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THE SECOND REPORT  
ON THE STATE  
OF THE WORLD'S  
**ANIMAL GENETIC RESOURCES FOR  
FOOD AND AGRICULTURE**

**FAO COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE**  
ASSESSMENTS • 2015



## Part 4 The state of the art

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Introduction

|                   |  |            |
|-------------------|--|------------|
| <b>SECTION A:</b> | <b>CHARACTERIZATION, INVENTORY<br/>AND MONITORING</b>      | <b>415</b> |
| 1                 | Introduction   | 415        |
| 2                 | Characterization as the basis for decision-making          | 416        |
| 3                 | Tools for characterization, surveying and monitoring       | 419        |
| 4                 | Information systems  | 423        |
| 5                 | Changes since 2005   | 426        |
| 6                 | Conclusions and research priorities                        | 427        |
|                   | References   | 429        |
| <br>              |  |            |
| <b>SECTION B:</b> | <b>MOLECULAR TOOLS FOR EXPLORING<br/>GENETIC DIVERSITY</b> | <b>431</b> |
| 1                 | Introduction   | 431        |
| 2                 | Developments in the use of DNA markers                     | 433        |
| 3                 | Characterization of within-population diversity            | 435        |
| 4                 | Characterization of between-population diversity           | 436        |
| 5                 | Molecular tools for targeting functional variation         | 437        |
| 6                 | The role of bioinformatics                                 | 440        |
| 7                 | Conclusions and research priorities                        | 441        |
|                   | References   | 442        |
| <br>              |  |            |
| <b>SECTION C:</b> | <b>BREEDING STRATEGIES AND PROGRAMMES</b>                  | <b>451</b> |
| 1                 | Introduction   | 451        |
| 2                 | Scientific and technological advances                      | 452        |
| 3                 | The elements of a breeding programme                       | 457        |
| 4                 | Breeding programmes in high-input systems                  | 459        |
| 5                 | Breeding programmes in low-input systems                   | 474        |
| 6                 | Conclusions and research priorities                        | 482        |
|                   | References   | 485        |
| <br>              |  |            |
| <b>SECTION D:</b> | <b>CONSERVATION</b>  | <b>497</b> |
| 1                 | Introduction   | 497        |
| 2                 | Planning a conservation strategy                           | 501        |
| 3                 | Identifying breeds at risk                                 | 501        |
| 4                 | Determining the conservation value of a breed              | 503        |
| 5                 | <i>In vivo</i> conservation                                | 504        |
| 6                 | Cryoconservation   | 511        |
| 7                 | Conclusions and research priorities                        | 522        |
|                   | References   | 523        |

|  |            |
|--|------------|
| <b>SECTION E: ECONOMICS OF ANIMAL GENETIC RESOURCES<br/>USE AND CONSERVATION</b> | <b>529</b> |
| 1 Introduction   | 529        |
| 2 Developments in animal genetic resources economics                             | 531        |
| 3 Challenges and opportunities   | 539        |
| References   | 541        |

## Part 5 Needs and challenges

---

|   |            |
|---|------------|
| Introduction  |            |
| <b>SECTION A: CHALLENGES POSED BY LIVESTOCK<br/>SECTOR TRENDS</b> | <b>553</b> |
| <b>SECTION B: CHARACTERIZATION AND MONITORING</b>                 | <b>555</b> |
| <b>SECTION C: SUSTAINABLE USE AND DEVELOPMENT</b>                 | <b>557</b> |
| <b>SECTION D: CONSERVATION</b>                                    | <b>559</b> |
| <b>SECTION E: POLICIES, INSTITUTIONS AND CAPACITY-BUILDING</b>    | <b>561</b> |

## Annexes (on CD-ROM and on the web at <http://www.fao.org/3/a-i4787e/index.html>)

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Country reports  
 Survey responses – national legal and policy frameworks  
 Reports from regional focal points and networks  
 Reports from international organizations  
 Thematic studies  
 Supplementary tables for Part 3  
 List of references reviewed for Part 4 Section E – Economics  
 of animal genetic resources use and conservation  
 List of authors, reviewers and their affiliations

## Part 4

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### THE STATE OF THE ART





# Introduction

This part of the report provides an overview of the state of the art in methodologies, tools and techniques for the management of animal genetic resources for food and agriculture (AnGR). There is no well-defined set of methodologies encompass by the phrase “management of AnGR”. However, it can be taken to encompasses all technical, policy and logistical operations involved in understanding and documenting AnGR (inventory, characterization, surveying and monitoring); using and developing AnGR; conserving AnGR; and ensuring fair and equitable access to AnGR and sharing of benefits from their utilization.

The sections contained in this part of the report – addressing, in turn, surveying, monitoring and characterization, molecular tools, breeding programmes, conservation and economic evaluation – are each intended to serve as updates of the equivalent sections in the first report on *The State of the World’s Animal Genetic Resources for Food and Agriculture*, published in 20007. They therefore focus in particular on developments over the last decade or so. Each section ends with an assessment of gaps in current knowledge and proposes priorities for future research.

## Section A

# Characterization, inventory and monitoring

## 1 Introduction

The Global Plan of Action for Animal Genetic Resources (FAO, 2007a) notes that:

*“Understanding the diversity, distribution, basic characteristics, comparative performance and the current status of each country’s animal genetic resources is essential for their efficient and sustainable use, development and conservation. Complete national inventories, supported by periodic monitoring of trends and associated risks, are a basic requirement for the effective management of animal genetic resources. Without such information, some breed populations and unique characteristics they contain may decline significantly, or be lost, before their value is recognized and measures taken to conserve them.”<sup>1</sup>*

The Convention on Biological Diversity calls on countries to identify and monitor their biodiversity, including agricultural biodiversity. It recognizes that these activities are fundamental to the conservation and sustainable use of genetic resources. It also calls for the identification and monitoring of factors that threaten or are likely to threaten biodiversity.<sup>2</sup>

Knowledge of animal genetic resources (AnGR) is fundamental to their sustainable use, development and conservation. As defined in the first report on *The State of the World’s Animal Genetic*

*Resources for Food and Agriculture* (first SoW-AnGR) (FAO, 2007b),

*“characterization of animal genetic resources 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”.*<sup>3</sup>

The objective of characterization is to increase knowledge of AnGR and their present, and potential future uses, in a wide variety of environments (FAO, 1984; Rege, 1992). Characterization activities should contribute to objective and reliable prediction of animal performance in defined environments, so as to allow a comparison of the potential performance of different types of AnGR within the various production systems found in a country or region.

The term “surveying” is typically used in the context of national efforts to obtain data on the size of breed<sup>4</sup> populations. However, there is no clear cut distinction between surveying and characterization. A “survey” may collect a range of different types of AnGR-related data, while characterization, broadly defined, includes the task of obtaining data

<sup>3</sup> FAO, 2007b, page 347.

<sup>4</sup> FAO (1999) defines breed as follows: “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.” This broad definition is a reflection of the difficulties involved in strictly defining the term “breed”. For further discussion of the breed concept, see FAO, 2007b, pages 339–340.

<sup>1</sup> FAO, 2007a, Paragraph 23, Introduction to Strategic Priority Area 1.

<sup>2</sup> Article 7 of the Convention on Biological Diversity (available at <http://www.cbd.int/convention/articles.shtml?a=cbd-07>).

## PART 4

on population sizes. A survey that provides, for the first time, sufficient data to estimate the size of a national breed population is often referred to as a “baseline survey” (FAO, 2011a). At national level, surveying and characterization comprise the identification and description of the respective country’s AnGR, including their population sizes and structures, geographical distributions and production environments, as well as threats to their survival. Monitoring is the process of documenting how the sizes and structures of breed populations – along with their geographical distributions and production environments and the threats that they face – change over time. Characterization is typically differentiated into two categories: phenotypic characterization and molecular characterization (see Box 4A1).

In addition to data collection, the process of characterization, surveying and monitoring also includes the systematic documentation of the information gathered, so as to allow easy access by stakeholders involved in the management of AnGR. Monitoring of breed populations is a prerequisite for the operation of the early warning and response systems for AnGR (FAO, 2008) called for in the Global Plan of Action (see Box 4A2).<sup>5</sup>

The first SoW-AnGR presented an overview of the significance of characterization, surveying and monitoring in AnGR management and the main activities involved. The material presented below updates this overview, drawing on guideline publications prepared by FAO during the intervening years (FAO, 2011a; 2011b; 2012a) and focusing particularly on recent developments.

## 2 Characterization as the basis for decision-making

Decision-making related to the management of AnGR requires reliable data. Figure 4A1 illustrates the basic decision-making steps involved

<sup>5</sup> FAO, 2007a, Strategic Priority 1: “Inventory and characterize animal genetic resources, monitor trends and risks associated with them, and establish country-based early-warning and response systems.”

### Box 4A1

#### Phenotypic and molecular characterization

The term “phenotypic characterization of animal genetic resources” generally refers to the process of identifying distinct breed populations and describing their external and production characteristics within given production environments – along with description of these production environments. The process involves desk work in terms of gathering existing data, as well as field work recording information (descriptions, photos and trait measurements) for a group of representative animals. The term “production environment”, in this context, refers not only to the “natural” environment (climate, terrain, etc.), but also to management practices and the uses to which the animals are put. Broadly defined, it can also be taken to include social and economic factors such as market orientation, marketing opportunities and gender issues. Recording the geographical distribution of breed populations is considered to be an integral part of phenotypic characterization.

Complementary procedures used to unravel the genetic basis of phenotypes, their patterns of inheritance from one generation to the next, within-breed genetic structure and levels of variability, and relationships between breeds are referred to as “molecular characterization” (or alternatively as “molecular genetic characterization” or simply “genetic characterization”). In this case, inferences are drawn from a representative sample of animals that have been subject to a genotyping procedure.

In essence, phenotypic and molecular characterization of animal genetic resource are used to measure and describe genetic diversity in these resources as a basis for understanding them and utilizing them sustainably.

in identifying a strategy for managing a breed population. Breeds are grouped into categories according to their risk of extinction (the orange rectangles in the figure) and this defines the types of actions taken to manage them. The octagons

## Box 4A2

**Elements of a country-based early warning and response system**

It has been recommended (FAO, 2008) that a country-based early warning system for animal genetic resources should include the following elements:

1. a facilitating policy and legal framework (specific requirements will depend on needs and circumstances of the respective country);
2. institutional arrangements (allocation of responsibility for coordinating the system, establishment of relevant advisory groups, stakeholder networks, etc.)
3. a monitoring system (arrangements for keeping track of breeds' risk statuses as they change over time);
4. a risk-status classification system (criteria that can be used to allocate breeds to risk-status categories);
5. data and information management systems (including a national animal genetic resources database);
6. a priority-setting mechanism (a system for determining which breeds should be prioritized for conservation if resources are limited);
7. Breed recovery teams and breed recovery plans (arrangements for the implementation of conservation measures, including plans to protect breeds from acute threats such as disease epidemics);
8. Regional and global collaboration (cooperation, for example, in the organization of conservation programmes for transboundary breeds or in the establishment of regional gene banks); and
9. National, regional and global reporting and communication.

