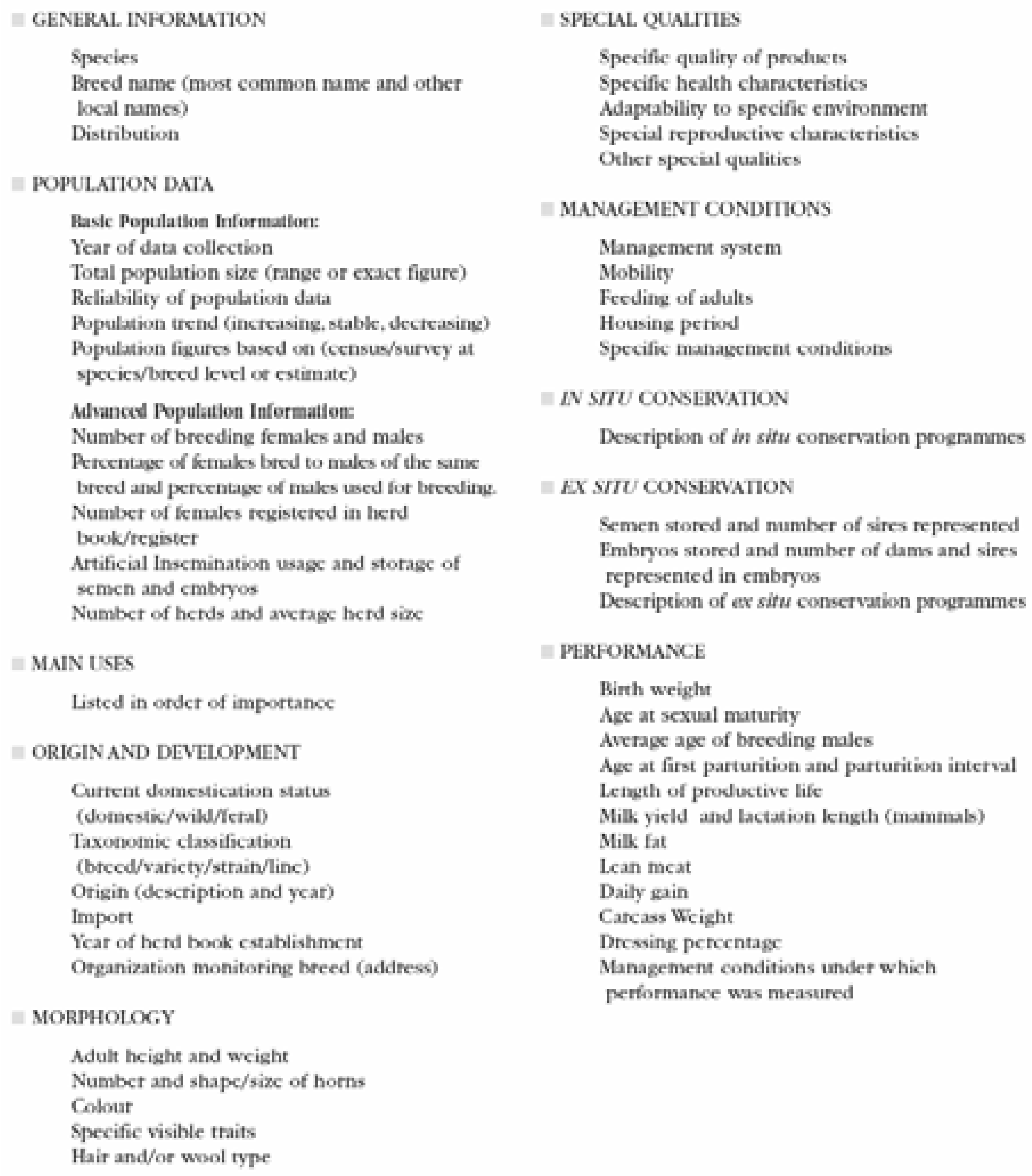
3 Tools for characterization

3.1 Surveying

Surveys are undertaken to systematically collect data needed to identify breed populations and describe their observable characteristics, geographical distribution, uses and general husbandry, as well as their production environments. Full baseline surveys need to be undertaken once; some elements of the survey may be repeated when significant changes are observed in the livestock sector.

As part of the effort to develop global databanks for the management of AnGR, FAO developed a comprehensive list of animal and environment descriptors to serve as a guide for standardized characterization activities at various levels (FAO, 1986a,b,c). However, these descriptors were far too complex for universal application. In recognition of this fact, FAO developed simplified formats for data collection for mammalian and avian species (see summary of data items in Tables 97 and 99). This was based on the experience of the EAAP, which started collecting data in the 1980s and later built the first computer-based information system known as EAAP–AGDB. ILRI, in collaboration with FAO (Rowlands *et al*., 2003) has developed and tested an approach for collecting and analysing on-farm breed-level information in Zimbabwe. The same approach has been applied in Ethiopia. A key lesson from this work was that logistic and time requirements for extensive livestock surveys, data management and analysis, can be grossly underestimated. It was also found that the outcomes of multivariate survey techniques need to be verified by complementary molecular genetic studies (Ayalew *et al*., 2004).

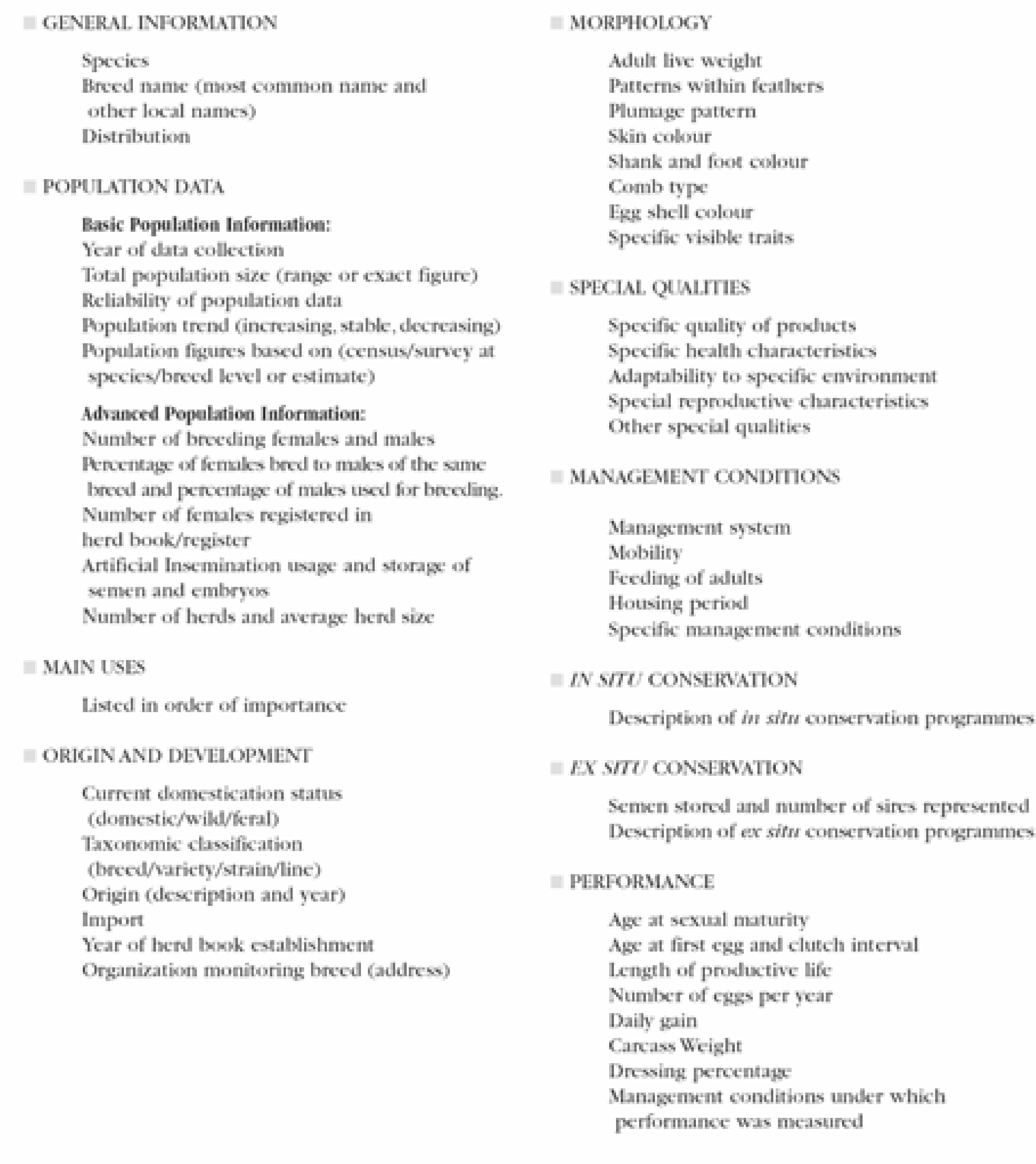
Table 97
Information recorded for mammalian species in the Global Databank for Animal Genetic Resources



- GENERAL INFORMATION
  - Species
  - Breed name (most common name and other local names)
  - Distribution
- POPULATION DATA
  - **Basic Population Information:**
  - Year of data collection
  - Total population size (range or exact figure)
  - Reliability of population data
  - Population trend (increasing, stable, decreasing)
  - Population figures based on (census/survey at species/breed level or estimate)
  - **Advanced Population Information:**
  - Number of breeding females and males
  - Percentage of females bred to males of the same breed and percentage of males used for breeding.
  - Number of females registered in herd book/register
  - Artificial Insemination usage and storage of semen and embryos
  - Number of herds and average herd size
- MAIN USES
  - Listed in order of importance
- ORIGIN AND DEVELOPMENT
  - Current domestication status (domestic/wild/feral)
  - Taxonomic classification (breed/variety/strain/line)
  - Origin (description and year)
  - Import
  - Year of herd book establishment
  - Organization monitoring breed (address)
- MORPHOLOGY
  - Adult height and weight
  - Number and shape/size of horns
  - Colour
  - Specific visible traits
  - Hair and/or wool type
- SPECIAL QUALITIES
  - Specific quality of products
  - Specific health characteristics
  - Adaptability to specific environment
  - Special reproductive characteristics
  - Other special qualities
- MANAGEMENT CONDITIONS
  - Management system
  - Mobility
  - Feeding of adults
  - Housing period
  - Specific management conditions
- *IN SITU* CONSERVATION
  - Description of *in situ* conservation programmes
- *EX SITU* CONSERVATION
  - Semen stored and number of sires represented
  - Embryos stored and number of dams and sires represented in embryos
  - Description of *ex situ* conservation programmes
- PERFORMANCE
  - Birth weight
  - Age at sexual maturity
  - Average age of breeding males
  - Age at first parturition and parturition interval
  - Length of productive life
  - Milk yield and lactation length (mammals)
  - Milk fat
  - Lean meat
  - Daily gain
  - Carcass Weight
  - Dressing percentage
  - Management conditions under which performance was measured

Source: FAO/UNEP (2000)

Table 98
Information recorded for avian species in the Global Databank for Animal Genetic Resources



- GENERAL INFORMATION
  - Species
  - Breed name (most common name and other local names)
  - Distribution
- POPULATION DATA

  Basic Population Information:
  - Year of data collection
  - Total population size (range or exact figure)
  - Reliability of population data
  - Population trend (increasing, stable, decreasing)
  - Population figures based on (census/survey at species/breed level or estimate)

  Advanced Population Information:
  - Number of breeding females and males
  - Percentage of females bred to males of the same breed and percentage of males used for breeding.
  - Number of females registered in herd book/register
  - Artificial Insemination usage and storage of semen and embryos
  - Number of herds and average herd size
- MAIN USES
  - Listed in order of importance
- ORIGIN AND DEVELOPMENT
  - Current domestication status (domestic/wild/feral)
  - Taxonomic classification (breed/variety/strain/line)
  - Origin (description and year)
  - Import
  - Year of herd book establishment
  - Organization monitoring breed (address)
- MORPHOLOGY
  - Adult live weight
  - Patterns within feathers
  - Plumage pattern
  - Skin colour
  - Shank and foot colour
  - Comb type
  - Egg shell colour
  - Specific visible traits
- SPECIAL QUALITIES
  - Specific quality of products
  - Specific health characteristics
  - Adaptability to specific environment
  - Special reproductive characteristics
  - Other special qualities
- MANAGEMENT CONDITIONS
  - Management system
  - Mobility
  - Feeding of adults
  - Housing period
  - Specific management conditions
- *IN SITU* CONSERVATION
  - Description of *in situ* conservation programmes
- *EX SITU* CONSERVATION
  - Semen stored and number of sires represented
  - Description of *ex situ* conservation programmes
- PERFORMANCE
  - Age at sexual maturity
  - Age at first egg and clutch interval
  - Length of productive life
  - Number of eggs per year
  - Daily gain
  - Carcass Weight
  - Dressing percentage
  - Management conditions under which performance was measured

Source: FAO/UNEP (2000)

Based on the Global Strategy for the Management of AnGR, ten categories of variables are covered in AnGR surveys, including basic and advanced breed population information, main uses of the breed, origin and development/evolution of the breed, typical morphological features, average performance levels, special characteristics, and ongoing conservation activities.

3.2 Monitoring

Changes in population size and structure need to be documented regularly for all breeds. This should be carried out on a yearly or biennial basis, as the application of modern reproductive technologies, global trade, market demands, and policies favouring particular breeds, can lead to rapid changes in the size and structure of breed populations.

Monitoring should be conducted at least once per generation of the species, particularly for breeds classified as at risk or potentially at risk. This requires surveys at intervals of about eight years for horses and donkeys, five years for cattle, buffalo, sheep and goats, three years for pigs and two years for poultry species.

At present, most national livestock censuses do not contain breed-level data, and so regular reporting of breed population numbers does not take place. Species and breeds that have been classified as at risk should be monitored on a regular basis. This monitoring should serve as the basis for national early warning.

Information collected during monitoring activities enables adjustments to be made to management plans for AnGR. Monitoring programmes need to be carefully designed so that they provide feedback to farmers, managers and other stakeholders. Monitoring approaches need to be flexible, and activities by different players need to be well coordinated, as different groups will monitor different parameters. For example, farmers may wish to monitor production parameters; resource managers may wish to monitor completion of breed inventories; and administrators may wish to monitor the cost-effectiveness of various programmes. Monitoring is also necessary to evaluate progress in the implementation of action plans, and to identify new priorities, issues and opportunities.

Monitoring can be an extremely expensive aspect of AnGR management. However, if countries are strategic in their approaches to monitoring, and take advantage of existing resources, it can be cost effective. For managing genetic resources at high risk, data on current population size and geographic location are required. For such populations, regular and simple quantification and reporting of actual population sizes by those directly involved may be adequate and achievable. Large and widely dispersed populations may require the establishment of stratified samples, where a portion of the population in each major geographical region of the country is monitored. Lack of easy-to-apply tools for collecting such data, general lack of trained persons to undertake assessments, and lack of awareness on the part of policy-makers and implementers regarding the importance of such information, represent important challenges.

In every country there may be opportunities to monitor AnGR by taking advantage of existing activities, and thereby avoiding significant additional costs. National livestock censuses offer good opportunities. It may also be possible to set up effective monitoring stations in locations where livestock are sold or traded, such as auctions and local markets. This approach can greatly reduce costs by bringing the livestock to the monitors. However, a focus on traded animals may not accurately reflect the structure of the target populations on the farms. In countries where farmer groups, breed societies, or herd or stud books exist, tracking registrations can be a very effective means to monitor particular breeds. There may also be opportunities to combine monitoring activities with the tasks of existing government offices. For example, wildlife biologists could assist in monitoring livestock populations as part of wildlife surveys. Health officials could record livestock population numbers by breed when conducting food-processing inspections or delivering veterinary services. All these options, however, have to be treated with caution and potential biases need to be considered. The value of the information obtainable on the basis of existing activities has to be weighed against the additional information, but also greater costs, associated with surveys specifically designed and conducted to monitor AnGR.

As a step towards the inclusion of breed-level data in national livestock censuses, the next World Programme for Census of Agriculture (produced by FAO every ten years to guide countries in conducting of their agricultural census) (FAO, 2006) encourages countries to collect and report livestock data at breed level.

3.3 Molecular genetic characterization

Molecular genetic characterization explores polymorphism in selected protein molecules and DNA markers in order to measure genetic variation at the population level. Because of the low level of polymorphism observed in proteins, and hence limited applicability in diversity studies, DNA-level polymorphisms are the markers of choice for molecular genetic characterization (see Section C).

The process of molecular genetic characterization comprises field sampling of biological material (often blood or hair root samples), laboratory extraction of DNA from the samples, DNA storage, laboratory assaying (e.g. genotyping or sequencing), data analysis, report writing, and maintenance of a molecular genetic information database. Sampling for molecular analysis may be combined with surveying and/or monitoring, as molecular information on its own cannot be used for utilization and conservation decisions.

Characterization at the molecular genetic level is undertaken mainly to explore genetic diversity within and between animal populations, and to determine genetic relationships among such populations. More specifically, the results from the laboratory work are used to:

- determine within and between-breed diversity parameters;
- identify the geographical locations of particular populations, and/or of admixture among populations of different genetic origins;
- provide information on evolutionary relationships (phylogenetic trees) and clarify centres of origin and migration routes;
- implement gene mapping activities, including identification of carriers of known genes;
- identify parentage and genetic relationships (e.g. DNA fingerprinting) within populations;
- support marker assisted genetic improvement of animal populations; and
- develop DNA repositories for research and development (Hanotte and Jianlin, 2005).
- In populations with limited or no information on pedigrees and population structure, molecular markers can also be used to estimate the effective population size (N_e).

In the absence of comprehensive breed characterization data and documentation of the origin of breeding populations, molecular marker information may provide the most easily obtainable estimates of genetic diversity within and between a given set of populations.

3.4 Information systems

Information systems or databases can serve a variety of different purposes, but collectively they contain important information for decision-making, research, training, planning and evaluation of programmes, progress reporting and public awareness. An information system normally includes hardware, software (applications), organized data (information) and facilities for communication. It can be operated either manually, electronically using computers, or through a combination of both. The information may be on a single desktop machine, or a network of computers. Alternatively, it may be on the Internet, allowing external access to view or, in case of interactive dynamic systems, update the information.

The overall purpose of information systems is to enable and support decision-making regarding the present value and potential future uses of AnGR, by a range of stakeholders, including policy-makers, development practitioners, farmers and researchers. Thus, they need to incorporate essential decision-support tools to meet the needs of stakeholders at subnational, national, subregional, regional and global levels. However, users operating at these different hierarchies or levels will each have different objectives, and be interested in different aspects of the data contained within the information system. For instance, users operating at regional or global levels will be more interested in the cross-border distribution of breeds, cross-border livestock markets, transboundary disease risks, and germplasm exchange across borders. Conversely, more relevant issues for users at national and subnational (local) levels are breed population size, herd/flock structures, production levels, and stressors associated with local environments. Linkages and information exchange between the hierarchies, as well as with external information sources can add value to information systems. Complementary databases may exchange information through a system of data transfer, or can serve as “gateways” to each other through electronic links via the Internet. For instance, national and subnational AnGR databases could be linked to geophysical databases (climate, soils, water or landscape). Functional linkages between these sets of data could lead to the generation of animal disease risk maps, and information on specific adaptations of particular breeds to stressful environments.

National databases of domestic animal diversity are essential planning tools. They present the current state of knowledge on the size, distribution, status, and utility value of AnGR. They allow access to information on planned and ongoing management activities. Moreover, they facilitate the identification of gaps in existing information.

At present, a number of public-domain electronic information systems for animal genetic diversity are globally accessible and contain data from more than one country. Two of these – DAD-IS and EFABIS (previously EAAP–AGDB) are related to the FAO global information system for AnGR. The Domestic Animal Genetic Resources Information System (DAGRIS), managed by ILRI is a database of synthesized research information from published and grey literature. Oklahoma State University’s Breeds of Livestock information system provides brief summaries of breed origins, characteristics and uses. The content of these information systems is described in Box 69.

Currently, the information resources have facilities for simple searches by country or breed only. Ideally, they should have as much research information as is available, and enable users to make informed judgements about the value of each item of information. If researchers and decision-makers are to have the information they require, the functionality of the existing information systems will need to be greatly increased, to allow extraction and customized analysis of various categories of information within and between data sources. The scope of data acquisition also needs to be expanded so that breed information can be linked to geographical information system (GIS)-based environment and production system mapping. This will allow poorly documented adaptation traits such as disease resistance to be predicted from past and current breed distribution and use (Gibson *et al*., 2007).

Information systems for AnGR have been developed and administered as global public goods, and have limited ability to attract investment from the private sector or major funding agencies. This explains the very limited information that the systems contain compared to that which is potentially possible and which would be necessary for them to effectively achieve their stated purposes. One possibility to circumvent such limitations is to establish functionalities for interconnectivity and interoperability between information systems. This has been achieved with FABISnet (a distributed information system for AnGR) which enables countries to set up national Web-based information systems that can exchange core data with the higher levels of the network – regional systems (such as EFABIS) and the global system (DAD-IS).

Box 69
Information systems at global level

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

The Domestic Animal Diversity Information System (DAD-IS) developed by FAO is the first globally accessible dynamic multilingual database of AnGR. It was initiated as a key communication and information tool for implementing the Global Strategy for the Management of AnGR, to assist countries and country networks in their respective programmes (FAO, 1999). Apart from country-level breed information and images, DAD-IS provides a virtual library containing a large number of selected technical and policy documents, including tools and guidelines for research related to AnGR. It offers Web-links to relevant electronic information resources. It also has a facility for the exchange of views and for addressing specific information requests, by linking a range of stakeholders: farmers, scientists, researchers, development practitioners and policy-makers.

DAD-IS provides a summary of national breed-level information on the origin, population, risk status, special characteristics, morphology and performance of breeds, as provided by FAO member countries. Currently, the database contains more than 14 000 national breed populations from 35 species and 181 countries. A key feature of DAD-IS is that it provides a country-secure information storage and communication tool. Each country decides when and what breed data are released through their officially designated contact person (the National Coordinator (NC) for the Management of AnGR). See Tables 97 and 98 for a summary of information recorded, stored and disseminated in the global breeds database contained in DAD-IS.

DAD-IS:3 has been rebuilt based on the same software and functionality as EFABIS (European Farm Animal Biodiversity Information System – http://efabis-eaap.tzv.fal.de), and with a similar interface. The software was developed within a European Union project in order to overcome the problem of incompatibility between EAAP–AGDB and DAD-IS. The new system allows for the creation of a network of distributed information systems with automatic data synchronization. Countries and regions are provided with tools to set up their own Web-based information systems. Information content and interface can be translated to any local language. The appearance of the interface can be adapted to reflect local flavours. Outside the core data structure, countries and regions may further define data structures that specifically reflect their needs. These specificities would not be synchronized with the higher-level information systems. Poland set up the first national information system under this new framework (http://efabis.izoo.krakow.pl), and defined additional structures to accommodate data on farmed fish and bees. NCs can enter breed information, images, publications, links to external Web sites, contact addresses and news into the system.

DAGRIS [http://dagris.ilri.cgiar.org/]

The Domestic Animal Genetic Resources Information System (DAGRIS) is developed and managed by the International Livestock Research Institute (ILRI). It was initiated in 1999 as a tool to collate research information available on global AnGR. In addition to containing information, obtained from a synthesis of the literature, on the origin, distribution, diversity, characteristics, present uses and status of indigenous breeds, DAGRIS is unique in that it includes complete references and abstracts of published or unpublished scientific literature pertaining to the breeds in the system. DAGRIS is designed to support research, training, public awareness, genetic improvement and conservation. Version I of the database was released on the Web in April 2003, and is also available on CD-ROM. Currently, the database contains over 19 200 trait records on 154 cattle, 98 sheep, and 62 goat breeds of Africa, plus 129 chicken ecotypes/breeds and 165 pig breeds of Africa and some Asian countries. The breed information pages in DAGRIS provide a Web link to the page for the corresponding breed in the FAO's DAD-IS system and vice versa.

The scope of DAGRIS is being expanded so that it will, in the near future, cover more species (turkeys, geese and ducks) and countries in Asia (Ayalew *et al.*, 2003). The priority next-steps for DAGRIS are: 1) development of a new module to allow all users to upload relevant research information into the database so that database administrators can capture and collate otherwise unavailable breed-level information; 2) development of GIS linkages in the database to allow georeferencing of as much of the breed-level information as possible; and 3) development of a template for a country module of DAGRIS to assist interested countries to further develop and customize the database.

Breeds of Livestock – Oklahoma State University [http://www.ansi.okstate.edu/breeds]

The Department of Animal Science of Oklahoma State University, in the United States of America, manages this information resource established in 1995. It provides a brief description of breeds in terms of origin, distribution, typical features, uses, and population status, along with photographs/images and key references for breed information. It presents a list of breeds from all over the world, with options to sort by region. As of January 2006, the database displayed a total of 1 063 breeds including 280 sheep, 262 cattle, 217 horse, 100 goat, 72 pig, 8 donkey, 8 buffalo, 6 camel, 4 reindeer, 1 llama, 1 yak, 64 chicken, 10 duck, 7 turkey, 7 goose, 1 guinea fowl and 1 black swan breeds. It also provides links to relevant information in its virtual livestock library. The aim is to expand the scope of the system, in terms of the number of breeds and the educational and scientific information it contains, through collaboration with individuals and universities from around the world. The submission of information (written material or images) on breeds not included in the list, or additional information on those already included, is welcome.

4 Conclusions

Adequate characterization of AnGR is a prerequisite for successful management programmes and for informed decision-making in national livestock development. Tools developed in the field of characterization should allow a strategic and coherent approach to identification, description and documentation of breed populations. Interest in such an approach is slowly emerging. Some aspects of characterization are increasingly being addressed. Molecular characterization has received particular attention. However, there is still a need for methods and tools to organize surveying and monitoring.

An important missing element in breed descriptions in many countries/regions, is a clear definition of the respective breeds to give them unique identity, and a description of the production environments to which they are adapted. A basic structure for the definition of production environments has been proposed, but needs to be reviewed and implemented. The existing breed-related information systems need to be further developed to allow easy information capture, processing, accessibility and interconnectivity.

Ideally, tools and methods for decision-making on AnGR management, as well as early warning and response tools, would be based on comprehensive information obtained using the methods described above. However, given that immediate action is required, there is a need for tools and methods that make effective use of incomplete information.

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SECTION C: MOLECULAR MARKERS – A TOOL FOR EXPLORING GENETIC DIVERSITY

DNA markers are useful in both basic (e.g. phylogenetic analysis and search for useful genes) and applied research (e.g. marker assisted selection, paternity testing and food traceability). This section focuses mainly on their application in characterization of AnGR diversity, and in the search for functional variants of relevant genes. It is important to note that RNA and proteins also contain key information, and therefore deserve parallel study; their role in the search for functional variants is also explored below.

1 Introduction

Diversity among organisms is a result of variations in DNA sequences and of environmental effects. Genetic variation is substantial, and each individual of a species, with the exception of monozygotic twins, possesses a unique DNA sequence. DNA variations are mutations resulting from substitution of single nucleotides (single nucleotide polymorphisms – SNPs), insertion or deletion of DNA fragments of various lengths (from a single to several thousand nucleotides), or duplication or inversion of DNA fragments. DNA variations are classified as "neutral" when they cause no change in metabolic or phenotypic traits, and hence are not subjected to positive, negative, or balancing selection; otherwise, they are referred to as "functional". Mutations in key nucleotides of a coding sequence may change the amino acid composition of a protein, and lead to new functional variants. Such variants may have an increased or decreased metabolic efficiency compared to the original "wild type", may lose their functionality completely, or even gain a novel function. Mutations in regulatory regions may affect levels and patterns of gene expression; for example, turning genes on/off or under/over-expressing proteins in specific tissues at different development or physiological stages.

Box 70
DNA, RNA and protein

DNA (deoxyribonucleic acid) is organized in pairs of chromosomes, each inherited from one of the parents. Each gene in an individual, therefore, has two copies, called alleles, one on each chromosome of a pair. In mammals, genes are scattered along chromosomes, separated by long, mainly repetitive, DNA sequences. Genes are formed by coding sequences (exons) separated by introns. The latter carry no protein coding information, but sometimes play a role in the regulation of gene expression. The instruction encoded by genes is put into action through two processes. The first is transcription (copy) of genetic information into another type of nucleic acid, RNA (ribonucleic acid). Both exons and introns are transcribed into a primary messenger RNA (mRNA) molecule. This molecule is then edited, a process which involves removing the introns, joining the exons together, and adding unique features to each end of the mRNA. A mature mRNA molecule is, thereby, created, which is then transported to structures known as ribosomes located in the cell cytoplasm. Ribosomes are made of ribosomal RNA (rRNA) and proteins, and provide sites for the second process – translation of the genetic information, previously copied to the mRNA, into a polypeptide (an entire protein or one of the chains of a protein complex). The mRNA molecule is read or translated three nucleotides (a codon) at a time. Complementarity between the mRNA codon and the anti-codon of a transfer RNA (tRNA) molecule which carries the corresponding amino acid to the ribosome ensures that the newly formed polypeptide contains the specific sequence of amino acids required.

Not all genes are translated into proteins; some express their function as RNA molecules (such as the rRNA and tRNA involved in translation). Recently, new roles of RNA in the process of mRNA editing and in the regulation of gene expression have been discovered (Storz *et al*., 2005; Aravin and Tuschl, 2005; Wienholds and Plasterk 2005). Indeed, non-coding RNAs appear to be key players in various regulatory processes (Bertone *et al*., 2004; Clop *et al*., 2006). Thus, three types of molecules are available for investigating genetic characteristics at cellular, tissue and whole organism levels: the DNA which contains the encoded instruction; the RNA which transfers the instructions to the cell "factory"; and the proteins which are built according to the instructions, and make functioning cells and organisms.

Although analysis of single types of biomolecules has proven extremely useful in understanding biological phenomena, the parallel large-scale investigation of DNA, RNA and proteins opens up new perspectives in the interpretation and modelling of the complexity of living organisms. New scientific disciplines with the suffix "–omics" are coming into existence. In these fields, recent advances in the preparation, identification and sequencing of DNA, RNA and proteins, and in large-scale data storage and analysis, are bringing about a revolution in our understanding. A global, integrated view of an entire set of biological molecules involved in complex biological processes is emerging. Structural genomics, transcriptomics and proteomics are followed by metabolomics, and interactomics among others, and at a still higher level of complexity, systems biology (Hood *et al*., 2004; Box 71).

Box 71
The new "–omics" scientific disciplines

Genomics charts genes and the genetic variations among individuals and groups. It provides an insight into the translation of genetic information to metabolic functions and phenotypic traits. It unveils biological processes and their interactions with environmental factors. Genomics involves the combination of a set of high-throughput technologies, such as proteomics and metabolomics, with the bioinformatic techniques that enable the processing, analysis and integration of large amounts of data.

Investigation of biological complexity is a new frontier which requires high-throughput molecular technology, high computer speed and memory, new approaches to data analysis, and integration of interdisciplinary expertise (Box 72).

Box 72
Recent developments in molecular biology

Current revolutionary developments in molecular biological research relevant to livestock breeding and genetic diversity conservation include: 1. establishment of the entire genome sequence of the most important livestock species; 2. development of technology to measure polymorphisms at loci spread all over the genome (e.g. methods to detect SNPs); and 3. development of microarray technology to measure gene transcription at a large scale. Information obtained through the sequencing of the entire genome (achieved for chickens and almost complete for pigs and cattle), integrated with SNP technology, will speed up the search for genes. Quantitative trait loci (QTL) mapping to identify chromosome regions influencing a target trait, the presence of candidate genes located in the same region, and investigation of their patterns of expression (e.g. by microarray and proteomic analyses) and their function across species, will come together to identify key genes and to unravel the complexity of physiological regulation for target traits.

See below for further discussion of these developments

2 The roles of molecular technologies in characterization

Information on genetic diversity is essential in optimizing both conservation and utilization strategies for AnGR. As resources for conservation are limited, prioritization is often necessary. New molecular tools hold the promise of allowing the identification of genes involved in a number of traits, including adaptive traits, and polymorphisms causing functional genetic variation (QTN – Quantitative Trait Nucleotides). However, we do not have sufficient knowledge to prioritize conservation choices on the basis of functional molecular diversity, and alternative measures are still needed. Phenotypic characterization provides a crude estimate of the average of the functional variants of genes carried by a given individual or population. However, the majority of phenotypes of the majority of livestock species are not recorded.

First role: In the absence of reliable phenotype and QTN data, or to complement the existing data, the most rapid and cost-effective measures of genetic diversity are obtained from the assay of polymorphisms using anonymous molecular genetic markers. Anonymous markers are likely to provide indirect information on functional genes for important traits, assuming that unique populations that have had a particular evolutionary history at the neutral markers (e.g. because of ancient isolation or independent domestication) are likely to carry unique variants of functional variations. Molecular techniques have also proved useful in the investigation of the origin and domestication of livestock species, and their subsequent migrations, as well as providing information on evolutionary relationships (phylogenetic trees), and identifying geographical areas of admixture among populations of different genetic origins. Subchapter 3.1 presents an outline of molecular techniques for the assessment of genetic diversity within and between breeds.

Second role: Effective population size (N_e) is an index that estimates the effective number of animals in a population that reproduce and contribute genes to the next generation. N_e is closely linked to the level of inbreeding and genetic drift in a population, and therefore is a critical indicator for assessing the degree of endangerment of populations (see Sections A and F). Traditional approaches to obtaining reliable estimates of N_e for breeding populations are based on pedigree data or censuses. The necessary data on variability of reproductive success and generation intervals are often not reliably available for populations in developing countries. Molecular approaches may, therefore, be a promising alternative (see subchapter 3.2 for further details).

Third role: A top priority in the management of AnGR is the conservation of breeds that have unique traits. Among these, the ability to live and produce in challenging conditions, and to resist infectious diseases are of major importance, particularly for developing countries. Complex traits, such as adaptation and disease resistance, are not visible or easily measurable. They can be investigated in experiments in which the animals are submitted to the specific environmental conditions or are infected with the relevant agent. However, such experiments are difficult and expensive to perform, and raise concerns about animal welfare. This is the reason why researchers are extremely interested in identifying genes controlling complex traits. Such genes can be sought by a number of different approaches. Tools being developed by modern research are described in subchapter 3.3.

3 Overview of molecular techniques

This section describes the most important molecular techniques currently being utilized and developed for the assessment of genetic diversity, and for targeting functional variation. Box 73 describes how DNA and RNA are extracted from biological material and prepared for analysis. The attributes of commonly used molecular markers are outlined in Box 74, and sampling (a very important aspect of molecular studies) is discussed in Box 75.

Box 73
Extraction and multiplication of DNA and RNA

The first step in DNA, RNA and protein analysis is extraction and purification from biological specimens. Several protocols and commercial kits are available. The strategies applied depend on the source material and the target molecule. For example, DNA extraction from whole blood or white cells is relatively easy, while its extraction from processed food is rather difficult. RNA extraction from pancreatic tissue is difficult because of very rapid post-mortem degradation in this organ. Purity of DNA, RNA and proteins is often a key neglected factor in obtaining reliable results. After isolating DNA (or RNA) from cells, the next step is to obtain thousands or millions of copies of a particular gene or piece of DNA. DNA fragment multiplication can be delegated to micro-organisms, typically *E. coli*, or accomplished *in vitro* using a polymerase chain reaction (PCR). This technique, which won the Nobel Prize for its inventor, Cary Mullis, exponentially amplifies any DNA segment of known sequence. The key component in a PCR reaction is the DNA polymerase isolated from *Thermus aquaticus*, a micro-organism adapted to live and multiply at very high temperature. This thermostable *Taq*- (after *Thermus aquaticus*) polymerase permits chain replication in cycles and produces a geometric growth in the number of copies of the target DNA. A PCR cycle includes three steps: i) DNA denaturation at 90–95 °C to separate the DNA into two single strands to serve as a template; ii) annealing of a pair of short single-strand oligonucleotides (primers) complementary to the target regions flanking the fragment of interest, at 45–65 °C; iii) extension or elongation of newly synthesized DNA strands led by primers and facilitated by the *Taq*-polymerase, at 72 °C. This cycle can be repeated, normally 25 to 45 times, to enable amplification of enough amplicons (a fragment of a gene or DNA synthesized using PCR) to be detected.

Protein polymorphisms were the first markers used for genetic studies in livestock. However, the number of polymorphic loci that can be assayed, and the level of polymorphisms observed at the loci are often low, which greatly limits their application in genetic diversity studies. With the development of new technologies, DNA polymorphisms have become the markers of choice for molecular-based surveys of genetic variation (Box 74).

Box 74
Commonly used DNA markers

Restriction fragment length polymorphisms (RFLPs) are identified using restriction enzymes that cleave the DNA only at precise “restriction sites” (e.g. EcoRI cleaves at the site defined by the palindrome sequence GAATTC). At present, the most frequent use of RFLPs is downstream of PCR (PCR–RFLP), to detect alleles that differ in sequence at a given restriction site. A gene fragment is first amplified using PCR, and then exposed to a specific restriction enzyme that cleaves only one of the allelic forms. The digested amplicons are generally resolved by electrophoresis.

Microsatellites or SSR (Simple Sequence Repeats) or STR (Simple Tandem Repeats) consist of a stretch of DNA a few nucleotides long –2 to 6 base pairs (bp) – repeated several times in tandem (e.g. CACACACACACACACA). They are spread over a eukaryote genome. Microsatellites are of relatively small size, and can, therefore, be easily amplified using PCR from DNA extracted from a variety of sources including blood, hair, skin or even faeces. Polymorphisms can be visualized on a sequencing gel, and the availability of automatic DNA sequencers allows high-throughput analysis of a large number of samples (Goldstein and Schlötterer, 1999; Jarne and Lagoda, 1996). Microsatellites are hypervariable; they often show tens of alleles at a locus that differ from each other in the numbers of the repeats. They are still the markers of choice for diversity studies as well as for parentage analysis and Quantitative Trait Loci (QTL) mapping, although this might be challenged in the near future with the development of cheap methods for the assay of SNPs. FAO has published recommendations for sets of microsatellite loci to be used for diversity studies for major livestock species, which were developed by the ISAG–AO Advisory Group on Animal Genetic Diversity (see DAD-IS library http://www.fao.org/dad-is/).

Minisatellites share the same characteristics as microsatellites, but the repeats are ten to a few hundreds bp long. Micro and minisatellites are also known as VNTRs (Variable Number of Tandem Repeats) polymorphisms.