*Note:* Further information on monitoring and conservation measures can be found in the relevant FAO guidelines (FAO, 2011a; 2012b; 2013).

provides the information necessary to evaluate a breed with respect to the various criteria upon which the categorization and management decisions are made.

Breed surveys will provide the bulk of the information needed to establish a breed's risk status. An effective baseline survey at national level will establish a reliable estimate of the size, structure and geographical distribution of the breed's population and regular monitoring will record how these change over time. If the breed is present in more than one country (i.e. a transboundary breed), national surveys in all countries where it is present will be needed in order to obtain an accurate estimate of its global population size (a breed's international distribution and global risk status may be factors to consider in decision-making at national level, but knowledge of these factors should clearly not be regarded as a prerequisite for action).

Analysis of data from molecular characterization studies allows inferences to be drawn not only on the present genetic structure of a breed population, but also on the breed's history (see Part 1 Section A). Molecular characterization can also be used to refine knowledge about transboundary populations by contributing to the identification of breeds that have different names but show little differentiation at the genetic level (see Part 4 Section B).

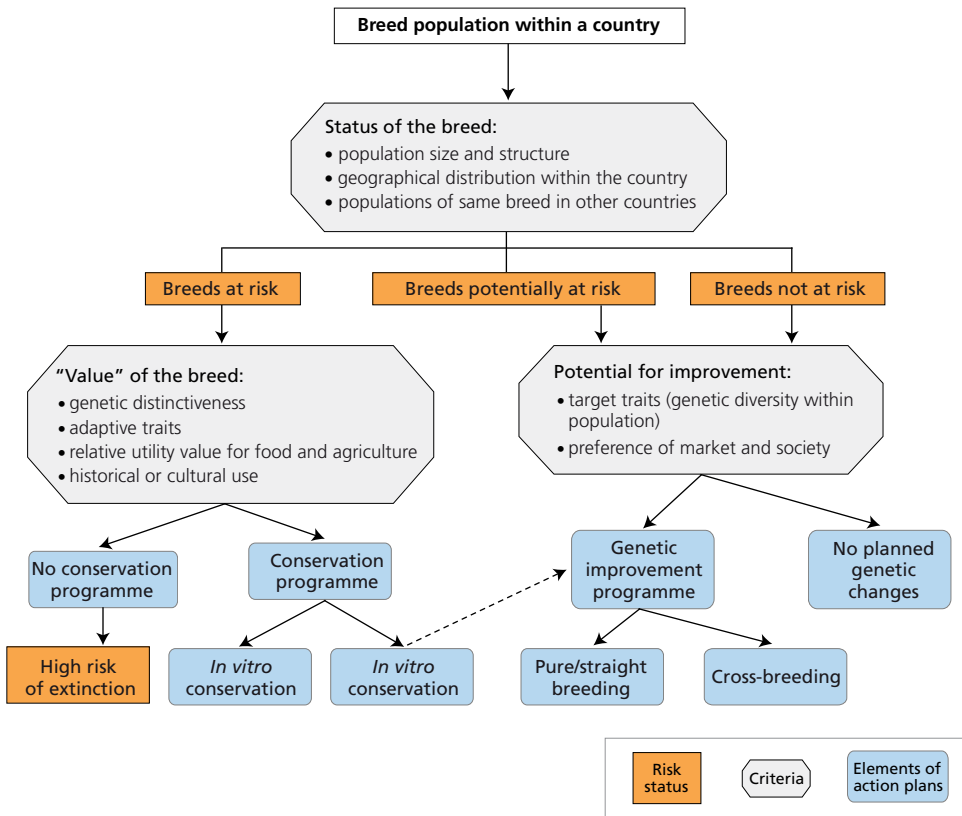
The relative utility value of a breed for food and agriculture will depend on a combination of factors and can be assessed on the basis of the results of phenotypic characterization studies that record performance, adaptability and product quality, along with descriptions of the production environments in which the animals are kept. Phenotypic characterization will also provide an indication of the breed's genetic distinctiveness, as unique traits can be expected to have a significant genetic basis. Molecular characterization can confirm this differentiation with respect to functional genes and extend it to "neutral" areas of the genome that are not subject to the forces of selection. A combination of phenotypic characterization (including information on production

in the figure list criteria considered when assigning breeds to risk categories and when determining the course of action to take. Characterization



## PART 4

FIGURE 4A1

**Management of breed populations – flow chart of decisions**

Source: FAO, 2007b.

environments) and molecular characterization will indicate a breed's adaptive traits and provide some indication of the biological basis for the observed characteristics. Studies will ideally also note any particular historical or cultural significance of the breeds targeted.

Molecular characterization can help in the evaluation of a breed's potential for genetic improvement. For simply inherited traits controlled by a single locus or a few well-defined loci, molecular analyses can determine whether a given breed carries the most favourable allele(s) and at what frequency. The situation is more complicated for

quantitative traits, because such traits are influenced by many genes – and few of these genes have been identified. However, genetic variation is essential for genetic improvement, and molecular characterization can be used to obtain a general assessment of a breed's genetic variability. An approach of this kind relies on the assumption that overall genetic variation (which includes variation for neutral loci that do not influence traits) is proportional to the variation for trait-influencing loci.

As noted above, description of the production environment is an essential element of phenotypic characterization. It can allow inferences

to be drawn regarding a breed's potential for improvement, particularly whether or not its genetic potential is being constrained by the environment (natural conditions or management capacity). Describing the production environment in which a breed has been raised for many years can also serve as an indirect means of characterizing its adaptive traits, based on the assumption that, over the years, the breed will have become adapted to the conditions in which it is kept. A description of the production environment in the broad sense may include an assessment of marketing opportunities and current and potential future demand for products or services provided by breeds and thereby provide information that can be used in planning their future management.

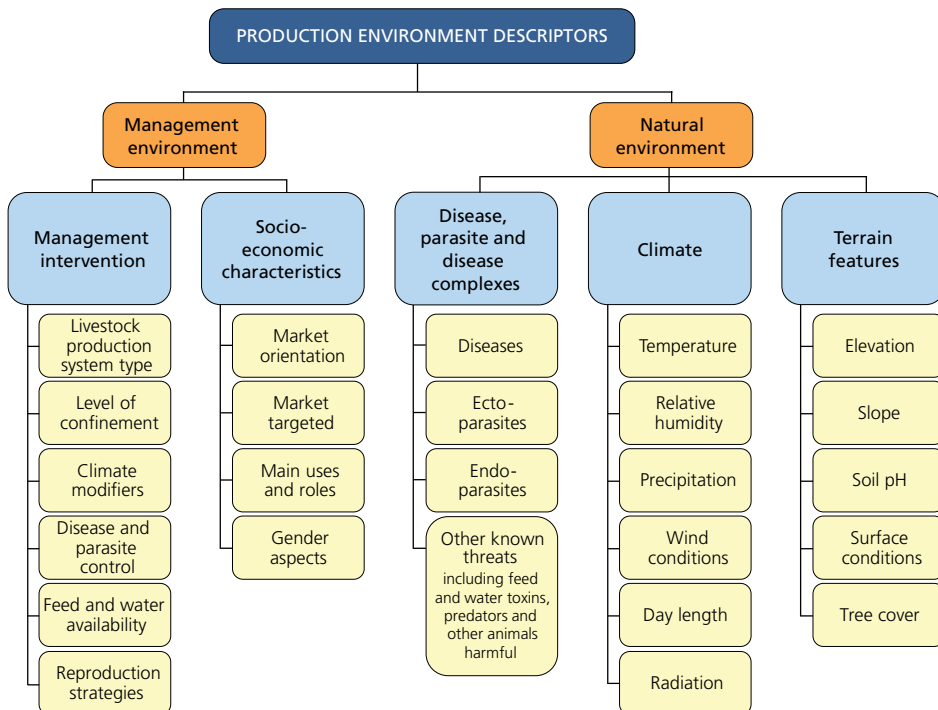
Knowledge of the production environments in which performance measurements are taken is, clearly, also essential if they are to be interpreted appropriately. A set of standard production environment descriptors has been developed for use in the Domestic Animal Diversity Information System (DAD-IS) (FAO, 2012a; FAO/WAAP, 2008). The main elements of the framework are shown in Figure 4A2.

### 3 Tools for characterization, surveying and monitoring

Since the first SoW-AnGR was prepared, FAO has developed and distributed technical guidelines on

FIGURE 4A2

**Descriptor system for production environments**



Source: FAO/WAAP, 2008.

## PART 4

surveying and monitoring (FAO, 2011a), phenotypic characterization (FAO, 2012a) and molecular characterization (FAO, 2011b). These guidelines describe in detail the tools recommended for use in the respective fields. They also describe some of the major developments that have occurred in the field of characterization in recent years.

The guidelines on surveying and monitoring provide advice on how to draw up a strategy for meeting national needs for data and information on AnGR. They also offer practical advice on how to plan and implement an AnGR survey – covering the whole process from planning the survey to disseminating the outputs and taking the first steps in translating results into action. A range of surveying methods are presented and advice is offered on how they can be combined and integrated within an effective strategy that addresses both the task of acquiring a baseline of data on AnGR and the subsequent task of monitoring changes over time. Box 4A3 provides brief descriptions of various methods or tools that can be used for surveying and monitoring.

When planning a survey or a surveying strategy, the appropriate choice of tools will depend on the specific objectives and on the circumstance in which the data will be collected (state of capacity to implement surveying activities, characteristics of the communities targeted, challenge posed by the rural landscape, availability of funding, etc.). Table 4A1 provides an overview of the suitability of different tools as methods for answering some of the basic questions that AnGR surveys attempt to address.

The guidelines on phenotypic characterization (FAO, 2012b) offer advice on how to conduct a well-targeted and cost-effective phenotypic characterization study and provide an overview of the concepts and approaches that underpin phenotypic characterization. They also provide practical guidance on planning and implementing field work, data management and data analysis. Generic data collection formats for phenotypic characterization of major livestock species, as well as a framework for recording data on breeds' production environments are also included.

To summarize briefly, phenotypic characterization encompasses the following activities (FAO, 2012b):

1. describing the geographical distribution of the targeted breeds and if possible the size and structure of their populations;
2. assessing the breeds' phenotypic characteristics, 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 productive and adaptive attributes;
3. obtaining images of typical adult males and females, as well as of herds or flocks in their typical production environments;
4. gathering information on the breeds' origin and development;
5. describing any known functional and genetic relationships with other breeds within or outside the respective country;
6. describing the biophysical and management environment(s) in which the breeds are kept;
7. documenting the breeds' responses to environmental stressors such as disease and parasite challenge, climatic extremes and poor feed quality, along with any other special characteristics related to adaptation; and
8. cataloguing any relevant indigenous knowledge (including gender-specific knowledge) related to the breeds and their management.

Many of these tasks can be accomplished through desk work or by consulting breeders or other stakeholders. The clearest exceptions are items 2 and 3, which require recording of data on a representative sample of live animals directly in their production environments.