Amplified fragment length polymorphisms (AFLPs) are a DNA fingerprinting technique which detects DNA restriction fragments by means of PCR amplification.

STS (Sequence Tagged Site) are DNA sequences that occur only once in a genome, in a known position. They needn’t be polymorphic and are used to build physical maps.

SNPs are variations at single nucleotides which do not change the overall length of the DNA sequence in the region. SNPs occur throughout the genome. They are highly abundant and are present at one SNP in every 1000 bp in the human genome (Sachinandam *et al*., 2001). Most SNPs are located in non-coding regions, and have no direct impact on the phenotype of an individual. However, some introduce mutations in expressed sequences or regions influencing gene expression (promoters, enhancers), and may induce changes in protein structure or regulation. These SNPs have the potential to detect functional genetic variation.

Box 75
Sampling genetic material

Sample collection is the first and the most important step in any diversity study. Ideally, samples should be unrelated and representative of the populations under investigation. Generally, the sampling of 30 to 50 well-chosen individuals per breed is considered sufficient to provide a first clue as to breed distinctiveness and within-breed diversity, if a sufficient number of independent markers is assayed (e.g. 20–30 microsatellites; Nei and Roychoudhury, 1974; Nei, 1978). However, the actual numbers required may vary from case to case, and may be even lower in the case of a highly inbred local population, and higher in a widely spread population divided into different ecotypes.

The choice of unrelated samples is quite straightforward in a well-defined breed, where it can be based on the herd book or pedigree record. Conversely, it can be rather difficult in a semi-feral population for which no written record is available. In this case, the use of a geographic criterion is highly recommendable, i.e. to collect a single or very few (unrelated) animals per flock from a number of flocks spread over a wide geographic area. The record of geographical coordinates, and photo-documentation of sampling sites, animals and flocks is extremely valuable – to check for cross-breeding in the case of unexpected outliers, or for identifying interesting geographic patterns of genetic diversity. A well-chosen set of samples is a long-lasting valuable resource, which can be used to produce meaningful results even with poor technology. Conversely, a biased sample will produce results that are distorted or difficult to understand even if the most advanced molecular tools are applied.

3.1 Techniques using DNA markers to assess genetic diversity

Nuclear DNA markers

A number of markers are now available to detect polymorphisms in nuclear DNA. In genetic diversity studies, the most frequently used markers are microsatellites.

Microsatellites

Currently, microsatellites (Box 74) are the most popular markers in livestock genetic characterization studies (Sunnucks, 2001). Their high mutation rate and codominant nature permit the estimation of within and between-breed genetic diversity, and genetic admixture among breeds even if they are closely related.

Some controversy has surrounded the choice of a mutation model – infinite allele or step-wise mutation model (Goldstein *et al*, 1995) – for microsatellite data analysis. However, simulation studies have shown that the infinite allele mutation model is generally valid for assessment of within-species diversity (Takezaki and Nei, 1996).

The mean number of alleles (MNA) per population, and observed and expected heterozygosity (Ho and He), are the most common parameters for assessing within-breed diversity. The simplest parameters for assessing diversity among breeds are the genetic differentiation or fixation indices. Several estimators have been proposed (e.g. F_{ST} and G_{ST}), the most widely used being F_{ST} (Weir and Basten, 1990), which measure the degree of genetic differentiation of subpopulations through calculation of the standardized variances in allele frequencies among populations. Statistical significance can be calculated for the F_{ST} values between pairs of populations (Weir and Cockerham, 1984) to test the null hypothesis of a lack of genetic differentiation between populations and, therefore, the partitioning of genetic diversity (e.g. Mburu *et al.*, 2003). Hierarchical analysis of molecular variance (AMOVA) (Excoffier *et al.*, 1992) can be performed to assess the distribution of diversity within and among groups of breeds.

Microsatellite data are also commonly used to assess genetic relationships between populations and individuals through the estimation of genetic distances (e.g. Beja-Pereira *et al.*, 2003; Ibeagha-Awemu *et al.*, 2004; Joshi *et al.*, 2004; Sodhi *et al.*, 2005; Tapio *et al.*, 2005). The most commonly used measure of genetic distances is Nei's standard genetic distance (D_S) (Nei, 1972). However, for closely related populations, where genetic drift is the main factor of genetic differentiation, as is often the case in livestock breeds, particularly in the developing world, the modified Cavalli-Sforza distance (D_A) is recommended (Nei *et al.*, 1983). Genetic relationship between breeds is often visualized through the reconstruction of a phylogeny, most often using the neighbour-joining (N-J) method (Saitou and Nei, 1987). However, a major drawback of phylogenetic tree reconstruction is that the evolution of lineages is assumed to be non-reticulate, i.e. lineages can diverge, but can never result from crosses between lineages. This assumption will rarely hold for livestock, where new breeds often originate from cross-breeding between two or more ancestral breeds. The visualization of the evolution of breeds provided by phylogenetic reconstruction must, therefore, be interpreted cautiously.

Multivariate analysis, and more recently Bayesian clustering approaches, have been suggested for admixture analysis of microsatellite data from different populations (Pritchard *et al.*, 2000). Probably the most comprehensive study of this type in livestock is a continent-wide study of African cattle (Hanotte *et al.*, 2002), which reveals the genetic signatures of the origins, secondary movements, and differentiation of African cattle pastoralism.

Molecular genetic data, in conjunction with, and complemented by, other sources such as archaeological evidence and written records, provide useful information on the origins and subsequent movements and developments of genetic diversity in livestock species. Mapping the origin of current genetic diversity potentially allows inferences to be made about where functional genetic variation might be found within a species for which only limited data on phenotypic variation exist.

Combined analysis of microsatellite data obtained in separate studies is highly desirable, but has rarely been possible. This is because most population genetic studies using DNA markers are limited to small numbers of breeds, often from a single country (Baumung *et al*., 2004). Often, different subsets of the FAO-recommended markers are used, and no standard samples are genotyped across projects. The application of different microsatellite genotyping systems causes variation between studies in the estimated size of alleles at the same loci. To promote the use of common markers, FAO is now proposing an updated, ranked list of microsatellite loci for the major livestock species.[3] FAO recommends the use of the markers in the order of ranking, to maximize the number of markers overlapping among independent investigations. For some species, DNA from standard animals is available. For example, aliquots of sheep and goat standard DNA used in the European Union (EU) Econogene project have been distributed to other large-scale projects in Asia and Africa, and can be requested through the Econogene Website (http://www.econogene.eu).

There are only a few examples of large-scale analyses of the genetic diversity of livestock species. Hillel *et al*. (2003) and SanCristobal *et al*. (2006a) investigated, respectively, chicken and pig diversity throughout Europe; Hanotte *et al*. (2002) obtained data on cattle at the scale of almost the entire African continent; Tapio *et al*. (2005) assessed sheep diversity at a large regional scale in northern European countries; and Cañon *et al*. (2006) studied goat diversity in Europe and the Near and Middle East. However, for most species, a comprehensive review is still lacking. Ongoing close coordination between large-scale projects promises the delivery of a global estimate of genetic diversity in the near future for some species such as sheep and goats. In the meantime, new methods of data analysis are being developed to permit the meta-analysis of datasets that have only a few breeds and no, or only a few, markers in common (Freeman *et al*., 2006). This global perspective on livestock diversity will be extremely valuable to reconstruct the origin and history of domestic animal populations and, indirectly, of human populations. It will also highlight regional and local hotspots of genetic diversity which may be targeted by conservation efforts.

SNPs

SNPs (Box 74) are used as an alternative to microsatellites in genetic diversity studies. Several technologies are available to detect and type SNP markers (see Syvänen, 2001, for a review). Being biallelic markers, SNPs have rather low information content, and larger numbers have to be used to reach the level of information obtained from a standard panel of 30 microsatellite loci. However, ever-evolving molecular technologies are increasing automation and decreasing the cost of SNP typing. This is likely, in the near future, to permit the parallel analysis of a large number of markers at a lower cost. With this perspective, large-scale projects are ongoing in several livestock species to identify millions (e.g. Wong *et al*., 2004) and validate several thousands of SNPs, and identify haplotype blocks in the genome. Like sequence information, SNPs permit a direct comparison and joint analysis of different experiments.

SNPs seem to be appealing markers to apply in the future for genetic diversity studies because they can easily be used in assessing either functional or neutral variation. However, the preliminary phase of SNP discovery or SNP selection from databases is critical. SNPs can be generated through various experimental protocols, such as. sequencing, single-stranded conformational polymorphism (SSCP) or denaturing high-performance liquid chromatography (DHPLC), or *in silico*, aligning and comparing multiple sequences of the same region from public genome and expressed sequence (EST) databases. When data have not been obtained randomly, standard estimators of population-genetic parameters cannot be applied. A frequent example is when SNPs initially identified in a small sample (panel) of individuals are then typed in a larger sample of chromosomes. By preferentially sampling SNPs at intermediate frequencies, such a protocol will bias the distribution of allelic frequencies compared to the expectation for a random sample. SNPs do hold promise for future application in population genetic analyses; however, statistical methods that can explicitly take into account each method of SNP discovery have to be developed (Nielsen and Signorovitch, 2003; Clark *et al*., 2005).

AFLPs

AFLPs are dominant biallelic markers (Vos *et al*., 1995). Variations at many loci can be arrayed simultaneously to detect single nucleotide variations of unknown genomic regions, in which a given

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[3] Lists and guidelines can be found in the DAD-IS library at http://fao.org/dad-is.

mutation may be frequently present in undetermined functional genes. However, a disadvantage is that they show a dominant mode of inheritance; this reduces their power in population-genetic analyses of within-breed diversity and inbreeding. Nevertheless, AFLP profiles are highly informative in assessing the relationship between breeds (Ajmone-Marsan *et al*., 2002; Negrini *et al*., 2006; De Marchi *et al*., 2006; SanCristobal *et al*., 2006b) and related species (Buntjer *et al*., 2002).

Mitochondrial DNA markers

Mitochondrial DNA (mtDNA) polymorphisms have been extensively used in phylogenetic and genetic diversity analyses. The haploid mtDNA, carried by the mitochondria in the cell cytoplasm, has a maternal mode of inheritance (individuals inherit the mtDNA from their dams and not from their sires) and a high mutation rate; it does not recombine. These characteristics enable evolutionary biologists to reconstruct evolutionary relationships between and within species by assessing the patterns of mutations in mtDNA. MtDNA markers may also provide a rapid way of detecting hybridization between livestock species or subspecies (e.g. Nijman *et al*., 2003).

The polymorphisms in the sequence of the hypervariable region of the D-loop or control region of mtDNA have contributed greatly to the identification of the wild progenitors of domestic species, the establishment of geographic patterns of genetic diversity, and the understanding of livestock domestication (see Bruford *et al*., 2003, for a review). For example, the Middle Eastern origin of modern European cattle was recently demonstrated by Troy *et al.* (2001). The study identified four maternal lineages in *Bos taurus* and also demonstrated the loss of bovine genetic variability during the human Neolithic migration out of the Fertile Crescent. In the same way, multiple maternal origins with three mtDNA lineages were highlighted in goats (Luikart *et al*., 2001), with Asia and the Fertile Crescent as possible centres of origin. Recently, a third mtDNA lineage was discovered in native Chinese sheep (Guo *et al*., 2005), a fourth in native Chinese goats (Chen *et al*., 2005), and a fifth in Chinese cattle (Lai *et al*., 2006). In Asian chickens, nine different mtDNA clades have been found (Liu *et al*., 2006), suggesting multiple origins in South and Southeast Asia. All these results indicate that our current knowledge of livestock domestication and genetic diversity remains far from complete. For further discussion of the origins of domestic livestock species see Part 1 – Section A.

3.2 Using markers to estimate effective population size

Hill (1981) suggested using gametic phase disequilibrium of DNA polymorphisms to estimate effective population size (N_e). This estimation can be based on genotypes for linked markers (microsatellites or SNPs). The expected correlation of allele frequencies at linked loci is a function of N_e and the recombination rate. N_e can, therefore, be estimated from the observed disequilibrium. Hayes *et al.* (2003) suggested a similar approach based on chromosome segment homozygosity, which, in addition, has the potential to estimate N_e for earlier generations, and therefore allows a judgement of whether an existing population was of increasing or decreasing size in the past. The study demonstrated, with example data sets, that the Holstein-Friesian cattle breed underwent a substantial reduction of N_e in the past, while the effective population size of the human population is increasing, which is in agreement with both census and pedigree studies.

3.3 Molecular tools for targeting functional variation

Approaches based on map position: quantitative trait loci (QTL) mapping

Genetic markers behave as Mendelian traits; in other words, they follow the laws of segregation and independent assortment first described by Mendel. Two genes that are located on the same chromosome are physically linked and tend to be inherited together. During meiosis, recombination between homologous chromosomes may break this linkage. The frequency of recombination between two genes located on the same chromosome depends of the distance between them. Recombination rate between markers is, therefore, an indication of their degree of linkage: the lower the recombination rate, the closer the markers. The construction of genetic maps exploits this characteristic to infer the likely order of markers and the distance between them.

Mapping exercises are generally accomplished following the co-segregation of polymorphic markers in structured experimental populations (e.g. F2 or backcross) or existing populations under selection programmes (families of full siblings or half siblings). Medium to high density genetic maps of a few hundred to a few thousand markers are available for most livestock species.

To identify a QTL for a given trait, a family segregating for the trait is genotyped with a set of mapped molecular markers evenly spread over the genome (Box 76). A number of statistical methods exist to infer the presence of a significant QTL at a given marker interval, but all rely on the fact that families possess a high level of linkage disequilibrium, i.e. large segments of chromosomes are transmitted without recombination from parents to progeny.

Box 76
QTL mapping

If a QTL for a target trait exists, the plus- and minus- variant allele of the unknown responsible gene (Q and q) will co-segregate with the alleles at a nearby M1 marker (M1 and m1) that we are able to genotype in the laboratory. Let us, for instance, hypothesize that M1 co-segregates with Q and m1 with q, that is M1 and Q are nearby on a same chromosome and m1 and q on the homologous chromosome (M1Q and m1q).

Let us also assume that an F2 population derived by the mating of heterozygous F1 individuals is genotyped. Following the genotyping, F2 progenies are grouped on the base of their marker genotype (M1M1 and m1m1; M2M2 and m2m2; ... MnMn and mnmn), and afterwards the average phenotype of the groups is compared. If no QTL is linked to a given marker (e.g. M2), then no significant difference will be detected between the average phenotypic value of the M2M2 and m2m2 progenies for the target trait. Conversely, when progenies are grouped by their genotype at the marker M1, then the group M1M1 will mostly be QQ at the QTL, and the group m1m1 will mostly be qq. In this case, a significant difference is observed between progeny averages, and therefore the presence of a QTL is detected. In species, such as poultry and pigs, where lines and breeds are commonly interbred commercially, this exercise can be accomplished in experimental populations (F2, BC) while in ruminants two (daughter design – DD) or three (grand-daughter design – GDD) generation pedigrees are generally used. In DD the segregation of markers heterozygous in a sire (generation I) is followed in the daughters (generation II) on which phenotypic data are collected. In GDD, the segregation of markers heterozygous in a grand-sire (generation I) are followed in his half-sib sons (generation II), whose phenotype is inferred from those of the grand-daughters (generation III).

The result of a QTL mapping experiment is the identification of a chromosome region, often spanning half of a chromosome, in which a significant effect is detected for the target trait. Modern research is actively using mapping to identify QTL influencing adaptive traits. Examples of such traits include, in chickens, increased resistance to Salmonella colonization and excretion (Tilquin *et al*., 2005), and susceptibility to develop pulmonary hypertension syndrome (Rabie *et al*., 2005); and in cattle, trypanotolerance (Hanotte *et al*., 2002).

The QTL mapping phase is generally followed by the refinement of the map position of the QTL (QTL fine mapping). To accomplish this task, additional markers, and above all additional recombination events in the target area, are analysed. A clever approach has recently been designed and applied to the fine mapping of a chromosome region on BTA14 carrying a significant QTL for milk fat percentage and other traits (Farnir *et al*., 2002). This approach exploits historical recombination in past generations to restrict the map position to a relatively small 3.8 cM (centimorgan) region, a size that has permitted the positional cloning of the gene (DGAT1) (Grisart *et al*., 2002).

Following fine mapping, the genes determining the performance trait can be sought among the genes that are located in the regions identified. Candidate genes may be sought in the same species (e.g. when a rich EST map is available or when the genome is fully sequenced) or in orthologous regions of a model organism for which complete genome information is available.

Occasionally, key information on gene function arrives from an unexpected source. This was the case with the myostatin gene, the function of which was first discovered in mice and then found to be located in cattle in the chromosomal region where the double-muscling gene had previously been mapped (McPherron and Lee, 1997).

It is clear that identifying the responsible gene (quantitative trait genes – QTG) and the functional mutation (QTN) of a complex trait is still a substantial task, and several approaches are needed to decrease the number of positional candidate genes. Information on gene function is fundamental in this respect. However, we are still ignorant about the possible function(s) of the majority of genes identified by genome and cDNA (complementary DNA) sequencing. This is why the investigation of patterns of gene expression may provide useful information, in combination with the positional approach previously described, to identify candidate genes for complex traits. This combined approach is referred to as genetical genomics (Haley and de Koning, 2006). New advances in the investigation of patterns of gene expression are described in the next section.

Alternative approaches are presently being investigated to detect adaptive genes using genetic markers (Box 77). They are now at the experimental stage, and only further research will permit an evaluation of their efficacy.

Box 77
The population genomics approach

An alternative approach to the identification of genome regions carrying relevant genes has recently been proposed. It consists of the detection of "selection signatures" via a "population genomics" approach (Black *et al*., 2001; Luikart *et al*., 2003). Three main principles of the population genomics approach to QTL mapping are that (1) neutral loci across the genome will be similarly affected by genetic drift, demography, and evolutionary history of populations; (2) loci under selection will often behave differently and, therefore, reveal "outlier" patterns of variation, loss of diversity (increase of diversity if the loci were under a balanced selection), linkage disequilibrium, and increased/decreased G_{st}/F_{st} indices; and (3) through hitchhiking effects selection will also influence linked markers, allowing the detection of a "selection signature" (outlier effects), which can often be detected by genotyping a large number of markers along a chromosome and identifying clusters of outliers. This approach utilizes phenotypic data at the breed level (or subpopulations within a breed), rather than at the individual level, and thereby nicely complements classical QTL mapping approaches within pedigrees.

The population genomics approach can also identify genes subjected to strong selection pressure and eventually fixed within breeds, and in particular, genes involved in adaptation to extreme environments, disease resistance etc. Many of these traits, which are of great importance to the sustainability of animal breeding, are difficult or impossible to investigate by classic QTL mapping or association study approaches. The potential of population genomics has recently been investigated from a theoretical point of view (Beaumont and Balding, 2004; Bamshad and Wooding, 2003), and through experimental work with different types of markers in natural populations (AFLPs: Campbell and Bernatchez, 2004; microsatellites: Kayser *et al*., 2003; SNPs: Akey *et al*., 2002). The approach has recently been applied within the Econogene project (http://lasig.epfl.ch/projets/econogene). In preliminary analyses, three SNPs in MYH1 (myosin 1), MEG3 (callypige), and CTSB (cathepsin B) genes in sheep have shown significant outlier behaviour (Pariset *et al*., 2006).

Within the same project, a novel approach based on Spatial Analysis Method (SAM) has been designed to detect signatures of natural selection within the genome of domestic and wild animals (Joost, 2006). Preliminary results obtained with this method are in agreement with those obtained by the application of theoretical models in population genetics, such as those developed by Beaumont and Balding (2004). SAM goes a step further compared to classical approaches, since it is designed to identify environmental parameters associated with selected markers.

The ultimate goal of QTL mapping is to identify the QTG, and eventually the QTN. Although only a few examples exist to date in livestock, these are the kind of mutations that could have a direct impact on marker assisted breeding and on conservation decision-making. Conservation models considering functional traits and mutation need to be developed, as an increasing number of QTG and QTN will be uncovered in the near future.

Investigating patterns of gene expression

In the past, the expression of specific traits, such as adaptation and resistance, could only be measured at the phenotypic level. Nowadays, the transcriptome (the ensemble of all transcripts in a cell or tissue), and the proteome (the ensemble of all proteins) can be directly investigated by high-throughput techniques, such as differential display (DD) (Liang and Pardee, 1992), cDNA-AFLP (Bachem *et al*., 1996), serial analysis of gene expression (SAGE) (Velculescu *et al*., 1995; 2000), mass spectrometry, and protein and DNA microarrays. These techniques represent a breakthrough in RNA and protein analysis, permitting the parallel analysis of virtually all genes expressed in a tissue at a given time. Thus, the techniques contribute to the decoding of the networks that are likely to underlie many complex traits.

-Omics technologies are often compared to turning on the light in front of a Michelangelo fresco rather than using a torch that permits a view only of parts of the whole. The overall view allows the meaning of the representation to be understood and its beauty to be appreciated. In reality, the power of these techniques is paralleled at present by the difficulty and cost involved in applying them and in analyzing the data produced. The isolation of homogeneous cell samples is rather difficult, and is an important prerequisite in many gene expression profiling studies. The large number of parallel assays results in low cost per assay, but at a high cost per experiment. Equipment is expensive, and high technical skill is needed in all experimental phases. This is in addition to the general difficulty in analysing RNA compared to DNA. RNA is very sensitive to degradation, and particular care has to be taken while extracting it from tissues that have a very active metabolism. Indeed, sample conservation and manipulation is one of the keys to success in RNA analysis experiments. The application of nanotechnologies to the analysis of biological molecules is opening up very promising perspectives in solving these problems (Sauer *et al.*, 2005).

Data handling is a further problem. Molecular datasets such as gene expression profiles can be produced in a relatively short time. However, the standardization of data between laboratories is needed for consistent analysis of different biological datasets. Agreements on standardization, as well as the creation of interconnected databases, are essential for the efficient analysis of molecular networks.

Transcript profiling

This section briefly describes SAGE and microarray techniques. Descriptions of other techniques may be found in a number of recent reviews (e.g. Donson *et al.*, 2002). SAGE generates complete expression profiles of tissues or cell lines. It involves the construction of total mRNA libraries which enable a quantitative analysis of the whole transcripts expressed or inactivated at particular steps of a cellular activation. It is based on three principles: (i) a short sequence tag (9–14 bp) obtained from a defined region within each mRNA transcript contains sufficient information to uniquely identify one specific transcript; (ii) sequence tags can be linked together to form long DNA molecules (concatemers) which can be cloned and sequenced – sequencing of the concatemer clones results in the quick identification of numerous individual tags; (iii) the expression level of the transcript is quantified by the number of times a particular tag is observed.

Microarrays can be used to compare, in a single experiment, the mRNA expression levels of several thousands of genes between two biological systems, for example, between animals in a normal and animals in a challenging environment. Microarray technology can also provide an understanding of the temporal and spatial patterns of expression of genes in response to a vast range of factors to which the organism is exposed.

Very small volumes of DNA solution are printed on a slide made of a non-porous material such as glass, creating spots that range from 100 to 150 μm in diameter. Currently, about 50 000 complementary DNAs (cDNAs) can be robotically spotted onto a microscope slide. DNA microarrays contain several hundreds of known genes, and a few thousands of unknown genes. The microarray is spotted with cDNA fragments or with prefabricated oligonucleotides. The latter option has the advantage of a higher specificity and reproducibility, but can be designed only when the sequence is known. Microarray use is based on the principle of “hybridization”, i.e. the exposure of two single-stranded DNA, or one DNA and one RNA, sequences to each other, followed by the measurement of the amount of double-stranded molecule formed. The expression of mRNA can be measured qualitatively and quantitatively. It indicates gene activity in a tissue, and is usually directly related to the protein production induced by this mRNA.

Gene expression profiling contributes to the understanding of biological mechanisms, and hence facilitates the identification of candidate genes. The pool of genes involved in the expression of trypanotolerance in cattle, for example, has been characterized by SAGE (Berthier *et al.*, 2003), and by cDNA microarray analysis (Hill *et al.*, 2005). The parallel investigation of the expression of many genes may permit the identification of master genes responsible for phenotypic traits that remain undetected by differential expression analysis. These master genes may, for instance, possess different alleles all expressed at the same level, which promote the expression of downstream genes with different efficiency. In this case, the master gene can be sought either by exploiting current knowledge of metabolic pathways, or via an expression QTL (eQTL) approach (Lan *et al.*, 2006). In this approach, the level of expression of the downstream genes is measured in a segregating population. The amount of transcript of each gene is treated as a phenotypic trait, and QTL that influence the gene expression can be sought using methodologies described above. It is worth noting that data analysis for the detection of QTL is still quite difficult to master. This is also true for transcript profiling techniques because of the many false signals that occur.

Protein profiling

The systematic study of protein structures, post-translational modifications, protein profiles, protein–protein, protein–nucleic acid, and protein–small molecule interactions, and the spatial and temporal expression of proteins in eukaryotic cells, are crucial to understanding complex biological phenomena. Proteins are essential to the structure of living cells and their functions.

The structure of a protein can be revealed by the diffraction of x-rays or by nuclear magnetic resonance spectroscopy. The first requires a large amount of crystalline protein, and this is often restrictive. In order to understand protein function and protein–protein interactions at the molecular level, it would be useful to determine the structure of all the proteins in a cell or organism. At present, however, this has not been achieved. Interestingly, the number of different protein variants arising from protein synthesis (alternative splicing and/or post-translational modifications) is significantly greater than the number of genes in a genome.

Mass spectrometry (an analytical technique for the determination of molecular mass) in combination with chromatographic or electrophoretic separation techniques, is currently the method of choice for identifying endogenous proteins in cells, characterizing post-translational modifications and determining protein abundance (Zhu *et al*., 2003). Two-dimensional gel electrophoresis is unique with respect to the large number of proteins (>10 000) that can be separated and visualized in a single experiment. Protein spots are cut from the gel, followed by proteolytic digestion, and proteins are then identified using mass spectrometry (Aebersold and Mann, 2003). However, standardization and automation of two-dimensional gel electrophoresis has proved difficult, and the use of the resulting protein patterns as proteomic reference maps has only been successful in a few cases. A complementary technique, liquid chromatography, is easier to automate, and it can be directly coupled to mass spectrometry. Affinity-based proteomic methods that are based on microarrays are an alternative approach to protein profiling (Lueking *et al*., 2003), and can also be used to detect protein–protein interactions. Such information is essential for algorithmic modelling of biological pathways. However, binding specificity remains a problem in the application of protein microarrays, because cross-reactivity cannot accurately be predicted. Alternative approaches exist for detecting protein–protein interactions such as the two hybrid system (Fields and Song, 1989). However, none of the currently used methods allow the quantitative detection of binding proteins, and it remains unclear to what extent the observed interactions are likely to represent the physiological protein–protein interactions.

Array-based methods have also been developed for detecting DNA–protein interaction *in vitro* and *in vivo* (see Sauer *et al*., 2005, for a review), and identifying unknown proteins binding to gene regulatory sequences. DNA microarrays are employed effectively for screening nuclear extracts for DNA-binding complexes, whereas protein microarrays are mainly used for identifying unknown DNA-binding proteins at proteome-wide level. In the future, these two techniques will reveal detailed insights into transcriptional regulatory networks.

Many methods of predicting the function of a protein are based on its homology to other proteins and its location inside the cell. Predictions of protein functions are rather complicated, and also require techniques to detect protein–protein interactions, and to detect the binding of proteins to other molecules, because proteins fulfil their functions in these binding processes.

4 The role of bioinformatics

Developing high-throughput technologies would be useless without the capacity to analyse the exponentially growing amount of biological data. These need to be stored in electronic databases (Box 78) associated with specific software designed to permit data update, interrogation and retrieval. Information must be easily accessible and interrogation-flexible, to allow the retrieval of information, that can be analysed to unravel metabolic pathways and the role of the proteins and genes involved.

Box 78
Databases of biological molecules

A number of databases exist which collect information on biological molecules:

DNA sequence databases:

- European Molecular Biology Lab (EMBL): http://www.ebi.ac.uk/embl/index.html
- GenBank: http://www.ncbi.nlm.nih.gov/
- DNA Data Bank of Japan (DDBJ): http://www.ddbj.nig.ac.jp

Protein databases:

- SWISS-PROT: http://www.expasy.ch/sprot/sprot-top.html
- Protein Information Resource (PIR): http://pir.georgetown.edu/pirwww/
- Protein Data Bank (PDB): http://www.rcsb.org/pdb/

Gene identification utility sites Bio-Portal

- GenomeWeb: http://www.hgmp.mrc.ac.uk/GenomeWeb/nuc-geneid.html
- BCM Search Launcher: http://searchlauncher.bcm.tmc.edu/
- MOLBIOL: http://www.molbiol.net/
- Pedro's BioMolecular Research tools: http://www.biophys.uni-duesseldorf.de/BioNet/Pedro/ research_tools.html
- ExPASy Molecular Biology Server: http://www.expasy.ch/

Databases of particular interest for domestic animals:

http://locus.jouy.inra.fr/cgi-bin/bovmap/intro.pl
http://www.cgd.csiro.au/cgd.html
http://www.ri.bbsrc.ac.uk/cgi-bin/arkdb/browsers/
http://www.marc.usda.gov/genome/genome.html
http://www.ncbi.nlm.nih.gov/genome/guide/pig/
http://www.ensembl.org/index.html
http://www.tigr.org/
http://omia.angis.org.au/
http://www.livestockgenomics.csiro.au/ibiss/
http://www.thearkdb.org/
http://www.hgsc.bcm.tmc.edu/projects/bovine/

Bioinformatics is crucial to combine information from different sources and generate new knowledge from existing data. It also has the potential to simulate the structure, function and dynamics of molecular systems, and is therefore helpful in formulating hypotheses and driving experimental work.

5 Conclusions

Molecular characterization can play a role in uncovering the history, and estimating the diversity, distinctiveness and population structure of AnGR. It can also serve as an aid in the genetic management of small populations, to avoid excessive inbreeding. A number of investigations have described within and between-population diversity – some at quite a large scale. However, these studies are fragmented and difficult to compare and integrate. Moreover, a comprehensive worldwide survey of relevant species has not been carried out. As such, it is of strategic importance to develop methods for combining existing, partially overlapping datasets, and to ensure the provision of standard samples and markers for future use as worldwide references. A network of facilities collecting samples of autochthonous germplasm, to be made available to the scientific community under appropriate regulation, would facilitate the implementation of a global survey.

Marker technologies are evolving, and it is likely that microsatellites will increasingly be complemented by SNPs. These markers hold great promise because of their large numbers in the genome, and their suitability for automation in production and scoring. However, the efficiency of SNPs for the investigation of diversity in animal species remains to be thoroughly explored. The subject should be approached with sufficient critical detachment to avoid the production of biased results.

Methods of data analysis are also evolving. New methods allow the study of diversity without *a priori* assumptions regarding the structure of the populations under investigation; the exploration of diversity to identify adaptive genes (e.g. using population genomics, see Box 77); and the integration of information from different sources, including socio-economic and environmental parameters, for setting conservation priorities (see Section F). The adoption of a correct sampling strategy and the systematic collection of phenotypic and environmental data, remain key requirements for exploiting the full potential of new technologies and approaches.

In addition to neutral variation, research is actively seeking genes that influence key traits. Disease resistance, production efficiency, and product quality are among the traits having high priority. A number of strategies and new high-throughput –omics technologies are used to this end. The identification of QTN offers new opportunities and challenges for AnGR management. Information on adaptive diversity complements that on phenotypic and neutral genetic diversity, and can be integrated into AnGR management and conservation decision-tools. The identification of unique alleles or combinations of alleles for adaptive traits in specific populations may reinforce the justification for their conservation and targeted utilization. Gene assisted selection also has the potential to decrease the selection efficiency gap currently existing between large populations raised in industrial production systems, and small local populations, where population genetic evaluation systems and breeding schemes cannot be effectively applied. Marker and gene assisted selection may not, however, always represent the best solution. These options need to be evaluated and optimized on a case-by-case basis, taking into account short and long-term effects on population structure and rates of inbreeding, and cost and benefits in environmental and socio-economic terms – in particular impacts on people's livelihoods.

As in the case of other advanced technologies, it is highly desirable that benefits of scientific advances in the field of molecular characterization are shared across the globe, thereby contributing to an improved understanding, utilization and conservation of the world's AnGR for the good of present and future human generations.

Box 79
Glossary: molecular markers

For the purpose of this section the following definitions are used:

Candidate gene: any gene that could plausibly cause differences in the observable characteristics of an animal (e.g. in disease resistance, milk protein production or growth). The gene may be a candidate because it is located in a particular chromosome region suspected of being involved in the control of the trait, or its protein product may suggest that it could be involved in controlling the trait (e.g. milk protein genes in milk protein production).

DNA: the genetic information in a genome is encoded in deoxyribonucleic acid (DNA), which is stored in the nucleus of a cell. DNA has two strands structured in a double helix which is made of a sugar (deoxiribose), phosphate, and four chemical bases – the nucleotides: adenine (A), guanine (G), cytosine (C) and thymine (T). An A on one strand always pairs with a T on the other through two hydrogen bonds, while a C always pairs with a G through three hydrogen bonds. The two strands are, therefore, complementary to each other.

Complementary DNA (cDNA): DNA sequences generated from the reverse transcription of mRNA sequences. This type of DNA includes exons and untranslated regions at the 5’ and 3’ ends of genes, but does not include intron DNA.

Genetic marker: a DNA polymorphism that can be easily detected by molecular or phenotypic analysis. The marker can be within a gene or in DNA with no known function. Because DNA segments that lie near each other on a chromosome tend to be inherited together, markers are often used as indirect ways of tracking the inheritance pattern of a gene that has not yet been identified, but whose approximate location is known.

Haplotype: a contraction of the phrase “haploid genotype”, is the genetic constitution of an individual chromosome. In the case of diploid organisms, the haplotype will contain one member of the pair of alleles for each site. It may refer to a set of markers (e.g. single nucleotide polymorphisms – SNPs) found to be statistically associated on a single chromosome. With this knowledge, it is thought that the identification of a few alleles of a haplotype block can unambiguously identify all other polymorphic sites in this region. Such information is very valuable for investigating the genetics behind complex traits.

Linkage: The association of genes and/or markers that lie near each other on a chromosome. Linked genes and markers tend to be inherited together.

Linkage disequilibrium (LD): is a term used in the study of population genetics for the non-random association of alleles at two or more loci, not necessarily on the same chromosome. It is not the same as linkage, which describes the association of two or more loci on a chromosome with limited recombination between them. LD describes a situation in which some combinations of alleles or genetic markers occur more or less frequently in a population than would be expected from a random formation of haplotypes from alleles based on their frequencies. Linkage disequilibrium is caused by fitness interactions between genes or by such non-adaptive processes as population structure, inbreeding, and stochastic effects. In population genetics, linkage disequilibrium is said to characterize the haplotype distribution at two or more loci.

Microarray technology: a new way of studying how large numbers of genes interact with each other and how a cell's regulatory networks control vast batteries of genes simultaneously. The method uses a robot to precisely apply tiny droplets containing functional DNA to glass slides. Researchers then attach fluorescent labels to mRNA or cDNA from the cell they are studying. The labelled probes are allowed to bind to cDNA strands on the slides. The slides are put into a scanning microscope that can measure the brightness of each fluorescent dot; brightness reveals how much of a specific mRNA is present, an indicator of how active it is.

Primer: a short (single strand) oligonucleotide sequence used in a polymerase chain reaction (PCR)

RNA: Ribonucleic acid is a single stranded nucleic acid consisting of three of the four bases present in DNA (A, C and G). T is, however, replaced by uracil (U).

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SECTION D: GENETIC IMPROVEMENT METHODS TO SUPPORT SUSTAINABLE UTILIZATION

1 Introduction

This section gives an overview of genetic improvement methods for sustainable use of AnGR. The first chapter describes the contexts for genetic improvement. As social and economic contexts are discussed extensively in other parts of the Report, they are only briefly described here. The scientific and technology-related context is described in greater detail. The second chapter discusses breeding strategies for genetic improvement, along with the elements of a straight-breeding programme. These elements involve planning, implementation and evaluation, and constitute a continuous and interactive process. Breeding programmes for the main livestock species in high-input systems are then reviewed. This includes a description not only of the breeding goals and the traits making up the selection criteria, but also the organization and the evolution of the breeding sector. This is followed by a description of breeding strategies for low-input systems, and those utilized in the context of breed conservation. This distinction is somewhat artificial as the situations and strategies sometimes overlap. Finally, some general conclusions are drawn.

2 The context for genetic improvement

Genetic improvement implies change. For a change to be an improvement, the overall effects of the change must bring positive benefits to the owners of the animals in question or to the owners' community. Moreover, to be an improvement, the effects of the change should bring positive benefits in both the short and the long term, or at minimum a short-term benefit should not result in long-term harm. As such, it is vital that the planning of genetic-improvement programmes takes careful account of the social, economic and environmental context in which they will operate. This can best be achieved by making these programmes an integral part of national livestock development plans, which should establish broad development objectives for each production environment.

2.1 Changing demand

Traditionally, livestock breeding has been of interest only to a small number of professionals: breeding company employees, farmers, and some animal scientists. However, food production is changing from being producer driven to consumer driven. Consumer confidence in the livestock industry has broken down in many countries (Lamb, 2001). Fears about the quality and safety, of animal products have been heightened in recent years by various crises: bovine spongiform encephalopathy (BSE), dioxin, and more recently, highly pathogenic avian influenza (HPAI). Welfare has also become an important element in consumers' perception of product quality especially in Europe (organic products and free-range animals). At the same time, the majority of consumers have become less connected to the countryside, and know less about farming. There is a growing demand for "natural" production, but often without a clear understanding of what this should encompass.

2.2 Diverse production environments

Sustainable production systems need to be tailored to account for physical, social and market conditions. For breeding organizations this raises the question of whether they should diversify their breeding objectives, or whether they should breed an animal that can do well under a wide range of environments (physical environment, management system and market conditions). To date, however, only limited insights into the underlying genetics of phenotypic adaptation to the environment have been achieved.

2.3 Increasing recognition of the importance of genetic diversity

Livestock breeding requires variability within and between populations if it is to improve the traits of interest. Genetic diversity is important to meet present requirements, but is especially important to meet future requirements. For example, a change of emphasis from high-input to low-input production systems will favour different breeds and different characteristics within breeds. More generally, the increasing importance given to factors such as animal welfare, environmental protection, distinctive product quality, human health and climate change, will require a wider range of criteria to be included in breeding programmes. These criteria are often met by local breeds. Thus, it is possible that the most appropriate strategies for managing these breeds may involve only limited genetic change. For example, it may be wise to maintain adaptation to the local environment and disease challenges – and even to maintain the level of a production trait, such as body size or milk production, if this is currently at or near an optimum level.