The guidelines on molecular characterization (FAO, 2011b) include a short overview of progress in molecular characterization of AnGR over the preceding two decades and prospects for the future. They also provide practical advice for researchers wishing to undertake a molecular characterization study. The guidelines emphasize the importance of obtaining high-quality and representative biological samples that yield

## Box 4A3

**Surveying and monitoring methods – a toolbox**

**Mapping expeditions:** The term “mapping expedition” is used to describe a set of journeys undertaken (with limited contact with local livestock-keeping communities) for the purpose of obtaining rudimentary information on the animal genetic resources (AnGR) within a given geographical area. A mapping expedition can be used to map the approximate distribution of particular breeds and species, and may serve to frame subsequent surveys that will use other methods. However, the lack of contact with livestock keepers will result in very little acquisition of knowledge on production systems, livestock-keeping communities or the uses of AnGR. Geographic information system (GIS) tools and knowledge of the links between landscape types and livestock production systems may help to focus the mapping expedition.

**Breed search tours:** A “breed search tour” aims to fill gaps in breed inventories and identify breeds to be targeted by more detailed characterization studies. It involves an expedition to a part of the country where the livestock population has not been thoroughly studied and where it is suspected that undocumented breeds may be present. Planning a survey of this type may involve studying sources of historical information about the livestock populations in the targeted area. A breed search tour can be a low-cost activity that takes up relatively little time. However, it is possible that no undocumented breeds will be found.

**Transects:** In some locations it may be possible to estimate the numbers and types of animals present by using transect methods similar to those that have been developed for surveying wildlife. The approach involves drawing transects, *a priori*, across the area targeted by the survey and then travelling along them. The animals observed along the transect are counted and complex statistical methods are then used to estimate the numbers of animals in the area as a whole.

**Aerial surveys:** Aerial surveys can be thought of as airborne mapping expeditions or transects. They are appropriate only for use in sparsely populated and open landscapes and can be relatively expensive because of the need for costly equipment and

highly skilled personnel. Despite these limitations, poor accessibility, the unpredictable movements of pastoralists’ herds and security uncertainties may justify the use of aerial surveys as a means of estimating the size and structure of livestock populations and their spatial and seasonal distributions. In some areas, such surveys may be the only realistic option for achieving systematic coverage and obtaining the data needed for comprehensive statistical analysis. The main weakness of aerial surveys is a lack of contact with local livestock keepers and with the animals themselves. However, they may provide a starting point for further surveying activities that provide more information on livestock-keeping communities and the causes behind the outcomes observed from the air.

**Household surveys:** A household survey involves collecting data from a random sample of households chosen from among all households meeting a specific set of criteria referred to as the “sampling frame”. The larger the sample as a fraction of the whole, the more accurate the survey will be as an estimator of the target group. Information is obtained via interviews, normally held face to face with household members. The interviews are commonly based on a questionnaire.

**Rapid appraisal:** The term “rapid appraisal” can be used to describe data collection activities that involve interaction with livestock keepers and/or other knowledgeable stakeholders, but are not based on formal sample-based surveys. Rapid appraisals are multidisciplinary in nature and normally require visits to the communities targeted. Triangulation – the use of several sources in order to validate the data obtained – is a key characteristic. A range of rapid-appraisal tools are available and they can be selected and combined to meet the objectives of particular surveys or surveying strategies. Group interviews and exercises can serve as an alternative, or as a complement, to interviews with individual livestock-keeping householders or other informants.

(Cont.)

## PART 4

Box 4A3 (Cont.)

**Surveying and monitoring methods – a toolbox**

**Key informants:** Key informants are individuals who are targeted because of their particular knowledge about some aspect of the location or production system targeted by the survey or because they have broad knowledge that can be drawn upon as an alternative or complement to conducting a survey of individual livestock keepers. Advantages of using key informants include the potential for obtaining a lot of information from a limited number of interviews and the potential for obtaining detailed information within the key informants' areas of expertise. Disadvantages of using key informants include the possibility that the key informants are insufficiently well-informed about the situation on the ground and the risk that the knowledge and opinions of the livestock keepers themselves, particularly marginalized groups, may be overlooked.

**Obtaining information from breed societies:** Breed societies, where they exist, can be considered a specific category of key informant. They are particularly useful for monitoring population size and structure and hence for identifying when breeds come to be

at risk of extinction. Breed societies can be asked to report at regular intervals on the numbers of breeding males and females that are registered in their herd/flock books or (where possible) to provide details of animal pedigrees. Obtaining data from breed societies is a rapid and relatively easy means to keep track of population trends. Breed societies will also be knowledgeable about breeds' geographical distributions, morphology, performance, uses, production environments, marketing and so on.

**Censuses:** In a technical sense, a census is a household survey of wide scope and in which all qualifying households are interviewed. Most countries implement national agricultural censuses once every ten years; they may also implement more specific livestock censuses. In some countries, national censuses are based on sampling rather than on complete enumeration of the target populations.

*Note:* Detailed descriptions of the methods and their advantages and disadvantages can be found in FAO (2011a).

standardized data that can be integrated into analyses on an international scale.

With respect to biological samples, the guidelines suggest the collection of samples from at least 40 animals from across the geographic range of the breed. Blood has traditionally been the most frequently sampled material, but tissue and hair are gaining in popularity. Equipment has been developed for sampling ear tissues during the process of tagging animals for identification purposes. This approach efficiently combines animal identification with sample collection and links the identification number of the animal to the container in which the tissue sample is captured and stored. The material in the sampling tubes can also be cryopreserved and stored in a gene bank for possible use in population regeneration through cloning via somatic cell nuclear transfer (FAO, 2012b).

Ideally, for maximum efficiency, phenotypic and molecular genetic characterization activities will be combined, so that body measurements and other relevant traits can be recorded from the same animals from which biological samples are taken. Recording geographic coordinates for each animal from which samples and measurements are taken facilitates the description of their production environments, as the coordinates can be linked to other georeferenced datasets. A simple method for the collection of phenotypic data based on images is described in Box 4A4.

A variety of biotechnological tools are available for assaying the DNA collected during molecular characterization. Lists of the standard International Society for Animal Genetics–FAO Advisory Group panels of microsatellite markers for nine common livestock species are included in the guidelines on molecular genetic characterization

TABLE 4A1

**Usefulness of different surveying and monitoring tools to address different survey questions**

| Surveying and monitoring tools   | Mapping expedition | Breed search tour | Transect <sup>1</sup> | Aerial survey | Rapid appraisal | Household survey | Census |
|--|--------------------|-------------------|-----------------------|---------------|-----------------|------------------|--------|
| <b>Identification and characterization</b>   |                    |                   |                       |               |                 |                  |        |
| Is Breed A present in the survey area and listed in the relevant breed inventory?    | *****              | *****             | *****                 | *             | ***             | *****            | ****   |
| What are the characteristic identifiers of Breed A?                                  | **                 | ***               | ***                   | *             | ****            | *****            | *      |
| Is Breed A part of a common gene pool that extends beyond national borders?          | **                 | ***               | *                     | *             | *****           | *****            | **     |
| How many animals of Breed A are there?   | *                  | **                | ****                  | **            | **              | *****            | ****   |
| What is the geographical distribution of Breed A?                                    | *****              | ***               | ***                   | **            | ***             | *****            | *****  |
| What role does the breed play within the production environment in which it is kept? | *                  | ***               | *                     | *             | ****            | *****            | **     |
| Is Breed A associated with a particular socio-economic or cultural group?            | *                  | ****              | *                     | *             | ***             | *****            | ***    |
| Does Breed A have any important adaptations or unique traits?                        | *                  | **                | *                     | *             | *****           | *****            | *      |
| What are the threats to Breed A?   | *                  | **                | **                    | *             | *****           | *****            | *      |
| <b>Monitoring</b>  |                    |                   |                       |               |                 |                  |        |
| Is Breed A increasing or decreasing in numbers?                                      | *                  | *                 | ****                  | **            | ****            | ***              | ****   |
| Is a recognized threat to Breed A increasing or decreasing?                          | *                  | *                 | **                    | *             | *****           | ***              | **     |

Note: The number of asterisks represents the usefulness of the tool: \* = of little use; \*\*\*\*\* = very useful.

<sup>1</sup> Assuming this approach is feasible in the respective production environment.

Source: FAO, 2011a.

(FAO, 2011b). These panels are, however, limited to the characterization of neutral genetic variability.

## 4 Information systems

The information gathered through characterization, surveying and monitoring activities is not useful unless a system is in place to ensure it is organized and made easily available to stakeholders. An information system normally includes data, hardware and software for the organization, analysis and storage of these data, and facilities for communication. Information

systems can be manual or automated and may or may not be publicly accessible. The most widely used systems are those that are publicly available on the internet.

The roster of public-domain electronic AnGR information systems that are globally accessible and contain data from more than one country has remained largely unchanged since the time the first SoW-AnGR was prepared. Two of these systems – the Domestic Animal Diversity Information System (DAD-IS)<sup>6</sup> and the European Farm Animal Biodiversity Information System (EFABIS)<sup>7</sup>

<sup>6</sup> <http://fao.org/DAD-IS>

<sup>7</sup> <http://efabis.tzv.fal.de/>

## PART 4

## Box 4A4

**A digital enumeration method for collecting phenotypic data for genome association**

Genomic science aimed at finding important adaptive genetic variations requires consistent data across animal populations. The ADAPMap\* Digital Phenotype Collection Method is a new method for obtaining consistent phenotypic data by digital enumeration of categorical and continuous values. It is an easy to use, low-cost procedure that involves the collection of data on health status indicators (anaemia status, age and weight), body measurements, shapes and coat colour and pattern via digital images, using mobile technology.

The method calls for six photos: four for body measurements and two for health indicators. The animal walks directly into the photo set and has to make only two right one-quarter turns to allow the first four photos (Shots 1 to 4) to be taken. The camera is positioned at the eye level of the animal at a distance of 3 m. The two health indicator photos are close-ups of the teeth (tooth age) (Shot 5) and eye (FAMACHA score\*\*) (Shot 6).

Novel calibration signs designed to affirm size and colour are made of sturdy, light-weight metal and dry-erase pens are used to record sample data captured

by the images. A field photo sampling kit (see photo) includes everything needed except the camera.

Twelve sampling teams have employed the method in 12 countries, sampling roughly 2 000 goats and collecting over 12 000 images. An ADAPMap Quick Start Guide was developed and proved valuable in enabling the sampling teams to set up the equipment and take the photos properly. Samplers generally had little difficulty applying the method; however, the FAMACHA and tooth shots were challenging.



Shot 1: Rear



Shot 2: Naked Goat



Shot 3: Sign



Shot 4: Front



Shot 5: Teeth



Shot 6: FAMACHA

(Cont.)



## Box 4A4 (Cont.)

**A digital enumeration method for collecting phenotypic data for genome association**

The method is designed to provide consistent phenotypic measurements that can be used in conjunction with DNA sampling to inform genomics research, guide animal selection for breeding programmes and facilitate animal genetic conservation decisions. It will enable countries to take advantage of state-of-the-art science and support them in identifying priority breeds for conservation. The data may be used in research, surveillance efforts to detect emerging animal health issues or as a tool for on-farm herd record keeping management and animal health care.

Simplification of the collection protocol is being explored. The associated digital phenotyping software under development could be integrated into other livestock software applications.

\*ADAPMap is an international project for characterization of goats on a global level that employs landscape genomics to study adaptation to local environments (see [www.goatadaptmap.org](http://www.goatadaptmap.org) for more information).

\*\*FAMACHA score is based on the colour of the inner eyelid and is used as indicator of the animal's level of anaemia.

Provided by Jennifer Woodward-Greene, Jason K. Kinser, Heather J. Huson, Tad S. Sonstegard, Johann (Hans) Sölkner, Iosif I. Vaisman and Curtis P. Van Tassel. The work is funded by USAID Feed the Future, the USDA and FAO

(previously EAAP-AGDB) – are part of a linked network of information systems (EFABISnet)<sup>8</sup>. Countries are able to set up their own national information systems (“nodes”) linked to EFABIS. Seventeen countries<sup>9</sup> (as of October 2014) operate national nodes that regularly exchange data with EFABIS, which in turn exchanges data with DAD-IS. The national nodes can be accessed via the web. In most cases the data are provided in English and the respective local language. In addition to the core data structure that is common to all the systems in the region, countries can add data structures that reflect their specific needs. Data pertaining to these national specificities are not synchronized with EFABIS. Similarly, EFABIS, is tailored to the specific requirements of the European region (e.g. it includes a register of cryobank material) and data pertaining to these specificities are not transferred to DAD-IS. The number of national breed populations for which some information is available in DAD-IS has increased by about 6 percent (from 14 017 in 2006 to 14 896 in 2014) and the proportion of breeds for which population data are recorded has increased from

42 to 59 percent (see Part 1 Section B for further information).

The Domestic Animal Genetic Resources Information System (DAGRIS)<sup>10</sup>, managed by the International Livestock Research Institute (ILRI), is based on a database of research information obtained from published and grey literature (DAGRIS, 2007). At the time the first SoW-AnGR was prepared, DAGRIS comprised a single central database. However, dispersed national units have now been established for some countries through an initiative known as “Country DAGRIS” (DAGRIS, 2013). Oklahoma State University’s Breeds of Livestock<sup>11</sup> information system (Oklahoma State University, 2005) provides brief summaries of breed origins, characteristics and uses. Although this resource is maintained, little new information has been added in recent years. Brazil, Canada and the United States of America are collaborating in the development of Animal-GRIN (the Animal Genetic Resources Information Network)<sup>12</sup> as a common platform for the management of AnGR-related data.<sup>13</sup> Wikipedia, the online

<sup>8</sup> <http://efabis.net>

<sup>9</sup> Austria, Bulgaria, Cyprus, Estonia, Finland, Greece, Hungary, Iceland, Ireland, Italy, Netherlands, Poland, Republic of Moldova, Slovenia, Slovakia, Switzerland, United Kingdom.

<sup>10</sup> <http://dagris.ilri.cgiar.org/>

<sup>11</sup> <http://www.ansi.okstate.edu/breeds/>

<sup>12</sup> [http://nrrc.ars.usda.gov/A-GRIN/main\\_webpage/ars?record\\_source=US](http://nrrc.ars.usda.gov/A-GRIN/main_webpage/ars?record_source=US)

<sup>13</sup> [http://nrrc.ars.usda.gov/A-GRIN/database\\_collaboration\\_page#](http://nrrc.ars.usda.gov/A-GRIN/database_collaboration_page#)



## PART 4

## Box 4A5

**Biogeoinformatics for the management of animal genetic resources**

The management of animal genetic resources requires data on population and evolutionary genetics and on animal husbandry practices, but also on the socio-economic and environmental conditions in the locations where animals are bred. The integration of these different types of information by means of geographical coordinates and geographic information systems (GIS) will facilitate the development of monitoring systems able to identify at-risk breeds and thereby support conservation prioritization. Supported by expert-based decision-making approaches, web-based platforms developed on the basis of expertise in biology, GIS and computer science are able to simultaneously assess animal demographics and the sustainability of breeding activities in areas of interest.

In parallel, and in conjunction with molecular genetic data, the use of geographical coordinates enables the use of livestock landscape genomics to seek regions of the genome influencing the ability of animals to cope with environmental variations. The approach can be used to identify key traits involved in parasite resistance, to support efforts to conserve the adaptive potential of locally adapted breeds and

even to increase adaptability in industrial breeds. Specific software developed at the interface of geographic, biological and computer sciences can be used to identify regions of the genome that may be under natural selection and involved in evolutionary processes such as local adaptation.

Biogeoinformatics has a crucial role to play in the characterization of animal genetic resources. It will not be possible to extract new knowledge from the data tsunami brought about by the advent of high-throughput molecular tools, new sources of high-resolution environmental data and new sources of socio-economic information unless efficient and easy-to-use computing tools are developed. If the discipline is to fulfil its potential in the coming decades, the livestock community will need to ensure that recording of geographical coordinates for any sampled animals is treated as a standard practice and thus that links can be made to information available in georeferenced databases.

Provided by Stéphane Joost, Solange Duruz and Sylvie Stucki.

encyclopedia,<sup>14</sup> has descriptive entries for many individual livestock breeds. Breeds are, clearly, not the main focus of this resource and the information available is not standardized.

Information systems for AnGR are 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 amount of information that they contain relative to what would potentially be possible – and would be necessary for them to achieve their stated purposes effectively.

<sup>14</sup> [http://en.wikipedia.org/wiki/Main\\_Page](http://en.wikipedia.org/wiki/Main_Page)

## 5 Changes since 2005

Developments in telecommunication technologies, expansion of their range of usage and decreases in their costs are creating greater potential for the use of these technologies in surveying and monitoring. However, adoption of these technologies for this purpose has been very limited. Increasing numbers of countries are exploiting telecommunication technologies to establish or enhance animal identification and traceability systems (FAO, 2015). However, in most cases these systems do not gather data on the breeds to which animals belong.

Advances in global positioning technologies and geographic information systems have created opportunities for more accurate and detailed

descriptions of breeds' production environments. Box 4A5 discusses some recent developments in this field. Various publicly available databases provide access to georeferenced data on the climate and other environmental measures such as soil type and vegetation. If the geographical coordinates of breed distributions have been recorded, they can be linked to these datasets as part of efforts to characterize breeds' production environments. Global positioning technologies and geographic information systems, along with advances in molecular genetic characterization have also facilitated the use of "landscape genomics" in the study of adaptation at molecular level.

Developments in the field of molecular genetic analysis since the time the first SoW-AnGR was prepared have been nothing short of revolutionary (details are provided in Part 4 Section B). Genome sequencing has become much more rapid and much less costly. Reference genome sequences have been established for all the major livestock species and several minor ones. The genomes of several thousand individual animals, most commonly cattle, have been sequenced. The single nucleotide polymorphisms (SNPs) identified through sequencing have become the basis for high-throughput genotyping assays with which tens of thousands of markers can be screened simultaneously. One shortcoming, however, is that development of these technologies for livestock has been driven by the commercial market. As a result, the tools have been created for, and are more applicable to, the species and breeds that are most common in industrialized countries (i.e. a limited number of international transboundary breeds).

As far as phenotypic characterization is concerned, genomic and other technological advances have increased opportunities and demands for so-called advanced characterization. Such studies involve relatively complex data-gathering activities, particularly repeated measurements over a period of time (e.g. weights of young animals to characterize growth rate), and often target novel traits related to the cost and efficiency of

production rather than to the quantity of output produced. The scientific community has recently realized that a lack of phenotypic information, rather than genomic information, has now become the limiting factor in the study of biological systems and processes. "Phenomics" – the study of phenotypes from a systematic perspective – has thus recently emerged as an important discipline. Phenomics involves the collection of data on multiple phenotypes, including "traditional" traits and biological indicator traits measured in an automated manner. Integration of phenomics concepts into phenotypic characterization, although not yet widely done, is likely to become more common in the future, especially as more effort is made to characterize breeds for complex phenotypes such as heat resistance and other forms of adaptation.

Characterization of rumen microbes is an emerging research topic that may assist in the reduction of greenhouse gas emissions (Box 4A6).

## 6 Conclusions and research priorities

Adequate surveying, monitoring and characterization of AnGR are prerequisites for successful management of these resources and for informed decision-making in national livestock development. A strategic and coherent approach is needed and all activities should be undertaken in close cooperation with livestock keepers and other stakeholders. There is still particular need to develop innovative methods and tools that take advantage of the potential of telecommunication networks (e.g. cellular phones and mobile internet) for use in surveying and monitoring. The political will to undertake surveying and monitoring at breed level is also essential. Most national livestock censuses and animal identification systems do not record information about breeds.

In many countries, comprehensive breed definitions that unambiguously distinguish different populations are often lacking. Also often lacking are descriptions of the production environments

## PART 4

## Box 4A6

**Rumen microbes: small but significant**

Rumen microbes play a central role in the nutrition, health and greenhouse gas emissions of ruminant animals. However, we do not know whether the rumen microbial community is the same in all ruminants, and how much host species, diet and geography influence the microbial community. The Global Rumen Census Project ([www.globalrumencensus.org.nz](http://www.globalrumencensus.org.nz)) was established to address this knowledge gap and aims to characterize the composition and diversity of rumen microbial communities. In total, 742 samples from a range of ruminants, and other mammals with similar digestive systems, were provided by collaborators from 58 research institutions in 33 countries ([www.globalrumencensus.org.nz/samples](http://www.globalrumencensus.org.nz/samples)). The samples encompassed a wide variety of species and breeds, including taurine cattle (Charolais, Cika, Hereford, Highland, Holstein, Icelandic, Korean Native, White Park, etc.), zebu cattle (Muturu, N'Dama, Nelore, White Fulani, etc.), goats (Creole, Red Sokoto, Saanen, etc.), deer, water buffalo (Murrah, Nili-Ravi, etc.), to name but a few. Samples from non-farmed ruminants were also included. The sampled animals were from a range of different production systems (small and large-scale commercial operations, research farms and the wild) and locations (temperate, tropical, high-altitude locations, etc.) and consumed a wide variety of diets, comprising many different forages and concentrate combinations of greatly differing quality.

As part of the Global Rumen Census Project, DNA was extracted from the samples, and bacterial, archaeal, protozoal and fungal marker genes were sequenced using a standardized pipeline. The dataset comprises 5 million bacterial, 1 million archaeal, 1 million protozoal and 15 000 fungal sequencing reads. Analysis of these data will allow the identification of factors that influence which taxa are present in the rumen and allow the following questions to be addressed:

- How much variation is there in rumen microbial communities?
- What is the extent of diversity in each microbial group?
- What novel groups are present?
- Is there a core microbial community?