2.4 Scientific and technological advances

Developments in genetic improvement methods

Quantitative genetics

A breeding scheme aims to achieve genetic improvement in the breeding goal through the selection of the animals that will produce the next generation. The breeding goal reflects the traits that the breeder aims to improve through selection. The rate of genetic improvement (ΔG) with respect to the breeding goal (and the underlying traits) depends on the amount of genetic variability in the population, the accuracy of the selection criteria, the intensity of selection, and the generation interval.

Maintenance of genetic variation is a condition for continuous genetic improvement. Genetic variation is lost by genetic drift and gained by mutation. Therefore, the minimum population size to maintain genetic variation is a function of the mutation rate (Hill, 2000). Selection experiments in laboratory animals have shown that substantial progress can be maintained for many generations, even in populations with an effective size well under 100, but that responses increase with population size (ibid.).

The loss of genetic variation within a breed is related to the rate of inbreeding (ΔF). In the absence of selection, ΔF is related directly to the number of sires and dams. In populations undergoing selection, this assumption is no longer valid because parents contribute unequally to the next generation. A general theory to predict rates of inbreeding in populations undergoing selection has recently been developed (Woolliams *et al.*, 1999; Woolliams and Bijma, 2000). This approach facilitates a deterministic optimization of short and long-term response in breeding schemes.

Research on the optimization of breeding schemes initially focused on genetic gain, while little attention was paid to inbreeding. It is now well accepted that constraining inbreeding is an important element of breeding schemes. Meuwissen (1997) developed a dynamic selection tool which maximizes genetic gain while restricting the rate of inbreeding. From a given set of selection candidates, the method allows the selection of a group of parents in which the genetic merit is maximized while the average coefficient of co-ancestry is constrained. Implementation of this method results in a dynamic breeding programme, in which the number of parents and the number of offspring per parent may vary, depending on the candidates available in a particular generation.

The accuracy of selection depends largely on the quality and the quantity of the performance records that are available. Genetic improvement can only be made if performance and pedigree are recorded. Based on these observations, the genetic merit of an individual is predicted and the animals with the highest predicted merit can be selected as parents.

It is well established that the method of choice for the genetic evaluation of linear traits (e.g. milk and egg production, body size and feed efficiency) is best linear unbiased prediction based on an animal model (BLUP-AM) (Simianer, 1994). The development of algorithms and software has meant that by today, in most countries and for most species, BLUP-AM is routinely used by breeding companies or in national-level breeding programmes. The limitations associated with applying simplistic single-trait models has led to the development of multiple-trait BLUP-AM evaluations based on sophisticated models (including, for example, maternal effects, herd × sire interactions or dominance genetic effects). This has been greatly facilitated by the increasing power of computers, and major advances in computational methods. The tendency now is to use all available information, including single test day records, records from cross-bred animals, and a wide geographical range (across countries). Significant difficulties associated with the use of increasingly complex models are a lack of robustness (especially when population size is limited) and computational problems. The challenge today is to develop tools to systematically validate the models used.

BLUP is optimum only when the true genetic parameters are known. Methods for unbiased estimation of (heterogeneous) variance components with large data sets have been developed. Restricted Maximum Likelihood (REML) applied to animal models is the method of preference. Quite a few important traits are not correctly described by linear models (e.g. traits based on scoring and survival). A wide variety of nonlinear mixed models have, therefore, been proposed: threshold models, survival models, models based on ranks, Poisson models etc. However, the benefits of using these nonlinear models remain to be proven.

The selection intensity reflects the proportion of animals that are needed as parents for the next generation. Reproductive capacity and techniques have an important influence on the number of parents that are needed for the production of the next generation, and thereby on the rate of genetic improvement. In poultry, high reproductive capacity means that about 2 and 10 percent of the male and female candidates, respectively, are retained as parents. In cattle, the introduction of AI has resulted in an enormous reduction in the number of sires. In dairy and beef cattle, the bulls used for AI and the cows with high genetic merit are the nucleus animals, and form less than 1 percent of the entire population.

The generation interval is the average time between two generations. In most populations, a number of age classes can be distinguished. The amount of information available differs between classes. In general, there is less information about the younger age classes than about older age classes. Consequently, the accuracy of estimates of breeding value is lower in the younger generations. However, the mean level of the estimated breeding value (EBV) of young age classes is higher than that of older age classes because of continuous genetic improvement in the population. Selection across age classes to obtain the highest selection differential is recommended (James, 1972). The fraction of animals selected from each age class depends on the differences in accuracy of the EBV between the age classes (Ducrocq and Quaas, 1988; Bijma *et al.*, 2001). The use of reproductive technologies may increase the amount of sib information available, and thereby increase the accuracy of the EBV of younger age classes (van Arendonk and Bijma, 2003). This will change the proportion of parents selected from the younger age classes, and therefore also influence the average generation interval. Thus, generation interval is primarily a result of selection among the available age classes.

Molecular genetics

Molecular genetics in livestock has been subject to extensive study during the last two decades. These studies are related to gene-based selection of Mendelian traits (mainly diseases and genetic defects), marker assisted selection and introgression. Furthermore, molecular information is increasingly used to assist breed conservation programmes and to improve understanding of the origin and domestication of livestock.

Gene-based selection. Increasing knowledge of the animals' genome increases the prospects for applying this technology and provides new tools with which to select for healthy animals. Initial applications are related to Mendelian traits. In cattle for example, DNA diagnosis is routinely utilized to eliminate genetic disorders such as bovine leukocyte adhesion deficiency (BLAD), deficiency of uridine monophosphate synthase (DUMPS) and complex vertebral malformation (CVM), as well as in selection for traits such as milk kappa-casein and double muscling.

In pigs, the best-known gene which has so far been used in commercial breeding is the “halothane” gene. It was known that a number of pigs could not handle stressful situations (e.g. transportation to the slaughterhouse). A (recessive) gene – a natural mutation, called the “halothane” gene – was found to be responsible for this defect. Using a DNA test that detects whether a pig has the "defective form" of the gene, it has been possible to eliminate this gene completely from several breeds (Fuji *et al.*, 1991).

Scrapie, the prion disease of sheep, is the most common natural form of transmissible spongiform encephalopathy (TSE), a group of diseases which also include Creutzfeldt-Jakob disease in humans and BSE in cattle. Genetic susceptibility to scrapie is strongly modulated by allelic variations at three different codons in the sheep PrP gene (Hunter, 1997). Breeding for scrapie resistance has, therefore, been considered an attractive option for the control of this disease (Dawson *et al.*, 1998; Smits *et al.*, 2000). This can be done by selecting for the allele that is associated with the greatest degree of resistance to scrapie (the ARR allele). As described in Part 1 – Section F: 4, breeding programmes to eliminate scrapie can pose a threat to rare breeds that have a low frequency of the resistant genotype.

Marker assisted selection. Most economically important traits in animal production are of a quantitative nature and are affected by a large number of genes (loci), a few of which have major effects, while the majority have small effects (Le Roy *et al.*, 1990; Andersson *et al.*, 1994). If a gene (locus) with a major effect can be identified, and if a molecular test can be designed, animals' genotypes at the locus can be used for selection. In other cases, a chromosomal region close to the gene of interest may be identified and used as a marker.

Mixed models of inheritance, which assume one or several identified segregating loci, and an additional polygenic component, have been developed. When genotypes at each identified locus are known, they can be treated as fixed effects in standard mixed-model techniques (Kennedy *et al.*, 1992). When only genotypes at linked markers are known, the uncertainty resulting from unknown haplotypes and recombination events has to be taken into account (Fernando and Grossman, 1989).

Extra genetic gain is usually to be expected if information on genes with medium to large effects is included in the genetic evaluation process. Numerous studies have investigated this problem in recent years. Results are not always comparable, because selection criteria differed between studies (i.e. from an index based on individual information to animal models), but they all indicate that knowledge of genotypes at quantitative trait loci generally improves short-term response to selection (Larzul *et al.*, 1997). Conversely, some discrepancies have been obtained for long-term response to selection – see Larzul *et al.* (1997). In less favourable situations where only genotypes at linked markers are known, results largely depend on the particular circumstances. Large gains can be expected when linkage disequilibrium exists at the population level (Lande and Thompson, 1990), and when traits are difficult to measure (e.g. disease resistance), sex limited (e.g. traits related to egg or milk production), expressed late in the lifespan of the animals (e.g. longevity and persistency in litter size), or measured after slaughtering (e.g. meat quality traits). In other cases, the advantage of marker assisted selection may be questionable.

Genes at the same or at different loci interact with each other in producing a phenotypic effect. It is seldom known how this occurs. When, by using statistical models, an apparent effect is assigned to a particular gene, such interaction is not taken into account. This explains, at least partly, why even when genes with major effects are identified, incorporating them (or their markers) into a selection programme may not achieve the desired results. Because of such interactions, there is often an apparent lack of consistency between different studies related to the use of genetic markers (Rocha *et al.*, 1998). To correctly assess the effect of a gene, the average effect over the possible genotypes in the population where the information is to be applied (weighted according to their frequencies) has to be considered.

Introgression is advocated mainly to improve disease resistance in a given population. If markers for the resistance gene(s) (or probe for the gene) are available, marker assisted selection may be used to simplify the process of introgression. Dekkers and Hospital (2002) discuss the use of repeated backcrosses to introgress a gene into a population. If the non-resistant breed is considered the recipient breed, and the breed that carries the resistance gene is considered the donor breed, introgression of the desirable gene from the donor breed to the recipient breed is accomplished by multiple backcrosses to the recipient breed, followed by one or more generations of intercrossing. The aim of the backcross generations is to generate individuals that carry one copy of the donor gene, but that are similar to the recipient breed for the rest of the genome. The aim of the intercrossing phase is to fix the donor gene. Marker information can enhance the effectiveness of the backcrossing phase of gene introgression strategies by identifying carriers of the target gene (foreground selection), and by enhancing recovery of the recipient genetic background (background selection). Generally, it is more feasible and economically sound to mate, in successive generations, pure-bred females of the recipient breed to cross-bred males that carry the desired gene, than to carry out the reverse process.

If the gene for resistance is dominant, its introgression into a population may be effective even without a molecular marker for the gene. If the gene for resistance is recessive (or co-dominant), markers are necessary. In cases where resistance is polygenic, introgression without genetic markers is not likely to be effective; by the time the genetic influence of the donor breed is high enough to give high levels of resistance, the desired characteristics of the recipient breed will probably have been lost. In fact, the development of a composite breed would be easier than the introgression of numerous genes into a recipient breed by backcrossing, even when genetic markers are available. Hanotte *et al.* (2003) mapped QTLs affecting trypanotolerance in a cross between the "tolerant" N'Dama and "non-tolerant" Boran cattle breeds. Results showed that at some of the putative QTLs associated with trypanotolerance, the allele associated with tolerance came from the non-tolerant cattle. It was concluded that "selection for trypanotolerance within an F2 cross between N'Dama and Boran cattle could produce a synthetic breed with higher trypanotolerance levels than currently exist in the parental breeds."

Conceptually, introgression through marker assisted selection could be accomplished even without exposure to the disease agent. It is, however, wise to test the resistance of animals with the desired genotype.

Molecular characterization of genetic diversity is helpful in the planning of conservation programmes and to develop understanding of the origin and domestication of livestock species. Better knowledge of genomic variation, together with the development of new quantitative genetic methods, may provide the means to link marker information to functional variation. For example, combination of molecular methods and pedigree analysis has been used to estimate the degree of genetic diversity in founder populations in thoroughbred horses (Cunningham *et al.*, 2001).

Developments in reproductive technologies

Reproductive technology has a direct effect on the rate of genetic improvement. For a given population size, a higher reproduction rate implies a lower number of breeding animals and, therefore, a higher intensity of selection. More offspring per breeding animal also allows more accurate estimation of breeding values. Another advantage of increasing reproductive rates is to disseminate superior genetic stock more quickly.

As reproductive technologies are extensively discussed elsewhere in the Report, this chapter focuses only on the use of AI and multiple ovulation and embryo transfer (MOET) in breeding programmes. For other techniques, only a brief description is provided here.

Artificial insemination The use of AI results in higher selection intensity, more accurate selection of males based on progeny testing and more accurate estimation of breeding value across herds. The latter is a result of exchange of semen between different nucleus herds, which facilitates the establishment of genetic links between them. AI is used by breeding organizations for most species. For species such as cattle that have low reproductive rates, progeny testing based on AI is a prerequisite for an accurate estimation of breeding values for traits of low heritability such as functional traits. AI allows faster dissemination of genetic superiority to the commercial population. Sixty to eighty percent of all the AI performed is carried out in cattle. A male identified as superior can leave thousands of progeny in different populations all over the world.

AI requires technical skills both at the AI centre and on the farm, as well as effective lines of communication between the two. However, in many countries, the majority of producers are smallholder farmers, and existing skills and infrastructure may be insufficient to allow the successful operation of AI services. The farmer has to be able to detect heat and have a means to contact the semen distribution centre, which then has to be able to serve within few hours. For extensive production systems, this is a labour-intensive process. Consequently, AI is unlikely to be used in extensive grazing systems for beef production. Similarly, AI is difficult to perform in sheep, and natural mating using superior males is still the dominant means of diffusing genetic improvement.

Use of AI affects the ownership structure of the breeding sector. Where AI is used, the ownership of the breeding animals is usually transferred to larger breeding organizations, such as cooperatives or private breeding companies. For the last twenty years in the developed world, AI centres have been responsible for the identification of young bulls for progeny testing, and for the marketing of semen from proven sires.

Multiple ovulation and embryo transfer Increasing the reproductive rate of females by MOET is mainly useful in species with low reproductive rates such as cattle. The benefits are higher selection intensity on the female side, and more accurate estimation of breeding values. As family sizes are larger, there is more information available on animals' sibs. This allows reasonably reliable breeding values to be obtained at a younger age, particularly when the traits are only recorded for one sex (female). In practice, this means that there is no need to wait for a progeny test to select males – they can be selected at younger age based on information on their half-sib sisters. The gain in generation interval is large, and compensates for the loss of selection accuracy that results from replacing a progeny test by a sib test. The ability to select at a young age, even among embryos, is the main reason of the application of MOET in pig breeding. Embryo transfer is also used to disseminate desirable genes from superior female animals with minimum disease risks, as animals do not need to be transported.

The use of MOET is costly and requires highly developed technical skills. The logistical challenge is that at the time of embryo transfer, a group of recipient cows needs to be available and synchronized. This can be done only in large centralized nucleus herds. In many cases, it may be better to invest resources in more basic prerequisites – performance and trait recording, extension and dissemination. This is all the more true as MOET seems less efficient than AI in enhancing genetic progress. In all cases, the introduction of AI and/or MOET has to be cost effective and accepted by the local farmers.

Semen and embryo freezing gives breeding organizations the opportunity to create genebanks as a back-up store of genetic diversity in breeding programmes. Moreover, cryopreservation of gametes and embryos facilitates international exchange and transport of genetic material in ruminants, and is a prerequisite for routine use of AI and ET on a world scale.

Cloning (somatic cells) is a new technology which is currently not being used commercially. This is partly for technical and economic reasons, and partly because there is no public desire for such developments at present. Cloning has potential application in the field of conservation, as other tissues may be easier to preserve than embryos.

Sexing of embryos or semen enables the production of larger numbers of animals of a particular sex. For example, preferences for male or female offspring are obvious in cattle – females for milk production, and males for beef production. Numerous attempts have been made to develop a reliable technology. Currently, it is possible to identify male and female embryos by various methods. However, with a few exceptions, this technology has not yet been widely used by breeders or farmers. Various attempts have been made to separate sperm based on their sex-determining characteristics. However, further advances are required before the technology can be applied on a large scale.

The use of the above-described reproductive and conservation techniques means that there is less need for the transportation of breeding animals. Furthermore, these technologies offer an opportunity to safeguard the health status of flocks and herds even when embryos originate from countries with a radically different health status.

2.5 Economic considerations

Any economic evaluation should consider both returns and costs. As animal breeding is a long-term process, returns on breeding decisions may be realized many years later. This is the case in dairy cattle for example. Furthermore, different costs and returns are realized at different times with different probabilities, and a number of considerations that may not be important for relatively short-term processes are sometimes of major importance in the longer term.

Until the advent of reproductive biotechnologies, the main cost elements of breeding programmes were trait measurement and recording, progeny testing and maintaining the breeding stock. Although the main objective of most recording systems is breeding, it should be noted that once available, the information is useful for other farm management decisions such as culling and predicting future production.

Animal breeding in the developed world has become more and more sophisticated and professionalized, and hence costly. Economic considerations are, therefore, driving most if not all breeding-related activities, and economic theory has been incorporated into this area. The bases for economic evaluation are profit, economic efficiency, or return on investment. When breeding goals have been developed by and for (groups of) producers, emphasis is put on profit maximization. In developing countries, markets are generally more local, but the same mechanism will apply. It is, therefore, advisable to opt for profit maximization, unless there are clear reasons to deviate from this strategy.

A critical economic consideration is: who will pay for the genetic improvement? This question is not particularly important when breeding nuclei, multipliers and commercial herds/flocks are fully integrated. However, in all other situations, where vertical integration does not exist, it is not unusual that those who invested in breeding activities are unable to adequately recoup their investment. This commonly provides justification for public sector involvement in one or more facets of genetic improvement.

Under a free market system, breeding organizations have to adapt to the demands of their customers – the commercial producers, who are normally only prepared to pay for improved breeding animals or semen if this will enhance their profits. However, it is interesting to note that even if a trend in breeding does not appear to be economically justified, it may continue for an extended period of time (Box 80). Under a government subsidized system, all or part of the costs of genetic efforts are paid for by taxpayers. In this case, breeding programmes should be subject to scrutiny to ensure that they truly produce some social benefits. Such benefits could include, for example, providing safer, more nutritious or less expensive products for the consumer, or reducing the negative environmental impacts of livestock production.

3 Elements of a breeding programme

The elements required in a breeding programme depend on the choice of the general breeding strategy. Thus, the first decision is which of the three main genetic improvement strategies should be applied: selection between breeds, selection within breeds or lines, or cross-breeding (Simm, 1998).

- Selection between breeds, the most radical option, is the substitution of a genetically inferior breed by a superior one. This can be done at once (when as in poultry the cost is not prohibitive) or gradually by repeated backcrossing with the superior breed (in large animals).

- Cross-breeding, the second fastest method, capitalizes on heterosis and complementarity between breeds' characteristics. Conventional cross-breeding systems (rotational systems and terminal sire-based systems) have been widely discussed (e.g. Gregory and Cundiff, 1980). The *inter se* mating of animals of newly developed composites has been suggested as an alternative form of cross-breeding (Dickerson, 1969; 1972).

- The third method, within-breed selection, gives the slowest genetic improvement, especially if the generation interval is long. However, this improvement is permanent and cumulative, which is not the case for cross-breeding programmes.

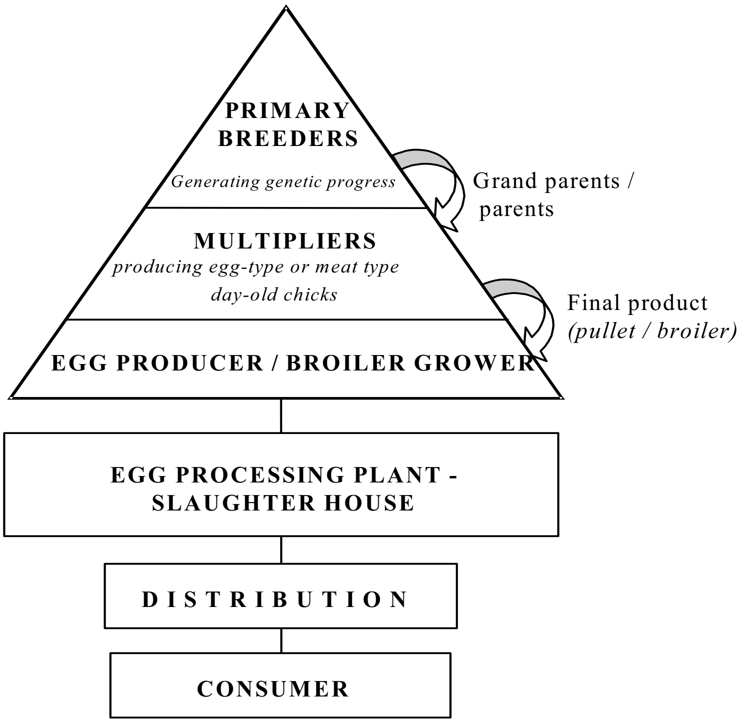
Gradual genetic improvement is the most sustainable form of improvement, as it gives the stakeholders time to adapt the production system to the intended change. When the traits of interest are numerous and/or some of them are antagonistic, different lines may be created, and maintained by within-line selection. These lines can then be crossed to produce commercial animals. This strategy is used in pig and poultry breeding.

Setting up a breeding programme involves the definition of a breeding goal (Groen, 2000) and the design of a scheme that is able to deliver genetic progress in line with this goal. In practice, it involves the management of people and resources as well as the application of the principles of genetics and animal breeding (Falconer and Mackay, 1996). Each aspect of the breeding programme involves many processes, individuals and sometimes institutions. Success depends on how well the available resources are harnessed and managed to achieve the goals of the stakeholders.

The stakeholders of a breeding programme are all those who are affected, in one way or another, by its success. These include the end users of the products of the programme (i.e. livestock producers), commercial companies and others who directly or indirectly invest in the scheme, government departments, breed societies, and those employed to implement the programme. Other stakeholders include ancillary beneficiaries such as suppliers, distributors, and sellers of by-products of the scheme.

Most programmes have a pyramidal structure (Simm, 1998), with varying number of tiers depending on the sophistication of the programme. At the apex of the pyramid is the nucleus where selection and breeding of the elite pedigree animals is concentrated. The multiplication of stock happens in the middle tiers. This is required when the number of nucleus animals is insufficient to satisfy the demands of commercial farmers. The bottom tier comprises the commercial units where the final product is disseminated. The pyramidal structure of the poultry breeding industry is illustrated in Figure 48.

Figure 48
Structure of the poultry breeding industry



The activities that constitute a breeding programme can be summarized in eight major steps (Simm, 1998):

- choice of breeding goal;
- choice of selection criteria;
- design of the breeding scheme;
- recording of the animals;
- genetic evaluation of the animals;
- selection and breeding;
- progress monitoring; and
- dissemination of genetic improvement.

These steps will be described in the following subchapters. However, the reader should be aware that planning, implementation and evaluation form a continuous process – the elements should be approached interactively rather than step-by-step. A further critical element is the need to document in detail all areas of the breeding plan and its execution over time.

3.1 Breeding goals

The breeding goal is a list of traits to be improved genetically. It should be in line with national agricultural development objectives, and appropriate for the production system for which it is defined and the breeds suited to the production system. A country's development objectives for agricultural production traditionally include economic variables, but should be extended to accommodate ethics, and other social aspects of human well-being. These objectives are used to formulate the breeding goals. Different tools are available to achieve this. The most common is the profit function. In theory, setting up a profit function is straightforward, especially in the case of within-breed selection programmes, as it is a linear function of the relative economic values of the traits to be improved. In practice, however, it is not easy to obtain these economic values, partly because they may vary in time and in space, and partly because of a lack of time, expertise, knowledge, resources etc. Thus, breeders manipulate the direction of change through trial and error based on perceived market demand and preference. Amer (2006) discusses other tools for formulating breeding goals such as the bio-economic model and the geneflow model.

Livestock improvement is measured relative to a given set of traits, generally referred to as "traits of economic importance". In reality, the traits and their economic importance vary as widely as the breeding programmes. For many livestock species, the traits of economic importance are those that affect the productivity, longevity, health and reproductive ability of the animals.

For most of the traits, the objective is a continuous improvement, but for some traits the goal is to reach intermediate values. Pharo and Pharo (2005) term these alternatives, respectively, breeding for a "direction" and for a "destination". An example of the latter is egg weight in laying hens. The market values eggs within a particular range of weights – for example, between 55 and 70 grams. Smaller eggs are not saleable and there is no premium for bigger ones. Given that egg size is correlated negatively to egg number, shell strength and hatchability, selecting for bigger eggs is not only a waste of selection intensity, it is also counter productive. Another example is body size. For meat animals, size at slaughter is an important determinant of value. Body size has a major effect on nutritional requirements, through its effect on maintenance requirements. It may also affect fertility. The latter (net fertility such as calf crop or lamb crop weaned) is a major determinant of biological efficiency and profitability. Since body size is associated with both costs and benefits, it is difficult to determine an optimum value, especially under grazing systems, because of the difficulty involved in adequately describing forage intake. Another consideration is that most slaughter markets discriminate against animals that fall outside a desired range of carcass (or live) weights. For example, the European market requires a minimum carcass weight, which cannot be met by some breeds (e.g. Sanga breeds from Namibia). Even if the current body size of these cattle is optimum with regard to biological efficiency, larger cattle may be more profitable.

The choice of the breeding goal may be a one-off activity, or one that is revised from time to time. The decision is taken by the breeders, with feedback from all tiers of the breeding pyramid. In poultry and pig breeding, this decision is taken by the top management of the breeding companies (research and development managers in agreement with technical and marketing or sales managers). In cattle breeding, the decision is taken at the apex nucleus, but usually in consultation with people in all other tiers including the commercial tier, in a way that reflects the ownership pattern of the programme.

The outcome of breeding programmes, particularly in dairy and beef cattle, is realized many years after selection decisions are made. Even in poultry, where the generation interval is shorter, a genetic change implemented in the nucleus will not be noticed at the commercial level in less than three years, at the earliest. This underlines the need to anticipate future demands when defining breeding goals.

In a competitive market like the poultry breeding industry, the identification of traits of interest and the focus of selection efforts is not only highly dependent on signals from the market place (i.e. the commercial producers), but also on the performance of the products of competing programmes.

3.2 Selection criteria

The breeding goal is distinct from the selection criteria that are used to take the decision as to which animals are to become the parents of the next generation. Usually, the decision involves the construction of a “selection index”. Measurements are taken in the candidate animals and their relatives, and are weighted according to index coefficients calculated to maximize the correlation between the selection index and the breeding goal. It should be emphasized that some of the breeding goal traits may differ from those used to construct the selection index. For example, pigs are selected for the fatness of their carcass – this is a breeding goal trait. However, it cannot be observed in selection candidates, as this would mean that they would have to be slaughtered. A predictor trait, the subcutaneous fat thickness measured ultrasonically, is therefore recorded. Where it is difficult or expensive to acquire information on the relationships between animals, and the traits are sufficiently heritable, selection can be based on individual performance (mass selection). The construction of the selection index is a technical issue, and requires personnel with the necessary expertise.

There are numerous circumstances in which at the moment of selection many traits that are not relevant to breeding goal trait list are considered. This can seriously decrease the actual selection intensity and, therefore, limits the genetic improvement. Sometimes this is acceptable (e.g. a genetic defect is a valid reason for culling). In other cases such criteria are doubtful (e.g. “body volume” as an indicator of productivity) or not recommendable (e.g. frame size or “dairyness”).

Box 80
The changing body size of beef cattle in United States of America

In 1900 the vast majority of beef cattle in the United States of America were Shorthorn, Hereford, or Angus. The cattle at the time were fairly large. Bulls of 1 100 kg and cows of 730 kg were common. Cattle were finished (fattened) primarily on grass, and there was some interest in producing cattle that would finish at a younger age and lighter weight. A trend developed for selecting for smaller-framed cattle that had greater apparent ability to fatten. Much of the selection was actually based on attempts to win in the show ring. Selection was effective, and major changes were achieved in the cattle population. After a few generations (the late 1920s and early 1930s) the cattle were probably of a more appropriate size for the production conditions under which they were kept. However, selection continued in the same direction, and by the 1950s the cattle in most highly regarded herds were much too small and predisposed to fattening to be profitable under any commercial management programme.

A major change in the United States beef industry began in the mid-1950s, with the development of large feedlots in the Great Plains states. To be profitable in these new feedlots, cattle had to be able to grow at a fairly high rate for a long feeding period (four or five months) without getting too fat. The small early fattening cattle which had previously been popular were not acceptable to the feedlot industry. Charolais and other continental European breeds became popular, and cattle of the British beef breeds were selected for increased size and growth. From the mid-1950s to the late 1960s, larger cattle were favoured as long as they were fairly compact in their conformation. However, by the late 1960s, larger cattle were favoured, even if they were taller and very different in their conformation from the popular cattle of the earlier period. Within a few years, cattle were being selected for larger frame size, even in the continental European breeds. This selection was also quite effective, and extremely large animals were produced.

In the mid to late 1980s, several of the major breeding organizations realized that the trend had gone too far, and moves were made to produce more moderate sized animals. In the last ten years, more breeders have recognized that intermediate size is preferable to extremes in any direction. However, they continue to be in the minority, and extremely large cattle have continued to be favoured in many major herds.

3.3 Design of the breeding schemes

Designing a breeding programme requires taking a range of decisions in a logical order. The designer of the programme should be aware that such a process evolves over time – from the simple to increasing levels of sophistication as organization and capacity develop. Most of the decisions involve determining how best to utilize present population structure to reliably generate the improvement and/or restructuring that is needed. Economic evaluation is an integral part of this process, and should be carried out both for the pre-implementation phase and for evaluating the change being realized when the programme is underway.

Investment decisions in the breeding programme should be assessed with respect to the three components contributing to the rate of genetic change: selection intensity, selection accuracy and generation interval. Based on these components, alternative scenarios are assessed. Theoretical knowledge of quantitative genetics is used to predict the gains to be expected from different scenarios (Falconer and Mackay, 1996). For this purpose, population genetic parameters such as heritability and phenotypic variation of the traits are needed to build up the selection index (reasonable assumptions can also be made) (Jiang *et al*., 1999). A suitable mating plan is then outlined. It must allow sufficient records to be obtained for genetic evaluation, and sufficient elite animals to be produced for the nucleus and for multiplication in the lower levels of the breeding pyramid. Note that in performing these activities, the designer of the programme is already in the optimization phase.

When designing the breeding programme, it should not be forgotten that most aspects are directly influenced by the reproductive rate of the breeding animals. A higher reproductive rate means that fewer breeding animals are needed. More offspring per breeding animal allows more accurate estimation of breeding value.

3.4 Data recording and management

Recording of performance data and pedigrees is the main driving force for genetic improvement. Abundant and accurate measurements lead to efficient selection. In practice, however, resources are limited. The question then is: which traits should be measured and on which animals? Preferably, the traits included in the breeding objective should be measured, but this will depend on the ease and cost of measurement. The nucleus animals, at least, should be measured for performance and pedigree.

The collection of performance data on which to base selection decisions is a vital component of any breeding programme, and it should be regarded as such, rather than as a by-product of recording systems primarily designed to assist short-term management (Bichard, 2002). The task of collecting, collating and using data in genetic evaluation requires good organization and considerable resources (Wickham, 2005; Olori *et al.*, 2005). In many instances, special schemes may need to be put in place to generate and record the required data. The cost and complexity of these schemes vary depending on the type of breeding organization, the type of traits, and the method of testing.

Type of breeding organization: pig and poultry breeding companies have in-house facilities for the collection and storage of all required data, whereas other breeding organizations may rely on resources owned by more than one stakeholder. For example, this is the case in a typical dairy cattle breeding programme (see subchapter 4.1).

Type of trait: when body weight of live animals is the trait of interest, all that is needed is a weighing scale. However, to measure feed efficiency in individual animals, more sophisticated equipment may be needed to allow the recording of individual feed intake.

Performance versus progeny or sib testing: in a performance-testing scheme, the traits of interest are recorded directly in every individual. For example, body weight and growth are often recorded over a fixed period during the lifespan of beef cattle, pigs, broiler chickens or turkeys. Basically, a cohort of animals is managed together under similar conditions over a period of time during which individual performance is measured. This can be done on the farm, or at a performance test station where cattle or pigs from different herds or farms are brought together for a direct comparison under the same conditions.

Sometimes, the information of interest may not be measurable directly in the selection candidate, either because the expression of the trait is sex-limited as in the case of milk and egg production, or because the traits can only be recorded after the death of the animal (e.g. carcass composition). In these circumstances, indirect recording by progeny and/or sib testing is required. This is also useful for traits with low heritability which may require several records to accurately evaluate an individual. Progeny testing refers to a scheme in which an individual is evaluated on the basis of performance records obtained from its progeny. It is mainly associated with males (Willis, 1991), as it is easier to generate large numbers of progeny from a single male than from a single female. Typically, not all males are progeny tested, but only the males born from “elite matings”. Progeny testing is very useful to increase selection accuracy for species with low reproductive rates, and to test genotype–environment interactions.

For many ruminant species, the cost of a central progeny testing facility may be prohibitive. It is, therefore, a common practice to involve as many farmers or commercial producers as possible. The farmers are encouraged to accept semen from a group of young sires to be used on a proportion of their female animals. Because the young sires are not of proven genetic merit, farmers involved in progeny testing often require good incentives to participate (Olori *et al.*, 2005). In these circumstances, the total costs (several hundred thousand US Dollars) are often borne by the owners of the young sire under test.

In addition to performance records, genetic evaluation in a breeding programme requires pedigree information. The quality of pedigree information depends on its depth and completeness. Whether the breeding objective involves genetic improvement or the prevention of extinction resulting from a loss of genetic variation, the pedigree of all breeding animals must be recorded and maintained.

When the resources are available, a centralized database with shared access has been shown to be beneficial and cost effective (Wickham, 2005; Olori *et al.*, 2005). The provision of comprehensive management-related information from such a system often serves as a stimulus for further participation in data recording schemes. The requirement for small breeding programmes may simply be a single personal computer with adequate spreadsheet, data management and reporting software, while national-level programmes may require a specialized department utilizing modern information technology (Grogan, 2005; Olori *et al.*, 2005).

3.5 Genetic evaluation

Progress in a breeding programme requires that animals of superior genotypes for the traits of interest are identified and selected to breed the next generation. Identifying these animals requires disentangling the environmental contribution from the phenotypic observation. This is accomplished by breeding value prediction or genetic evaluation. This is a core activity in every breeding programme.

The genetic evaluation should be reliable. BLUP methodology, applied to a variety of models depending on the traits and data available, has become the standard method for nearly all species. The evaluation should also be available in time to make the best use of the investment in data collection and database management. A genetic evaluation system using BLUP relies on good data measurement and structure. If these prerequisites are in place, investment in BLUP is usually highly cost effective.

Across-herd evaluation has the advantage of allowing fair comparisons of predicted breeding values (PBVs) of animals in different herds, which leads to selection of more animals from the genetically superior herds. To do this, genetic links (usage of animals across herds and across years) are critical. In order to use the information from different herds, an adequate organizational structure is needed. This can be achieved through close collaboration between breeders, their associations, and universities or research centres. Unique identification for all animals that supply data for the breeding scheme is essential. The data analysts, with guidance and assistance from breed association personnel, assign animals to contemporary groups (groups of animals of about the same age that are raised together with the same treatment). This assignment may be critical for accurate genetic evaluation. The breeders submit data to the association, and after checking for obvious errors, the information is forwarded to the evaluation team for analysis. For ruminants, the evaluations are performed once or twice a year, but for pig and poultry meat programmes, where the selection is performed on a monthly, weekly or bi-weekly basis, evaluations are run continuously.

The results of the genetic predictions (PBV and aggregate indices) are typically printed on the animals' registration certificates. It is common to print PBVs in sale and semen catalogues. This means that the end users (farmers) have to understand and accept the EBVs that are produced, and know how to use them. There is no sense in running a genetic evaluation if the results are left untouched by the end users.

A typical genetic evaluation unit requires both qualified staff, and adequate material resources to carry out data analysis and produce suitable reports to facilitate selection decisions. Many large-scale breeding programmes have a dedicated genetic evaluation unit in-house. However, it is also easy to contract this evaluation out to an external institution. Many universities and research centres provide a genetic evaluation service for national and non-national breeding programmes. Such services can cover several different breeds or species, as the principle of genetic evaluation and the software involved will be similar in each case. Perhaps, the most popular genetic evaluation unit with international repute is the International Bull Evaluation Service (INTERBULL). The centre, which is based at the Swedish Agricultural University in Uppsala, was set up as a permanent subcommittee of the International Committee for Animal Recording (ICAR), and provides international genetic evaluation to facilitate the comparison and selection of dairy bulls on an international scale. Another example is BREEDPLAN, a commercial beef cattle genetic evaluation service with an operational base in Australia, which has clients in many countries.

3.6 Selection and mating

Selection should predominantly be based on the selection criterion. From each sex, as few breeding animals as possible should be selected to maximize selection intensity, with the only restrictions being the number of animals required for a minimum population size, and the number needed for reproductive purposes. As reproductive rates of males are generally much higher than those of females, far fewer breeding males than females are normally selected.

Selection candidates may be of different ages, and thus unequal amounts of information may be available about them. For example, older males may have a progeny test, while for younger ones, their own performance, or that of their dam or sibs, will be the only information available. If BLUP is used, such candidates can be easily and fairly compared. Selecting more animals with accurate EBVs, and only the very best animals with less accurate EBVs, is probably the best approach.

It is widely accepted that the use of family information, as occurs in BLUP, increases the probability of co-selection of close relatives, which in turn leads to increased inbreeding. Various methods are used to reduce inbreeding while maintaining high rates of genetic gain. All these methods are based on the same principle – reducing the average relationship between the individuals selected. Computer programmes have been developed to optimize selection decisions for a given list of candidates for which pedigree information and EBVs are available. Ad hoc methods to control inbreeding include selecting a sufficient number of males, as the rate of inbreeding depends on effective population size; not overusing the males within the nucleus; restricting the number of close relatives selected, especially the number of males selected per family; limiting the number of females mated to each male; and avoiding mating between full and half sibs. These simple rules have been quite effective in maintaining a low level of inbreeding in commercial poultry and pig breeding.

Mating of selected animals may or may not be at random. In the latter case, the very best of the selected males are mated to the very best of the selected females – this is known as assortative mating. The average genetic value of the progeny born in the next generation does not change, but there will be more variance among the progeny. When multiple traits are included in the breeding objective, assortative mating may be useful – matching qualities in different parents for different traits.