Interrogation of sample (meta-)data will allow the identification of factors that influence which taxa are present in the rumen.

Many of the rumen microbes have not been adequately characterized, often due to a lack of available representative cultures. A second project with collaborators from 14 countries, the Hungate1000 ([www.hungate1000.org.nz](http://www.hungate1000.org.nz)), aims to generate a reference set of rumen microbial genome sequences from cultivated rumen bacteria and archaea, together with representatives of rumen anaerobic fungi and ciliate protozoa. Data from the Global Rumen Census are being used to inform the selection of candidates for isolation and genome sequencing. The Hungate1000 project currently has genome sequencing in progress for more than 280 microbial cultures (<http://www.hungate1000.org.nz/genomes.html>). Results will be used to initiate genome-based research aimed at understanding rumen function, feed conversion efficiency, methanogenesis and plant cell wall degradation in order to find a balance between food production and greenhouse gas emissions. Results from both projects will aid the analysis of future rumen microbiome studies.

Both projects are funded by the New Zealand Government in support of the Livestock Research Group of the Global Research Alliance on Agricultural Greenhouse Gases (<http://www.globalresearchalliance.org>) to support international efforts to develop methane mitigation and rumen adaptation technologies.

Provided by Gemma Henderson, Peter H. Janssen, Adrian Cookson, Sinead Leahy and Bill Kelly.

in which breeds are kept and in which they achieve given levels of performance. FAO is cooperating with several countries to collect such information, but recording has yet to be implemented on a wide scale.

With regard to research priorities, the first SoW-AnGR noted that growing interest in issues such as animal welfare, distinctive product qualities, human–health effects, the environmental impacts of livestock production and the efficiency of resource utilization meant that there was a need for characterization studies to target traits relevant to these concerns. Specific priorities identified included research into the robustness of different breeds, as measured by the extent of genotype–environment interactions, and into the genetic basis of robustness and disease resistance, including infection mechanisms and host–pathogen interactions. These priorities remain relevant. More generally, there is a need to improve understanding of the contributions that different types of livestock make to the economy and to rural development, including not only the supply of marketed products, but also the provision of regulating, habitat and cultural ecosystem services (see Part 1 Section D and Part 4 Section E for further discussion of ecosystem services). Studies that investigate the links between the characteristics of specific breeds and the supply of niche products and ecosystem services may also be significant in the planning of conservation measures, given that functions of this kind are increasingly being regarded as potential means of keeping at-risk breeds in use (see Part 3 Section D and Part 4 Section D).

Lack of phenotypic data has always been a constraint in developing countries, but advances in genomics and interest in new traits have meant that phenotyping has now become the main limiting factor in characterization in both developing and developed countries. Methods for measuring phenotypic characteristics associated with health, fitness, adaptability and the provision of ecosystem services need to be improved.

There is a need to develop cheap and efficient tools for monitoring AnGR populations, including

monitoring of their geographic distributions. It is possible that in the era of the internet and crowd sourcing it may be possible to develop more participatory approaches to the collection of AnGR-related data. This would require forms of organization that differ from those used in conventional top-down surveying and monitoring programmes. Investigating the feasibility of using such approaches would be likely to require input from the social sciences.

Ideally, decision-making in AnGR management would be based on comprehensive information. However, given that immediate action is required, there is a need to develop tools and methods that make effective use of the information that is presently available.

Existing AnGR information systems have relatively little functionality beyond simple searches by country or breed. There is a need to create user-friendly tools that allow stakeholders to access the data they require and conduct customized analyses. However, information systems are only as good as the information they contain. Insertion of missing data and regular updating and correction of existing data are essential. This process would be facilitated by the development of specific software applications that reduce the work associated with data input. Georeferencing of AnGR-related data needs to be expanded and made routine, so as to allow these data to be linked to georeferenced geophysical and agro-ecological data and to provide more precise information about the current and past geographic distributions of specific AnGR. Finally, given that no single information system can gather and store all relevant data, the interconnectivity and interoperability of information systems and databases need to be further developed.

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## Section B

# Molecular tools for exploring genetic diversity

## 1 Introduction

Recent advances in the field of genomic technology have constituted a major innovation in livestock production. The increasing availability of molecular tools is deeply affecting the ways in which livestock species are studied and managed. This section provides an overview of recent developments related to molecular tools and their use, focusing particularly on the period since the first report on *The State of the World's Animal Genetic Resources for Food and Agriculture* (first SoW-AnGR) (FAO, 2007) was prepared.

The first SoW-AnGR noted that the main roles of molecular technologies in the characterization of AnGR include:

- assessing functional and neutral genetic variability within and between populations, including investigation of their history (domestication, expansion or reduction of the population size, migrations, introgression episodes, etc.);
- assessing the current state of a population in terms of risks related to inbreeding and genetic drift, using estimators such as effective population size; and
- genetic characterization of traits (e.g. physical appearance, productivity, disease resistance and other adaptability traits) specific to given populations.

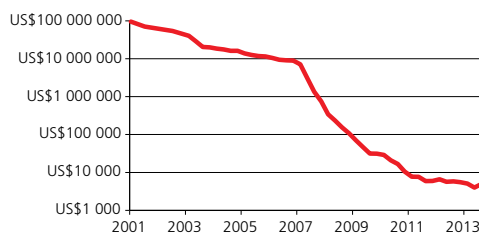
The report highlighted the following three ongoing developments in molecular biology as being particularly relevant to AnGR management:

- the establishment of whole genome sequences for various livestock species;

- the development of technologies for measuring polymorphisms at loci spread across the entire genome; and
- the development of technologies for measuring gene transcription and expression on a large scale.

Since the first SoW-AnGR was prepared, the list of species whose genomes have been sequenced has continued to grow. It now includes chicken (2004), sheep (2010), cattle (2009), horse (2009), pig (2012), rabbit (2009), turkey (2009) and goat (2013). The costs of genotyping and sequencing have declined sharply during this period (Figure 4B1). High-density SNP arrays, allowing the simultaneous assay of several tens of thousands to several hundreds of thousands of SNPs, are available for use in livestock species at a cost of US\$100 or less if a relatively large number of individuals are sequenced. Genomes

FIGURE 4B1  
Change in cost per genome sequenced in humans



Note: Costs expressed on a logarithmic scale.

Source: Based on data from National Human Genome Research Institute ([http://www.genome.gov/pages/der/sequencing\\_costs\\_jul2014.xlsx](http://www.genome.gov/pages/der/sequencing_costs_jul2014.xlsx); accessed January 2015).

## PART 4

## Box 4B1

**From DNA to phenotype**

The genome of livestock species is organized in pairs of chromosomes, each inherited from one of the parents and chemically made up of large molecules of DNA (deoxyribonucleic acid). Each gene in an individual, therefore, has two copies, known as alleles, one on each chromosome of a pair (with the exception of non-paired sex chromosomes). Chromosomes comprise genes and intergenic regions. The former encode proteins and other products. The latter, which represent the majority of the genome, are believed to play various regulatory roles (The ENCODE Project Consortium, 2012). Genes typically consist of coding sequences (exons) separated by introns and accompanied by regulatory elements. Like intergenic regions, introns carry no protein-coding information, but sometimes play a role in the regulation of gene expression.

Nucleic acids are strands of smaller molecules called nucleotides. DNA has four types of nucleotide (adenine, cytosine, guanine and thymine). The instruction encoded in a gene depends on the sequence in which these nucleotides are ordered. This sequence information is put into action in two steps. The first is the 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 molecule. In the second step, these molecules (transcripts) are edited and eventually translated into proteins (particular three-nucleotide sequences correspond to particular amino acids, the molecules that constitute a protein). Gene expression is highly tissue-specific and time-dependent. Not all genes are translated into proteins; some express their function as non-coding RNA molecules that play important roles in protein synthesis

(transfer RNA and ribosomal RNA) and various regulatory processes (microRNA and long non-coding RNA, two types of regulatory RNA that differ in terms of the number of nucleotides they consist of – approximately 20 and more than 200 nucleotides, respectively).

Phenotypic differences between individuals, populations and species are a consequence both of environmental effects (including epigenetic mechanisms – see Box 4B5) and of variations in DNA sequences. These variations may be caused by point mutations leading to the substitution of single nucleotides (single nucleotide polymorphisms – SNPs), insertions, deletions, duplications, copy number variations or inversions of DNA fragments. If SNPs are in exons, different alleles may lead either to the same amino acid (synonymous SNPs) or to a different amino acid (non-synonymous SNPs) being included in the resulting protein. DNA variations can be classified as “functional” or “neutral”. In the case of functional variation, changes in the sequence of nucleotides in the DNA molecule induce changes in the phenotypic function of the organism. In the case of neutral variation, a change in the DNA sequence does not give rise to any change in function.

Because genes or SNPs that lie near each other on a chromosome (i.e. are physically “linked” to each other) tend to be inherited together, a neutral variant can be associated with a functional one. In addition, this interdependence between linked genes means that the various combinations of their alleles are not distributed randomly (a phenomenon termed “linkage disequilibrium”). Linkage and linkage disequilibrium allow the use of one site of polymorphism as a “genetic marker” for polymorphism in a nearby region.

can be sequenced for less than US\$3 000 each with moderate coverage (e.g. “eight-fold” coverage – meaning that, on average, each position in the genome is sequenced eight times). Sequencing smaller fractions of genomes (restriction site associated DNA sequencing – RAD-Seq) can be used directly in the characterization of

individual animals (this is termed “genotyping by sequencing”) (De Donato *et al.*, 2013). Similarly, the development of tools capable of assaying a high density of transcripts and even direct transcriptome sequencing (also known as “RNA-seq” – short for RNA sequencing), has increased capacity to study gene expression and hence to unravel

the complex physiological regulation of target traits (D'Alessandro and Zola, 2012).

## 2 Developments in the use of DNA markers

Progress in sequencing techniques and the opportunities offered by the development of high-density marker arrays have considerably improved the availability of DNA information over the last ten years, both in terms of the number of markers identified and in terms of the cost of genotyping.

Until recently, microsatellites remained one of the most popular types of marker in genetic characterization studies (Lenstra *et al.*, 2012), used for example in projects such as “GlobalDiv”, which ran from 2007 to 2010 and combined microsatellite datasets from various diversity studies from different parts of the world (Ajmone-Marsan *et al.*, 2010). Microsatellite data continue to be used, especially in developing countries (e.g. Abdullah *et al.*, 2012; Azam *et al.*, 2012) and in the context of conservation and priority setting at regional level (e.g. Medugorac *et al.*, 2011; Ginja *et al.*, 2013). However, they are increasingly being superseded by the use of SNP marker arrays. With the advent of next-generation sequencing, mitogenomics (analysis of the whole mitochondrial genome rather than a limited fragment of mitochondrial DNA) can be routinely used in livestock species, including less intensively studied species such as goats (Doro *et al.*, 2014) and horses (Achilli *et al.*, 2012). The recent generation of whole genome reference sequences for many livestock species has allowed “population genetics” to become “population genomics”. Population genomics uses large sets of SNPs to study specific variations across the genome and determine how they have been shaped by the history (e.g. changes in population size, selection, and cross-breeding) of livestock populations. SNPs can be assigned to various classes (neutral vs. genic, intron vs. exon or synonymous vs. non-synonymous), which provides opportunities for more detailed analysis of diversity. The past decade has also witnessed

a revolution in sequencing technologies that has led to the development of various platforms for DNA and RNA sequencing, known collectively as next-generation sequencing technologies (see Metzker, 2010 and Davey *et al.*, 2011 for reviews). These tools can rapidly (in a few days or weeks) provide sequence data in the form of short reads (sequenced DNA fragments between 100 and 400 base pairs long on average) that collectively cover the whole genome of a sample (or the transcriptome of a particular organ) several times. Identifying SNPs from this type of data is relatively easy, provided that a reference sequence has been established (Nielsen *et al.*, 2011), which is the case for most livestock species. Methods have also been developed for SNP discovery in newly sequenced species (Norman *et al.*, 2013) and these approaches may prove useful for less common livestock species.

High-density SNP panels are now widely used for genome-wide association studies (GWAS), genomic prediction and population genomic analyses. However, the preliminary phase, i.e. SNP discovery or SNP selection from databases, is critical. If data have not been obtained randomly, standard estimators of population genetic parameters should be applied with caution. Non-random selection may occur if SNP sets are derived for use on a given set of breeds but later used on other breeds or if SNP sets are filtered to meet certain criteria (e.g. a minimum allele frequency).

Many current tools are affected by both these factors, as they have been developed primarily using widely used international transboundary breeds and with the use of SNP-filtering criteria. Such protocols bias the distribution of allelic frequencies relative to what would be expected in a random sample. The resulting inaccuracy in estimation of genetic parameters is known as “ascertainment bias”. Bias caused by problems of this kind is probably present in most commercial and ready-to-use medium- and high-density SNP panels currently available for use in livestock species. Unbiased estimates of the absolute genetic diversity (i.e. the nucleotide diversity) of a population can, in theory, be



## PART 4

## Box 4B2

**Glossary: genetic markers**

**Genetic marker:** a DNA sequence variation that is informative with respect to a specific location (locus) on a particular chromosome.

**Microsatellites:** segments of DNA characterized by a variable number of copies (typically 5 to 50) of sequence motifs of around two to five bases (referred to as a repeat unit). At any one locus (site in the genome), there are usually several different “alleles” in a population, each allele identifiable by the number of repeat units detected via polymerase chain reaction (PCR). Many microsatellites have a large degree of polymorphism. In many species, they were the first standard marker technology used to characterize diversity. However, due to their comparatively infrequent presence across the genome, inconsistent reproducibility across laboratories and genotyping platforms, and higher genotyping cost per locus, microsatellites are being replaced by other technologies.

**Single-nucleotide polymorphism (SNP):** a DNA sequence variation that results from a change in the nucleotide at a single location in the genome. SNPs usually have only two alleles. They may represent either neutral or functional genetic diversity and generally occur throughout the genome. In most species, SNPs occur, on average, once in every 100 to 300 positions in the DNA sequence. For most major livestock species, commercial arrays are available that allow substantial numbers of SNPs (from a few hundreds to over a million) to be genotyped in a single reaction at a low cost per marker. SNP arrays are now

routinely used as more informative alternatives to microsatellite panels in genetic diversity studies.

**Markers of sex-specific inheritance:** certain parts of the genome have sex-specific inheritance. Mitochondrial DNA is passed from the mother to the offspring. The Y-chromosome in mammals is inherited from father to son, while the W-chromosome in birds is inherited from mother to daughter. This class of markers can include both SNPs and other sequence variations and has been instrumental in identifying wild ancestors, localizing domestication centres and reconstructing colonization and trading routes.

**Sequence variation:** with the emergence of whole-genome sequencing, the entire variation present in the DNA sequence is now available as a potential source of marker information. This variation comprises SNPs and insertions and deletions (InDels) (loss or gain of one or more nucleotides relative to the species reference sequence), duplications, copy number variations (CNVs) (variation in the number of copies of sections of the DNA) or inversions of DNA fragments. Sequencing can be performed on a whole genome basis or only for specific parts of the genome (e.g. the exome or genome fractions used for genotyping by sequencing). Whole-genome sequences will be the ultimate source of genetic diversity information, as they harbour the motifs responsible for genetic differences between breeds. However, efficient management, use and storage of this information will require, in addition to sequencing capacities, substantial development of resources in bioinformatics (methods, tools and hardware).

obtained only via whole genome sequencing. Statistical approaches that explicitly account for the methods used in SNP discovery and sample preparation have been developed for use when undertaking various kinds of population genetics analyses with SNPs (Nielsen *et al.*, 2011; Kofler *et al.*, 2011). Large-scale projects have also started to harvest genome-wide information for use in characterizing livestock populations at national

or international scale, including studies on cattle (Gauthier *et al.*, 2010), sheep (Kijas *et al.*, 2012), horses (McCue *et al.* 2012; Orlando *et al.*, 2013), pigs (Groenen *et al.*, 2010), chickens (Weigend *et al.*, 2015) and goats (Dong *et al.*, 2013).

It is important to note that although cost per SNP is low relative to microsatellites (and decreases with the number of SNPs analysed) the costs of high-density assays – currently (2015)

US\$50 to US\$200 and depending heavily on the number of arrays purchased – are nonetheless prohibitive for many applications. Costs continue to decline, however, and financially realistic options are likely to eventually become available for most situations. This being said, even if lower cost genotyping assays become available, the bioinformatic infrastructure in most developing countries will still require further development. Both the sheer amount of raw data and the complexity of analytical models are several orders of magnitude larger than those associated with microsatellite-based analyses. This is true for work with SNP array data, but even more so for work with sequence data.

Further studies are in the process of identifying millions of SNPs and haplotypes (specific allelic combinations for a given set of loci) and also other sequence variants such as insertion–deletion polymorphisms (InDels) and copy number variants (CNV) (see Box 4B2 for explanations of these terms). Novel sequencing technologies are continuously evolving, accompanied by a drop in cost per sequenced genome (see Figure 4B1). Allele frequency differences and diversity measures derived from them can be obtained inexpensively by sequencing pooled DNA from multiple individuals from a population (e.g. Qanbari *et al.*, 2012). Sooner or later, sequence-based approaches will become the standard methodology for generating data for use in livestock diversity studies.

Marker information will become even more useful when linked to biological background information available in specialized databases. Information about marked genes and their functions is available in the Ensembl database<sup>1</sup> (among others) for many livestock species. Information on quantitative trait loci (QTL) is collected in the AnimalQTL database<sup>2</sup> and genomic pathway information is available through KEGG.<sup>3</sup> In human genetics, the Encode project<sup>4</sup> is

systematically annotating functional elements in the genome, and similar initiatives are emerging in other species, including livestock (Andersson *et al.*, 2015). On this basis it can, for example, be judged whether observed between-breed diversity in a given genomic region is purely neutral and has been generated by genetic drift or is of functional relevance and may have been caused by selection. Making systematic use of such information will allow a shift from a purely statistical assessment of genetic diversity to a more informative functional approach.

### 3 Characterization of within-population diversity

Classical estimators of genetic variability (heterozygosity, F-statistics, etc.) are still commonly used. However, some are not adapted for use with biallelic markers (e.g. number of alleles per locus, which is invariably equal to two for biallelic markers). As the use of SNPs has become more common, so has the use of individual and population genomic indicators of diversity and similarity, such as coancestry and inbreeding (Meuwissen and Goddard, 2001; Keller *et al.*, 2011; Saura *et al.*, 2013; Curik *et al.*, 2014). Some of these indicators make it possible to test whether inbreeding effects are more or less important in specific genomic locations, or whether inbreeding comes from a more or less distant common ancestor (e.g. Ferenčaković *et al.*, 2013). Estimators of genetic variability can also be used in conservation decision-making as a means of optimizing the choice of breeding animals so as to minimize the loss of genetic variability (Oldenbroek, 2007).

In parallel, several methods of estimating present and past effective population sizes have been developed or improved, based either on the correlation between allele frequencies (linkage disequilibrium) or on runs of homozygosity (Sved, 1971; Hill, 1981; Hayes *et al.*, 2003; Waples, 2006; Li and Durbin, 2011; Hillestad *et al.*, 2014). These approaches have been increasingly applied in livestock, including cattle (de Roos *et al.*, 2008;

<sup>1</sup> <http://www.ensembl.org>

<sup>2</sup> <http://www.animalgenome.org/cgi-bin/QTLdb/index>

<sup>3</sup> <http://www.genome.jp/kegg>

<sup>4</sup> <http://www.genome.gov/encode>

## PART 4

Flury *et al.*, 2010), sheep (Kijas *et al.*, 2012), pigs (Uimari and Tapio, 2011), chickens (Qanbari *et al.*, 2010) and horses (Corbin *et al.*, 2010). It should be noted, however, that the widely used approach suggested by Sved (1971) has some methodological shortcomings (Sved, 2008) and is especially sensitive to non-random samples of SNPs (Corbin *et al.*, 2012; Ober *et al.*, 2013).

At the time the first SoW-AnGR was prepared, it was generally considered that because of the limited number of markers available it was more efficient to use genealogical information than molecular information in conservation decision-making (Fernandez *et al.*, 2005). This appears no longer to be the case. Commercial SNP arrays are now affordable and provide estimates of genetic relationships that account for the random segregation and recombination of chromosomes that occur during inheritance from parents to offspring. Because marker-based information provides better estimates of genetic relationships than pedigree data, inclusion of genomic data is likely to increase the efficiency of conservation schemes (Hasler *et al.*, 2011; Toro *et al.*, 2014).

#### 4 Characterization of between-population diversity

Relationships between populations have long been assessed through the estimation of genetic distances, which are often used to construct phylogenetic trees to visually infer genetic relationships. However, a major drawback of reconstructing phylogenetic trees is that the evolution of lineages is assumed to be non-reticulate, i.e. it is assumed that while lineages may diverge, they never result from crosses between lineages. There is therefore a tendency for these methods to be replaced by alternative graphical networks or other approaches such as Bayesian clustering methods or multivariate analysis (Bertorelle *et al.*, 2004). One of the most popular model-based Bayesian approaches in current use is the model-based clustering method developed by Pritchard *et al.* (2000) (STRUCTURE software), although alternatives are available (e.g. Alexander

*et al.*, 2009). The approach uses Monte Carlo Markov chain simulation to assign individuals to a chosen number of clusters (populations), inferring genetic origins without *a priori* knowledge or assumptions. This is a particularly important consideration in livestock populations, where unsuspected admixture may have occurred. The approach is, however, not without limits. For example, inferred clusters may not always be ancestral, but rather related to highly inbred populations ("inbreeding bias") or to populations over-represented in the dataset ("sampling bias") (Lenstra *et al.*, 2012). Multivariate analysis approaches are interesting alternatives to model-based approaches, as they are generally assumption-free methods and are specifically designed for summarizing large and complex datasets into a small number of synthetic variables (Jombart *et al.*, 2010). These various approaches are usually applied to microsatellite or SNP marker information. They have been extensively used in livestock studies, either independently or (because of the complementary information they may provide) in parallel (Muchadeyi *et al.*, 2007; Leroy *et al.*, 2009; Gautier *et al.*, 2010; Kijas *et al.*, 2012). Methods have been developed over the last few years that use dense haplotype data to unravel fine-scale population structure (Lawson *et al.*, 2012) or apply advanced admixture analysis in order to infer the presence and historical timing of admixture events among human populations (Patterson *et al.*, 2012; Pickrell and Pritchard, 2012; Hellenthal *et al.*, 2014).