Any mating strategy will require sufficient facilities. For natural mating, animals to be mated have to be put together in the same paddock, but separated from other animals of reproductive age. AI can be used, but also requires a range of resources and expertise (semen collection, freezing and/or storing, and insemination).

3.7 Progress monitoring

This involves the periodic evaluation of the programme with respect to progress towards the desired goal. If necessary, it leads to a reassessment of the goal and/or the breeding strategy. Monitoring is also important to ensure early detection of undesired effects of the selection process, such as increased susceptibility to diseases or a reduction in genetic variation.

To assess progress, phenotypic and genetic trends are usually obtained by regressing average annual phenotypic and breeding values on year of birth. In addition to this information, breeders run regular internal and external performance testing. An external testing scheme needs to cover a wide range of production environments to ensure that selected animals can perform well under a wide range of conditions. Other sources of information, and probably the most important, are field results and feedback from customers. Ultimately, the customer is the best judge of the work done.

3.8 Dissemination of genetic progress

The value of superior individuals is limited if they do not efficiently contribute to the improvement of the gene pool of the whole target population. The wide impact of genetic improvement depends on the dissemination of genetic material. Reproductive technologies, especially AI, are very important in this respect. However, their impact varies between species. In sheep and goat breeding, the exchange of genetic material largely depends on trade in live animals. In the case of cattle, AI allows bulls selected in the nucleus to be used across the whole population. In principle, there is no problem in allowing an exceptional bull to have many progeny throughout the population. However, performing AI using semen from bulls from the same family very intensively will ultimately lead to inbreeding.

It should be possible to apply the elements described above even under basic conditions. Breeding structures do not necessarily require sophisticated systems of data recording and genetic evaluation, nor do they initially require use of reproductive technologies. The breeding structure should be determined in accordance with what is possible and what is optimum. Environmental or infrastructure restrictions, tradition, and socio-economic conditions have to be considered when planning breeding programmes.

4 Breeding programmes in high-input systems

In high-input systems, continuous genetic improvement is generated mainly by straight-breeding within a breed or line. In the case of ruminants, this is largely a result of the strong position and active work of breeding associations, and of the spectacular results obtained by this method. Cross-breeding is used to realize the benefits of hybrid vigour (heterosis) and complementarity. In poultry and pigs, breeders concentrate their efforts on within-breed or line selection, and use cross-breeding to capitalize on heterosis for fitness traits and on complementarity for other traits.

The number of livestock breeding companies in the world is relatively low, but they are of great economic significance. They increasingly operate on a global scale. As the following subchapters will illustrate, the structure, including the ownership, of breeding organizations differs greatly between species.

4.1 Dairy and beef cattle breeding

Selection criteria

In dairy cattle, the average milk, fat and protein production per cow per year has increased enormously in the past decades as a result of the widespread use of breeds such as the Holstein-Friesian and intensive within-breed selection. This increase is also a reflection of the fact that productivity has for many years been an important selection objective, with selection mainly being based on production and morphological traits.

Recent years have seen a growing concern on the part of consumers about animal welfare issues, and about the use of antibiotics in livestock production. Breeding organizations have also realized that selecting solely for product output per animal leads to a deterioration of animals' health and reproductive performance, increased metabolic stress and reduced longevity (Rauw *et al*., 1998). As a result, emphasis on functional traits has increased, and less attention is paid to product output. Selection for functional traits is now based on direct recording of these traits rather than through type traits. Breeding values for a wide range of functional traits have been developed and applied in most countries. This enables breeding organizations and farmers to pay direct attention to these traits in their selection decisions.

Box 81
Calving problems in Belgian White Blue cattle

In beef cattle, the demand for high-quality meat has led to the use of breeds, such as the Belgian White Blue, that have extreme phenotypes. However, this breed has an extremely high rate of caesarean sections (Lips *et al*., 2001). In the short term, this rate cannot be significantly reduced. The extreme muscularity of the Belgian White Blue is mainly caused by the myostatin gene, a single autosomal recessive gene which is located on chromosome 2. It is, therefore, questionable whether a reduction in calving difficulties can be realized while maintaining the extreme muscularity. Because of this, as well as the obvious animal welfare concerns, the future of the breed is questionable.

Breeders face difficulties in two areas – breeding (including recording) and marketing. With regard to breeding, there are problems associated with correlated responses to selection. In most cattle breeding programmes, an aggregate index is constructed that includes traits such as growth, milk yield, fertility, conformation, number of somatic cells in the milk, calving ease and duration of productive lifespan (for more details see Table 99). In dairy cattle, the main focus has been (and is still) put on milk yield, despite the negative genetic correlations between milk yield and reproduction and health-related traits. Undesired side-effects have, therefore, been observed – including lower fertility, and greater susceptibility to mastitis, leg problems and ketosis.

In beef cattle and in sheep, selection for growth has led to higher birth weights and increasing risk of birth problems. Higher growth rates can also be expected to increase the mature size of breeding females. This may result in lower reproductive rates if larger animals are unable to meet their nutritional requirements because of limitations in the quantity or quality of the available forage. These undesired effects can be avoided, or at least reduced, by increasing the weight of functional traits within selection indices. This supposes that these traits can be directly measured. Recording of functional traits often remains an important bottleneck hindering their inclusion in breeding schemes. This is illustrated by the example of efficiency of feed utilization. Recording feed intake in a large number of animals is currently impossible – preventing efficient selection for this trait.

Box 82
Cross-breeding to address inbreeding-related problems in Holstein cattle

The Holstein breed, which is composed almost completely of American Holstein genes, has largely replaced other breeds of dairy cattle throughout much of the world. Production and conformation traits have been emphasized in the breeding of Holsteins because of moderately high heritability and ease of data collection. However, female fertility, calving ease, calf mortality, health and survival have been ignored until very recently. Problems related to functional traits, coupled with increased inbreeding on an international scale, have resulted in tremendous interest in cross-breeding among commercial dairy producers. Pure-bred sires will continue to be sought to breed almost all dairy heifers and cows for cross-breeding. Most cross-breeding systems with dairy cattle will make use of three breeds to optimize the average level of heterosis across generations.

For further information see Hansen (2006)

There are also problems related to marketing. For milk, good management practices have been in place in many countries for a long time, and product quality has a direct impact on the price paid to producers. In the case of meat, however, traceability and organization in the production chain has traditionally been poor. This limits opportunities to improve quality. In general, farmers are not rewarded for meat quality, and often only poorly rewarded for carcass quality.

Table 99
Breeding objectives in ruminants

Objectives/product	Criteria	Further specification
Production traits		
Milk	Quantity	Milk carrier production
	Contents/quality	% protein, % fat, somatic cell count, milk coagulation
Beef	Growth rate	At different ages
	Carcass quality	Fat content, bone/meat ratio
	Meat quality	Tenderness, juiciness
Wool	Quantity	
	Fibre quality	Length, diameter
Functional traits		
Health and welfare	Genetic defects	BLAD, MF and CVM
	Mastitis incidence	
	Udder conformation	Udder attachment, udder depth and teat traits
	Feet and leg problems	
	Locomotion	Indicator of hoof disorders
Reproduction efficiency	Female fertility	Showing heat, pregnancy rate
	Male fertility	Non-return rate
	Calving ease	Direct and maternal effects, still births
	Number of live offspring	
Feed Efficiency	Feed conversion efficiency	
	Milk production persistency	
Workability	Milkability	Milking speed
	Behaviour	
Longevity	Functional herd life	

Box 83
Norwegian Red Cattle - selection for functional traits

The Norwegian Red (NRF) is a high-producing dairy cattle breed in which fertility and health have been included in a selection index (known as the Total Merit Index) which has been in operation since the 1970s. The case of the NRF provides a practical illustration that production and functional traits can be successfully balanced in a sustainable breeding programme. This achievement has been based on an effective recording system and a willingness to place sufficient weight on the functional traits. The programme is run by GENO, a cooperative owned and managed by Norwegian dairy farmers. Currently, ten traits are included in the Total Merit Index. The following list shows the relative weight given to each:

Milk index	0.24
Mastitis resistance	0.22
Fertility	0.15
Udder	0.15
Beef (growth rate)	0.09
Legs	0.06
Temperament	0.04
Other diseases	0.03
Stillbirths	0.01
Calving ease	0.01

Photo credit: Erling Fimland

Key features of the programme include the fact that more than 95 percent of herds participate in the recording system and are on a computerized mating plan, 90 percent of matings are carried out using AI, and there is 40 percent use of test bulls. All diagnosis and health registration is carried out by veterinarians, and databases are maintained for pedigree and AI-related information. About 120 young bulls are tested annually with progeny groups of 250 to 300 daughters – thus enabling the inclusion of traits with low heritability (such as mastitis with a heritability of 0.03 and other diseases with 0.01) while still providing a selection index with high accuracy.

Milk production per lactation in the best herds exceeds 10 000 kg, with the top cows producing more than 16 000 kg. The genetic trend is positive with respect to fertility – the average 60 day non-return rate in the population is 73.4 percent. Between 1999 and 2005 incidence of mastitis in NRF cows was reduced from 28 percent to 21 percent, and it is estimated that of this reduction 0.35 percent per year was the result of genetic improvement. Major calving difficulties are reported in less than 2 percent of calvings, and less than 3 percent of calves are stillborn.

The sustainability of the breeding programme is promoted by a number of factors:

Both production and function are expressed by many traits, and they are both strongly weighted in the breeding strategy.

Many different combinations can result in a high total breeding value. This allows for the selection of animals from different breeding lines and, thus, automatically reduces the risk of inbreeding.

The breeding work is based on data from ordinary dairy herds, which guarantees that the breeding programme produces animals that are well adapted to normal production conditions.

Provided by Erling Fimland
For further information, see: http://www.geno.no/genonett/presentasjonsdel/engelsk/default.asp?menyvalg_id=418

Organization and evolution of the breeding sector

Because of the low reproductive rate, the long generation interval and the large amount of space required to house each animal, cattle breeding has a more complex and more open organizational structure than poultry or pig breeding. Gene flow can occur both from the breeder to the producer and vice versa. Information resources are shared between players at different levels. In a typical dairy cattle breeding programme, pedigree information is often recorded, owned and managed by breed societies, while milk production records are owned by farmers, but collected and managed by milk recording organizations. Information on fertility and reproductive performance are kept by companies that provide AI services, while health information generally resides with veterinarians. Often, these organizations are in decentralized locations and may store information in different systems.

Because cattle production is a major traditional agricultural enterprise and because breeding has a major impact on this enterprise, cattle breeding programmes have more input from government agencies than do poultry or pig breeding, and therefore have a country-specific outlook. Most programmes were either initiated or sustained with support or grants from national government agencies (Wickham, 2005). Organizations such as the Animal Improvement Programs Laboratory (AIPL) of the United States Department of Agriculture (USDA), Canadian Dairy Network (CDN), Cr-Delta in the Netherlands, and l'Institut de l'Elevage (IE) in France, play major roles in cattle breeding programmes in their respective countries, especially in data management and genetic evaluation. This is also the case for breed societies, which have played a major role in maintaining and enhancing the integrity of their respective breeds. The success of the Holstein-Friesian, which is by far the dominant sire breed in most dairy herds in the Western world, is testimony to the activities of the World Holstein-Friesian Federation (WHFF). The formation of herd books with dedicated members and the importance of show ring performance (which are strictly within-breed affairs) have helped sustain pure-breed development and the maintenance of all major breeds of dairy and beef cattle.

The selection programmes conducted by AI centres have developed from local to national schemes, and are increasingly operating internationally. The dissemination of genetic material from "superior" animals is now global. It is predicted that within the next ten to 15 years AI centres will become unified into a few worldwide breeding companies, such as now exist in the pig and poultry sectors. For example, in the early 1990s the "Genus" breeding programme was the major cattle programme in the United Kingdom. Over the years, Genus has merged with ABS genetics from the United States of America to form a global company, which now supplies bovine genetics from a variety of dairy and beef cattle breeds to over 70 countries. More recently, Genus bought Sygen, a biotech company.

Breeding programmes in cattle rely on commercial producers to generate sufficient data for genetic evaluation. Data recording, therefore, takes place in all tiers of the breeding pyramid. This requirement is greatest in the case of dairy programmes, which require large progeny groups for the accurate evaluation of bulls (especially for traits with low heritability), or in beef cattle to be able to estimate direct and maternal effects. The use of AI to disseminate semen across many herds is prevalent, and this helps to facilitate the comparison of animals raised in different environments. AI also enables higher intensity in the selection of males.

Successful selection within dairy cattle breeds is the result of well-organized programmes for the measurement of production, testing of young bulls and effective genetic evaluation. The high level of feeding in commercial dairy production allows a high proportion of a cow's genetic potential to be expressed, which in turn allows selection to be particularly effective.

Cross-breeding studies with dairy cattle have consistently found significant levels of heterosis between dairy breeds for milk production, fertility and survival traits. However, successful long-term selection for high levels of milk production in the Holstein-Friesian has led to the widespread use of straight-bred animals of this breed. However, increasing pressure from commercial producers, who are suffering losses related to poor fertility and longevity, and the need for flexibility in product development is likely in the future to lead to increased development of hybrid cattle at the breeding programme level.

Cross-breeding applied to beef cattle is often undertaken without a well-designed programme. In beef cattle, cross-breeding programmes are difficult to implement in herds that use fewer than four bulls. Even for larger operations, managing the herds separately, as is required in organized cross-breeding programmes, can be difficult (Gregory *et al.*, 1999).

In cattle, the introduction of AI has resulted in an enormous reduction of the number of sires and contributed to the exchange of genetic material between regions and countries. Through AI, bulls selected in the nucleus are used in the general population. As a result of the high reproductive rate of sires, the selection of bulls contributes 70 percent to total genetic change in dairy and beef cattle populations.

4.2 Sheep and goat breeding

Selection criteria

Sheep and goats are kept for meat, milk, and wool or fibre (see Table 99 for corresponding breeding goals). Sheep milk is an important product in Mediterranean countries. It is mainly transformed into a variety of cheeses (e.g. Roquefort, Fiore Sardo, Pecorino Romano and Feta). Milk production and quality are important breeding criteria. Milk sheep may also be bred for growth rate, reproductive traits such as twinning rate, and type traits such as udder shape (Mavrogenis, 2000). Conversely, in northwestern Europe, meat is the most significant product obtained from sheep. Specific breeding objectives will depend on the production environment (e.g. mountain vs. lowland), and may include growth rates, carcass quality, reproductive performance and maternal abilities. Commercial wool production is dominated by Australia and New Zealand with their specialized flocks of straight-bred fine-wool sheep of the Merino type. Although the animals all descend from the Merino sheep of Spain, different strains have been developed over the years. The need for animals adapted to specific environmental conditions has shaped breed development. In Australia, for example, different strains of Merino have been bred for their adaptation to the environment in different parts of the country. With respect to wool production, criteria for selection normally include clean fleece weight and fibre diameter. Increasing economic importance of meat relative to wool has led to a shifting of breeding objectives towards criteria such as reproduction rate and sale weight.

In Mediterranean countries, in South Asia, and in parts of Latin America and Africa, goats are mainly kept for their milk. In Mediterranean countries and in Latin America, goat milk is often used for cheese production, whereas in Africa and South Asia, it is consumed raw or acidified. In other parts of Asia and Africa, goats are kept mainly for meat production. In these regions very little supplemental feeding is provided, and browse provides a significant amount of the nutritional requirements. The animals are of moderate to small size, and of moderate to light muscling. An exception is the development of the Boer goat for meat production in South Africa. The breed has been introduced to other countries in Africa and to other parts of the world such as Australia.

Organization of the breeding sector

Major breeding programmes for fine-wool sheep are based in the southern hemisphere (Australia and New Zealand). These programmes are based on straight-breeding. However, in fine-wool sheep operations where a significant part of the income is from lambs (for slaughter), self-contained F1 production has been used. Under this type of programme, all ewes are straight-bred for fine wool. A large fraction of the selected ewes are mated to fine-wool rams to produce replacement females. The remaining ewes are mated to terminal sires and all the lambs are sold.

In the case of meat sheep breeding, the average size of flocks is generally too small to allow intensive within-flock selection. This problem has been overcome through cooperative breeding schemes. Nucleus breeding schemes are well established (e.g. James, 1977), but sire-referencing schemes (SRS) have recently gained popularity. In SRS, genetic links are created between flocks by mutual use of specific rams (reference sires). These connections allow comparable across-flock genetic evaluation, offering a larger pool of candidates for selection for collective goals. About two-thirds of performance-recorded sheep in the United Kingdom, including all of the major specialized meat breeds, now belong to these schemes (Lewis and Simm, 2002).

Cross-breeding is the basis of the stratified sheep industry of the United Kingdom (Simm, 1998). The system functions on the basis of a loose structure involving several breed societies, government agencies and other institutions. Traditional hill breeds such as the Scottish Blackface are straight-bred under the harsh production conditions of the hills. Ewes from these pure breeds are sold to farmers in "upland" areas (where the climate is less harsh and there is better grazing). Here, they are crossed with rams from intermediate crossing breeds such the Blueface Leicester. F1 Females are sold for breeding in lowland flocks where they are mated to terminal-sire breeds such as the Suffolk and the Texel. Most data recording and genetic evaluation aim at improving the terminal-sire breeds to produce rams of superior genetic quality. Data recording and genetic evaluations are carried out by commercial operations such as Signet or by research institutions supported by public funds.

Most dairy goats are in developing countries. However, breeding programmes are concentrated mainly in Europe and North America. The French selection programme, based on AI with frozen semen and oestrus synchronization (60 000 goats inseminated/year), and the Norwegian programme, based on rotation of sires in several herds (buck circles), are examples of organized progeny testing programmes. They include a formal definition of selection objectives and organized mating to produce young sires and their progeny. Probably, the best example of a structured meat goat breeding programme is that run by the Boer Goat Breeders' Association of Australia. Cashmere and mohair production is based on straight-breeding of the respective breeds. There is almost no cross-breeding involving Angoras.

4.3 Pig and poultry breeding

Selection criteria in pigs

As in the case of ruminants, pig breeding programmes have been very successful in achieving genetic improvement of economically important traits, especially daily gain, backfat thickness, feed efficiency and, during the last decade, litter size (for more details see Table 100). At present, the goal is to breed for more robust and efficient animals to meet different environmental conditions. This implies finding an adequate strategy to deal with genotype × environment interaction, and the placing of more emphasis on secondary traits which have up to the present been of negligible economic importance. Secondary traits include piglet survival, interval between weaning and first oestrus, longevity of sows, conformation (especially legs), vitality of pigs until slaughter weight, meat colour and drip loss. The health of the pigs is becoming more important. This means not only improving the sanitary status in breeding farms, but also selecting for general disease resistance under commercial conditions.

Table100
Breeding objectives in pigs

Objectives	Criteria	Further specification
Production traits		
	Growth rate	At different ages
	Carcass weight	
	Carcass quality	Uniformity, leanness of carcass
	Meat quality	Water holding capacity, colour, flavour
Functional traits		
Health and welfare	General resistance	Robustness
	Vital piglets	Maternal ability, Teat number
	Survival of pigs	
	Stress	Elimination of stress (halothane) gene in dam lines, and where possible, in male lines
	Congenital effects	Example: Atresia Ani, Cryptorchism, Splay leg, Hermaphrodism and Hernia
	Leg problems	Leg weakness and lameness.
Efficiency	Litter size	Number of slaughter pigs per sow per year
	Feed conversion efficiency	
Longevity	Functional herd life	Lifetime production with minimal health problems

As in the case of ruminants, there are some difficulties involved in implementing efficient selection for "functional" traits. There are still no appropriate tools to select for better resistance to diseases or to reduce metabolic disorders. Sufficient knowledge of the genetic aspects of welfare is lacking. Stress recording methods need to be improved – for example, through the use of non-invasive methods for measuring stress-indicating parameters, determination of catecholamine levels, and heart-rate recording on under-skin chips. Improved knowledge of the cognitive abilities and coping strategies of pigs might enable individual characteristics to become indicative of ability to adapt to various housing conditions and social challenges, and could be included in selection criteria. Additionally, there is a need for further assessment of the impact of selection for specific disease resistance and welfare objectives.

Selection criteria in poultry

Laying hens have been selected mainly for productivity. Over several decades, breeding programmes were refined, and more and more traits were included in the selection objectives. Today, the main selection objectives are: the number of saleable eggs per hen housed per year, efficiency of converting feed into eggs, external and internal egg quality, and adaptability to different environments (for more details see Table 101).

Table 101
Breeding objectives in poultry

Objectives/product	Criteria	Further specification
Production traits		
Egg	Egg number	Number of saleable eggs per hen
	External egg quality	Average egg weight, shell strength and colour
	Internal egg quality	Egg composition (yolk/albumen ratio), firmness of albumen and freedom from inclusions (blood and meat spots).
Meat	Growth rate	Weight gain; age at market weight
	Carcass quality	"Yield" in terms of valuable parts, especially breast meat; select against breast blisters and other defects to reduce condemnation rate
Functional traits		
Health and welfare	Disease resistance	Not routinely used
	Monofactorial genetic defects	
	Leg problems in broilers and turkeys	
	Osteoporosis in laying hens	
	Heart and lung insufficiency	Incidence of "sudden death syndrome" and ascites in broilers and "round heart" in turkeys
	Cannibalism, feather pecking	
Feed efficiency	Feed consumption per – kg egg mass in laying hens, – kg weight gain in broilers and turkeys Residual feed consumption	
Longevity	Length of productive life	

For poultry meat, substantial genetic improvements in terms of market weight at a younger age and correlated feed efficiency have been achieved by simple mass selection for juvenile growth rate and "conformation". During the 1970s, direct selection for efficient feed conversion was introduced. During the last two decades, the emphasis of selection has shifted increasingly to traits that are of primary importance to processing plants – breast meat yield, total carcass value, efficiency of lean meat production, uniformity of product, and low mortality and condemnation rates. The development of specialized male and female lines, and the introduction of controlled feeding of parents, are effective tools to overcome the negative correlation between juvenile growth rate and reproductive traits.

The most obvious challenges for the poultry industry are related to diseases. Primary breeding companies have eliminated egg-transmitted disease agents such as leucosis virus, mycoplasms and salmonella from their elite stock, and continue to monitor freedom from these problems. Other diseases such as Marek's disease, *E. coli*, *Campylobacter coli*, and highly pathogenic avian influenza are more difficult to control.

In the field of animal welfare, the main challenges for breeders are to adapt laying hens to alternative management systems – for example, to reduce feather pecking and cannibalism in non-cage systems (pecking and cannibalism are also serious problems for turkeys and waterfowl), and to reduce the incidence of cardio-vascular insufficiencies (sudden death syndrome and ascites) and leg problems in broilers and turkeys. However, the causes of these problems are probably multifactorial, and further research is required.

Organization and evolution of pig and poultry breeding sectors

The modern poultry industry has a typical hierarchical structure with several distinct tiers. Breeding companies, based mainly in Europe and North America with subsidiaries in major production regions, own the pure lines. They have to keep the whole production chain in mind – hatcheries, egg and meat poultry growers, processing plants, retailers and consumers. Hatcheries (multipliers) are located near population centres around the world. They receive either parents or grandparents from the breeders as day-old chicks, and produce the final crosses for egg producers and broiler, turkey or duck growers. Today, egg processing plants, slaughterhouses and feed suppliers have developed contractual relationships with egg producers and poultry growers, which provide the latter with better financial security, but at the cost of reduced initiative and freedom.

The pig sector has a similar pyramidal structure, which is largely the result of the introduction of cross-breeding, AI and specialized breeding farms. However, some differences exist between the pig and the poultry sectors. For example, a pig producer will typically obtain the "commercial" animals by mating sows from a specialized dam line and boars from a specialized sire line – both genders being bought from the breeding company (and not from a multiplier as in poultry).

In contrast to poultry, there are still breeding associations for pigs, and national genetic evaluation is performed. While genetic evaluations for the large breeding companies may be performed in-house, genetic evaluations at the pure-breed level are conducted by governmental institutions (e.g. by the National Swine Registry in the United States of America) or breed associations.

Pig and poultry breeding schemes are sometimes referred to as "commercial" breeding programmes because of the corporate ownership structure of these companies. Over the years, these programmes have amalgamated to become large corporations. In poultry, for example, only two to three groups of primary breeders account for about 90 percent of the layers, broilers and turkeys produced annually. Furthermore, some of these companies are owned by the same group. The pig breeding industry has more breeding companies and fewer large ones (such as PIC and Monsanto), but is following the same trend. The recent entry of the giant Monsanto into this sector is a clear indication of this tendency. Because of the competitive nature of the business and the high level of investment, "commercial" breeding companies are usually at the forefront in the application of technologies. These leading companies are on the verge of incorporating genomic information in their breeding programmes, at a time when many breeders are merely discussing the feasibility of the approach.

The activities of these commercial breeding companies are characterized by the following features:

- Pedigree selection occurs in the nucleus only.
- Selection is strictly within specialized lines (or breeds). These lines are designated as sire and dam lines and are selected with different intensities. In poultry bred for meat and in pigs, male lines are selected for growth and lean meat production, while female lines are selected for reproduction. New lines are constantly developed either by crossing between existing lines or by further selection in a given direction.
- The final product is a cross between two or more pure-bred lines.

For economic reasons, each breeding company will sell under several trademarks (accumulated through acquisitions and fusions), but will in fact only have a limited number of differentiated products. Indeed, pig or poultry breeding companies develop lines to meet few (two or three) breeding goals, which vary depending on the extent of their global market share and the degree of variation in the production environments in which the clients operate. For example, a breeder may develop a high-yielding, fast-growing line for use under high-input conditions where superior-quality feed allows the expression of the animals' full genetic potential, and a line for more challenging environments that is more "robust", but has lower performance for production traits.

5 Breeding programmes in low-input systems

5.1 Description of low-input systems

Many of the world's livestock will continue to be kept by smallholders and pastoralists. These producers often have limited access to external inputs and to commodity markets. Even if external inputs are locally available, there is usually little cash available for their purchase. To quote LPPS and Köhler-Rollefson (2005), "Cash products are often of secondary importance, especially in marginal and remote areas. Traditional breeds generate an array of benefits that are more difficult to grasp and to quantify than outputs of meat, milk, eggs or wool. These include their contribution to social cohesion and identity, their fulfilment of ritual and religious needs, their role in nutrient recycling and as providers of energy, and their capacity to serve as savings bank and insurance against droughts and other natural calamities."

The livestock owned by smallholders and pastoralists may be autochthonous or originate from early introductions of exotic breeds to the area. Traditional livestock keepers have no technical training in genetics and many are illiterate. However, they possess valuable local knowledge about breeds and their management. They have breeding goals and strategies even if they are not "formalized" or written down. For example, they may share breeding males (they seldom have more than one of a given species) with their neighbours or the entire community.

In conclusion, formalizing genetic improvement in these conditions is a challenging, but definitely not an impossible or inappropriate, task.

Box 84
Community-based sheep management in the Peruvian Andes

Agriculture in the central Andes of Peru is severely limited by low temperatures and drought, and most rural households depend on livestock for their income. Rangeland sheep are economically the most important species, and are used as a source of food, as a means of obtaining goods through exchange, and to generate cash through the sale of live animals or wool. To a lesser extent they are also used for cultural activities, recreation and tourism. Criollo sheep represent 60 percent of the Peruvian sheep population. They are mainly raised on family farms and by individual farmers, who value the local breed highly. A dual-purpose breed, developed from a cross between Criollo sheep and Corriedale sheep imported from Argentina, Australia, Chile, New Zealand and Uruguay between 1935 and 1954, is also available. Peasant farmers maintain both the Criollo and the composite breed.

In this part of Peru, peasant communities have organized themselves independently to improve the management of their sheep, with little support from the government. Multicommunal and communal enterprises, cooperatives, as well as family and individual farms, are common. Farmers exchange genetic material, experiences and technologies. Multicommunal and communal enterprises have far higher production rates than individual farmers. They have successfully set up participatory breed improvement programmes based on open-nucleus schemes, are technically efficient, keep their pastures in good condition, and use some of their profits to improve the social well-being of their members – for example, by buying school materials, selling milk and meat at reduced prices, and providing assistance to the elderly.

Provided by Kim-Ahn Tempelman
For further information see FAO (2007)

Box 85
Genetic improvement of an indigenous livestock breed – Boran cattle in Kenya

The Boran, a medium-sized cattle breed of East African origin, is the breed most widely kept primarily for beef production in the semi-arid zones of Kenya. Commercial ranchers prefer the Boran to *Bos taurus* breeds because of their relative adaptability to the local environment – achieved through generations of natural and artificial selection in conditions of high ambient temperature, poor feed quality, and high disease and parasite challenge. Boran genetic material is recommended as a means of improving beef production in other indigenous and exotic breeds in the tropics. Genetic exports to Zambia, the United Republic of Tanzania, Uganda, Australia and the United States of America occurred from the 1970s to the 1990s. Export of Boran embryos to Zimbabwe and South Africa took place during 1994 and 2000.

This market potential has been an incentive for farmers to improve the breed. By the 1970s, the Boran had undergone cross-breeding with *B. taurus* types, backcrossing, and within-breed selection (which was mainly based on visual appraisal guided by experience). During the 1970s a recording scheme was initiated. Producers sent animal performance records routinely to the Livestock Recording Centre (LRC) for genetic evaluation. However, because of inconsistency and delays in the release of evaluation results, and the expenses associated with recording, most producers opted out of the scheme. In 1998, a bull performance testing project was implemented by the National Beef Research Centre in an attempt to evaluate bulls across various herds. However, the performance testing could not be sustained because of a lack of funds.

Recently, breeding objectives for Boran production systems have been developed. Systems are classified according to the sale age of the animals (24 or 36 months), levels of input (low, medium or high), and final goal (beef or dual purpose). Traits of economic importance have been identified, and genetic parameters have been estimated for some of them. These traits include sale weight for steers and heifers, dressing percentage, consumable meat percentage, milk yield in dual purpose production systems, cow weight, cow weaning rate, cow survival rate, post-weaning survival rate, and feed intake of steers, heifers and cows.

Genetic improvement of the Boran in Kenya is facilitated by the Boran Cattle Breeders' Society (BCBS). Membership of the society is restricted to farmers keeping Boran cattle, and other interested stakeholders. At present, the activities of the society focus on administration, maintaining breed standards, and searching for new markets for both beef and genetic material. Farmers are still independent with respect to selection and genetic improvement. Occasional exchange of genetic material between herds as a means of preventing inbreeding is probably the only form of interaction between farms. On most farms, selection focuses largely on weaning weights and calving interval. To evaluate their animals, some farmers have purchased various computer programmes to enable them to re-orientate on-farm performance recording to suit their management purposes.

The BCBS is among the most active breeders' associations in Kenya. It is not at present subsidized financially, but is involved in strategic cooperation with the LRC which stores and evaluates performance records for those producers still participating in the recording scheme. The BCBS also cooperates with the National Agricultural Research System in the exchange of information – especially on nutrition and breeding. Research aimed at developing appropriate genetic improvement programmes for the Boran and updating the current ones is ongoing.

Provided by Alexander Kahi
For more information on the Boran cattle and BCBS, see http://www.borankenya.org

5.2 Breeding strategies

It is important to keep in mind that whatever strategy is considered, it will be successful only if certain conditions are met. Meeting these conditions does not guarantee success, but neglecting them will certainly lead to failure. The owners of the livestock should be involved as much as possible, and preferably from the very beginning of the programme. The social structure of the region and the objectives of the producers should be carefully taken into consideration. The whole system, and not only one element of it, needs to be considered. For example, when considering a cross-breeding scheme in a remote area, it is necessary to ensure that the progeny of cross-bred animals are viable in these conditions.

The programme should be as simple as possible. In some cases it may be feasible to cross-breed individual females to males from other breeds that are available in the vicinity, but programmes that require continuous use of males of more than one breed are not feasible under low-input systems.

Box 86
A llama breeding programme in Ayopaya, Bolivia

In the high Andes of Bolivia, llama keeping is an important and integral part of the mixed farming practised by rural households. Llamas provide smallholders with dung, meat and fibre; they are used as pack animals and also play an important social role. Llamas, as an autochthonous species, contribute to maintaining the ecological balance of the fragile local ecosystem. There are two main types of llama – the "Kh'ara" type and the wool type known as "Th'ampulli".

The region of Ayopaya (department of Cochabamba) where the breeding programme takes place is situated at 4 000 to 5 000 metres above sea level in the eastern Cordillera of the Andes. Because of the geographical conditions and very basic infrastructure, the region is difficult to access.

In 1998, a breeding programme for llamas was jointly initiated by the 120-member local producers association ORPACA (Organización de Productores Agropecuarios de Calientes), the NGO ASAR (Asociación de Servicios Rurales y Artesanales) and two universities (University Mayor de San Simon, Cochabamba, and University of Hohenheim, Germany). Initial funding was assured by the above-mentioned institutions. Continuation of the programme critically depends on securing external funding.

As a first step, the production system was studied by participative observation and the use of questionnaires. The phenotype of 2 183 llamas, of the Th'ampulli type, was also characterized. The process revealed that the llamas possess fibre of extraordinarily high quality – 91.7 percent fine fibres and a fibre diameter averaging 21.08 µm. This fibre quality is unmatched by other llama populations in Bolivia. The animals, therefore, constitute a unique genetic resource. Interviews with representatives of the textile industry and traders provided information on the economic potential of the fleece. The performance of identified llamas was recorded and breeding parameters estimated. A mating centre run by ASAR to which members of ORPACA bring their females for service was established in Calientes in 1999. Selected males are kept at the centre during the mating season. The phenotypic evaluation of the males aims to identify animals with uniform fleece colour; a straight back, legs and neck; testicles that are of equal size and not too small; and no congenital defects. Six communities within a radius of about 15 km are served by the mating centre. Performance data for the offspring are recorded by trained farmers.

Llamas in Ayopaya region

Photo credit: Michaela Nürnberg

Restraining llamas for transport

Photo credit: Michaela Nürnberg

Functions of llamas and breeding objectives are being recorded, ranked and valued jointly with the llama keepers. In a stepwise procedure, the breeding programme is being adapted to meet the breeders' preferences, the market conditions, and the biological constraints. Genetic progress has not yet been evaluated because of the llama's long generation interval.

Linear measurements on llamas

Photo credit: Javier Delgado

Deworming during sire selection at Milluni

Photo credit: André Markemann

Llama herd (of Emeterio Campos) in Ayopaya region

Photo credit: André Markemann

Provided by: Angelika Stemmer, André Markemann, Marianna Siegmund-Schultze, Anne Valle Zárate
Further information can be obtained from the following sources: Alandia (2003); Delgado Santivañez (2003); Markemann (forthcoming): Nürnberg, M. (2005); Wurzinger (2005), or from: Prof. Dr Anne Valle Zárate, Institute of Animal Production in the Tropics and Subtropics, University of Hohenheim, 70593 Stuttgart, Germany. E-mail: inst480a@uni-hohenheim.de

Breeding strategies

Determining the breeding objectives is the most important and difficult task in any genetic improvement programme, and there is even less margin for error in low-input systems. The questions that need to be considered under these conditions include: what (if anything) should be changed, and what would actually be an improvement in these conditions?

A low-input system is also a low-output system, but this does not necessarily mean low productivity. For the low-input system, it is inadequate to think of genetic improvement only in terms of increases in output traits, such as body weight, milk or egg production, or fleece weight. Efficiency is also a key criterion. Unfortunately, very little is known about the genetic improvement of intrinsic efficiency. Increased efficiency is usually measured in terms of increased gross efficiency. The increased gross efficiency observed in high-producing animals results from the fact that a lower proportion of the animals' nutrient intake is used for maintenance, and a correspondingly higher proportion is used for production. This does not mean that the animal needs less feed to achieve a given level of performance.

Box 87
Pastoralists' breeding criteria – insights from a community member

The East African pastoralists of the Karamoja cluster[4] keep a range of livestock including Zebu cattle, Small East African goats, Persian Black Head sheep, grey donkeys and light brown dromedaries. Some also keep indigenous chickens. Uses of livestock are diverse, and include food; a store of wealth, and a currency against which other commodities can be valued; a source of recreation and prestige; a means for the payment of debts, fines and compensations; a means of transport and agricultural traction; a source of skins and fibres; and a source of dung for fuel, fertilizer or building. Livestock also have many cultural roles such as being given to the bride's family at the time of marriage. They are also slaughtered at the time of rituals associated with births; funerals; the onset of transhumance; rain-making; averting bad omens, epidemics or enemy attack; cleansing ceremonies; or curing an ailment on the prescription of a village herbalist.

Criteria for breeding decisions are multifaceted, and reflect the interaction of social, economic and ecological factors. They include not only productivity, but also the taste of meat, blood, and milk; agreeable temperament; coat colour; religious requirements; disease and parasite resistance; mothering instincts; walking ability; tolerance of droughts; survival on meagre feed; and tolerance of extremes of temperature or precipitation.

Criteria for breeding decisions (in order of importance)

A breeding bull should:

be active and agile – so as to serve all the females in the herd in a given breeding period (it is considered that such bulls are tolerant of diseases and parasites, and that diseases in them are easily detected);

produce offspring that can maintain their body weight (and milk yield in the case of females) even during periods of feed shortage;

have large body size and weight – important for marketability and status, but be not too heavy to perform its breeding functions;

be tall, with a wide chest and straight back – again to meet breeding functions;

have the coat colour or horn configuration identified with the owner[5] or the community;

have a coat colour and quality suitable for marketing or other uses;

have good temperament – aggressive[6] towards predators, but not towards other livestock or humans;

bulls kept to breed offspring for draught purposes should have large body weight, and be strong and tractable;

breeding bulls should stay in the owner's herd, graze well, and not be fond of roaming or fighting other bulls.

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[4] "Karamoja Cluster": The entire Ateker people in Uganda, Kenya, Ethiopia and the Sudan who generally share a common livelihood. "Ateker" people: (variously called "Ngitunga/Itunga" = the people). The people with a common origin living in Uganda (NgiKarimojong including Pokot, Iteso), Kenya (NgiTurukana; Itesio, Pokot); Ethiopia (NgiNyangatom/NgiDongiro) and in the Sudan (NgiToposa) and their neighbours; who speak similar languages and refer to their clans as Ateker (pl. Ngatekerin / Atekerin). Some clans of Ateker people are spread all over Karamoja cluster.

[5] Pastoralists also base their own name on the colour or horn configuration of their favorite bulls. This is typical in the Karamoja Cluster. Such names have the prefix Apa- which means "the owner of the bull with a ... coat colour/horn configuration". For instance, the name "ApaLongor" means "the man with a bull with a brownish coat colour". The favourite breeding bull receives many privileges from the owner such as being adorned with a bell, or prompt treatment when ill.