Recently, a growing number of methods for combining genomic information with information from other sources, often related to the environments where animals are raised, have been developed (Pariset *et al.*, 2012). Landscape genomics is an approach that aims to use various methods (e.g. estimation of molecular distance, Bayesian and multivariate analyses) to identify environmental factors that shape genetic variability. For example, a study on Vietnamese goats showed that social organization and husbandry practices were as important as geographical distance in shaping genetic structure (Berthouly *et al.*, 2009). The increasing density of markers genotyped may also allow these approaches to be used to identify chromosomal

regions and genes likely to be subject to positive selection linked to the environment. Finally, knowledge of the history of livestock populations has greatly increased in the last ten years, based on the development of new methods and the increasing availability of large sets of markers (see Part 1 Section A). For instance, a recent study on horse breeds (Wallner *et al.*, 2013) showed that the diversity of the paternally inherited Y-chromosome was very low in comparison to that of maternally inherited mitochondrial DNA haplotypes, a finding consistent with the disproportionate use of a limited number of popular stallions over recent centuries. Genome-wide panels of markers also make it possible to discriminate areas of the genome whose variation has increased or decreased through history in relation to specific gene function.

## 5 Molecular tools for targeting functional variation

Recent advances in genomics have clearly improved our capacity to characterize functional variation in livestock species. Detection and mapping of QTLs, i.e. markers physically linked to a genomic variant that underlies variation in a quantitative trait, have benefited from increased genome coverage, as well as from the development of new methodologies. In particular, the use of sequence data may allow causative polymorphism to be targeted directly instead of via QTLs. The molecular background of various breed-specific traits has been the subject of numerous investigations (Table 4B1) (see also Box 4B3). The molecular analysis of adaptive variation has also improved knowledge of the possible adverse effects of selection on the health and productivity of animals. For example:

- Several gene variants are pathogenic or confer sterility in homozygous animals. For instance, myostatin deficiency caused by mutations in the *MSTN* (myostatin) gene hinders the delivery of calves (Bellinger *et al.*, 2005).
- Gene variants exhibiting clear antagonism between milk yield and fertility (increasing

the former while decreasing the latter) have been identified in cattle (Kadri *et al.*, 2014).

- The use of only a few top sires promotes inbreeding and thus increased homozygosity. This effect, which inevitably increases the proportion of offspring that have recessive genetic defects, can be assessed using neutral genetic markers (Lenstra *et al.*, 2012). Several pathogenic mutations in livestock species, most of which are recessive, have been identified. They surpass in number the gene variants known to be involved in economic traits (Nicholas *et al.*, 2012).
- Significant deficiency or complete absence of individuals homozygous for a given haplotype may indicate the presence of a recessive genetic defect causing early embryonic mortality. This concept has been successfully used in the identification of possible causes of reduced fertility in various cattle populations (Fritz *et al.*, 2013).

International consortia have provided large amounts of data on SNPs and other variants. For example, the “1 000 bull genomes project” (Daetwyler *et al.*, 2014) identified 28.3 million variants, related, *inter alia*, to coat colour, embryonic loss and production traits. However, it is still difficult to obtain genome sequences for a large number of animals at an affordable price. Methods have therefore been developed that can be used to “impute” or infer the genotypes of individual animals for which information is sparse (e.g. obtained using low- or medium-density SNP chips) from information on a subset of individuals that have been sequenced (e.g. those studied in the above-mentioned 1 000 bull genomes project) (Jansen *et al.*, 2013).

Although the study of animal genetic diversity has typically concentrated on direct differences in genomes, the impact of genetic diversity on the expression of genes may be relevant, especially as interest grows in functional genetic diversity relative to neutral genetic diversity. Since the mid-1990s, the widespread use of DNA microarrays and serial analysis of gene expression (SAGE), both of which provide a snapshot of actively expressed

## PART 4

## Box 4B3

**How genetic tools helped to solve the mystery of the origin of the Booroola gene**

Exceptionally high litter size in an Australian Merino flock kept at the Booroola Estate in Cooma, New South Wales, attracted the attention of scientists from the Australian Commonwealth Scientific and Industrial Research Organization (CSIRO). Initial analysis of ewes' pedigrees and performance records led to a hypothesis regarding the segregation of a major gene affecting this trait and increasing litter size in carriers. This hypothesis was first substantiated by analysis of litter-size segregation in families (Piper and Bindon, 1982). The origin of the high-fecundity gene in the low-prolific Merino population, however, remained a mystery until Professor Helen Newton Turner found evidence that ancestors of the Booroola flock could have had some admixture of Indian Bengal sheep brought to Australia from Calcutta in the 1790s (Turner, 1983). The hypothetical major gene increasing litter size was named Fecundity Booroola (*FecB*).

The first genetic markers linked to the *FecB* locus were discovered by a New Zealand team led by Professor Grant Montgomery (Montgomery, 1993). Further research led to the conclusion that the Booroola gene is located on the sixth chromosome. The first molecular test, devised to enable the introgression of the *FecB* mutation into the Romney breed, was based on the polymorphism of three microsatellite sequences (Lord *et al.*, 1998).

The real breakthrough with respect to the physiological basis for increased fecundity happened in 2001, when teams from AgResearch (New Zealand), INRA (France) and Edinburgh University (United Kingdom) independently discovered that carriers of the Booroola gene have a mutation in the bone morphogenetic protein receptor 1B gene (*BMPR-1B*). The Booroola gene (*FecB*) is a dominant autosomal gene with an additive effect on ovulation rate.

**Garole sheep of Bengal**

Photo credit: Kanhaiya M. Chavan.

The discovery of the mutation and the development of the molecular test enabled the identification of the mutation in the Garole sheep of Bengal, a breed that is well known for its large litter sizes – thus supporting Professor Turner's theory. At present, the *BMPR-1B* mutation has been found in a number of breeds that have high fecundity. The list includes Javanese Thin Tail sheep (Davis, 2009) and some Chinese breeds such as the Huyang, Small Tail Han (STH), Cele, Duolang and Chinese Merino (Hua and Yang, 2009). It seems that the original mutation took place in Mongolian Fat Tail sheep and was introgressed into Chinese breeds and later into the Indian Garole and Javanese breeds as a result of the movement of people and animals along the Silk Road.

So the mystery was solved thanks to the persistence of scientists and development of technology. Over time, the *FecB* mutation has been introgressed into about 40 breeds, all around the world (Walkden-Brown *et al.*, 2008).

Provided by Elżbieta Martyniuk.

genes and transcripts in a biological sample, has facilitated high-throughput molecular studies of the transcriptome. Microarray experiments

provide a cost-effective means of studying the transcriptome, and the bioinformatic and statistical analyses (referred to as "analysis pipelines")

TABLE 4B1

**Examples of non-disease phenotypes specific to one or more livestock breeds**

| Species/breed(s)                        | Phenotype                      | Gene or locus                                       | Reference   |
|---|--------------------------------|---|---|
| <b>Cattle</b>                           |                                |   |   |
| French                                  | Dairy traits                   | Several candidate genes                             | Flori <i>et al.</i> , 2009                              |
| Several                                 | Dairy and beef traits          | Several candidate genes                             | Rothammer <i>et al.</i> , 2013                          |
| Danish Red                              | High milk yield, low fertility | Deletion removing <i>RNASEH2</i> *                  | Kadri <i>et al.</i> , 2014                              |
| Several                                 | Milk protein content           | <i>ABCG2</i> +                                      | Braunschweig, 2010                                      |
| Several                                 | Muscular hypertrophy           | <i>MSTN</i> * (different mutations)                 | Nicholas and Hobbs, 2012; O'Rourke <i>et al.</i> , 2013 |
| Holstein                                | Stature                        | <i>PLAG1-CHCHD7</i> intergenic                      | Karim <i>et al.</i> , 2011                              |
| Dexter                                  | Short stature                  | <i>ACAN</i> #                                       | Cavanagh <i>et al.</i> , 2007                           |
| Dutch Belted<br>Galloway<br>Swiss Brown | Belted pattern                 | <i>HES1</i> (candidate gene)                        | Drogemuller <i>et al.</i> , 2010                        |
| <b>Sheep</b>                            |                                |   |   |
| Several                                 | Litter size                    | <i>GDF9</i> * ( <i>FecG</i> , different mutations)  | Vage <i>et al.</i> , 2013                               |
| Several                                 | Litter size                    | <i>BMP15</i> * ( <i>FecX</i> , different mutations) | Nicholas and Hobbs, 2012                                |
| Several                                 | Litter size                    | <i>BMPR1B</i> (Booroola, <i>FecB</i> )              | Davis <i>et al.</i> , 2006                              |
| Lacaune                                 | Litter size                    | <i>B4GALNT2</i> ( <i>FecL</i> )                     | Drouilhet <i>et al.</i> , 2013                          |
| Texel and others                        | Muscular hypertrophy           | <i>MSTN</i> (= <i>GDF8</i> )                        | Clop <i>et al.</i> , 2006                               |
| Dorset                                  | Muscular hypertrophy           | <i>CLPG</i> *                                       | Braunschweig, 2010                                      |
| <b>Pig</b>                              |                                |   |   |
| European                                | Muscle growth                  | <i>IGF2</i>   | Braunschweig, 2010                                      |
| <b>Horse</b>                            |                                |   |   |
| Quarter                                 | Type I muscle fibres           | <i>MSTN</i>   | Petersen <i>et al.</i> , 2013                           |
| Several                                 | Endurance                      | <i>GYS1</i> #                                       | McCoy <i>et al.</i> , 2014                              |
| <b>Chicken</b>                          |                                |   |   |
| Several                                 | Naked neck                     | <i>BMP12</i>  | Mou <i>et al.</i> , 2011                                |
| Several                                 | Frizzle feather                | <i>KRT75</i>  | Ng <i>et al.</i> , 2012                                 |
| Several                                 | Silky feather                  | <i>PDSS2</i>  | Feng <i>et al.</i> , 2014                               |
| Several                                 | Comb shape                     | <i>MNR2</i>   | Imsland <i>et al.</i> , 2012                            |

Note: Several mutations may already have played a role in more general adaptation to domestication (see Part 1, Section A, Table 1A2).  
 # causative gene variant is pathogenic or confers sterility if homozygous; \* recent gene mutation; + ATP-binding cassette, sub-family G (WHITE), member 2.