[6] Indiscriminate aggression is unacceptable in livestock, even if other traits are favourable.

Female breeding animals should:

have a stable high milk yield that is not only tasty and has ample butterfat content, but is also able to maintain healthy and quick growth of the offspring;

be able to calve regularly and produce quick-growing offspring;

be tolerant of disease, heat, cold and long droughts;

survive on little feed and maintain high milk yield, particularly in the dry season when the feed quantity and quality is low;

the udder should be wide and the teats always complete;

cows should be docile to humans and other livestock, but aggressive towards predators;

small stock (goats, sheep) should regularly give birth to twins.[7]

The world should appreciate the role pastoralists play in sustainably utilizing their uniquely adapted breeds. Not only do these animals provide food and income security for their keepers, but they also contribute to the maintenance of genetic diversity, thereby providing a resource for future genetic improvement programmes. In this regard, pastoralists need appropriate support from livestock services provided by national governments, civil society organizations and the international community.

Provided by Thomas Loquang (member of the Karimojong pastoralist community)
For further information see: Loquang (2003); Loquang (2006a); Loquang (2006b); Loquang and Köhler-Rollefson (2005)

Selection based on residual feed intake (RFI) has been proposed as a means of improving intrinsic efficiency. This is an important criterion for all species and all production systems. Genetic selection to reduce RFI can result in animals that eat less without sacrificing growth or production performance (Herd *et al*., 1997; Richardson *et al*., 1998). For example, in contrast to the ratio of weight gain/feed intake, residual feed consumption is relatively independent of growth. RFI is therefore a more sensitive and precise measurement of feed utilization (Sainz and Paulino, 2004).

Box 88
The Bororo Zebu of the WoDaaBe in Niger – selection for reliability in an extreme environment

This example refers to cattle breeding in a specialized pastoral system in Niger. The WoDaaBe are full-time cattle keepers. Marketing livestock is the cornerstone of their livelihood strategy. Their herds contribute a substantial proportion of national cattle exports, particularly to the large markets of Nigeria where Bororo animals sell at a premium.

"Extreme environment" here refers to a combination of a harsh ecosystem characterized by stochastic events, and comparatively poor access to both primary resources and external inputs. WoDaaBe herders exploit a semi-arid territory characterized by erratic and unpredictable rainfall. In an ordinary year, fresh grass is available for only two to three months at any given location. Access to forage, water and services requires a degree of purchasing power and negotiation with neighbouring economic actors competing for these resources. The WoDaaBe are usually on the weaker side in these transactions.

It has been proposed that the concept of "reliability" is key to understanding the management strategies of pastoralists under such conditions (Roe *et al*., 1998). "High-reliability" pastoral systems are geared to the active management of hazards rather than their avoidance, with the aim of ensuring a steady flow of livestock production. In these systems, breeding has to be closely interconnected with the environment and the production strategy. The main goal of the WoDaaBe is to maximize the health and reproductive capacity of the herd throughout the year. Their management system aims to ensure that the animals eat the highest possible amount of the richest possible diet all year round (cf. Schareika, 2003). This involves specialized labour, focusing on managing the diversity and variability of both grazing resources and livestock capabilities.

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[7] Please note that it is a taboo for small ruminants to deliver twins at the first delivery. It is allowed only in the subsequent births. Similarly, it is a taboo for cattle to deliver twins whether at the first or subsequent delivery. Any such situations (births of twins) would lead to the animals concerned being slaughtered by stoning or beating. An animal in this situation is said to have become a witch and as such should be promptly eliminated!

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photos provided by Saverio Krätli

The nutritional value of the range is maximized by moving the herd across zones that show spatially and temporally heterogeneous distribution of fodder. Additionally, the animals' capacity as feeders is stretched beyond the natural level. While feeding capacity has in part a genetic base (for example the enzymatic system or the size and conformation of the mouth), it can also be greatly affected by learning, based on individual experience and imitation between social partners (for example efficient trekking and grazing behaviour and diet preferences). Animals' feeding motivation is manipulated through optimizing their digestive feedback, and ensuring best fodder quality and preferred foraging conditions. A carefully diversified diet of grasses and browses is favoured, in order to correct nutritional imbalances which, particularly during the dry season, could keep feeding motivation low by triggering negative digestive feedback. The dry-season watering regime is also tailored in order to hone cattle's digestive performance to meet the herders' long-term strategic goal of maximizing reproduction.

The production strategy is very demanding on both people and the herd. With the onset of the dry season, while other pastoral groups sharing the same ecosystem move closer to water points, where water is more accessible but pasture is poor, the WoDaaBe move in the opposite direction, trying to keep their camps close to prime fodder. This results in long-distance mobility and a watering regime which, at the peak of the hot season, often involves journeys of 25–30 kilometres to reach the well, with the herd drinking every third day.

It is, therefore, essential to the WoDaaBe's production strategy that functional behavioural patterns are maintained within the herd. Consequently, their breeding system focuses on fostering social organization and interaction within the herd. It encourages sharing of animals' feeding competence across the breeding network, and tries to guarantee, the genetic and "cultural" continuity of successful cattle lineages within the network. These lineages have proved capable of prospering under the WoDaaBe's herd management system, and over a long enough period to have included episodes of severe stress. The breeding strategy focuses on ensuring the reliability of the herd's reproductive performance, more than on maximizing individual performance in specific traits.

Breeding involves selective mating of cows with matched sires, and a marketing policy that targets unproductive cows. Less than 2 percent of the males are used for reproduction. Close monitoring of the herd allows early detection of oestrus and ensures that more than 95 percent of births result from match-making with selected males. A different sire is used for almost every oestrus of a particular cow, with an overall ratio of about one sire every four births. Pedigree sires are borrowed across large networks of (often related) breeders. Sire borrowing remains frequent (affecting about half the births) even when a breeder owns pedigree sires of his own. Match-making with non-pedigree sires, owned or borrowed, affects about 12 percent of births. Both practices are maintained explicitly in order to preserve variability. Matrilineal genealogies and the sire of each animal in the herd are usually remembered, together with pedigrees of special sires, and the identity and owner of all borrowed sires.

A cow's productivity depends heavily on how well the animal responds to the management system. By adopting a production strategy that manipulates the animals' experience of the ecosystem, the herder exposes his animals to diverse natural environments involving particular combinations of favourable and unfavourable foraging and watering conditions. Over the years, some cows prosper and produce a numerous progeny while others die, or struggle and are sold. In this way, the WoDaaBe are able to harness natural selection pressure for their breeding purposes.

Provided by Saverio Krätli
For more information see: Krätli (2007)

Data recording in low-input systems

The absence of a credible recording scheme and resources for adequate data storage and management hinder the development of sustainable breeding programmes in low-input systems. Running a computerized database can be expensive and may require specialized skills. The absence of technical skills and financial resources has been identified as the main obstacle to the establishment of sustainable animal recording systems in many African countries (Djemali, 2005). Continuous advances in information technology mean that data recording devices are becoming cheaper and offer greater potential for recording in low-input systems. The use of hand-held devices, laptops and the

Internet could make it easier for small numbers of people to gather and transmit large amounts of data from remote locations to a central database. Such a database could be based in a university or a government department. Provision of facilities of this type is one way in which governments or donor agencies could facilitate the development of breeding programmes for low-input systems in developing countries.

Box 89
Community-driven breeding programmes for local pig breeds in north Viet Nam

In the mountainous areas of Northwest Viet Nam, livestock breeding and management programmes, can contribute to improving rural livelihoods if they respect the production objectives, intensity and resource-availability of the area's resource-poor smallholder mixed farming systems. The local Ban pig which shows considerable hardiness, but has a low reproductive and growth performance is increasingly being replaced by higher-yielding Vietnamese Mong Cai sows from the Red River Delta.

In a collaborative project between the National Institute of Animal Husbandry (NIAH) Hanoi and the University of Hohenheim, Germany[8], community-based pig breeding programmes have been established in seven villages, differing in terms of their remoteness and market access.

A total of 176 households currently participate in the programmes. On-farm performance testing schemes have been developed. Farmers are provided with data sheets on which they record the performance of their pigs (mainly date of farrowing and number of piglets). Vietnamese and German researchers cross-check data and collect additional data by weighing and identifying animals when they visit the villages. Specially trained farmers enter the data into the project databank using the PigChamp® software and researchers analyse the data.

Farmers in Viet Nam often receive money for their participation in projects; in the case of this project, compensations are gradually being reduced. Results are fed back to farmers at seminars/training modules, and are further used to optimize breeding (gilt selection and optimization of mating plans). In order to ensure long- term sustainability, local partners such as the province Department of Agriculture and Rural Development (DARD) and the sub-Department of Animal Health of Son La province, are actively involved and trained. Cooperation with provincial extension services will be strengthened in the current project phase. In earlier phases, the service's strong orientation towards intensive management in favoured regions meant that exchanges were limited. Financial support for the future of the project seems to be available thanks to NIAH's official mandate to carry out projects on AnGR conservation. Moreover, the marketing element of the current project is aimed at ensuring long-term economic viability.

Initial performance testing results indicate that Mong Cai and their cross-bred offspring (sired by exotic boars) are more suited to semi-intensive, market-oriented production conditions, where the higher levels of inputs needed to achieve higher production can be provided. They seem to be less robust in the harsh upland climates and under conditions of low and varying input intensity. Ban pigs are only suited for the extensive conditions of subsistence-oriented resource-poor farming. As the project continues, efforts are being made to further develop breeding goals, to optimize stratified breeding programmes, and to implement marketing programmes. Close to town, lean meat is produced from the cross-bred offspring of Mong Cai sows. Production of Ban pigs continues in remote locations with pure or cross-bred animals marketed as a branded speciality – contributing to the "conservation through use" of this local breed.

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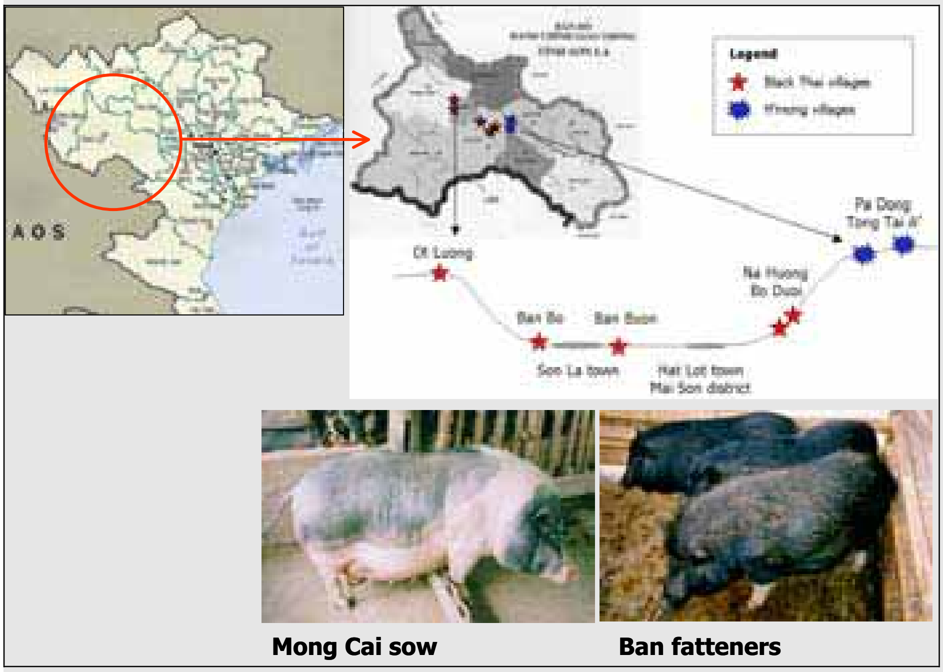
[8] *Funded by the German Research Association (DFG) in the frame of the Thai-Vietnamese-German collaborative research programme SFB 564 and by the Ministry of Science and Technology, Viet Nam.*

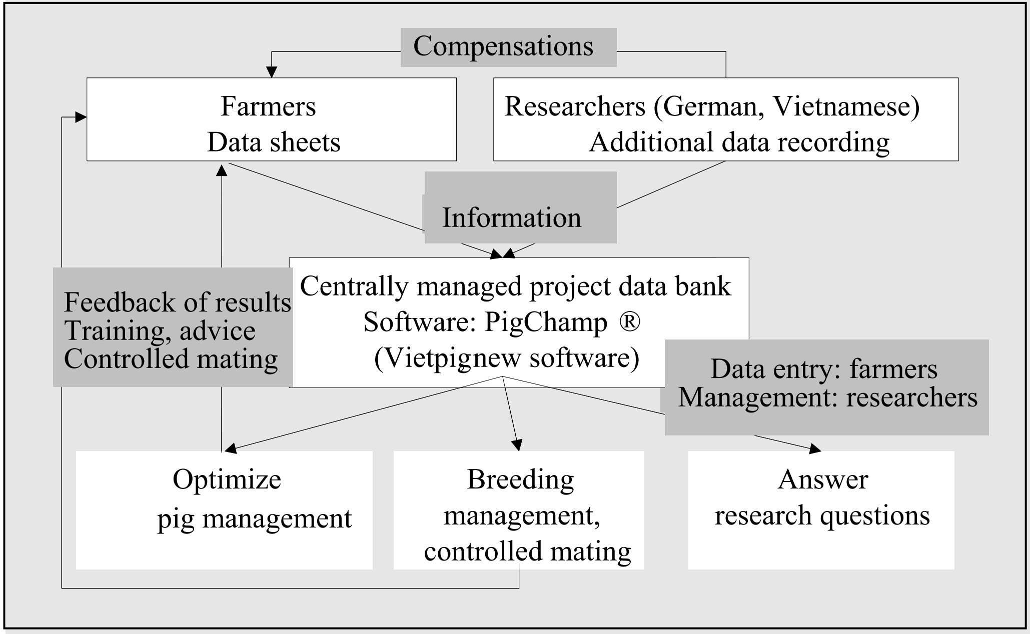
Schematic view of the study region



Mong Cai sow **Ban fatteners**

photos provided by Ute Lemke

Data and resource flow in the on-farm performance testing schemes



Weighing of pigs in Pa Dong, Mai Son district

Photo credit: Regina Rößler

Pigs in Song Ma district

Photo credit: Pham Thi Thanh Hoa

Provided by Ute Lemke and Anne Valle Zárate
Further information can be obtained from the following sources: Huyen, et al. (2005); Lemke, (2006); Rößler. (2005), or from: Prof Dr Anne Valle Zárate, Institute of Animal Production in the Tropics and Subtropics, University of Hohenheim, 70593 Stuttgart, Germany. E-mail: inst480a@uni-hohenheim.de

Breeding schemes

If genetic change is justified, how can it be achieved? The choice is between straight or cross-breeding, but choosing the appropriate option is far from simple.

In low-input systems, adaptation to the environment is a prerequisite for improved efficiency. This is a matter of great importance, as intervention to reduce environmental stresses (supplementary feeding, parasite treatments or other management inputs) is often unaffordable. In these circumstances, straight-breeding to improve well-adapted indigenous breeds may be an option. Implementing a straight-breeding programme is a long-term undertaking, requiring considerable resources, good organization, and (most of all) commitment of all stakeholders. These requirements tend to be lacking under low-input systems in the developing world, and programmes that do exist are only of a very limited scope. For example, most controlled breeding of the West African Dwarf Goat has been in research institutions (especially in those in Nigeria) (Odubote, 1992).

Cross-breeding with an exotic breed may appear to be a more rapid means to improve performance with a minimal increase in inputs. However, the higher performance of the cross-breeds is accompanied by higher nutritional and management requirements (disease control, housing etc.).

Therefore, any system that incorporates higher-performing cross-bred animals will require (among other needs) more feed resources – which in many cases can only be achieved by maintaining a smaller number of animals.

If, after careful analysis, cross-breeding is considered to be a better option than straight-breeding the local breed, the programme should be developed in a way that can be sustained with locally available inputs. Cross-breeding with an exotic (non-adapted) breed presents particular difficulties. Even if the F1 animals are sufficiently adapted, the pure-bred exotic males will usually be under environmental stress, and this will often result in a reduced reproductive life. Even if the male of the exotic breed can be successfully maintained, the backcross resulting from mating F1 females with the exotic males will almost always lack adequate adaptation to the area. Therefore, the F1 females should preferably be mated to adapted-breed sires.

One option under these conditions is to use F1 males, generation after generation. Under such a system, the original local females are mated to F1 males, resulting in offspring that are 1/4 exotic. These quarter-blood females are, in turn, mated to F1 males, resulting in females that are 3/8 exotic. After a few generations the animals would be very close to half exotic. This system introduces exotic influence into the population, but never uses or produces any animals that are more than half exotic.

Box 90
The cost of heterosis

Heterosis has sometimes been referred to as a free opportunity for increased profitability. Although it may be worth more than it costs, heterosis is not free. It involves at least two types of costs.

First, there is the cost involved in meeting the nutritional requirement for the additional performance. The higher performance of the cross-bred animal tends to reduce the cost per unit of production, because the cost for maintenance becomes a smaller fraction of the total requirement, but there is a cost for the extra production.

A second type of cost is associated with potential changes in population structure. These costs may include (1) reductions in the size (and a corresponding increase in the level of inbreeding) of an original pure-bred population which occurs because of the need to accommodate the cross-bred population, and (2) a reduced opportunity to select for female productivity in a population where some of the cross-bred females are not considered to be candidates for selection (as in any terminal-sire system).

Another option for cross-breeding under low-input systems is to cross different breeds that are well adapted to the production conditions. The obvious advantage of such programmes is the ability to maintain and produce the breeding stock in the area without additional inputs. It would be logical to assume that such crosses would produce less-productive animals and/or exhibit less heterosis than crosses between a local and an exotic breed. However, Gregory *et al*. (1985) report estimates of heterosis for weight of calf weaned per cow of 24 percent between Boran and Ankole cattle, and 25 percent between Boran and Small East African Zebu.

With any cross-breeding scheme it is important to consider the whole system and all outputs produced. Commenting the value of the European dairy–Zebu F1 cow for milk production in the tropics, LPPS and Köhler-Rollefson (2005) write “in India, many owners of cross-bred cows cannot see a use for male calves, so let them die.”

Box 91
Nigeria’s Village Poultry Improvement Scheme

A Village Poultry Improvement Scheme aimed at upgrading the indigenous breed of chicken with improved exotic breeds (Rhode Island Red, Light Sussex and Australorp) was initiated in Nigeria around 1950 (Anwo, 1989). The strategy was to cull all indigenous males and replace them with improved imported breeds in a “cockerel exchange programme” (Bessei, 1987). This scheme failed because the cross-bred chicks, though better in performance, could not survive in the semi-wild extensive backyard production system under which the indigenous chickens were raised. Another major drawback was that breed replacement resulted in a rapid loss in genetic variation and narrowing of the available AnGR.

Box 92
A community-based and participatory dairy goat cross-breeding programme in a low-input smallholder system in the eastern highlands of Kenya

FARM Africa’s Meru project in Kenya provides an example of a comprehensive and flexible cross-breeding programme. Improved goat genotypes accompanied by improved husbandry practices have been adopted by very poor farmers with incomes well below US$1 per person per day. The local goats (Galla and East African) were proving difficult to maintain on small and declining farm sizes (0.25 to 1.5 acres), and the farmers had started to abandon goat production. Consequently, the cross-breeding programme aimed to provide more docile and productive animals. Sixty-eight female and 62 male British Toggenburg goats were imported from the United Kingdom and crossed with indigenous goats: the Toggenburgs providing the dairy potential and the local goats providing adaptability. Previous introductions and trials had indicated that Toggenburgs were better adapted than other exotic dairy breeds such as Saanens or Anglo-Nubians.

The project adopted a group and community-based approach. The farmers established the project’s rules, by-laws and mechanisms. It was linked to the government, NARS, and international research institutes, which provided training in husbandry (housing, nutrition, fodder production, record keeping and healthcare), group dynamics, marketing and entrepreneurship.

Farmer groups initially comprised 20 to 25 members, but some lost members over time while others grew. Four such groups were linked in a unit (mainly for administrative and monitoring purposes), with representatives being elected to a larger body the Meru Goat Breeders’ Association (MGBA). Small (one buck and four does) breeder units were provided (as a loan to be paid back in kind) to one group member, who produced the Toggenburgs (T) needed for breeding stock. One pure-bred Toggenburg buck was provided to each farmer group and kept in a buck station, maintained by another group member. Local does were brought to the buck station for service. The resulting F1 female cross-breeds were backcrossed to unrelated Toggenburg bucks to produce ¾ Toggenburg and ¼ Local (L) animals. These were evaluated, and superior males selected to start new buck stations, where they were used to serve unrelated females of similar genetic composition (¾ T and ¼ L). Initial trials had shown that such does produced adequate amounts of both milk and meat, and were reasonably adapted to the local conditions. Through the MGBA, which also registered the cross-breeds with the Kenya Stud Book, groups rotated the bucks every 1 to 1.5 years to avoid inbreeding. Farmers who wished to further upgrade towards the Toggenburg had the opportunity to do so by further backcrossing the ¾ T females to unrelated pure T bucks.

Project statistics 1996 to 2004

	1996	1997	1998	1999	2000	2001	2002	2003	2004
New farmer groups	10	34	20	6	12	10	7	18	8
New buck stations	10	34	10	11	6	16	14	3	22
New breeders units	5	20	25	10	12	6	2	4	7
Buck services		809	1994	3376	3936	3892	3253	5660	6500
Families participating	250	1100	1125	1400	1550	1700	2050	2050	2650
Cross-breeds produced		990	2894	3241	3817	3736	4187	5865	7200

Source: FARM-Africa Dairy Goat and Animal Healthcare Project; six-monthly reports January 1996–June 2004.

Two years after FARM Africa’s pull-out the number of operating groups has continued to increase. In 2006 the MGBA has 3 450 members, all of whom keep improved goats which produce between 1.5 and 3.5 litres of milk per day. The group produces about 3 500 litres of milk daily, some of which is processed and packaged for sale. Member families own more than 35 000 improved goats of which 30 percent have reliable pedigree and performance records. The performance records are used for calculating growth rates and milk yields. These data were formerly processed by FARM-Africa. After the phasing out of the project, MGBA has been encouraged to establish collaboration with universities and research institutions to support them in data processing. Most of the owners of the improved goats are no longer “poor”. Some have used profits from goat production to purchase one or two dairy cows, build better houses and educate their children. Production of yoghurt and fresh pasteurized milk (adding value) is indicative of scope for further developments.

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The features that made the scheme successful include:

a farmer-based approach since its inception;

an emphasis on capacity building so that farmers can manage the programme;

availability of locally produced breeding material;

a group approach – farmers train each other and share experiences;

capacity building for extension staff, farmer-centred extension messages, and participatory approaches; and

the community-based establishment of breeder units and buck stations.

The scheme has ensured that after the end of “the project”, farmers are not reliant on government services. Breeding stock is supplied by farmers themselves, and a parallel animal healthcare service has also been established by training community-based animal health workers, with links to more qualified paraveterinarians and veterinarians. An integrated fodder and reforestation programme was also established.

Provided by Okeyo Mwai and Camillus O. Ahuya
For further reading see: Ahuya et al. (2004); Ahuya et al. (2005); Okeyo (1997)

6 Breeding in the context of conservation

Conservation programmes for AnGR are discussed in greater detail elsewhere in this Report. The following discussion, therefore, focuses on aspects of breeding that need to be considered when implementing conservation measures. A conservation programme may simply aim at ensuring the survival of a population through monitoring and maintaining its integrity, or a programme may also have the objective of improving the performance of the population.

6.1 Methods for monitoring small populations

FAO has produced several publications on the management of at-risk small populations. These documents provide a more extensive review of the subject. Where the objective is merely to ensure the survival of the population and the maintenance of its integrity (as a pure population), the conservation strategy is limited to monitoring the population, and ensuring that the following criteria are within acceptable limits:

Inbreeding: is the result of mating related animals. In a small population, all animals in future generations will come to be related to each other, and mating among these animals will result in inbreeding. The genetic effect of inbreeding is increased homozygosity – the animal receives the same alleles from both its parents. The degree of inbreeding and homozygosity in future generations can be predicted from the population size.

Effective population size: As there is almost always a much smaller number of breeding males than breeding females, the number of breeding males is the more important factor determining the amount of inbreeding. The effective population size (N_e) is a function of the number of breeding males and breeding females. If N_m represents the number of breeding males and N_f represents the number of breeding females, effective population size can be calculated as:

$N_e = (4N_mN_f) / (N_m + N_f)$

If the number of breeding males is the same as the number of breeding females, the effective population size is the same as the actual population size; if the numbers of males and females are different, the effective population size is less than the actual population size. If the number of breeding females is much larger than the number of males, the effective population size will be slightly less than four times the number of males.

A decrease in effective population size in livestock populations can be observed in two situations. The first and most obvious case is when the actual population size decreases. This can result from the replacement of a significant proportion of a breed with breeding animals of another breed, or from cross-breeding a significant fraction of the breed.

The second situation is when a particularly popular sire and his sons and other descendents are heavily used. From the time of the first establishment of breed societies up to the mid-1900s, much of the popularity of particular sires came about as a result of success in the show ring. In more recent times, predicted genetic value for particular traits has been the decisive factor. In dairy cattle, selection was for many years almost entirely focused on milk yield. Hansen (2001) reports that although over 300 000 head were registered by the Holstein Association USA Inc. in 2000, the effective population size was only 37 head. Using pedigree records of cattle born in 2001, Cleveland *et al.* (2005) report an estimated effective population size in the American Hereford of 85 head. The American Hereford Association registered over 75 000 head in 2001.

Relationship between the rate of inbreeding (ΔF) and effective population size (N_e) The level of inbreeding in a given population is dependent on effective population size rather than actual population size. The increase in the level of inbreeding per generation is expected to be $1/2N_e$. This is the increase expected per generation if each animal produces an equal number of offspring, and the animals in the initial population are not related to each other. If these assumptions are not met, the degree of inbreeding will be higher. Based on this relationship, Gregory *et al.* (1999) recommend that at least 20 to 25 sires be used per generation. This would also be a reasonable number to be used in the conservation of a breed. The use of 25 sires per generation would result in a rate of increase in inbreeding of about 0.5 percent per generation.

While the loss of effective population size is an important issue in the conservation of AnGR, it is interesting to note that successful breeders have always accepted some level of inbreeding in their programmes. These breeders established herds or flocks that met their standards – the animals produced in these closed herds or flocks inevitably came to be closely related, and inbreeding resulted (Hazelton, 1939).

6.2 Conservation through breeding

The objectives of a conservation programme may include not only ensuring the survival and integrity of the target population, but also improving its reproductive rate and performance while maintaining its specific adaptive features. Much of the above discussion of breeding strategy for low-input systems is likely to be applicable in these circumstances. This subchapter focuses on the potential risks associated with cross-breeding in the context of breed conservation.

One option to safeguard a breed is to use it as one of the components of a cross-breeding programme. However, any use of pure-bred females to produce cross-breeds will reduce the population size unless there is a reproductive surplus of females. In many cases, the environmental and management conditions do not allow for much reproductive surplus – especially in cattle, which have low reproductive rates. As such, most of the females that are raised must be retained as breeding animals in order to maintain the size of the population. In fact, the largest effect comes from the requirement for a smaller number of indigenous breeding males, brought about by the smaller number of indigenous females that are being used to produce pure-bred offspring. A logical starting point for consideration of a cross-breeding programme is, therefore, to estimate the amount of reproductive surplus in females. This can be measured in terms of the fraction of young females that are available for slaughter or for sale out of the programme (or region). As an example, for fairly well-managed beef herds in temperate areas, about 40 percent of the heifer calves are needed for replacements in order to maintain the size of the herd.

With knowledge of the reproductive surplus of females, and knowledge of the fraction of the total population that is currently made up of cross-breeds, the fraction of pure-breeds that can be utilized to produce F1s without further decreasing the population size of the pure breed can be calculated. As an example, if there is a 20 percent reproductive surplus of females and the current population is composed of 50 percent pure-breeds and 50 percent cross-breeds (includes any pure-bred females that are currently being used for cross-breeding), the population could move towards a composition of slightly more than 50 percent pure-breeds producing pure-breeds, slightly more than 20 percent pure-breeds producing F1s, and slightly less than 30 percent F1 females, without any further reduction in the size of the pure-bred population that is producing pure-breeds. These values assume that none of the females produced by the F1 females are retained as breeding females; in reality, this would probably never occur.

7 Conclusions

Breeding methods and organization vary greatly between industrialized commercial production systems and subsistence-oriented low external input systems. The current organization of the breeding sector is a result of a long evolutionary process. The latest development is the spread of the industrialized breeding model, characteristic of the poultry sector, to other species.

The industrialized breeding model uses state of the art techniques for genetic improvement. Breeding programmes are based mainly on straight-breeding and vary according to the characteristics of the species. Breeding companies market their animals worldwide. This tendency, which is well established among "commercial" pig and poultry breeders, is increasingly the case for beef and dairy cattle. To select for robust animals that are able to cope with different environments, breeders run selection programmes across different environments and management systems. However, it is not possible to have animals that produce well everywhere and under all conditions. As such, different breeds or lines may be developed to meet demands in high-input systems. To date, little is known about the genetic aspects of adaptation. Scientists and breeding companies are expected to explore these matters further in their research and their breeding programmes in the coming years.

In low external input production systems, animals kept by smallholders represent an important element of household food security and of the social fabric of village communities. To a large extent, smallholders and pastoralists keep local breeds. Genetic improvement in these conditions is a challenging, but not impossible, task. Detailed guidelines for the design and execution of sustainable breed utilization and improvement programmes for low external input systems are being developed and validated. Straight-breeding to adjust a local breed to the changing needs of producers is the most viable option not only to keep it in production and hence safeguard it, but also to improve food security and alleviate poverty. Another option is to use it as a component of a well-planned cross-breeding programme. In conjunction with the introduction of a breeding programme, attention should be given to the improvement of management conditions and husbandry practices.

A common tendency in research related to breeding programmes for all species is an increasing focus on functional traits – in response to the growing importance given to factors such as animal welfare, environmental protection, distinctive product qualities and human health. Examples of functional traits include robustness, disease resistance and behavioural traits, fertility, efficiency of feed utilization, calving ease and milkability. Generally, considered as secondary traits in high-input systems, functional traits are of great importance in low-input systems. Recording of functional traits, however, still remains an important bottleneck which hinders their inclusion in breeding schemes. Information is lacking on the genetic basis of disease resistance, welfare, robustness and adaptation to different environments. Nevertheless, the dairy cattle and pig industries have started to use DNA typing of single genes and genomics (SNPs) to screen breeding animals. This will support the expected shift towards breeding for functional and lifetime productivity traits.

Because of the tendency for reduced use of chemical medications in the developed world, animals are required to have better resistance, or at least tolerance, to particular diseases and parasites. However, for economic and animal welfare reasons, it is very difficult to select for such animals using classical quantitative genetic approaches. High expectations are therefore placed on genomics. Some applications are already in use to eliminate genetic disorders with Mendelian inheritance. In the case of the more complex resistance traits for which genetic markers have been identified, such as Marek's disease in poultry and *E. coli* in pigs, few if any breeding companies have implemented DNA-based selection.

Welfare has become an important element in consumers' perception of product quality, especially in Europe. The main challenges for breeders are to select for better temperament, and reduce foot and leg problems and the incidence of cardio-vascular problems (in poultry kept for meat production). The causes of these problems are multifactorial.

The increasing importance of functional traits will require inclusion of a wider range of criteria in breeding programmes. Some of these criteria may be best met by local breeds. Characterization (phenotypic and molecular) and assessment of these breeds for important traits may allow the detection of some that have unique features. Their further development through breeding programmes would ensure that they remain available for future generations. Unfortunately, the reality is a continuous loss of breeds and lines. The developed world (where the majority of concerted genetic improvement efforts are occurring) contributes directly or indirectly to this loss by concentrating on a very small number of breeds. The deletion of genetic lines that accompanies the worldwide reduction in the number of breeding companies via buy-outs has also played a major role.

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SECTION E: METHODS FOR ECONOMIC VALUATION

1 Introduction

The large number of AnGR at risk in developing countries, together with the limited financial resources available for conservation and sustainable use, means that economic analysis can play an important role in ensuring an appropriate focus for conservation and genetic improvement efforts. In this regard, important tasks include, *inter alia*:

- determining the economic contribution that AnGR make to various sectors of society;
- supporting the assessment of priorities through the identification of cost-effective measures which might be taken to conserve livestock diversity; and
- assisting in the design of economic incentives and institutional arrangements for the promotion of AnGR conservation by individual farmers or communities.

Swanson (1997) notes that human societies have been expanding and developing over time through a process involving biodiversity depletion. This process can be understood in terms of a trade-off between maintaining the stock of diverse biological resources, and the benefits to human society derived from the depletion of this stock. AnGR erosion can, thus, be seen in terms of the replacement of the existing slate of livestock with a small range of specialized “improved” breeds. Such replacement occurs not only through substitution, but also through cross-breeding and the elimination of livestock because of production system changes. Genotype choices and threats to AnGR, therefore, need to be understood in the context of the evolution of production systems (including biophysical, socio-economic and markets changes). See Part 2 for a further discussion of trends in livestock production systems.

From an economic point of view, AnGR erosion can be seen as a result of drivers generating a bias towards investment in specialized genotypes, which in turn results in under-investment in a more diverse set of breeds. Economic rationality suggests that investment decisions will be determined by the relative profitability of the two options (assuming risk neutrality and well-functioning markets). However, from a farmer’s perspective, the relevant rates of return are those that accrue to him/her rather than to society or the world as a whole. To the farmer, the loss of a local breed will appear to be economically rational in a situation where the returns from the activities that lead to the loss are higher than those from activities compatible with genetic resource conservation – especially as returns from the latter may consist of non-market benefits that accrue to people other than the farmer. This divergence will be further compounded by the existence of distortions in the values of inputs and outputs such that they do not reflect their economic scarcity.

The above-described divergence between private and public returns is important. As Pearce and Moran (1994) note, the recognition of the broader total economic value (TEV – see Box 93) of natural assets can be instrumental in altering decisions about their use, particularly in investment decisions that present a clear choice between erosion/destruction or conservation. When the activity of biodiversity (and genetic resource) conservation generates economic values that are not captured in the market place, the result of this “failure” is a distortion in which the incentives are against genetic resource conservation, and in favour of the economic activities that erode such resources. Such outcomes are, from an economic viewpoint, associated with market failure (i.e. distortions arising from the “missing markets” in the external benefits generated by biodiversity conservation); intervention failure (i.e. distortions caused by government actions in intervening in the workings of the market place, even where those appear to serve some social purpose); and/or global appropriation failures (i.e. the absence of markets/mechanisms to capture globally important external values). Note that global missing markets can co-exist with local market failure and intervention failure. The loss of biodiversity and genetic resources is a case in point.

Box 93
Economic values

Livestock keepers benefit from the conservation of livestock diversity because of their need for animals that are able to produce in diverse agro-ecosystems, and fulfil a range of functions. In addition to supplying products for sale or home consumption, livestock provide input functions related to other farm/household activities. Livestock provide manure to enhance crop yields, transport for inputs and products, and also serve for traction. Where rural financial and insurance markets are not well developed, they enable farm families to smooth variation in income and consumption levels over time. Livestock constitute savings and insurance, buffering against crop failure and cyclical patterns in crop-related income. They enable families to accumulate capital and diversify, and serve a range of sociocultural roles related to the status and the obligations of their owners (Jahnke, 1982; Anderson, 2003). Livestock also play a role in the maintenance of ecosystems; for example, managed grazing is increasingly viewed as an important tool for conservation.

The values mentioned in the above paragraph are components of direct or indirect use value. Other values are not related to use, but simply to the existence of the breeds (existence and bequest values). Another type of value arises from the notion of uncertainty about the future. The latter result from the motivation to avert risk (option value), and from the irreversibility of the loss of a breed and the related loss of information.

The "Total Economic Value" (TEV) is formally equal to the sum of all direct and indirect use values plus non-use and option values: TEV = DUV + IUV + OV + BV + XV where:

Direct Use Values (DUV) are the benefits resulting from*, inter alia*, actual uses, such as for food, fertilizer and hides, as well as cultural/ritual uses.

Indirect Use Values (IUV) are the benefits deriving from ecosystem functions. For example, some animals play a key role in the dispersion of certain plant species.

Option Values (OV) are derived from the value given to safeguarding an asset for the option of using it at a future date. It is a kind of insurance value (given uncertainty about the future and risk aversion) against the occurrence of, for example, a new animal disease or drought/climate change. Subtly different from, but related to, option values are quasi-option values. The latter relates to the extra value attached to future information made available through the preservation of a resource. Quasi-option values arise from the irreversible nature of breed loss (after which no further learning can take place); they are not related to the risk aversion of the decision makers.

Bequest Values (BV) measure the benefit accruing to any individual from the knowledge that others might benefit from a resource in the future; and

Existence Values (XV) are derived simply from the satisfaction of knowing that a particular asset exists (e.g. blue whales, capybaras or N´Dama cattle).

Some asset values may overlap between these categories, and double counting has to be avoided. Attempts to isolate option, bequest and existence values can be problematic. Underlying principles and procedures for such valuation are still debated.

Sources: adapted from Arrow and Fisher (1974); Jahnke, (1982); Pearce and Moran, (1994); Anderson, (2003); Roosen et al., (2005)

It is apparent from the above typology of values that current economic decisions are largely based on the first category, direct use values, although the other categories may be of equal or greater importance. For example, it has been estimated that approximately 80 percent of the value of livestock in low-input developing-country systems can be attributed to non-market roles, while only 20 percent is attributable to direct production outputs. By contrast, over 90 percent of the value of livestock in high-input developed-country production systems is attributable to the latter (Gibson and Pullin, 2005). By focusing exclusively on direct use values, biodiversity and genetic resource conservation are likely to be consistently undervalued, resulting in a bias towards activities that are incompatible with their conservation.

2 Development of methodologies for economic analysis

Although there is a large body of literature on the economic benefits of improved breeds in intensive (largely developed-country) commercial agriculture, the importance of indigenous breeds and trait values in the subsistence production systems typical of developing countries have been much less studied. There is an extensive amount of conceptual and theoretical literature concerning sources of value arising from genetic resources and biodiversity in general (usually referring to plants and wild animals). However, it is only since an FAO/ILRI workshop (ILRI, 1999) identified potential AnGR valuation methodologies, and subsequent initiatives by ILRI (Economics of AnGR Conservation and

Sustainable Use Programme) and its partners to test these methodologies, that significant research into the matter has been carried out.

Such tools and their findings have, as yet, rarely been put to use in situations that influence policy-making and farmer livelihoods. Further research is urgently needed to better understand implications for genotype preferences of an increasingly dynamic context characterized by, *inter alia*:

- globalization of markets;
- climate change and environmental degradation;
- the occurrence of new epidemic animal diseases;
- developments in the field of biotechnology; and
- policy developments related to the Convention on Biological Diversity.

Global efforts to eradicate poverty, as embodied in the Millennium Development Goals, also require an improved understanding of the potential contributions of alternative genotypes to poverty alleviation, in order to improve pro-poor targeting of AnGR programmes. In this context, research supporting institutional innovations and technology-adoption also play an important role. Such areas are critical for the management of AnGR and have important socio-economic dimensions.

There are a number of reasons for the relatively slow development of the economics of AnGR, including: the fact that the measurement of the benefits of germplasm diversity to livestock development is difficult; the limited availability of the data required to carry out economic analysis; and the importance of considering non-market values of livestock – obtaining such data frequently requires the modification of economic techniques for use in conjunction with participatory and rapid rural appraisal methods.

Despite the difficulties, there are a range of analytical techniques from other areas of economics that can be adapted for carrying out such analyses. These methodologies are reviewed by Drucker *et al.* (2001) who broadly categorize them into three (non-mutually exclusive) groups on the basis of the practical purpose for which they may be used (see Table 102):

- group 1) determining the actual economic importance of the breed at risk;
- group 2) determining the costs and benefits of AnGR conservation programmes, and targeting farmers for participation; and
- group 3) priority setting in AnGR breeding programmes.

A number of these methodologies have significant conceptual shortcomings and intensive data requirements (see Drucker *et al.*, 2001 for a detailed description). However, they have been shown to produce useful estimates of the values that are placed on market, non-market and potential breed attributes of the type useful for designing breeding and conservation strategies. The following section presents an overview of the methodologies. The objective is both to show the potential usefulness of the methodologies, as well as to provide information (inevitably location-specific) on the economic importance of indigenous AnGR. To this end, a number of specific studies are presented as illustrative examples of the application of the various tools. Many of the findings give useful insights into the value of particular indigenous livestock breeds within the production systems studied. Salient conclusions are highlighted at the start of each subsection. A more detailed overview can be found in Drucker *et al.* (2005), and an annotated bibliography of literature in this field is provided by Zambrano *et al.* (2005).

Table 102
Overview of valuation methodologies

Valuation methodology	Purpose	Contribution to conservation and sustainable use of AnGR
Group 1: Methodologies for determining the actual economic importance of the breed (mostly of interest to policy makers and breeders, as well as some farmers)		
Aggregate Demand & Supply	Identify value of breed to society.	Value potential losses associated with AnGR loss.
Cross-sectional Farm and Household	Identify value of breed to society.	Value potential losses associated with AnGR loss.
Aggregated Productivity Model	Determine farmer net returns by breed.	Justify economic importance of given breed in the context of multiple limiting inputs.
IPR and Contracts	Market creation and support for "fair and equitable" sharing of AnGR benefits.	Generate funds and incentives for AnGR conservation.
Contingent Valuation Methodologies I (e.g. dichotomous choice, contingent ranking, choice experiments)	Determine farmer trait value preferences and net returns by breed.	Justify economic importance of given breed.
Market Share I	Indicate current market value of a given breed.	Justify economic importance of given breed.
Group 2: Methodologies for determining the costs and benefits of AnGR conservation programmes and for targeting farmers for participation (mostly of interest to policy makers and farmers)		
Contingent Valuation Methodologies II (e.g. dichotomous choice, contingent ranking, choice experiments)	Identify society's willingness to pay (WTP) for the conservation of AnGR. Identify farmer willingness to accept (WTA) compensation for raising indigenous AnGR instead of exotics.	Define maximum economically justified conservation costs.
Production Loss Averted	Indicate magnitude of potential production losses in the absence of AnGR conservation.	Justify conservation programme costs of at least this magnitude.
Opportunity Cost	Identify cost of maintaining AnGR diversity.	Define opportunity cost of AnGR conservation programme.
Market Share II	Indication of current market value of a given breed.	Justify conservation programme costs.
Least Cost	Identify cost-efficient programme for the conservation of AnGR.	Define minimum cost of conservation programme.
Safe Minimum Standard	Assess trade-offs involved in maintaining a minimum viable population.	Define opportunity cost of AnGR conservation programme.
Group 3: Methodologies for priority setting in AnGR breeding programmes (mostly of interest to farmers and breeders)		
Evaluation of Breeding Programme	Identify net economic benefits of stock improvements.	Maximize economic benefits of conserved AnGR.
Genetic Production Function	Identify net economic benefits of stock improvements.	Maximize expected economic benefits of conserved AnGR.
Hedonic	Identify trait values.	Value potential losses associated with AnGR loss. Understand breed preferences.
Farm Simulation Model	Model improved animal characteristics on farm economics.	Maximize economic benefits of conserved AnGR.

Source: adapted from Drucker et al. (2001)

3 Application of economic methodologies in AnGR management

The following examples are presented in the context of the classification presented in Table 102.

3.1 Value of livestock genetic resources to farmers[9]

- Adaptive traits and non-income functions form important components of the total value of indigenous-breed animals to livestock keepers.
- Conventional productivity evaluation criteria are inadequate to evaluate subsistence livestock production and have tended to overestimate the benefits of breed substitution.

Tano *et al*. (2003) and Scarpa *et al*. (2003a; 2003b) used stated preference choice experiments (CE) to value the phenotypic traits expressed in indigenous breeds of livestock. Adaptive traits and non-income functions are shown to form important components of the total value of the animals to livestock keepers. In the study carried out by Tano *et al*. (2003) in West Africa, for example, the most important traits for incorporation into the goals of breed improvement programme were found to be disease resistance, fitness for traction, and reproductive performance. Beef and milk production were less important. The results of these studies also show that it is possible to investigate values of genetically determined traits that are currently not widely recognized in livestock populations, but are desirable candidates for breeding or conservation programmes (e.g. disease resistance).

Karugia *et al*. (2001) used an aggregate demand and supply approach covering both national and farm levels. They argue that conventional economic evaluations of cross-breeding programmes have overestimated their benefits by ignoring subsidies, the increased costs of management such as veterinary support services, and the higher levels of risk and socio-environmental costs associated with the loss of the indigenous genotypes. Applied to dairy farming in Kenya, the results suggest that at the national-level, cross-breeding has had an overall positive impact on society's welfare (based on a consumer/producer surplus measure), although taking important social cost components into account substantially lowers the net benefits. Farm-level performance is, however, little improved under "traditional" production systems by replacing the indigenous Zebu with exotic breeds.

Comparing the performance of different genotypes (indigenous goats vs. exotic crosses), Ayalew *et al*. (2003) come to a similar conclusion. The secondary importance of meat and milk production traits in many production systems leads these authors to argue that conventional criteria for the evaluation of productivity are inadequate for subsistence livestock production systems, because:

- they fail to capture non-marketable benefits of the livestock; and
- the core concept of a single limiting input is inappropriate to subsistence production, as multiple limiting inputs (livestock, labour, land) are involved in the production process.

The study involved the use of an aggregated productivity model to evaluate subsistence goat production in the eastern Ethiopian highlands. The results show that indigenous goat flocks generated significantly higher net benefits under improved than under traditional management, which challenges the prevailing notion that indigenous livestock do not adequately respond to improvements in the level of management. Furthermore, it is shown that under the subsistence mode of production considered, the premise that cross-bred goats are more productive and beneficial than the indigenous goats is wrong. The model, thus, not only underlines the value of indigenous AnGR to farmers, but also provides a more realistic platform upon which to propose sound improvement interventions.

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[9] using Group 1 valuation methodologies (see Table 102)

3.2 Costs and benefits of conservation[10]

- The costs of implementing an *in situ* breed conservation programme may be relatively small, both when compared to the size of subsidies currently being provided to the commercial livestock sector, and with regard to the benefits of conservation. However, few such conservation initiatives exist, and even where the value of indigenous breeds has been recognized and support mechanisms implemented, significant shortcomings can be identified.
- Similar work regarding the costs and benefits of the *ex situ* (cryo)conservation of livestock remains limited. However, under the assumption that technical feasibility brings the cost of cryoconservation and regeneration of livestock species to within the same level of magnitude as that of plants, extensive conservation efforts would be justified on economic grounds.

In situ conservation

Cicia *et al*. (2003) show that a dichotomous choice stated preference approach can be used to estimate the benefits of establishing a conservation programme for the threatened Italian Pentro horse. A bio-economic model was used to estimate the costs associated with conservation, and a cost–benefit analysis was subsequently realized. Benefit estimates were based on society's willingness to pay for conservation and, therefore, may be associated, in this particular case, with an existence value. The results not only show a large positive net present value associated with the proposed conservation activity (benefit/cost ratio > 2.9), but also show that this approach is a useful decision-support tool for policy-makers involved in allocating scarce funds to a growing number of animal breeds facing extinction.

A case study of the endangered Box Keken pig breed in Yucatan, Mexico revealed large net present values associated with conservation (Drucker and Anderson, 2004). Three methodologies for valuing the benefits of conservation and sustainable use of the breed – market share, production loss averted and contingent valuation (consumer taste test) – were tested and critically assessed. The costs of conservation were estimated with the use of contingent valuation (producer choice experiment) and least cost/opportunity cost approaches. A shortcoming of the first two techniques for valuing the benefits is that they are not based on consumer surplus measures, i.e. do not account for price changes and substitution possibilities should breed loss occur. Despite the identified shortcomings, and the fact that values can only be approximated, the study indicates that the benefits of conservation clearly outweigh the costs in this case (Table 103).

Table 103
Conservation benefits and costs under a range of valuation methodologies – the case of the Box Keken pig (Yucatan, Mexico)

Valuation Methodologies*	Measure of Conservation and Sustainable Use Benefits US$ *per annum*	Measure of Conservation Costs US$ *per annum*
Market share	US$490 000	
Production loss averted (Yucatan State only)	US$1.1 million	
Contingent valuation (consumer taste test)	US$1.3 million	
Contingent valuation (producer choice experiment) and least cost/opportunity cost approach		US$2 500–3 500

Source: Drucker and Anderson (2004)
**See Table 102*

Even where the value of indigenous breeds has been recognized and support mechanisms implemented, significant failings can be identified. Signorello and Pappalardo (2003), in an examination of livestock biodiversity conservation measures and their potential costs in the EU, report that many breeds at risk of extinction according to the FAO World Watch List are not covered by

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[10] using Group 2 valuation methodologies (see Table 102)

support payments as they do not appear in countries' Rural Development Plans. Furthermore, the results show that where payments are made, they do not take into account the different extinction risks faced by the different breeds. Moreover, payment levels are inadequate, meaning that it can still remain unprofitable to rear indigenous breeds. Ideally, support payments should be set at a level that reflects society's willingness to pay for conservation, but this is not usually the case and may not always be necessary to ensure profitability.

The lack of adequate incentives for the conservation of indigenous breeds is despite the fact that conservation costs have been shown, in a number of case studies described by Drucker (2006), to be relatively small. Drawing on the safe minimum standards (SMS) literature, the framework used in this study assumes that the benefits of indigenous livestock breed conservation can be maintained, as long as a minimum viable population of the breed is maintained. In general, the costs of implementing an SMS are made up of the opportunity cost differential (if any exists) of maintaining the indigenous breed rather than an exotic or cross-breed. In addition, the administrative and technical support costs of the conservation programme also need to be accounted for. Empirical cost estimates were obtained using data from economic case studies (Italy and Mexico), based on an SMS that is equivalent to the FAO measure of "not at risk", i.e. approximately 1 000 breeding animals. The results support the hypothesis that the costs of implementing an SMS are low (depending on the species/breed and location, these ranged from between approximately Euro 3 000 and 425 000 *per annum*), both when compared with the size of subsidies currently being provided to the livestock sector (less than 1 percent of the total subsidy) and with regard to the benefits of conservation (benefit/cost ratio greater than 2.9). The costs proved to be lowest in the developing country, which is encouraging given that an estimated 70 percent of the livestock breeds existing today are in developing countries, and that this is where the risk of loss is highest (Rege and Gibson, 2003).

More extensive quantification of the components required to determine SMS costs nevertheless needs to be undertaken before it can be applied in practice. Such economic valuation needs to cover both the full range of breeds/species being considered, and ensure that as many as possible of the elements making up their total economic value are accounted for.

Ex situ conservation

Similar work regarding the costs and benefits of the *ex situ* (cryo)conservation of livestock remains limited. Cryopreservation technologies for livestock, although advancing rapidly, are still well-developed only for a handful of species. Nevertheless, Gollin and Evenson (2003) argue that assuming that technical feasibility brings the cost of cryoconservation and regeneration of livestock species to within the same level of magnitude as that of plants, "there cannot be much doubt that the economics would justify extensive conservation efforts" (i.e. probable option values are likely to be much higher than conservation costs).

3.3 Targeting of farmers for participation in *in situ* breed conservation programmes[11]

- *In situ* conservation programmes play a crucial role in the context of AnGR.
- Household characteristics play an important role in determining differences in farmers' breed preferences. This additional information can be of use in designing cost-effective conservation programmes.

Wollny (2003) argues that community-based management approaches are likely to be required to play an increasingly important role in strategies that aim to improve food security and to alleviate poverty through the conservation of AnGR. This is because the utilization of indigenous livestock populations depends, in large part, on the ability of communities to decide on and implement appropriate breeding strategies. The community-based management of AnGR is also considered to play a critical role in poverty alleviation (FAO, 2003).

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[11] using Group 2 valuation methodologies (see Table 102)

In the context of crops (Meng 1997), proposed that conservation programmes should target those households that are the most likely to continue to maintain local varieties. As these households will be the least costly to incorporate into a conservation programme, a "least cost" programme can be identified. The cost of an *in situ* conservation programme can, thus, be expressed as the cost necessary to raise the comparative advantage of such breeds above that of competing breeds, species, or off-farm activities. A relatively small investment may suffice to maintain their advantage in a particular farming system.

This conceptual approach to identifying low-cost conservation strategies has recently been applied to estimate conservation costs for creole pigs in Mexico (Scarpa *et al*., 2003b; Drucker and Anderson, 2004) and Boran cattle in Ethiopia (Zander *et al*., forthcoming).

Scarpa *et al*. (2003b) show that for creole pigs in Mexico, the respondent's age, years of schooling, size of the household, and the number of economically active members of the household, were important factors in explaining breed trait preferences. Younger, less-educated, and lower-income households placed relatively higher values on the attributes of indigenous piglets compared to exotics and their crosses (Drucker and Anderson, 2004). Pattison's (2002) findings further corroborate these results. In the context of a ten-year conservation programme that would bring the creole pig population to a sustainable size considered "not at risk" under the FAO classification system; the findings indicate that small, less well-off households would require lower levels of compensation, or even (in 65 percent of cases) no compensation at all. The premise of this set of studies is that continued conservation of genetic resource diversity on-farm makes most economic sense in those locations where both society and the farmers who maintain it benefit the most.

Mendelsohn (2003) argues that where there is a divergence between private (farmer) and public values, conservationists must first make the case for why society should be willing to pay to protect apparently "unprofitable" AnGR, and then must design conservation programmes that will effectively protect what society treasures.

3.4 Priority setting in livestock conservation programmes[12]

- Conservation policy needs to promote cost-efficient strategies, and this can be achieved through the development of "Weitzman-type" decision-support tools. Such tools permit the allocation of a given budget among a set of breeds such that the expected amount of between-breed diversity conserved is maximized.

Simianer *et al*. (2003) and Reist-Marti *et al*. (2003) provide one of the few examples of the conceptual development of a decision-support tool in the field of AnGR. Recognizing the large number of indigenous livestock breeds that are currently threatened, and the fact that not all can be saved given limited conservation budgets, a framework is elaborated for the allocation of a given budget among a set of breeds so that the expected amount of between-breed diversity conserved is maximized. Drawing on Weitzman (1993) it is argued that the optimum criterion for a conservation scheme is to maximize the expected total utility of the set of breeds, which is a weighted sum of diversity, extinction probabilities and breed conservation costs (see Section F: 8.2 for further discussion of this approach). Drawing on Group 2 valuation methodologies (see Table 102) is currently postulated as a means of estimating conservation costs. However, Group 1 methodologies could be used should a livelihoods rather than a conservation cost approach be adopted. Both this, and the original Weitzman study, used measures of diversity based on genetic distances. Note, however, that alternative measures of diversity could also be used – for example, measures that include both between and within-breed diversity (Ollivier and Foully, 2005) or those drawing on functional diversity, based on the existence of unique attributes in certain breeds (see Brock and Xepapadeas (2003) for a plant genetic resource illustration). Implications for the choice of breeds for inclusion in conservation programmes may well differ depending on how the diversity index is constructed and the overall goal of the conservation programme (conservation of genetic diversity *per se*, maximizing the number of unique traits conserved, or maximizing the livelihood contribution of the livestock diversity conserved). Where

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[12] using Group 2 valuation methodologies (see Table 102)

such models are sufficiently specified and essential data on key parameters are available (currently lacking for conservation costs and benefits or contribution to livelihoods), the framework can be used for rational decision-making on a global scale. See section F:8 for further discussion of methods for priority setting in conservation.

3.5 Priority setting in livestock-breeding strategies[13]

- Economic analysis has demonstrated the magnitude of the contribution of genetic selection, for example using selection indices, to increased production.
- Methods are needed not only to account for the current set of economic objectives, but also to include foreseeable and even unpredictable future needs.
- Hedonic[14] approaches are useful to evaluate the importance of certain attributes or characteristics to the value of animals or animal products including their influence on selection strategies.

Breeding programmes have long used a selection index as a device for multiple-trait selection in livestock. For example, Mitchell *et al.* (1982) measured the value of genetic contributions to pig improvement in the United Kingdom by determining the heritability of important characteristics, and isolating the genetic contributions to improved performance. Using linear regression techniques to compare control and improved groups over time, they found that the returns were substantial, with costs in the region of £2 million *per annum* relative to benefits of £100 million *per annum*. The use of cross-breeding in commercial production was estimated to contribute approximately £16 million *per annum*. Farm-level simulation models have been built for several species under high-input management, and have also focused on valuing heritable trait gain.

Smith (1985), in the context of the importance of accounting for option values in genetic production function models, argues that genetic selection based on the current set of economic objectives is suboptimal in an intertemporal context. Instead, given uncertainty about future needs, selection should be "directed to cater for foreseeable and even unpredictable futures" (Smith, 1985, p. 411). In particular, Smith (1984) advocates the storage of stocks with traits that are currently not economically desirable because of temporary market demands and/or production conditions (e.g. market or grading requirements, carcass or product composition, special behavioural adaptations to current husbandry conditions).

Using hedonic approaches, Jabbar *et al.* (1998) show that in Nigeria, although there were some differences in prices that were solely because of breed, most variation in prices was because of such variables as wither height and girth circumference that vary from animal to animal within breeds. Variation because of type of animal or month of transaction was also greater than that because of breed. Jabbar and Diedhiou (2003) show that a hedonic approach used to determine livestock keepers' breeding practices and breed preferences in southwest Nigeria, confirms a strong trend away from trypanotolerant breeds. Richards and Jeffrey (1995) identify the value of relevant production and type traits for dairy bulls in Alberta, Canada. A hedonic valuation model is estimated, which models semen price as a function of individual production and longevity characteristics for a sample of Holstein-Friesian bulls.

3.6 General policy analysis development[15]

The current rapid rate of loss of AnGR diversity is the result of a number of underlying factors. While, in some cases, changes in production systems and consumer preferences reflect the natural evolution of developing economies and markets, in other cases, production systems, breed choice and consumer

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[13] using Group 3 valuation methodologies (see Table 102)

[14] Hedonic approaches are based on the idea that the total value of an animal can be decomposed into the values of individual characteristics. Statistical methods are used to estimate the contribution of each characteristic to the total value based on the market prices paid for animals with different combinations of characteristics

[15] potentially using Group 2, as well as Group 1 valuation methodologies (see Table 102)

preferences have been distorted by local, national and international policy. Such distortions may arise from macroeconomic interventions (e.g. exchange and interest rates); regulatory and pricing policy (e.g. taxation, price controls, market and trade regulations); investment policy (e.g. infrastructure development); and institutional policy (e.g. land ownership and genetic resource property rights). While the impact of policy factors on AnGR is readily discernable in broad terms, little is known about their relative importance.

4 Implications for policies and future research

The above studies reveal not only that there are a range of methodologies that can be used to value livestock keeper breed/trait preferences, but that they can be of use in designing policies that counter the present trend towards marginalization of indigenous breeds. In particular, it becomes possible to, *inter alia* (Drucker and Anderson, 2004):

- recognize the importance that livestock keepers place on adaptive traits and non-income functions, and the need to consider these in breeding programme design;
- identify those breeds that are a priority for participation in cost-efficient diversity-maximizing conservation programmes; and
- contrast the costs involved with the large benefits non-livestock keepers place on breed conservation.

Nevertheless, as recent advances in economic valuation for livestock genetic resources have eased some (but by no means all) methodological/analytical constraints, the issue of data availability has become relatively more critical. Data requirements imply the need to *inter alia*:

- measure breed performance parameters;
- characterize actual and potential breeding systems;
- identify uses and farmers' trait preferences (including eliciting the values that farmers place on specific market/non-market traits and the trade-offs they are willing to make between traits) for local breeds under different production systems, as well as the forces influencing such factors and the use of alternative breeds;
- identify factors affecting livestock demand and prices, including the impact of policy-induced changes in agricultural commodity (e.g. forage/crop) prices and external (e.g. veterinary) input costs in the context of different breed use;
- carry out *ex ante* analysis of the effects on livelihoods of using alternative breeds, together with constraints to adoption and potential access/dissemination mechanisms;
- consider the role of such factors as land tenure, agricultural potential, population density, market access and integration, licensing requirements, tax regimes, credit and extension programmes and education; and
- improve understanding of the importance of continued access and trade in livestock germplasm for research and development purposes, together with the nature of the costs and benefits arising from AnGR research.

Despite a wealth of livestock production data at the national level, such information tends to be limited to the principal breeds and largely ignores important non-market contributions. Information on local breeds in developing countries is extremely limited. Initiatives such as FAO's DAD-IS and ILRI's DAGRIS systems are supporting national-level programmes.

The challenge is now to raise awareness regarding the important role of economic analysis in improving farm AnGR conservation and sustainable use. National capacities must also be strengthened in order to enable the application of the relevant methodologies/decision-support tools, and to integrate them into the wider national livestock development process. In this way, further work on the economics of AnGR (including in dynamic systems evolution contexts and integrated with other components of agrobiodiversity), and the subsequent design of appropriate incentive mechanisms, can be applied in contexts where the results can be taken up so as to actively benefit farmers and support the work of national researchers and policy-makers.

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SECTION F: METHODS FOR CONSERVATION

1 Introduction

Breed development is a dynamic process of genetic change driven by environmental conditions and selection by humans, the latter being shaped by the culture and the economic situation. The fact that ecosystems are dynamic and complex and that human preferences change, has resulted in the evolution of breeds and, until recently, a net increase in diversity over time. However, in the past 100 years there has been a net loss of diversity resulting from an increase in the rate of extinction of breeds and varieties. In Europe and the Caucasus alone, 481 mammalian and 39 avian breeds have already become extinct, and another 624 mammalian and 481 avian breeds are at risk. Losses have been accelerated by rapid intensification of livestock production, a failure to evaluate local breeds, and inappropriate breed replacement or cross-breeding facilitated by the availability of high-performing breeds and reproductive biotechnologies (Box 95).

Box 94
Glossary: conservation

For the purpose of this Report, the following definitions are used:

Conservation of animal genetic resources: refers to all human activities including strategies, plans, policies and actions undertaken to ensure that the diversity of animal genetic resources being maintained to contribute to food and agricultural production and productivity, or to maintain other values of these resources (ecological, cultural) now and in the future.

In situ **conservation**: refers to conservation of livestock through continued use by livestock keepers in the production system in which the livestock evolved or are now normally found and bred.

Ex situ in vivo **conservation**: refers to conservation 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.

Ex situ in vitro **conservation**: refers to conservation external to the living animal in an artificial environment, under cryogenic conditions including, *inter alia*, the cryoconservation of embryos, semen, oocytes, somatic cells or tissues having the potential to reconstitute live animals (including animals for gene introgression and synthetic breeds) at a later date.

Box 95
Red Maasai sheep – accelerating threats

The Red Maasai, renowned for its hardiness and disease resistance, especially its resistance to gastrointestinal parasites, is predominantly kept by Maasai pastoralists, as well as by the neighbouring tribes in the semi-arid regions of Kenya and the United Republic of Tanzania. A number of research projects have demonstrated the breed's resistance to diseases, and high productivity under extremely challenging environments, where other breeds, such as the introduced Dorper perform very poorly. Until the mid-1970s, pure-bred Red Maasai were ubiquitous throughout the pastoral lands of Kenya, probably numbering several million head. In the mid-1970s, a subsidized dissemination programme for Dorper rams was established in Kenya. Widespread indiscriminate cross-breeding followed. No instruction was provided to farmers about how to maintain a continuous cross-breeding programme and many farmers continued crossing their flocks to Dorpers, which subsequently proved unsuitable in many production areas. In 1992, and again more recently, the International Livestock Research Institute undertook an extensive search in Kenya and northern parts of the United Republic of Tanzania, but was only able to locate a very small number of pure-bred animals. The Institute was able to establish a small "pure-bred" flock, but this flock later showed some levels of genetic contamination. The Red Maasai breed is clearly threatened, but the livestock databases DAD-IS and DAGRIS do not identify the breed as threatened, and the breed does not appear in the World Watch List (FAO/UNEP 2000). This is related to the current inability of the systems to document the dilution of breeds.

Provided by John Gibson

While the loss of livestock genetic diversity has greatly increased in recent decades, the extent of the problem has still not been fully evaluated. Information on AnGR provided by FAO member countries is made available to the public in the DAD-IS database. Although a specific call for information on extinct breeds was made in 1999 before compiling the third edition of the World Watch List (FAO/UNEP, 2000), the lists of extinct breeds are probably not complete – uncharacterized local populations in rapidly developing regions of the world may have disappeared without being recorded. Reasons for extinction are either not documented or not readily accessible and, therefore, have not been thoroughly analysed. The risk status of many breeds can only be estimated, as breed population census data are often missing or unreliable. The lack of knowledge hinders concerted actions and the setting of conservation priorities.

2 Arguments for conservation

The ratification of the Convention on Biological Diversity (CBD) by 188 states indicates a growing international commitment to sustain and protect biodiversity. The CBD calls for conservation and sustainable use of all components of biological diversity including those used for agriculture and forestry. Recognizing the importance of genetic level diversity it provides a mandate to conserve genetic resources for food and agriculture. Article 2 specifically recognizes "domesticated and cultivated species" as an important component of global biological diversity.

However, it has been noted that "while a significant international consensus regarding policy has apparently emerged, this consensus is not grounded in a consensually accepted value theory to explain why biodiversity protection, however strongly supported, should be a top priority of environmental policy" (Norton, 2000 in FAO, 2003, p. 105). For example, the argument for maintaining biological diversity for its own sake can be contrasted with the view that in the absence of a clear case for the utility of a breed, its loss should not be of much concern. This chapter presents an overview of the different lines of argument put forward in favour of conservation. The rationale of a conservation programme may include a combination of the following arguments:

2.1 Arguments related to the past

Livestock breeds reflect the cultural and historical identity of the communities that developed them, and have been an integral part of the livelihood 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.

A further argument relates to the fact that breed development, especially in species with longer generation intervals, will often have involved considerable investments in terms of time, financial expenditure and/or institutional resources. Moreover, historical processes may have given rise to unique outputs that could not easily be recreated. According to this point of view, the decision to abandon such breeds should, therefore, not be taken lightly. There is also a historical dimension to the development of adaptive traits – the longer an animal population has been exposed to an environmental challenge, the greater the possibility that specific adaptive traits have evolved. Areas with climatic extremes or particular disease conditions have given rise to genetically adapted and unique local stocks. These breeds have co-evolved with a particular environment and farming system, and represent an accumulation of both genetic stock, and associated husbandry practices and local knowledge.

2.2 Safeguarding for future needs

"Predicting the future is a risky business at best, particularly where human activities are involved" (Clark, 1995 in Tisdell, 2003, p. 369).

It is notoriously difficult to predict the future, and people's expectations are highly diverse. Very negative expectations may at times be more related to unsubstantiated fears than to rational arguments. However, a strong case for concern about the loss of AnGR diversity can be put forward: "From a long-term point of view, it is possible that concentration on high yielding environmentally sensitive breeds will create a serious problem for the sustainability of livestock production ... it is possible that farmers will lose their ability to manipulate natural environmental conditions. If all environmentally tolerant breeds are lost in the interim, the level of livestock production could collapse." (Tisdell, 2003, p. 373). Unforeseen developments may be brought about by changes in the ecosystem, in market demands and associated regulations, by changes in the availability of external inputs, by emerging disease challenges, or by a combination of these factors. Global climate change and the evolution of resistance in pathogens and parasites to chemical control are almost certain to affect future livestock production systems, though the nature of the changes remains unclear (FAO, 1992). The possibility of catastrophic losses of AnGR resulting from major disease epidemics, war, bioterrorism or civil unrest, indicates a need to have a secure reserve, such as a genebank, for breeds that are of great economic importance at present. The uncertainty of future needs, in combination with the irreversible nature of events such as species or breed extinction, highlights the need to safeguard the option value[17] of diversity.

Examples of previously unforeseen needs include the trend among developed-world animal breeders away from production-oriented genetic improvement to focus more on adaptation, disease resistance and feed efficiency. In some developed countries, the importance of conservation grazing has reached an extent that few would have foreseen forty years ago when rare breeds began to be used for this purpose. In the United Kingdom, over 600 conservation sites are grazed (although not all with rare or traditional breeds) and as many as 1 000 sites would benefit from such grazing (Small, 2004). Specific breeds which were once under threat but have now proved to be of economic importance include the Piétrain pig. This very lean breed, which is now used in a large number of commercial cross-breeding programmes, was hardly known outside the Brabant province of Belgium prior to 1950. It almost became extinct during the Second World War when fat animals were in demand (Vergotte de Lantsheere *et al*., 1974). Another example is the Lleyn sheep breed from Wales, which during the 1960s was in serious decline and had a population size of only 500 pure-bred ewes (Box 96). The breed has become increasingly popular among sheep farmers in the United Kingdom in recent years and its population has grown to over 230 000. The Wiltshire Horn, another British breed that was once in decline, is also attracting interest because of changing market conditions. The breed sheds its wool – a desirable characteristic when shearing costs can exceed the price obtained for the fleece.

Opportunities provided by future developments in biotechnology also need to be considered. Emerging reproductive and genetic technologies already provide greatly increased opportunities to identify and utilize the genetic variation of AnGR, and such technologies are expected to show major advances in future. If diverse AnGR remain available, such technologies should make it possible for developing countries to close the productivity gap with developed countries by selectively combining the best features of different breeds.

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[17] The option value of diversity is the value given to safeguarding an asset for the option of using it at a future date.

It is widely accepted that the future option value of AnGR provides a strong reason for conserving AnGR. It is reasonable to assume that changing circumstances and rapidly advancing technologies will require the use of conserved AnGR in the future.

Box 96
Lleyn sheep of Wales – revival in fortunes in tune with modern demands

In the course of the last half century the Lleyn sheep breed of northwest Wales has progressed from the brink of extinction to a breed of widespread national importance in the British sheep industry. Following the Second World War, the breed retreated from the considerable local importance that it had in the first half of the century, and by the 1960s there were a mere seven pure-bred flocks and 500 ewes. In contrast, by 2006 the number of pure breeders exceeds 1 000 spread throughout the United Kingdom, and regional Society sales involve the annual trading of many thousands of Lleyn sheep.

This revival was achieved through the determination and enthusiasm of an initially small group of twelve local breeders and supportive advisers. They set up a breed society in 1970 to coordinate breeding policy, register pure-bred flocks and grade up cross-bred sheep (by repeated backcrossing using Lleyn rams). The chief attributes of the breed from the start were its medium size, mothering ability (in its hey-day it was milked after weaning the lamb) and prolificacy, as well as meat and wool quality. An added attraction for flock biosecurity was the suitability of the Lleyn for “closed flock” operations in which the only animals purchased are top-quality rams.

These attributes were intensified by organized breeding, partly through the operation of a New Zealand-type nucleus group breeding scheme, involving objective recording (Meat and Livestock Commission) and fast generation turnover. The resulting wide appeal of easily handled ewes, convenient for large and small flock owners, coupled with efficient utilization of expensive land, was fostered by the support of the Breed Society. This involved shrewd marketing, with well-organized breed sales and information provision for prospective buyers and member breeders.

Another important element, as the breed rapidly extended its geographical coverage, was the encouragement given to local devolution. Groups or clubs have been formed on a countrywide basis, currently seven clubs in all, although the parent breed society has maintained its coordinating role and its link with the home base in northwest Wales.

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Photo credit: David Cragg

Provided by J B Owen
For further information on the breed see: http://www.lleynsheep.com

2.3 Arguments related to the present situation

The importance of maintaining threatened AnGR does not necessarily relate only to their potential future use under changed circumstances. There are a number of reasons why the use of these resources may be sub-optimal at present. These reasons fall into three main categories: deficits in information, market failures and policy distortions (Mendelsohn, 2003). There are large gaps in knowledge regarding the characteristics of local breeds and their traits or genes that may be important for production, research purposes or to meet other human needs (Oldenbroek, 1999). Imperfect information may lead to the overestimation of the performance of a breed within a particular production environment where its introduction is being considered, and hence an inappropriate decision regarding its adoption. It is, of course, also possible that imperfect information could lead to farmers unnecessarily retaining their indigenous breed and not adopting alternative breeds that would improve their livelihoods.

Policy distortions can put less intensive production systems at a disadvantage and provide disincentives for efficient resource allocation. A narrow focus on more productive breeds may be favoured by policies such as subsidized grain imports, free or subsidized support services (e.g. AI) or support prices for livestock products, which stimulate the intensification processes. For example, in some rapidly industrializing Asian countries important capital subsidies have clearly favoured an industrial mode of development; cheap capital has led to investments in large commercial units associated with high input use and uniform products. Furthermore, development or emergency programmes sometimes promote exotic breeds from donor countries. Finally, political instability and policies unfavourable to vulnerable livestock keeping populations may inhibit the efficient use of AnGR (Tisdell, 2003).

Markets may not accurately represent external costs or benefits. Examples of external costs include negative environmental impacts, and undesirable effects on income distribution and equity. External benefits associated with certain breeds may, for example, include their contribution to landscape management. Mendelsohn (2003, p. 10) suggests that: "Conservationists must focus on what the market will not do. They must identify and quantify the potential social benefits of AnGR that have been abandoned by the market."

The preservation of diversity, including within-breed diversity, serves to maintain stability in production systems. Diverse populations show greater ability to survive, produce and reproduce under conditions of fluctuating feed resources and water supply; extremes of temperature, humidity and other climatic factors; and low levels of management (FAO, 1992). There is evidence that they are also less susceptible to catastrophic epidemics (Springbett *et al*., 2003). In general, genetically uniform populations are less able to respond to strong selection pressures resulting from environmental changes. Maintaining breed diversity enables people to exploit diverse ecological or economic niches. This is particularly the case in marginal and environmentally fragile areas, such as drylands, where most livestock kept by poor farmers are located, and which are characterized by great diversity and high levels of risk.

Arguments for existence and bequest values for AnGR,[18] remove the need to identify tangible or non-tangible benefits as a justification for conservation. "Biological diversity has intrinsic value and should be conserved for its own sake to the maximum extent possible, regardless of whether any given component can be shown to produce tangible economic benefits" (FAO, 2003, p. 104). However, the development of breeds within domesticated species is primarily the product of human intervention to meet human objectives and values. The argument that the current diversity should be preserved on the grounds of its existence value is, therefore, perhaps more difficult to defend than in the case of the biodiversity of natural ecosystems.

Arguments and capacities for conservation vary from region to region. In Western societies, traditions and cultural values are important driving forces which ensure the development of conservation measures for rare breeds and promote the emergence of niche markets for livestock products. By contrast, in the developing world, the immediate concerns are for food security and economic development. However, most developing countries are already in a process of economic evolution, and their economies can be expected to become sufficiently developed to support conservation based on cultural heritage and other such drivers at some point in the future. There is a need to ensure that AnGR are not lost before this self-supporting stage is reached.

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[18] The existence value is derived from the satisfaction of knowing that a particular asset exists; a bequest value is the benefit accruing to any individual from the knowledge that others might benefit from the resource in the future.

3 The unit of conservation

A critical first step in the design of AnGR conservation programmes is to decide what is to be conserved. At the molecular genetic level, the genetic diversity present within a livestock species is a reflection of allelic diversity (i.e. differences in DNA sequences) across the 25 000 or so genes (i.e. functional DNA regions) affecting animal development and performance. Conceptually, therefore, the most basic unit of conservation is the allele. An objective might be to design conservation programmes that will both allow maintenance of a preponderance of the alleles that are currently present within a species, as well as providing for the normal accumulation and potential retention of the newly arising mutant alleles which are the fuel for continued animal evolution and improvement. Allelic diversity could, in theory, be quantified by enumeration of the number and frequencies of the various alleles, but for the moment this is an impossible task. In defining the unit of conservation, it must further be recognized that alleles do not act in isolation, and that animal performance in most cases is properly viewed as a result of the interactions of alleles present across the genome. Thus, the process of genetic resource development involves the creation of allelic combinations that support specific desired levels of animal performance and adaptation. Efficient genetic resource conservation, therefore, involves the creation of structures that allow for maintenance of existing genetic combinations of known adaptive or productive value, and for easy access to these combinations to support future animal production needs.

Existing livestock breeds are less genetically uniform than most varieties of crop plants, but nonetheless represent the realization of a diverse set of adaptive processes. The population structure of the major livestock species up to the mid-twentieth century conformed closely to the population structure predicted to maximize evolutionary potential. There were many partially isolated subpopulations (the breeds), maintained under diverse conditions, but with periodic exchange of animals among populations and periodic recombination of breeds to yield new genetic combinations. Thus, adoption of the breed as the unit of conservation is expected to maximize the maintenance of evolutionary potential within livestock species, and likewise to maximize access to a broad array of allelic combinations.

4 Conservation of plant versus animal genetic resources

Organization and implementation of the SoW-AnGR assessment process was based on the lessons learnt from the global assessment of plant genetic resources (PGR) and the resulting Report on the State of the World's Plant Genetic Resources (FAO, 1998a). Accordingly, the SoW-AnGR process focused on both the preparation of the first Report, and the initiation of actions at national level arising from the process of Country Report preparation. Nevertheless, approaches for conservation of PGR cannot be directly applied to AnGR.

In traditional production systems, plant and animal genetic resources are used in comparable ways. Locally adapted breeds and varieties predominate; seed for planting, and breeding animals are drawn from the farmers' fields, herds and flocks, and genetic diversity within resulting landraces is substantial. Most breeding and development activities are "participatory" (FAO, 1998a) in the sense that decisions regarding the seeds to save for planting and the animals to retain for breeding are made by farmers rather than professional plant and animal breeders. However, intensification of agriculture has resulted in important changes in patterns of genetic resource utilization and development. In plants, intensification of crop production has generally been accompanied by emergence of a strongly institutionalized and centralized seed production sector dominated by publicly funded national and international centres, and private firms. In contrast, the intensification of the livestock sector is currently much less advanced, and has been a result of, rather than a prerequisite for, economic development. The animal breeding sector is far less centralized and institutionalized than the plant seed sector, although there has been substantial movement towards centralization in the poultry, pig and, to a more limited extent, dairy cattle sectors. Direct involvement of farmers in animal breeding remains substantial for the other livestock sectors, and AnGR utilization and further development remains strongly "participatory" in certain production environments. The different structures of the seed and seedstock sectors in plants and animals have important implications for the conservation of global genetic resources.

Table 104 compares a number of biological, operational, and institutional factors that influence conservation activities in plants and animals. Biological differences clearly require different approaches to conservation, but perhaps the most significant difference between the crop and livestock sectors involves institutional capacity for genetic resource management. Many of the institutions of the seed sector already maintain extensive collections of PGR, and actively contribute to the development and release of plant varieties. The databases of the World Information and Early Warning System on Plant Genetic Resources (WIEWS) record the location of over 5.5 million PGR accessions, in some 1 410 *ex situ* collections around the world (FAO, 2004).

Establishing a genebank for animals involves long-term storage of gametes, embryos or somatic cells in liquid nitrogen. Technical aspects of such *in vitro* conservation in animals are discussed in detail below, but costs to collect, cryoconserve and subsequently reconstitute animal germplasm are many times greater per preserved genome than costs to collect, store and subsequently utilize seeds. Moreover, funding to support the conservation of animal germplasm has been insufficient. As a result, AnGR conservation has much more heavily emphasized *in situ* approaches. However, with the exception of a small number of developed countries, there has been little action to establish *in situ* conservation programmes, and the long-term sustainability of such schemes remains uncertain.

DAD-IS lists 4 956 extant mammalian breeds and 1 970 extant avian breeds. Few of these are well represented in *in vitro* collections and almost none have been sampled at levels consistent with FAO (1998b) guidelines for *in vitro* sampling. Very substantial resources would be required to develop *in vitro* collections of even the most endangered of these nearly 7 000 livestock breeds. For example, the FAO (1998b) Guidelines for Management of Small Populations at Risk recommend collection of frozen semen from at least 25 males per breed, and use of semen from these males on an additional 25 females per breed to produce frozen embryos. For cattle, with 300 endangered breeds, cryoconservation of semen from 7 500 males and approximately 100 000 embryos would be required. Policy guidelines for ownership, use and management of *in vitro* collections are yet to be developed.

Table 104
Comparisons of biological, operational, and institutional factors influencing plant and animal genetic resources conservation

Factor	Plants	Animals
Economic value of production per individual	Low to very low	Moderate to high
Reproductive rate (number of progeny per individual per generation)	High to very high (1000s)	Very low (<10) to moderate (<200) except for males of species (mainly cattle) where widespread use of artificial insemination is feasible (10 000s)
Generation interval	0.25 to 1 year	1 to 8 years
Within-line genetic diversity	Very limited in most plant varieties	Very substantial in most livestock breeds
Cost to record performance of an individual or family	Very low to low	High to very high
Cost to assess adaptation or disease resistance for an individual or family	Very low to moderate	Very high
Ability to conserve diversity of wild relatives under natural conditions	Common for plants	Rare in animal species
Ability to self-fertilize and develop inbred lines	Possible and routine in many species	Self-fertilization is not possible; due to depression, high levels of inbreeding have to be avoided; in specific cases inbred lines are used for crossing
Clonal propagation	Possible and routine for many species	Technically feasible but too inefficient even for most research purposes
Ability to collect germplasm	Simple in most cases	Technically feasible but requires facilities and trained personal
Ability to store germplasm *in vitro*	Seed storage in cool conditions is feasible for most species; a few species require tissue culture; in some cases cultures can be stored in liquid nitrogen	Feasible for male gametes of most species and female gametes of some species; storage of embryos is feasible for most mammalian species, but at much greater cost compared to spermatozoa; material from all species must be stored in liquid nitrogen
Requirements for regeneration of stored material	Most require periodic restoration to replenish stored material and maintain viability	Essentially permanent storage
Cost of extracting, regenerating, and testing material from a genebank	Relatively easy and with relatively low cost; tens of thousands of accessions are extracted and tested annually	Both regeneration and testing are difficult and time consuming; there has been little experience with the extraction and use of stored material
Status and scope of genebanks	Extensive collections at several locations globally include millions of accessions for hundreds of species mainly involving seed storage with relatively low collection and storage costs	Restricted to a small number of developed countries, mainly involving frozen semen
Ongoing collection of wild and indigenous germplasm	Lower levels than in past years, but still a significant effort, especially for neglected species	Very little activity, especially in the developing world
Institutional support for conservation	Substantial, well-organized, and stable	Limited, often poorly organized, some exception in developed countries

In the table, "plants" refers specifically to the annual plants that dominate food and agricultural production, but it is recognized that long-lived perennial plants such as trees have significant elements in common with animals. Similarly, "animals" include both relatively fecund species such as chickens, which have some elements in common with plants (e.g. the potential for annual replacement of commercial flocks), and very extensively managed, long-lived species such as the dromedary.

Institutional capacity for AnGR conservation is limited, with only a few national *ex situ* collections existing, mainly in developed countries. Among the institutions of the Consultative Group on International Agricultural Research (CGIAR), only the International Livestock Research Institute (ILRI) and the International Center for Agricultural Research in the Dry Areas (ICARDA) actively address issues of better management of AnGR, and neither institution has an active programme for long-term storage of germplasm. Ownership of AnGR resides almost exclusively in the private sector. A substantial enhancement of global capacity for conservation and better use of AnGR, with new institutional models and collaboration among public institutions and between public institutions and private farmers, may therefore be required if the recommendations of the SoW-AnGR process are to be implemented.

5 Information for conservation decisions

Setting priorities for AnGR conservation requires a process that enables the identification of breeds that contribute most to global genetic diversity and have the greatest potential to contribute to efficient future utilization and further development of that diversity. Additional criteria, such as cultural or heritage values of a breed, will also affect priorities for conservation.

Assessing the likely genetic diversity present in a set of breeds may be based on a variety of criteria, including:

- trait diversity, which is diversity in the recognizable combinations of phenotypic characteristics that define breed identity;
- molecular genetic diversity, based on objective measurements of genetic relationships among breeds at the DNA level; and
- evidence for past genetic isolation as a result of either geographical isolation or of breeding policies and cultural preferences applied in the communities where the breeds were developed.

Trait diversity is based on heritable phenotypic differences among breeds. When breeds are compared under comparable environmental conditions, trait diversity is necessarily indicative of underlying functional genetic diversity. For this reason, breeds that possess unique or distinctive trait combinations should be given high priority for conservation, because their unique phenotypic characteristics necessarily reflect unique underlying genetic combinations. Trait diversity expressed at the level of complex quantitative traits such as disease resistance, milk production or growth rate is generally given higher priority in conservation decisions than trait diversity associated with simply inherited traits such as coat or plumage colour, horn shape or body type. These simply inherited traits can be changed rapidly in response to owner preferences, whereas differences in complex quantitative traits generally involve larger numbers of genes, take longer to change, and therefore have greater potential to reflect underlying genetic diversity.

Direct measures of molecular genetic relationships among breeds are increasingly becoming available and also provide an indication of genetic diversity. These measurements are based on variation in DNA sequences, usually in neutral regions of the DNA that are not thought to influence animal performance or phenotype. For this reason, molecular measures of genetic diversity reflect differences in evolutionary history, but provide only indirect indications of genetic diversity in functional or potentially functional regions of the DNA. Breeds that appear closely related based on allelic frequencies at neutral loci may nonetheless differ importantly at functional loci as a result of divergent selection histories. For example, genetic distance information, derived using few randomly selected genetic markers does not provide information on specific genetic variations such as the double-muscling allele in Belgian Blue cattle, or the dwarf gene in the Dexter (Williams, 2004). For this reason, trait diversity generally warrants first consideration in choosing candidates for conservation.

However, phenotypically similar breeds may evolve as a result of different genetic mechanisms, and measures of molecular genetic diversity can aid the identification of breeds that are superficially similar but genetically distinct. Conservation of genetically unique breeds is, likewise, justified because these breeds are more likely to exhibit functional genetic diversity for traits previously unmeasured or unexpressed, but that may be of future importance in new markets, with exposure to new diseases, or under different production conditions.

Box 97
Decision-making in conservation and utilization – use of genetic diversity data

It is only recently that the value of genetic diversity data in conservation and utilization of AnGR has been recognized and applied. The Global Environment Facility (GEF) is supporting a project on conservation of trypanotolerant cattle, sheep and goats in four West African countries, which started in 2005. In much of the region, the purity of trypanotolerant breeds has been diluted by past cross-breeding with non-trypanotolerant breeds. However, this lack of purity is not immediately obvious in the appearance of the animals. Molecular genetic markers are being used to map the diversity of these breeds and identify the most pure populations which will then be the focus of conservation and further development. Meanwhile, an ongoing International Atomic Energy Agency (IAEA) programme is mapping molecular genetic diversity among Asian sheep and goat breeds. The genetic diversity data will then be combined with phenotype data to identify breeds in which different mechanisms of resistance to the same disease have evolved. These breeds will then be crossed, and molecular genetic markers used to map the genes controlling resistance in order to confirm that different breeds have evolved different mechanisms of resistance. If this is confirmed, these different mechanisms can be used in further genetic improvement programmes.

Provided by John Gibson

Measures of molecular genetic diversity are attractive as a basis for conservation decisions because they yield quantitative measures of relatedness which can, in turn, be used to assess genetic diversity within a set of breeds. In contrast, trait diversity is more difficult to quantify objectively, especially for quantitative traits and for small groups of breeds. Past efforts to quantify phenotypic differences have focused mainly on morphological measures at species or subspecies levels in natural populations. In the absence of widespread access to molecular genetic information, results had value as indicators of evolutionary distance, but are less useful in domestic animals where artificial selection can lead to rapid morphological changes, such as those observed in domestic dogs or fancy poultry. Objective assessment of genetic diversity at functional or potentially functional sites will, thus, require further development of objective methods to combine information on trait and molecular genetic diversity (see Section F: 8).

Historical information or evidence of long-term genetic isolation can be used in the absence of information on trait or molecular genetic diversity, but can also be misleading. Population genetics theory shows that very low levels of movement of animals between seemingly isolated populations can effectively prevent meaningful genetic differentiation. Thus, breeds with a history of genetic isolation are important candidates for careful trait and molecular genetic characterization, but final decisions on genetic uniqueness are better made using more objective tools. It should be recognized, however, that livestock breeds developed as a result of cultural preferences in isolated rural communities may be an important part of community identity and heritage. Conservation of such breeds may merit consideration as part of broader community development efforts, regardless of their predicted value as a unique global genetic resource.

Box 98
Spatial analysis of genetic diversity

The mapping of molecular genetic information in a Geographic Information System (GIS) allows a spatial analysis of the genetic information. GIS can be used to study spatial structures, distribution and distance of genetic data; to simulate animal population migrations in the landscape; to visualize and analyse geographic population structures; to define diversity zones; to detect areas of genetic differentiation; and to examine the interaction between environment and genetic variants.

The Econogene project (http://lasig.epfl.ch/projets/econogene/) was designed to combine molecular genetics with spatial analysis to document the spatial distribution and environmental correlates of genetic diversity among small ruminants in Europe. DNA was sampled from over 3 000 animals spread from Portugal to eastern Turkey. A set of 30 microsatellites, 100 AFLPs and 30 SNPs were assayed on these animals and more than 100 environmental variables were recorded. Geovisualization (GVIS) tools were then used to observe the patterns of physical association between various components of genetic variation and spatially varying environmental factors. Such visualizations led to the development of hypotheses for causative associations between environmental and anthropic factors and genetic variation. For example, the association of alleles of several molecular markers with selected environmental variables was tested. The testing included a set of AFLP molecular markers, which were not related to any specific trait, and a variety of environmental variables (mean temperature, diurnal temperature range, relative humidity, sunshine, ground frost frequency, wet day frequency, wind speed and precipitation). Three AFLP markers were found to be significantly associated with one or more variables, probably pointing to adaptation to a humid environment (e.g. coefficient of variation of precipitation, number of wet days, relative humidity, sunshine and mean diurnal temperature range).

The results were compared with those obtained with the application of a completely independent population genetics method. Two genetic markers were indicated to be under selection by both approaches, validating 31 percent of the significant associations identified by the spatial analysis. These results are particularly encouraging as they seem to validate an approach which is independent of any population genetics model (see Joost, 2005, for further details).

Provided by Paolo Ajmone Marsan and the ECONOGENE Consortium

6 *In vivo* conservation

The term "*in vivo* conservation" describes conservation of live animals and encompasses *in situ* and *ex situ in vivo* conservation methods.

6.1 Background

Conservation of AnGR takes place in a wide variety of contexts, varying in terms of species, breed, geographic region, and farming, social and economic systems. Conservation can also have a wide variety of objectives. Emphasis may be placed on the conservation of genetic resources or diversity *per se*; on the environmental services through which livestock contribute to the conservation of the wider ecosystem; on the socio-economic consequences of conservation; or on the cultural significance of maintaining particular livestock breeds. Approaches to the conservation of AnGR can differ significantly in their capacity to achieve the various conservation objectives, and in terms of their applicability in different contexts.

It is possible to view *in vivo* conservation techniques as subsuming a spectrum of different approaches: at the *in situ* end of the spectrum is the maintenance of breeds within their original production systems, while the extreme *ex situ in vivo* approach is to keep the breeds in zoos. Ranged between the two extremes are: maintaining the species under farm conditions but outside the environment in which they evolved; the maintenance of limited numbers of animals in special-purpose conservation farms, in experimental or educational herds; and keeping breeds for pasture or landscape management within protected areas. Faced with the diversity of potential conservation measures, it is sometimes difficult to make a clear distinction between *in situ* and *ex situ in vivo* approaches. For instance, governmental stations can be considered as applying *in situ* or *ex situ in vivo* conservation methods depending on location and husbandry practices.

There is no single prescription for a successful conservation programme. Numerous breed conservation activities have been undertaken, particularly since the 1980s. However, almost no attempts have been undertaken to analyse adequately the factors underlying the success or failure of *in vivo* conservation programmes. Such analyses are also constrained by the limited availability of data.

6.2 Genetic management of populations

Detailed discussions of many of the requirements for genetic management of populations can be found in Oldenbroek (1999).

Small populations and genetic variation

Whenever breeds are conserved *in vivo*, whether *in situ* or *ex situ*, they should be managed in ways that maintain their genetic variation in the long term. It is well known that a small population size may lead to loss of allelic diversity and an increase in inbreeding. Maintaining sufficient effective population sizes to preserve genetic variation is a central theme of long-term breed management. Apart from increasing the number of animals in the population, management techniques to maintain genetic diversity include maintaining a narrow sex-ratio. This is because even if the number of females in the population is large, high-intensity selection schemes can reduce the number of breeding males considerably, and result in a small effective population size and consequent high inbreeding increments. Another method is to minimize variance in the numbers of progeny produced by individual breeding animals, which reduces the average relationship among the animals available for breeding in the next generation.

The population should also be large enough to allow natural selection to purge deleterious mutations which could otherwise accumulate in the population as a result of genetic drift. It is significant for the management of small breeding populations that there is a threshold effective population size below which the fitness of the population decreases steadily. Based on the most recent estimates of mutation rates, this threshold of effective population size is considered to be between 50 and 100. The minimum population size required will therefore be above 50.

Another possible management technique is the use of cryoconserved genetic material in *in vivo* conservation schemes in order to increase the effective population size. The combined use of molecular genetic and pedigree information has also been proposed. Such techniques, however, require substantial expertise and expense, and may be too costly for many countries. Most of the theoretical and implementation models that have been developed refer to pedigree populations with a high degree of herd and animal management. Such models are likely only to be relevant for a limited number of species in a limited number of countries. Management schemes that can be implemented in populations with limited genealogical information have been developed (Raoul *et al*., 2004). However, field testing and further methodological development is needed to adapt them to situations with limited organizational capacity and funding.

Selection in local breeds

Breeds are dynamic, undergoing continuous genetic change in response to environmental factors and active selection by livestock keepers. The indigenous breeds of the developing world are rarely subject to modern breeding techniques. However, selection programmes can increase the frequency of genes desirable for the productivity and profitability of local breeds. Such measures will undoubtedly be required if local breeds are to remain a viable livelihood option for the farmers who maintain them. Selection schemes need to take into account the maintenance of genetic variation within the breed and the risks associated with high rates of inbreeding. Traits under selection need to be accurately recorded, and the highest responses to selection result from the use of statistical genetic estimates of breeding value. Controlled breeding, based on estimates of breeding value, result in inbreeding rates two to four times higher than those that result from random selection of parents. However, techniques have been developed to optimize selection so that a suitable balance between inbreeding and genetic improvement can be achieved. Such methods should be of particular advantage in small populations, but there has been little work on how they should best be applied in developing-country situations. As a broad generalization, genetic improvement in local breeds will often involve a greater emphasis on characteristics contributing to low production costs, and the environmental and cultural values of the associated farming systems.[19] Traits proposed for selection will need to be accurately evaluated for their genetic relationships with traits that determine the conservation value of the breed, so that possible negative effects on key adaptation traits are avoided.

6.3 Self-sustaining strategies for local breeds

The sustainability of a given breed is affected by many factors including: cultural, social and food demand changes; transformation of the food production chain; changes to policies and national and international legal frameworks affecting the importation of germplasm and livestock products; economic development; and technological changes. In most cases, it is a combination of changes in production systems and lack of current economic profitability that plays the major role in the decline of a breed. The question arises: what options are available to halt and reverse the process of breed decline? Possible options for achieving self-sustainability are described below.

Identification and promotion of quality products

Many local breeds are able to provide unique products that may be of a higher quality than those obtained from high-output commercial breeds. Local breeds and their products may also be valued as a characteristic part of traditional farming systems. Moreover, many local breeds have long played a central role in the social and cultural life of rural populations – including religious and civic traditions, folklore, gastronomy, specialized products and handicrafts (Gandini and Villa, 2003).

These characteristics can potentially be a basis for diversified livestock production, and increased profitability for local breeds. Conservation objectives have been promoted both through direct subsidy (see below), and through the promotion of high-value specialized products. The latter approach has been particularly successful in Mediterranean areas, where the diversity of breeds and production systems is still associated with a variety of animal products, food preferences and cultural traditions. Unfortunately, even in this part of the world, it is probable that the majority of such relationships that were present in the mid-nineteenth century have been lost. The strategy is supported by current European certification systems for agricultural products, such as the PDO (Protected Designation of Origin) and the PGI (Protected Geographical Indication), and also by the development of specific commercial brands.

In case of Europe, these conservation efforts are implemented within a highly developed economy that can support diverse high-value products, and actions to support cultural and environmental goals. Opportunities to apply such approaches are likely to be more limited in less-developed economies; but examples do exist, such as the higher price achieved for meat from native Creole pigs in Yucatan, Mexico, and for native chicken meat in several Asian and African countries. As economies develop, the cultural identity of breeds is likely to become more important as an aspect of marketing and as a policy goal, and hence offer greater opportunities for the achievement of breed self-sustainability.

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[19] A greater focus on disease resistance, feed efficiency and general adaptation is also being applied to genetic improvement of more commercially oriented breeds, driven by concerns about possible failure of existing disease control measures, Legislated reduction or elimination of the use of antibiotics, and concerns about the costs of external inputs, particularly related to the use of fossil fuels.

Box 99
In situ conservation of the Norwegian Feral Sheep

The Norwegian Feral Sheep is a remnant of the sheep populations kept in Norway during the days of the Vikings. In 1995, it was confirmed that the breed was threatened with extinction. There were an estimated 2 000 animals in the country at that time, mostly kept in western Norway.

A few committed individuals, centred on an active and long-established sheep breeding community in Austevoll in the county of Hordaland, decided to try to save the Feral Sheep and develop a niche industry based on the breed. In June 1995, the Norwegian Feral Sheep Association was established. The association is a nationwide, cooperatively managed society with about 300 members. The objectives of the association are to conserve the breed and improve its profitability, by adapting production methods and products to market demands, and by raising public awareness.

Photo credit: Erling Fimland

The association quickly established a set of production standards which had to be met if products were to be certified under the “Feral Sheep” label. These standards include both a breed description, and certain requirements regarding production methods. An important aspect of the association’s producer standards is also to safeguard traditional farming methods, which are a continuation of the way in which Feral Sheep have been kept in Norway for centuries. Requirements specify that the sheep are kept outdoors all year round, and that they have access to a protective shed if there is no natural shelter available. As a rule, the use of feed concentrates is also prohibited. Meat from the Feral Sheep has been welcomed by consumers. The characterful, tasty meat is regarded as a fashionable niche product. Another important aim of the breeding association is to maintain the coastal heathlands and other cultural landscapes. These landscapes, with grazing Feral Sheep, are increasingly popular attractions for tourists.

In 2003, only eight years after the first conservation measures were introduced, the Feral Sheep population exceeded 20 000 animals. Most Feral Sheep are still found in western Norway, but there are initiatives to introduce this special form of sheep farming in the coastal regions of central and northern Norway, as part of the development of rural industries in these areas.

Provided by Erling Fimland

Ecological services

Breeds adapted to local production conditions are often the best suited to provide environmental services such as landscape management, including the stimulation of desired types of vegetation growth, fire or avalanche control, and keeping power line and wildlife corridors free of brush (thereby reducing herbicide use). There may be opportunities even in less-developed economies to sustain a variety of culturally important breeds through ecological and cultural tourism, or other novel approaches to income generation for livestock keepers. An example might be the use of local cattle to maintain healthy ecosystems that promote increased animal density and diversity in large wildlife parks. The challenge is to translate such breed services into economic rewards for the livestock keepers.

Incentive measures

A lack of profitability relative to other breeds, and hence a lack of popularity with farmers, is frequently a reason for the decline of a breed's population numbers. One potential approach to conservation is to offer farmers financial incentives to compensate them for income that they forgo by keeping the less profitable breed. This approach is only feasible where resources are sufficient and there is political will to expend public funds to meet conservation objectives; where breed characterization is sufficient to allow breed populations to be identified and classified according to their risk status; and where the institutional capacity is in place to allow eligible farmers to be identified, to monitor their activities, and to administer payments. It is perhaps not surprising that incentive schemes for breed conservation have largely been restricted to Europe. Schemes have been in place in the EU since 1992 (for a further discussion of EU legislation covering incentive payments see Part 3 – Section E: 3). Such incentives have halted the decline of some, but not all local breeds. A number of national-level schemes have also been put in place, again mostly in Europe (see Box 100 for examples). Even where successful, the longer-term sustainability of such incentive systems is questionable. It seems worthwhile to investigate the use of more specific incentives; in Europe for example, the elimination of milk production quotas for endangered breeds might promote their wider use. In general, economic incentives should be designed to accelerate the achievement of breed self-sustainability rather than merely to provide temporary economic support.

Box 100
Examples of incentive payment schemes at the national level

In the United Kingdom, the Traditional Breeds Incentive scheme run by English Nature (a government nature conservation agency) covers livestock kept at, or adjacent to, sites of special scientific interest (English Nature, 2004). The premise is that traditional breeds are often better adapted to grazing the herbage found at these sites, and thus do a better job where grazing is required for conservation purposes. Here, the objective is broader than simply preserving the breeds *per se*, and the incentive payments to the farmers can be regarded, in part, as payments for the broader environmental services provided.

In Croatia registered breeders of locally-adapted endangered breeds receive state subsidies totalling around US$650 000 *per annum* (CR Croatia, 2003). Fourteen breeds including Istrian cattle, Slavonian-Podolian cattle, Posavina horse, Murinsulaner horse, Turopolje pig, Black Slavonian pig, Istrian sheep, Ruda sheep, Zagorje turkey and some donkey breeds are covered by the scheme. Similarly, in Serbia and Montenegro, the Department for Animal and Plant Genetic Resources of the Ministry of Agriculture operates a payment scheme for supporting the on-farm conservation of locally adapted breeds of horses, cattle, pigs and sheep (Marczin, 2005).

In Myanmar, population numbers of Shwe Ni Gyi cattle were increased through the provision of subsidized semen, and the payment of a small amount (equivalent to US$1) to owners when they registered a pure-bred animal (Steane *et al*., 2002).

Utilization in production systems

Higher productivity resulting from genetic improvement of local breeds can imply higher intensity of management and the need for supporting infrastructure. Conversely, improvement in production systems and infrastructure can stimulate improvement of the local breed and/or the importation of new breeds. Such development can be both an opportunity and threat to the maintenance of local breeds. For example, indiscriminate cross-breeding can be a major threat. However, if properly structured, cross-breeding can lead to maintenance of the local breed, for example, as a highly adapted and efficient dam breed in a recurrent cross-breeding programme. Unfortunately, little is known about how to improve production systems and infrastructure such that the livelihoods of local people are improved and food security is achieved while also conserving indigenous AnGR.

Box 101
An index of economic development potential for targeting *in situ* conservation investments

The Econogene project combines molecular analysis of biodiversity, with socio-economics and geostatistics in order to address the conservation of sheep and goat genetic resources and rural development in marginal agrosystems across Europe. Samples of genetic material were collected in seventeen countries in Europe and the Near and Middle East. (http://lasig.epfl.ch/projets/econogene/)

One of the objectives was to help make expenditure of funds more effective. The project developed an index of development potential, provided as a simple tool that can be used to determine where public money can best be spent to maximize response. Application is possible at different levels: from a single farm up to a region. The index is a weighted sum of three sub-indexes that evaluate, (1) the economic characteristics of the firm/farm (single or average from a region), (2) the social characteristics of the firm/farm, (3) marketing strategies. Each sub-index is based on a variety of inputs. In the case of the Econogene study of EU sheep and goat breeds, the relative weights in the economic development index were 50 percent for the economic dimension, 30 percent for the social dimension, and the remaining 20 percent for marketing strategies. The index does not include environmental factors, such as climatic conditions, availability of agricultural land or pasture, or public administration factors. These factors can affect outcomes when the policy tools are applied, but the index evaluates only the economic potential resulting from the characteristics and behaviour of the private sector.

Provided by Paolo Ajmone Marsan and the ECONOGENE Consortium

6.4 *In situ* versus *ex situ* approaches to *in vivo* conservation

Given the intimate and complex relationships between indigenous communities, environments and livestock, and a widespread lack of breeding services and infrastructure, community-based management of AnGR is seen as a solution (Köhler-Rollefson, 2004), and is widely promoted by NGOs. Certainly, such community-based approaches to conservation seem the preferable option if they support further development of the breed and its ability to enhance livelihoods. Many of the conservation strategies based on high-value products or production services, discussed above, have been built around community-based, *in situ* conservation. It has to be ensured that maintaining local breeds will enhance the short and long-term livelihoods of the communities that keep them. If this is not the case, such strategies will prove unsustainable as the communities will eventually switch to alternative breeds that provide better livelihoods.

Community-based management approaches do exist in the developing world. The example described in Box 102 illustrates that even where traditional production systems are threatened, progress can be made towards the achievement of goals such as, managing communal grazing areas, improving genetic resources and strengthening social development. However, the example from Nepal (Box 103) shows that as production conditions change, the introduction of imported genetic resources can sometimes be a viable option for small-scale livestock keepers. While in this case the livelihoods of the farmers have been improved, the local buffalo genetic resources are no longer being utilized. The example illustrates that achieving strategies that simultaneously improve livelihoods and achieve conservation objectives will often be a challenge.

Box 102
Community-based *in situ* conservation programme – a case from Patagonia

Photo credit: María Rosa Lanari

Neuquén criollo goats are the main source of income and animal protein for many households in the north of Neuquén province in Argentine Patagonia. The goats are well adapted to the transhumant movements which have traditionally shaped the lives of the goat keepers or *crianceros*. The sustainability of the system is, however, threatened by changes restricting livestock movements, notably the fencing of traditional grazing areas. Prospects of education, employment and better housing offered by more urbanized lives also promote sedenterization. Attempts during the 1980s to introduce Angora and Anglo-Nubian goats for fibre and milk production proved unsuccessful because of the harsh environment. Nonetheless, indiscriminate cross-breeding poses a threat to the local genetic resources.

A programme for the conservation and improvement of the Neuquén criollo goat was established in 2001 under the auspices of the Instituto Nacional de Tecnología Agropecuaria (INTA) and the provincial Agricultural Bureau. Organizational and technological innovations which promote the continuance of the traditional system under changed circumstances have been introduced. The goat keepers have been involved in the programme since its inception through the establishment of producers' associations which play a leading role in the development and diffusion of new technologies.

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Genetic improvement work is oriented towards conserving the breed's genetic variability, hardiness and productive efficiency within the framework of the traditional system. The programme is developing a system for providing improved strains of local ecotypes based on selection criteria proposed by the *crianceros* themselves. Preferences are for large but compact animals that provide good meat yield and can withstand extreme environments. The *crianceros* also pay attention to does' suitability for breeding and kidding. A preference for white goats is related to the marketing of the hair. Conversely, goats with coloured coats are considered easier to manage in snow-covered pastures. This preference is strongest in areas where snow lies longest. Further developments include measures to increase the value of goat products. Kid meat is now sold under a distinct "geographical indication". This commercial–legal innovation enhances the profitability of the traditional product of the system. A newer undertaking for the goat keepers is the harvesting of cashmere. Recent studies of the fibre from the breed have revealed the potential of this product. The *crianceros* have been provided with combs and trained to harvest and classify the fibre.

The aim is, thus, to forestall the breed's genetic dilution as part of integrated efforts to preserve the underlying production system. The goat breed, the local environment, the culture and traditional practices of the *crianceros* are regarded as valuable assets that can be used to enhance the development of this rural area.

Provided by María Rosa Lanari
For further information see FAO (2007a)

Box 103
Changes in production systems leading to replacement of local buffaloes – a case from Nepal

Parcelling out of available grazing land as a result of population growth has had a large impact on traditional livestock farming systems in the Mid-Hills of Nepal. Rural households with access to growing urban markets have replaced low-yielding local cattle and buffaloes with high-yielding dairy buffaloes that can be stall-fed. In less than 30 years, more than 95 percent of farm households in the study area have replaced their local cattle and Lime buffaloes with one to three high-yielding Murah milk buffaloes from the Indian lowlands. About 65 percent of households buy new animals in lactation each year, selling the dry ones for rebreeding or meat. The imported buffaloes are bred in the Indian lowlands, and selected by Indian traders, who transport them to the highlands of Nepal and purchase the dry animals. These private traders have played a much more important part than the government in promoting the utilization of higher-yielding animals. The local buffalo and cattle breeds will remain important in more remote rural areas where they continue to provide draft power and give enough milk for family subsistence.

Initial obstacles to managing the newly introduced breed have been overcome, and farmers no longer wish to return to using the local animals. Farmers have kept improved buffaloes successfully on a prolonged basis, and have been rewarded with an improved standard of living. Their priority now is to further develop breeding strategies for the Murah buffaloes to achieve even better productivity. This requires collaboration between the breeders of Nepal and India.

Socio-economic changes led farmers to abandon traditional farming practices and to seek alternatives. The new management strategies have provided higher economic returns, and farmers have come to favour an introduced breed over their local animals. This case study shows that as production conditions change, new breeds with different characteristics sometimes provide farmers with a better livelihood option than local breeds.

Provided by Kim-Anh Tempelman
For further information see FAO (2007b)

Although *in situ* conservation is the most frequently adopted conservation method in Europe, there are also several examples of *ex situ in vivo* conservation programmes, in farm parks and in a few cases in zoos. In the United Kingdom there are currently 17 Rare Breeds Survival Trust Approved Centres[20]. One such farm, the Cotswold Farm Park[21], attracts over 100 000 visitors annually. In Germany, Falge (1996) reported 124 institutions maintaining animals of 187 breeds and nine livestock species. Similar institutions exist in many other parts of Europe, for example, in Italy, France and Spain, and also in North America. A particularly valuable role of farm parks is that they contribute to public awareness of AnGR conservation. For some species, such as poultry, enthusiastic hobby-breeder organizations play a role in conserving local breeds. The first example of a protected area focused on rare domestic breeds was in Hungary, where native breeds are conserved on the Puszta (an area of grassy wetlands and plains in eastern part of the country). Such schemes are now found in other parts of Europe and elsewhere.

In the developing world, the most commonly observed *ex situ in vivo* conservation activities are in herds or flocks maintained by state-owned institutions. The evidence provided by the Country Reports

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[20] http://www.rbst.org.uk/html/approved_centres.html
[21] http://www.cotswoldfarmpark.co.uk

suggests that there is insufficient information to determine how sustainable such conservation programmes will be. It seems that virtually all *ex situ in vivo* conservation in the developing world is used to support ongoing use of the AnGR by farmers – raising the question of whether *ex situ in vivo* conservation is likely to be a viable approach to conservation of AnGR that are no longer in current use. There is very clearly a need to develop a far greater understanding of how to design and implement sustainable *in vivo* conservation, particularly in the developing world.

7 Current status and future prospects for cryoconservation

From the early development of AI in the mid-1940s to the most recent potential offered by DNA storage and transfer, reproductive biotechnologies have been instrumental in the transfer of genetic material *in vivo* and *in vitro*. The techniques that are currently accessible and economically feasible for *in vitro* conservation of AnGR are those for cryoconservation of reproductive cells, embryos and tissues. Materials conserved using these techniques may preserve their liveability and functional state for decades or even centuries. However, because of the relatively short period during which the technologies have been in existence, a precise evaluation of this putative longevity remains to be established. More recent biotechnologies, including cloning, transgenesis and transfer of somatic material, have great potential for future applications in AnGR conservation, but at present they are only accessible to a few laboratories. The low reliability and extremely high costs of these technologies are two factors likely to limit their use in AnGR conservation in the coming years. This chapter, therefore, focuses primarily on current state-of-the-art reproductive biotechnologies that are economically and technically accessible in most geographical areas. Previously published documents such as the "Guidelines for development of national farm animal genetic resources management plans" (FAO, 1998c) and "Guidelines for the constitution of national cryoconservation programmes for farm animals" (ERFP, 2003) provide more details about applications.

7.1 Gametes

Semen

Semen from all mammalian livestock species has been successfully frozen in past years, as has semen from some poultry species (chickens, geese). Freezing procedures for semen cryoconservation are species-specific, but the general procedures are as follows:

- following collection, semen is diluted in a suitable ionic (salt) or non-ionic (sugar) solution adjusted to near physiological osmolarity;
- suitable cryoprotectant is added – glycerol is most commonly used, but Dimethyl Sulfoxide (DMSO), Dimethylacetamide (DMA) or Dimethylformamide (DMF) are, depending on the species, of high practical interest;
- diluted semen is cooled, sampled and then frozen in liquid nitrogen (-196 °C);
- individual semen doses are generally frozen in straws rather than pellets to guarantee optimal sanitary conditions and permanent identification of each dose.

Following AI with frozen and thawed semen, global conception rates average 50–65 percent in more than 110 million yearly first-service inseminations in cattle; 70–80 percent in more than 40 million inseminations in pigs; 50–80 percent (intrauterine) or 55–65 percent (cervical) in more than 120 000 inseminations in goats; 50–80 percent (intrauterine) or 55–60 percent (cervical) in more than 50 000 inseminations in sheep; and 35–40 percent in more than 5 000 inseminations in horses (Ericksson *et al*., 2002; Thibier, 2005; G. Decuadro, personal communication, 2005). Results in chickens reveal large between and within-breed variability in the range of 10–90 percent (Brillard and Blesbois, 2003).

The number of semen doses that need to be stored is a function of the number of doses required per parturition or hatching, the expected lifetime production of fertile refounder females, and the number of males and females desired in the reconstructed population. Where semen is used to reconstruct breeds by backcrossing, some percentage of the genes from the female population used in the backcross will remain in the reconstructed breed. For example, five generations of backcrossing are needed to obtain animals carrying over 95 percent of the genotype of the breed restored from the frozen semen. Sufficient semen must be stored to produce the number of backcross generations required. In avian species in which females bear ZW heterochromosomes (males are ZZ), genes carried by the W chromosome cannot be transferred through standard semen cryoconservation. Moreover, in all species, some cytoplasmic effects of the donor breed may be lost or altered. Notwithstanding these limitations, this technique should be seen as playing a predominant role in the *ex situ in vitro* conservation of AnGR, because of the availability of advanced and reliable technology and the ease of application. However, if the number of doses available per male is low or if the number of females that can be obtained per dam is low, then the re-establishment of the breed via embryo transfer is, where possible, more desirable as a means of ensuring full recovery of the initial genes.

Oocytes

In the case of birds, despite interesting technical developments, hatched chicks have not yet been successfully obtained from eggs that have been frozen and thawed. This is, in part, because of the huge amount of lipid present in the vitellus. In contrast, embryos from some mammalian livestock species can be produced *in vitro* from matured oocytes collected at slaughter or from live females by ovum pick-up. Such oocytes can be frozen for prolonged periods prior to *in vitro* fertilization (IVF) to produce embryos. Two methods of freezing can be distinguished based on the rapidity of the freezing procedures. Slow-freezing procedures are currently feasible in cattle and potentially applicable in sheep and goats, but success rates in obtaining progeny remain extremely low (less than 10 percent). In part, this is a result of the limited success rate of embryo transfer, and high embryo mortality following fertilization. Moreover, such techniques, which require oocyte maturation prior to IVF, must be performed by highly qualified technicians. Ultra-rapid freezing procedures, also called vitrification, are currently developed experimentally to limit damage to the oocyte resulting from chilling injuries or the toxicity of cryoprotectants. Most protocols use high concentrations of cryoprotectants and sugars to remove water from the cells. This limits intracellular ice formation and, therefore prevents ice injuries to the oocyte. Promising results have been obtained in cattle. However, working procedures which would make the cryoconservation of oocytes useful for the preservation of AnGR remain to be validated on a large scale.

7.2 Embryos

In contrast to avian species, embryos of virtually all mammals can be successfully frozen, thawed and then transferred into recipient females to produce progeny. Currently, however, widespread use of embryo cryoconservation is limited to cattle, sheep and goats. Embryo collection in pigs requires the sacrifice of the female, and the procedure remains experimental in equine species. A number of factors including the method of embryo collection (biopsied, produced *in vitro*, or cloned), and stage of maturation, greatly affect the probability of obtaining live progeny. A variety of protocols to freeze and thaw embryos from livestock have been proposed, and as in the case of oocytes, they can be classified into two major categories based on the rapidity of freezing procedures.

In slow freezing approaches, equilibration of cryoprotectants and solutes between the medium surrounding the embryo and its intracellular compartments occurs slowly, thus limiting the risks of membrane rupture due to intracellular ice formation. Upon thawing, embryos are transferred into recipient females with or without removal of the cryoprotectant. Internationally, such techniques are at present the most commonly used in cattle, sheep and goats. Success rates at parturition vary depending on the species, genetic origin, source (*in vivo* or *in vitro*), and stage of development of the embryos. Embryos cryoconserved at an early stage of their development result in lower parturition rates than embryos cryoconserved at a more advanced stage (Massip, 2001).

Fast freezing (vitrification) techniques involve ultra-rapid cooling and freezing of embryos in a very small amount of suspending medium in which cryoprotectant and other solutes (sugars) are generally at high concentrations. Embryos from several mammalian species (cattle, sheep and goats) have been successfully vitrified and transferred. Survival rates of 59 and 64 percent have been observed in sheep and goat embryos, respectively, using the so-called pulled-straw vitrification technique (Cognié *et al.*, 2003).

Embryo preservation techniques are of particular interest with respect to the cryoconservation of AnGR because they allow full recovery of the initial genome. Slow freezing rates require expensive programmable freezers, but offer more flexibility to untrained technicians because of the relatively long intervals between the two steps of the procedure. In contrast, vitrification requires only limited equipment, but highly trained technicians.

7.3 Cryoconservation of somatic cells and somatic cell cloning

Since the creation of Dolly the sheep, the first animal created by cloning of somatic cells, the technology has been shown to work for most mammals in which it has been tested, However, it has not been applied successfully in birds. The current state of the technology is costly, with extremely low success rates. If reconstitution of live animals from somatic cells is developed to the point where it becomes both reliable and cheap, preservation of somatic cells would become an attractive option for cryoconservation of AnGR. Its main advantage would be that it would be possible to choose exactly which animals to conserve, and later to reconstitute a population of clones of these animals. Unlike in the case of preserved embryos, the cytoplasmic DNA is not preserved in animals derived from somatic cells. Collection of somatic cells is, however, far simpler than collection of embryos, and it would be feasible to collect samples extensively from field populations. The current costs of developing somatic cell cultures, and uncertainty about future prospects for producing live animals from the preserved cells, mean that somatic-cell conservation is unlikely to be a priority in species where cryoconservation of gametes and embryos is well developed. However, cryoconservation of somatic cells would be a prudent back up where cryoconservation of gametes and embryos is not feasible or has low success rates.

Table 105 provides an overview of the feasibility of the above-discussed techniques in the major livestock species.

Table 105
Current status of cryoconservation techniques by species

Species	Semen	Oocytes	Embryos	Somatic Cells
Cattle	+	+	+	+
Sheep	+	0*	+	0
Goat	+	0	+	0
Horse	+	0	0	0
Pig	+	0	0	0
Rabbit	+	0	+	0
Chicken	+	-	-	-

*+ routine techniques available; 0 positive research results; - not feasible in the current state of art; * cryoconservation of the whole ovary*

Box 104
Revival of the native Red and White Friesian cattle in the Netherlands

In 1800, the cattle population in the province of Friesland consisted mainly of Red Pied cattle. Many red ancestors were imported from Denmark and Germany after widespread losses caused by rinderpest. Since 1879, the Friesian Cattle herd book had registered a Red and White phenotype, but pushed by export markets, black and white animals progressively became more popular than the original red and white. In 1970, only 50 farmers owning a total of 2 500 cattle joined the Association of Red and White Friesian Cattle Breeders. Within a short period, the sustained import of Holstein-Friesians from United States of America and Canada resulted in a further decline of the population, so that only 21 Red and White individuals (4 males and 17 females) were remaining in 1993. A group of owners started the Foundation for Native Red and White Friesian Cattle. In collaboration with the newly created Genebank for Animals, a breeding programme was developed. Semen from sires preserved in the genebank in the 1970s and 1980s was used to breed females under a contract system. Male progeny were raised by breeders, who were granted a subsidy from the genebank. Semen from these males was collected, frozen and later used under new contracts. The breed increased in number, reaching 256 registered living females and 12 living males in 2004. Currently, a total of 11 780 semen doses from 43 bulls are stored in the genebank and kept available for AI. The majority of cows are raised by hobbyists for milk production.

Provided by Kor Oldenbroek

Box 105
Revival of the Enderby cattle in New Zealand

The case of the Enderby Island cattle illustrates that it is possible to resurrect breeds from extremely limited genetic material. However, it also shows that the process is complicated and requires a lot of time and resources.

Enderby is a small island situated 320 kilometres to the south of New Zealand. Cattle were first brought to the island in 1894, when one W.J. Moffett of Invercargill took up a pastoral lease and landed nine shorthorns. By the 1930s, farming on the island had been abandoned, but the cattle remained as a feral herd. After 100 years surviving Enderby's harsh climate and a diet of scrub and seaweed, the cattle were hardy, small, stocky and well adapted. In 1991, to help preserve the local wildlife, the Enderby cattle were shot. Sperm and oocytes from the dead animals were collected for cryoconservation, but attempts to fertilize the oocytes failed and it appeared that the Enderby breed had been wiped out forever.

The following year, members of the New Zealand Rare Breeds Conservation Society (NZRBCS), discovered a cow and a calf on the island. The animals were captured by helicopter and shipped to New Zealand. The subsequent death of the calf meant that "Lady", as the cow became known, was the last of the Enderby cattle. Attempts to produce a calf, through artificial insemination and MOET, using the cryoconserved semen taken from the bulls killed on the island, did not prove successful. Again it appeared that the breed faced extinction. However, in 1997 NZRBCS in collaboration with AgResearch successfully produced a calf, Elsie, cloned from a sample of Lady's somatic cells. Four more cloned heifers were born the following year. Meanwhile, efforts to produce an Enderby bull through *in vitro* fertilization using the cryoconserved semen and oocytes taken from Lady had also proved successful, with the birth of "Derby". Two of the clones later died, but in 2002 two more Enderby calves were born through natural mating of the cloned heifers and Derby.

For more details see Historical Timeline of the Auckland Islands; NZRBCS, (2002); Wells, (2004)

7.4 Choice of genetic material

Techniques to cryoconserve gametes and embryos are, extensively used for commercial purposes in most domesticated mammals; there are a few exceptions such as transfer of frozen embryos in equines and pigs (Thibier, 2004). In the case of cryoconservation programmes devoted to AnGR management, one major issue is to store sufficient biological material to allow the reconstruction of individual animals or populations bearing the desired traits. The choice of donor origin, number of donor individuals and type of material to be cryoconserved are, therefore, crucial if investments are to be of long-term benefit. Useful recommendations regarding these matters are available from the following sources: Blackburn (2004), ERFP (2003) and Danchin-Burge *et al*. (2002).

7.5 Security in genebanks

Genebanks for AnGR germplasm must provide technically secure storage and meet strict zoosanitary requirements.

Technical security

Loss of liquid nitrogen for any period of time (literally minutes) can lead to complete loss of the cryoconserved material. Storage of cryoconserved materials in two separate containers, and preferably two separate locations, limits the risk of losses resulting from accidental failure to maintain liquid nitrogen.

Biosecurity

Materials of animal origin including fluids, gametes and embryos may carry pathogens capable of surviving cryoconservation. While additional research is needed to further assess risks of transmission through genebanking, biosecurity recommendations provided by the Terrestrial Animal Health Code of the World Organization for Animal Health (OIE) are universally applicable. Meeting the requirements of the code presents severe difficulties for many countries. It makes movement of germplasm from disease-affected to disease-free areas extremely difficult. It can also mean that samples that do not meet the code's requirements cannot be stored in the same facility as samples that do. Such issues could provide a substantial obstacle to the establishment of national, regional and international cryoconservation banks. Special structures and possibly some special exemptions to existing codes will be required.

8 Resource allocation strategies in conservation

8.1 Methods for setting priorities

A clear definition of objectives is crucial for all conservation activities. One criterion that will often be considered important is the preservation of genetic diversity. However, conserving as much diversity as possible will rarely be the sole objective. Other factors such as conservation of certain special traits (e.g. disease tolerance), and ecological or cultural values of breeds, also have to be taken into account. The objective is, therefore, to maximize the utility of a set of breeds, where utility is a weighted combination of measures of diversity and other traits/values. Definition of weights requires the valuation of diversity relative to the other criteria considered.

Another important consideration is the degree of endangerment of the breeds in question. This can be quantified in the form of an extinction probability. The parameter is mainly determined by the effective population size, and the demographic trend (i.e. whether the population size is increasing or decreasing), but should also take into account other factors such as geographic distribution, implementation of breeding programmes, specific ecological, cultural or religious functions, and risk from external threats (Reist-Marti *et al.*, 2003).

Various methods for combining different criteria have been proposed for prioritizing breeds to be targeted by conservation programmes. Ruane (2000), for example, proposed a method to be followed by a group of experts identifying breed priorities at the national level. The following seven criteria are included in the framework:

species (i.e. breeds from which species are to be included in the priority setting exercise?);

degree of endangerment;

traits of current economic value;

special landscape values;

traits of current scientific value;

cultural and historic value; and

genetic uniqueness.

It is suggested that breeds with high degrees of endangerment should be given priority. If it is necessary to prioritize among highly endangered breeds, it is then suggested that the extent to which the breeds meet the other listed criteria should be taken into account. It may be necessary to assign weights to the various criteria in order to allow further differentiation of priority ranks. The relative importance to be given to each criterion would be decided by the expert group.

Hall (2004) put forward a framework based on both genetic and functional diversity, using British and Irish breeds of sheep and cattle as an example. Each breed under consideration was compared to every other breed in terms of functional and genetic distinctiveness. The genetic component was assessed on the basis of the history of the breed and the likelihood of significant gene flow within the last 200 years. The functional component related to the economic, social and cultural functions of the breed. In cattle, functional distinctiveness was assessed subjectively, but this was more difficult to do in the case of sheep. As such, mean fibre fineness, almost the only parameter that had been measured in a comparable way across the breeds in the study, was used as an indicator of functional distinctiveness in sheep breeds. Breeds that scored highly both for functional and genetic distinctiveness were considered to be the most appropriate for inclusion in a list of priorities.

The Rare Breeds Survival Trust in the United Kingdom has also established a set of criteria for recognition of “rare breeds” which require special attention in terms of conservation measures (Mansbridge, 2004). The length of time for which a breed has existed, the number of female animals, and the breed’s geographical distribution are taken into account.

8.2 Optimization strategies for planning conservation programmes

Efficient conservation programmes should use available monetary or non-monetary resources in such a way that the conservation objective is maximized. The questions to be answered are:

- For which breeds within the species under consideration should conservation programmes be implemented?
- What share of the total conservation budget should be allocated to each of the chosen breeds?
- Which conservation programmes should be implemented for any chosen breed?

If it is assumed that the objective of the conservation measures being considered is to conserve as much genetic diversity between breeds as possible, then the following method may be used to identify priority breeds (Simianer, 2002).

The total diversity of an existing set of breeds can be calculated, as can the contribution of each breed to the total diversity. Extinction probabilities and the diversity of different subsets of breeds are used to calculate what is referred to as the “expected diversity” (Box 106). This is the diversity expected at the end of the planning horizon assuming that no conservation activities are undertaken. It may happen that at the end of the planning horizon some of the most endangered breeds will have become extinct. If, however, conservation efforts are undertaken, the extinction probability of breeds will be reduced and the expected diversity will increase. The amount of change in the expected diversity as a function of the change in the extinction probability of a particular breed is referred to as the breed’s “marginal diversity”. This marginal diversity reflects the breed’s phylogenetic position. It also indicates whether closely related breeds are safe from extinction, but is independent of the breed’s own extinction probability.

The conservation priority of a breed has been shown to be proportional to its “diversity conservation potential” (Box 106) – a measure which reflects the additional amount of diversity that would be conserved if a breed were made completely safe from extinction. A high conservation potential can either result from a high degree of endangerment, or from a high marginal diversity.

The parameters discussed here (marginal diversity, conservation potential etc.) are elements of the general diversity theory put forward by Weitzman (1992; 1993), which has attracted considerable interest as a framework for decision-making in livestock conservation. The approach does not require that Weitzman's diversity metric, which is diversity between breeds, is the quantity maximized. The methodology can be applied to any objective function, including more comprehensive diversity metrics or utilities (in the sense of a weighted sum of a diversity component and other values).

Box 106
Glossary: objective decision aids

Diversity: numeric quantification of the amount of genetic variability in a set of breeds, ideally covering both the diversity within and between breeds.

Utility: numeric quantification of the total value of a set of breeds, e.g. a weighted sum of diversity and various economic value components.

Diversity contribution: the amount that the existence of a breed contributes to the diversity of the whole set of breeds.

Extinction probability: the probability that a breed becomes extinct within a defined planning horizon (often 50 to 100 years). The extinction probability can take values between 0 (breed is completely safe) and 1 (extinction is certain).

Expected diversity: the projection of the actual diversity to the end of a planning horizon, combining the actual diversity with extinction probabilities. The expected diversity reflects the amount of diversity to be expected if no conservation efforts are made.

Marginal diversity: reflects the change of expected diversity of the total set of breeds if the extinction probability of a breed is modified (e.g. through conservation measures).

Diversity conservation potential: a quantity proportional to the product of the marginal diversity and the extinction probability. This parameter approximately reflects how much the expected diversity can be increased if a breed is made completely safe. Weitzman (1993) suggested that this measure is the "single most useful [breed] alert indicator".

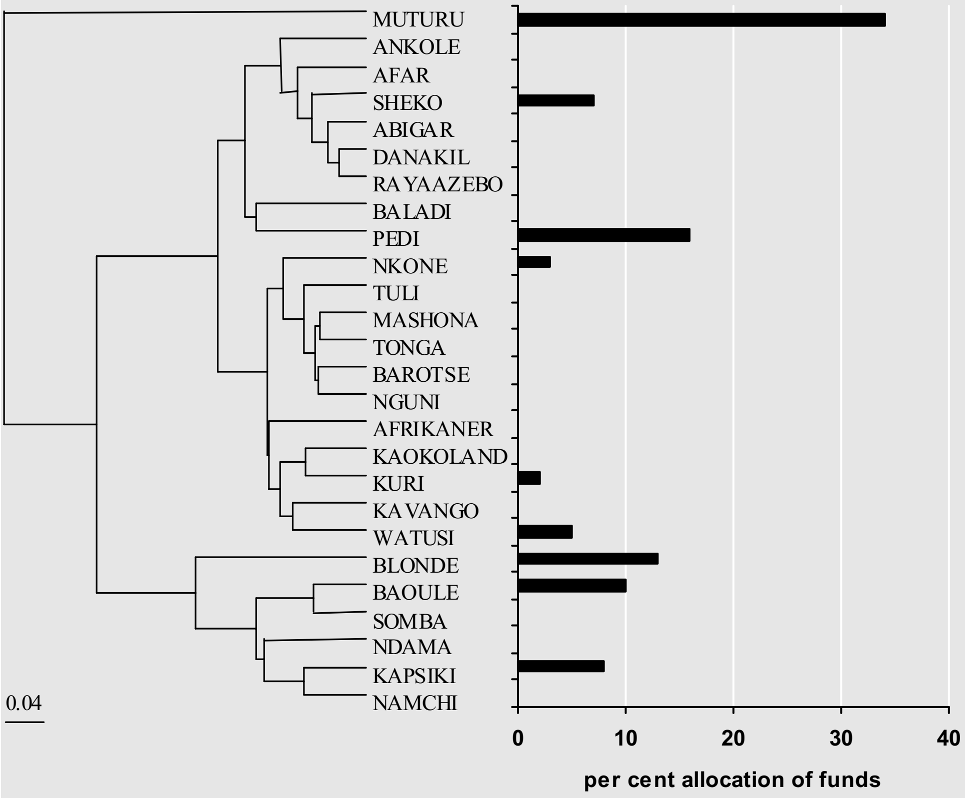
If utility rather than diversity is to be maximized, "utility contribution", "expected utility", "marginal utility" and "utility conservation potential" are the relevant terms, and the word "diversity" in the above definitions should be replaced by "utility."

Source: adapted from Simianer (2005)

Box 107 describes an example in which an optimum allocation of conservation funds could increase cost efficiency by almost 60 percent compared to that achieved using simplistic approaches.

Box 107
Optimum allocation of conservation funds – an example featuring African cattle breeds

Simianer (2002) illustrated the application of an optimum allocation scheme to a set of 26 African taurine and Sanga cattle breeds for which estimates of genetic distances (based on 15 microsatellites) and extinction probabilities had been calculated. Using the extinction probabilities, the expected loss of diversity in the absence of conservation over the assumed planning horizon of 50 years was estimated to be 43.6 percent of the current diversity. It was assumed that a conservation budget was available which, if allocated equally across all breeds, would prevent 10 percent of the expected loss of diversity. If this same total budget is allocated to the conservation of only the three most endangered breeds, the diversity conserved decreases slightly to 9 percent of the expected loss, and so is 10 percent less efficient than allocating funds equally across breeds. With an optimum allocation scheme based on Weitzman's diversity concept, 10 of the 26 breeds receive funds, with 34 percent of the funds being used for Muturu and only 2 percent for Kuri (see figure).



With the optimum allocation strategy, the expected loss of diversity is reduced by 15.7 per cent. This is 57 percent more efficient than allocating funds equally across breeds. The same impact on diversity as the uniform allocation strategy could be achieved with an optimum allocation of only 52 percent of the available funds. The example illustrates that optimum allocation can substantially increase the efficiency of use of conservation funds.

Provided by Henner Simianer

Defining conservation priorities by ranking breeds according to their conservation potential assumes that conservation costs are roughly identical between breeds. More precisely, the assumption is that opportunity costs for the reduction of the extinction probability by one unit are uniform across breeds. This of course is not true: reducing the extinction probability from, say, 0.8 to 0.7 (i.e. by 12.5 percent) can be achieved by relatively simple means and is much cheaper than reducing the extinction probability from 0.2 to 0.1 (i.e. by 50 percent).

For a more detailed and realistic analysis it is necessary to define the cost of particular conservation activities (e.g. establishing cryoconservation, or giving subsidies to farmers to maintain an *in situ* population of a breed at risk), and also to assess the effect of such activities in terms of a reduction in the extinction probability of the respective breed. If allocation of resources is undertaken in an international context, different cost levels, technical standards, and currency exchange rates need to be taken into account: it may well be the case that cryoconservation is established as a routine application in one country, while in another country, the required infrastructure would first have to be developed. Another consideration is that labour costs for *in vivo* conservation schemes may differ substantially between countries.

A conservation scheme always has a number of costs which will vary markedly between species and countries. The fixed costs are those required to establish and run the scheme as such (e.g. establishing a cryoconservation centre), while variable costs depend on the number of animals included and the type of genetic material (semen, oocytes or embryos) conserved in the scheme. Different conservation schemes vary in terms of the level of the fixed cost and the variable cost per genetic unit conserved. If this cost structure can be modelled with sufficient accuracy, optimum allocation schemes will not only assign a share of the conservation budget to a certain breed, but will also indicate which of the available conservation techniques will be most cost effective for this breed.

Since optimum allocation procedures are based on mathematical optimization, it is relatively simple to include certain restrictions or side conditions. This could relate to geographic balance, i.e. require that conservation activities are implemented in all parts of the target region. It could also force the optimum solution to avoid the loss of certain special traits by putting a high penalty on solutions in which, for example, all trypanotolerant cattle breeds become extinct.

Other strategies to find the optimum pattern of resource allocation are restricted to more specific decision-making problems. Eding *et al.* (2002) suggested the selection of a so-called core set of breeds based on marker estimated kinships. A core set can be thought of as a live or cryoconserved mixed population, which is constituted of various proportions of different breeds. The breed contributions to the core set are derived in such a way, that the expected diversity of the total core set is maximized. The advantage of this approach is that it combines between and within-breed diversity. However, it does not take into account the degree of risk faced by particular breeds, which limits its usefulness to special cases of decision-making, such as finding the optimum design for a cryoconservation programme with limited storage capacity.

Resource allocation for the efficient conservation of AnGR diversity requires good information on the phylogenetic substructure of a species, on factors affecting the degree of threat faced by the breeds considered, and on any special values that the breeds may have. A substantial knowledge of potential conservation programmes, including their costs, is also required. The more complete and reliable this information, the more cost-effective the design of the optimum conservation programme will be. Further work is required to resolve the question of what are the most appropriate factors to be optimized in conservation efforts, because use of different factors may lead to different conservation decisions. Substantial further work is also required to develop tools that will assist the maximization of a diverse range of measures of diversity and utility.

Final decisions on investments in conservation will be driven by many economic, social and political factors. Thus, the decision-aids described above should be regarded as tools to allow decision-makers a better understanding of the consequences of alternative investment strategies for conservation.

9 Conclusions

Traditions and cultural values are important driving forces for conservation in Western societies, and are also becoming increasingly important in some developing countries. Another strong motivation that is shared by many stakeholders is safeguarding as much diversity as possible for an unpredictable future.

Conceptually, the most basic unit of diversity is the allele, and thus, from a scientific point of view, one definition of maintaining genetic diversity could be considered to be maintaining high allelic diversity. This would avoid the problems associated with scientifically defining a breed. At present, however, molecular measures of genetic diversity provide only indirect indications of genetic diversity in functional or potentially functional regions of the DNA. Thus, the best proxy for functional diversity remains the diversity of breeds or distinct populations that have developed in distinct environments, and possess different production and functional traits. Furthermore, cultural arguments for conservation are linked to breeds not to genes. Nevertheless, there is a need to develop objective criteria to decide whether a certain breed is of unique scientific value, or whether, for example, it could be substituted by a neighbouring population. This requires the combination of all available information on breed characteristics, origin and geographical distribution. Wherever possible, additional information, including results from molecular characterization, should be also considered.

In vivo and *in vitro* conservation methods are clearly distinct in terms of what they can achieve. Preserving live animals allows further evolution of the breeds in interaction with the environment, while *in vitro* conservation preserves the current genetic status. *In vitro* methods provide an important back-up strategy when *in vivo* conservation cannot be established or cannot conserve the necessary population size. It may also be the only option in the case of emergencies such as disease outbreaks or wars. The past focus on cryoconservation as a supporting tool for breeding programmes has led to technically sound solutions for the main livestock species. However, there is an urgent need to develop standard procedures for all livestock species. Freezing tissue samples seems an appealing method, because of the ease with which the genetic material can be sampled. However, the difficulty of reproducing living animals from these samples suggests that it should be regarded as a method of last resort.

It is interesting to note that it has long been accepted that international genebanks financed by the international community should preserve plant genetic diversity. The Global Trust Fund Initiative aims to create the framework for long-term financial support for these genebanks to make them independent of the short-term financial priorities of the host institutions. Furthermore, the Norwegian government has offered to provide a last resort for PGR, which will be put in place in 2007 (Box 108).

Box 108
The Svalbard Global Seed Vault: an international seed depository in the Arctic

The Government of Norway recently initiated planning for the construction of the Svalbard Global Seed Vault to serve as an ultimate "fail-safe" back-up facility for genebanks. The facility will be established near the town of Longyearbyen, on Svalbard, at 78 degrees North and will open in the spring of 2008.

The depository will be large enough to conserve a copy of all distinct accessions now held in genebanks around the world, with additional space available for new collections. It will be located in a "vault", carved out of solid rock inside a mountain, and lined with reinforced concrete. There will be an air-lock door for moisture control, and a number of robust security devices. The remote location, the presence of Norwegian authorities, and the occasional wandering polar bear, will combine to make this facility the most secure and reliable in the world. Under normal conditions, collections will be housed at approximately -18 °C. However, as the vault will be located in permafrost, long-term electricity failures would only result in the temperature gradually rising to -3.5 °C.

The town of Longyearbyen, a dropping-off point for expeditions to the North Pole, is served by daily flights, and has excellent infrastructure and power supplies utilizing locally procured coal.

The seed depository will not be a "genebank" in the normal sense of the term. Instead, it will be intended to house distinct accessions that are already conserved and duplicated in two traditional genebanks that would serve as the source of seed for plant breeders and researchers. Materials from the depository, stored in "black-box" conditions, would be available only when all other copies had been lost, in keeping with the intention of providing a safe and secure facility that could provide protection for plant genetic resources for food and agriculture in the case of large-scale catastrophes such as nuclear war, or major acts of terrorism.

Participation in the scheme will be purely voluntary. Management will be "passive" the depository will not engage in characterization, evaluation, regeneration or other similar activities. The Nordic Gene Bank will be responsible for placing materials in the depository and retrieving them as necessary. It already has its back-up collection in another facility at Svalbard, and duplicate collections from SADC are also currently stored there. Due to the necessity of keeping management operations and costs at a minimum, and in keeping with the intention of constructing a facility that will function without day-to-day human involvement, the depository will only be in the position to accept properly packaged orthodox seed. As the facility will be designed for the international community, Norway will not claim any ownership over the seeds stored there.

The FAO Commission on Genetic Resources has warmly welcomed the Norwegian initiative, and many countries, as well as centres of the CGIAR, have already signalled their desire to make use of the depository.

Provided by Cary Fowler

In general, it takes much longer to create a livestock breed than to create a plant variety – for some breeds it has taken centuries. However, the global community seems to be much less prepared to invest the necessary time, energy and money in safeguarding this heritage. Nonetheless, it is a global responsibility to ensure that valuable resources are maintained – a responsibility that includes all genetic resources for food and agriculture.

The analysis of *in vivo* conservation methods indicates that the distinction between *in situ* and *ex situ in vivo* conservation methods is not clear cut. It may, therefore, be appropriate to consider *in vivo* conservation methods as a continuum: ranging from conserving animals in their original production environment, (*in situ* conservation as defined above), to the extreme *ex situ* situation of conserving livestock breeds in zoos. While there is clearly a preference for maintaining livestock breeds in the production environments, in which they were developed, it is important to carefully evaluate whether conservation objectives might also be achieved in an *ex situ* context. This will clearly depend on the species and on the specific *ex situ* conditions. In the developing world, most reported examples of *ex situ* conservation are linked to *in situ* populations, and it appears doubtful whether they are independently viable.

While methodologies to maintain maximum diversity in small populations have been developed, implementation strategies for maintaining at-risk breeds in traditional production systems are rare. Various successful examples have been reported from developed countries and from some developing countries. In developed countries, several possibilities, such as niche markets, conservation grazing or subsidies, have been employed to increase the economic viability of endangered breeds. Conversely, in developing countries the only successful examples reported are linked to consumer or market demands for specific or traditional products. However, these practical examples of what has been achieved have not yet led to (scientific) concepts or models for implementation strategies. Furthermore, no reliable estimates of the costs and benefits of conservation strategies are available. Attempts to optimize the allocation of conservation funds are based on crude assumptions on the cost side, and use rather simplistic objective functions. The development of more complex objective functions is constrained by the difficulties of quantifying desirable functional traits to be included.

The scientific concepts which are available for certain aspects of conservation have been developed mainly in the context of breeding programmes. Genuine research in the field of conservation of livestock genetic diversity (probably with the exception of molecular methods) is still in its early stages.

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SECTION G: RESEARCH PRIORITIES

In this section, priorities for research and development are identified based on the expert analysis of the state of the art in AnGR management. The priorities have been identified in order to fill gaps in knowledge and provide the tools required to develop and implement management programmes more effectively, efficiently and sustainably. The rationale for the research and development priorities has been set out in the earlier sections, and only the briefest description is presented here.

1 Information for effective utilization and conservation

A major obstacle to decision-making in utilization and conservation of AnGR is the shortage of information on key traits and performance of local or indigenous AnGR, and the lack of reliable data on population size and structure. The following research tasks have to be completed so that researchers, policy-makers, decision-makers and advisors to farming communities have the information they require to make appropriate recommendations and take appropriate decisions for the conservation and utilization of AnGR.

- Improved methods and greater use of phenotypic characterization: is required in order to assign livestock populations to the appropriate breeds, and to overcome a lack of information regarding key adaptation traits of indigenous AnGR.
- Production environment descriptors: need to be refined and implemented in existing AnGR information systems to indicate the environment to which particular breeds are suited, and as a proxy for adaptation traits.
- Improved methods of risk definition and monitoring: methods for estimating probability of extinction are poorly developed and need substantial further research. Improved monitoring methods have to be linked to regular entry of data on population size and structure into information systems to ensure that they remain up to date and relevant.

2 Information systems

Existing information systems have relatively little functionality beyond simple searches by country or breed. The functionality needs to be extended to provide stakeholders with the information they require in a more aggregated and user friendly way.

- Regular updating and correction of existing data, and completion of missing data: should be facilitated by system routines.
- Information system functionality: needs to be improved and expanded to allow extraction and customized analysis of phenotype and molecular genetic data within and between data sources. To supply such functionality will require development of improved methods of analyzing and interpreting diverse forms of genetic diversity data (molecular and phenotype).
- Georeferencing of AnGR information systems: to allow access to multilayered geophysical information linked to attributes of AnGR (specific adaptation), and to provide precise information about current and past geographic location and distribution of AnGR.
- Interconnectivity and interoperability between information resources/databases: options and modalities need to be further developed.

3 Molecular methods

Opportunities for utilizing molecular techniques in the management of AnGR are going to increase in the near future. However, the costs and benefits of applying these technologies, and, hence, appropriate strategies for their utilization, will vary depending on local conditions.

- Improved understanding of genetic diversity in the main livestock species: comprehensive assessments of genetic diversity using molecular genetic markers are required. This needs to be achieved in ways that maximize the value of the large amount of data which exist at present but are in fragmented form. Improved sampling methods will be needed, along with the development and supply of international reference samples. Results need to be entered into publicly accessible information systems.
- Worldwide identification of variants in genes for key traits.
- Enhanced understanding of the genetic basis of adaptive traits: explore the potential of new and emerging technologies to reveal the genetic basis of disease resistance, adaptation to difficult environments and production efficiency. Such understanding may provide new routes for conventional and transformative genetic improvement.
- Development of methods for the integration of molecular information into conservation and breeding programmes: methods have to be adapted to different environmental, agricultural and socio-economic circumstances.

4 Characterization

The increasing importance given to animal welfare, distinctive product qualities, human health concerns, improving the efficiency of resource utilization, and reducing environmental impact will require a wider range of selection criteria in future breeding programmes. To date, little is known about the genetic aspects of adaptation.

- Develop and apply methods for molecular and phenotypic characterization and for the capturing of knowledge associated with the breed and its management. Additionally, methods to assess the extent of genetic dilution of a breed need to be well developed. Linking the outcome of such research to regular inventories will inform decision-making about risk status and measures to be taken to halt the decline of genetic diversity.
- Understanding robustness: the value of different breeds with respect to robustness, as measured by reduction in genotype–environment interactions, needs to be determined; genes that explain variation in robustness and factors contributing to homeostatic imbalance under a given husbandry system or management practice need to be defined.
- Improved understanding of disease resistance: infection mechanisms and host–pathogen interactions need to be studied.

5 Genetic improvement methods

There is little information on how to adapt breeding strategies to low external input environments with little or no organizational infrastructure. In this regard, selection for functional traits such as robustness, disease resistance, behavioural traits, and efficiency of feed utilization are particularly relevant. Guidance is also needed for the initial decision as to whether to implement genetic improvement programmes.

- Detailed guidelines for the design of genetic improvement programmes in low external input systems: need to be developed and validated. These should include the development of breeding and production objectives in relation to national goals and policies and the role of adaptive traits.
- Development of stable cross-breeding systems with a role for native breeds.
- Simulation tools to predict the consequences of introducing exotic breeds into local populations should be developed (part of genetic impact assessment).

- Selection for disease resistance, where determining genes have been identified: strategies of how to implement DNA-based selection without compromising production traits should be developed.
- Selection for welfare traits: a clear definition of welfare traits is needed for each species; methods for the measurement of stress and psychological status (aggression, discomfort and frustration) need to be improved; and selection methods for more appropriate temperament, reduction of foot and leg problems, and incidence of cardio-vascular problems (in poultry raised for meat) need to be developed.
- Selection for increased efficiency of feed utilization: better knowledge of nutrient (e.g. amino acid) requirements under different conditions and genetic variation in digestion of specific amino acids and phosphorus is needed.

6 Conservation methods

There is little experience in establishing conservation programmes that will be sustainable in less developed countries, or in how to operate conservation programmes that operate across a number of countries, or regionally rather than nationally. Research is required better to understand the socioeconomic, infrastructural, technical and policy constraints to the establishment and sustaining of conservation programmes.

- *In situ in vivo* conservation methods: research and development is required to understand how to implement *in situ in vivo* conservation in ways that are sustainable, maximize livestock keepers' livelihoods and support development objectives.
- *Ex situ in vivo* conservation methods: there is a need to identify approaches to *ex situ in vivo* conservation in the developing world that are closer to being self-sustaining, and thereby less vulnerable to collapse than are approaches that are heavily dependent on state support.
- Sampling and storage for genetic material for backup systems related to breeding programmes: methods are required to optimize ongoing sampling and storage in systems where the primary objective is to provide a backup to ongoing genetic improvement programmes.
- Cryoconservation and reproduction techniques: improved effectiveness and expanded access to cryopreservation and reproductive techniques for gametes and embryos are required for species for which the technologies already exist. The technologies also need to be extended to other species. Cheap and effective somatic cloning would substantially improve the safety and cost-effectiveness of *in vitro* conservation.
- Policy, legislative and zoosanitary frameworks for *in vitro* conservation: research and development is required to identify the policy, legislative and zoosanitary frameworks that will permit storage and promote access to AnGR held in national and multinational genebanks.

7 Decision-support tools for conservation

Tools to analyse complex data and optimize resource use, and to design programmes that assist researchers, policy makers and advisors better to understand the consequences of decisions, as well as to optimize such decisions are required. Since conservation will often involve utilization and improvement of the genetic resources, such decision aids need to include aids to the design and operation of breeding programmes. The following are the key areas for research and development:

- Methods for resource optimization: research is required into how to combine information of varying degrees of uncertainty to optimize the choice of AnGR for conservation, and the allocation of resources for conservation.

- Optimization tools: user friendly tools for optimization of resource allocation in conservation need to be developed, and these tools need to be included within the next generation of information systems.
- Early warning and response mechanisms: with defined triggers and actions need to be developed for use at country level.

8 Economic analysis

In relation to individual conservation and utilization decisions, improved methods that can be used in a wide range of situations to accurately value individual AnGR and the various characteristics of AnGR which might be conserved or improved are required. It is important to continue to field-test promising valuation methods, and to systematically apply proven ones to different traits, breeds and species across diverse production systems. In addition, it will be necessary to facilitate application of the methodologies and results at regional and national levels, thereby providing opportunities for influencing policy decisions related to conservation and sustainable use. A detailed costing of conservation alternatives across a wide spectrum of situations is needed to assist countries and other agencies to make decisions on cost-effective conservation programmes. Analytical methods are required to define the global benefits of AnGR conservation. This will require:

- Identifying uses and farmers' trait preferences for local breeds under different production systems: this analysis should include a systems evolution perspective as well as the forces influencing such factors and the use of alternative breeds. This will necessarily include measuring breed performance parameters, in addition to characterizing actual and potential breeding systems.
- Carrying out market analysis for livestock breeds and their products, and cost–benefit analysis of breeding programmes: this will guide decision-making whether to embark on structured breeding programmes with local breeds.
- Carrying out *ex ante* analyses of the effects on livelihoods of using alternative breeds: this will support pro-poor targeting of interventions, together with constraints to adoption, and potential access/dissemination mechanisms.
- Estimation of the costs of alternative conservation strategies: choice of the appropriate balance of conservation strategies will depend on the costs of alternative approaches. The costs of a given conservation approach will vary markedly between countries and regions, depending not just on local costs for various inputs, but also on the levels of existing infrastructure and accessible expertise.
- Developing and applying decision-support tools for prioritization of breeds: these tools should identify best options for cost-efficient diversity-maximizing conservation programmes.

9 Access and benefit sharing

Access and benefit sharing in the field of the exchange and use of AnGR is a matter of increasing international debate, the outcomes of which will have a large impact on the willingness of various states, agencies, institutions and companies to invest in the conservation and further development of AnGR. It is necessary to ensure that the anticipated international debates on the subject are well informed, and that effective decisions can be taken. Detailed analyses are required to improve understanding of the relationship between access and trade in livestock germplasm, and research and development, along with an assessment of the costs and benefits arising from such research. The need for, and the potential impacts of, frameworks for access and benefit sharing of conserved AnGR need to be assessed. Better information on the costs and benefits of past movements of AnGR would provide a valuable background to such analysis. This requires:

- Assessment of how to improve public and community use of biodiversity (e.g. improved community-based management of AnGR), including through the enhancement of existing benefit sharing at local level.
- Improved understanding of the significance of national regulatory interventions (i.e. macroeconomic interventions, regulatory and pricing policy, investment policy, institutional policy and animal disease control protocols).
- Ensuring current and future benefits from global flows of livestock germplasm: design of mechanisms at national and international levels to protect and enhance existing forms of benefit sharing, and assessment of needs in relation to future scenarios which might affect or change flows and the share of benefits.
- Explore the legal and technical framework for the setting up of a genebank of AnGR, including wild relatives, to be used for research purposes.