Sources: Braunschweig, 2010; Nicholas and Hobbs, 2012.

used to transform raw microarray data into interpretable results are now well established (Ritchie *et al.*, 2015). Since the time the first SoW-AnGR was prepared, the development of high-throughput sequencing in the field of transcriptomic analysis (RNA sequencing or RNA-seq) has led to radical changes (Mortazavi *et al.*, 2008), primarily

because RNA-seq approaches do not necessarily require prior knowledge of a genome sequence or annotation (identification of locations and functions of coding regions within a genome) and can therefore be used even in poorly characterized organisms. In addition, it enables a wide range of novel applications, including detection

## PART 4

of weakly expressed genes and alternative splicing isoforms (variations in the proteins translated from the same gene) (Wang *et al.*, 2008; Pan *et al.*, 2008), variable assembly of transcripts (Trapnell *et al.*, 2010; Guttman *et al.*, 2010; Robertson *et al.*, 2010; Grabherr *et al.*, 2011; Schulz *et al.*, 2012) and allele-specific expression (Skelly *et al.*, 2011).

Recent comparisons have indicated good overall agreement among results obtained using microarrays, quantitative PCR (polymerase chain reaction) and RNA-seq across different sequencing platforms (Zhao *et al.*, 2014; Trapnell *et al.*, 2013; Nookaew *et al.* 2012; Liu *et al.*, 2011). However, although microarrays and RNA-seq are both used to characterize transcriptional activity, the experimental, bioinformatic and analytical steps associated with the two differ considerably (Oshlack *et al.*, 2010). In particular, RNA-seq experiments generate much more data than alternative transcriptomic approaches and require more sophisticated analyses and therefore greater technical capacity in bioinformatics and biostatistics (e.g. Langmead and Salzberg, 2012; Grabherr *et al.*, 2011; Oshlack and Wakefield, 2009; Zhou *et al.*, 2014). The analytical processes of transcriptomics constitute a major area of research in bioinformatics and statistics.

In recent years, studies using RNA-seq to examine genetic variation in gene expression have been undertaken in cattle (Li *et al.*, 2011), chickens (Endale Ahanda *et al.*, 2014; Davis *et al.*, 2015) and pigs (Corominas *et al.* 2013; Fischer *et al.*, 2015). The objectives of these studies have included the identification of candidate genes influencing phenotypic differences and the study of differences in gene expression associated with specific SNPs.

## 6 The role of bioinformatics

The successful use of high-throughput technologies in the study of genetic diversity is largely contingent on the availability of support and expertise in bioinformatics and statistics. Increasingly large and complex datasets need to be

understood, organized, quantified, and analysed. Developing and applying the methods and software tools needed to do this requires appropriate computing resources (including sufficient computational power and memory to store and manipulate large data files) and programming skills. For example, genome sequencing and RNA-seq studies often require the services of a dedicated bioinformatics team to pre-process the data, including raw-data quality control and sequence alignment or assembly, in addition to biostatisticians for eventual data analysis. Bioinformatic support is often also an integral part of the development, maintenance and interrogation of biological databases.

An increasing number of well-documented and open-access bioinformatics and statistical tools are available online. For example, the Bioconductor project<sup>5</sup> is an open-source open-development software project that develops and provides widespread access to a diverse set of well-documented statistical and graphical analysis tools (written in the R programming language) for high-throughput genomic data. In addition, an increasing number of free and publicly accessible resources (e.g. the Galaxy project,<sup>6</sup> an open web-based platform) are available to facilitate bioinformatic analyses without the need for extensive programming knowledge.

It is highly desirable that when researchers gather large-scale genomic data for a given project they make them freely available to other researchers once the initial analyses have been completed. Increasingly, scientific journals and research-funding organizations request that data underlying publications or generated in publicly funded projects be deposited in open repositories. This kind of open-source policy will generate a large quantity and variety of reference data, across species and breeds, that can be used for increasingly comprehensive and informative diversity studies.

<sup>5</sup> <http://master.bioconductor.org>

<sup>6</sup> <http://galaxyproject.org>



## 7 Conclusions and research priorities

The world of genetics has been revolutionized over the last decade with the advent of massive parallel sequencing and high-throughput genotyping technologies. Other technologies and opportunities are on the way (see Box 4B4). These developments have opened many opportunities to utilize molecular techniques in the management of AnGR. However, while these technologies facilitate the sequencing of complete genomes or the genotyping of high-density SNP panels at moderate cost, they have not completely replaced traditional molecular markers such as microsatellites, mainly because of their still relatively high costs and the additional skills needed to analyse the enormous amount of data they produce. Low-cost alternatives, such as low-density SNP panels, that allow genetic variants scattered across the genome to be queried and can feasibly be used in small and medium-sized laboratories are in development, but remain to be implemented in practice.

Understanding of genetic diversity needs to be improved, even in the most widely used livestock species. For example, comprehensive assessments of genetic diversity using molecular genetic markers need to be extended to locally adapted breeds, particularly those with small population sizes. The value of the large quantities of data that currently exist in fragmented form needs to be maximized (e.g. by undertaking meta-analyses and by making as much data as possible publicly available for use by breeders, researchers and policy-makers). Improvements in sequencing and genotyping technologies have already provided standards that can be used as references for further genotyping and sequencing studies. Reference genomes, biological background information and population genotypic data are still not available for some species, but sequencing efforts currently underway in laboratories around the world will soon fill these gaps. For most populations and production systems, taking full advantage of the opportunities that

### Box 4B4

#### What are the promises of the post-genomic era?

Over the last twenty years, the use of molecular tools has acquired paramount importance in animal breeding through the development of genetic tests, as well as the implementation of genomic selection in a growing number of species. The role of molecular tools is expected to continue expanding. Potential developments include:

- increased use of whole-genome sequencing for genomic selection, identification of new functional variants (allowing selection on new traits) and analysis of genetic diversity;
- the use of epigenetics (see Box 4B5) in the study of environment  $\times$  genome interactions to provide insight into complex traits, especially those related to development;
- the use of meta-genomic studies that consider the gut microbiome to enable the optimization of the rumen microbial ecosystem for better feed-conversion efficiency; and
- combining genomics with other advanced biotechnologies, such as *in vitro* embryo transfer (selecting breeding candidates at the embryo stage) and genetic engineering (introducing genes of interest into the genome or even directly editing the genome through novel technologies such as the CRISPR/Cas system), which may bring about major changes in the way animals are raised and selected.

Some of these developments would, clearly, raise social and ethical concerns that would need to be addressed before putting them into practice.

Sources: Gonzalez-Recio, 2012; Hayes *et al.*, 2013.

advances in genomics have created for the study of genetic diversity will also require new and additional phenotypic data.

Understanding of the genetic basis of adaptive traits also needs to be improved. Potential approaches include the use of new technologies, such as genome sequencing and geographic



## PART 4

## Box 4B5

**The reality and promises of epigenetics for animal production**

The term “epigenetics” refers to mechanisms that cause variation of gene activity and are based not on variation in the nucleotide sequence but on chemical modifications of DNA and chromatin, for instance, affecting the degree of chromatin compaction or the accessibility of regulatory sequences to transcription factors.

Epigenetic processes occur during cell, tissue and organismal differentiation processes such as gametogenesis, embryo genome activation, X-chromosome inactivation and genomic imprinting (the differential expression of certain genes depending on which parent they come from). Epigenetic modifications driven by environmental factors, such as diet, stress and disease, form a molecular memory (transient or permanent) that adapts the organism and programmes signalling and metabolic pathways appropriate for particular conditions. Epigenetic marks are meiotically and mitotically inherited and the epigenome represents an additional level in genotype–phenotype mapping.

As epigenetic variation explains part of the so-called missing heritability (i.e. the part of genetic variation not explained by individual genes), there may be interest in using epigenetics in livestock breeding, for instance through genomic imprinting and metabolic programming (stimulation of early development to influence later physiological outcome). Particularly in cross-breeding schemes, imprinting offers new opportunities to establish dam and sire lines with enhanced production performances and maternal abilities and to produce cross-breeds according to market requirements. The interaction between genetic (breed) and environmental factors such as diets and management practices is key to the use of epigenetics in animal breeding. Extensive knowledge of epigenetic mechanisms and gene regulation will, in future, offer new opportunities in livestock breeding in relation to environment–genome–epigenome interactions.

Provided by Klaus Wimmers.

information systems, in combination with new data-capture methods (e.g. remote sensing, image analysis and mid-infrared technology) and analytical approaches (e.g. landscape genetics approach), to facilitate the identification of signatures of natural selection reflecting local adaptation to diseases and other environmental conditions. This is of particular importance in the light of climate change. There is a need to develop methods for integrating molecular information into conservation and breeding programmes, and these methods need to be adapted to different environmental, agricultural and socio-economic circumstances. Tackling this task will be a challenge and will require substantial additional data (on genotypes, phenotypes and production environments). Greater international collaboration in data collection, analysis and interpretation will be essential.

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## Section C

# Breeding strategies and programmes

## 1 Introduction

This section serves as an update of the overview of the state of the art in genetic improvement methods presented in the first report on *The State of the World's Animal Genetic Resources for Food and Agriculture* (first SoW-AnGR) (FAO, 2007a).<sup>1</sup> The importance of appropriate breeding strategies and programmes is highlighted throughout the Global Plan of Action for Animal Genetic Resources (FAO, 2007b), particularly in Strategic Priority Area 2, Sustainable Use and Development. The material presented in the first SoW-AnGR included an overview of the “context for genetic improvement”, which described both the factors influencing the objectives of breeding programmes (market demands, wider societal concerns about the nature and impacts of livestock production, the need to provide animals suitable for a diverse range of production environments, growing recognition of the importance of maintaining genetic diversity in livestock populations, etc.) and the latest scientific and technological developments in the field. This was followed by a description of the various activities or “elements” that make up a breeding programme and then by a review of the current state of breeding programmes by production system (high input vs. low input) and by species. Much of this material remains relevant. While the livestock sector is continuously evolving (see Part 2), the challenges that breeding programmes have to contend with remain broadly similar to those that existed at the time the first SoW-AnGR was prepared (2005/2006). Similarly,

the basic constituent elements of a typical breeding programme have not changed.

This update largely follows the same structure as that described above for the first SoW-AnGR. Emphasis is given to recent developments, but each subsection aims to provide sufficient background information (where relevant, a short recapitulation of the material presented in the first report) to make it comprehensible, in standalone form, to the non-specialist reader. High-input systems are again treated separately from low-input systems. These terms can be defined in various ways, but for the purposes of this section, “high-input systems” is used to refer to systems in which external inputs such as supplementary feeds, veterinary medicines and advanced breeding and reproductive technologies are relatively easily obtainable and widely used (precise levels of use will depend on the particular circumstances) and “low-input systems” to systems where the use of such technologies is more limited, often because of factors such as inaccessibility, unaffordability, lack of relevant knowledge or lack of organizational capacity. Departures from the structure of the first SoW-AnGR include separate subsections on sheep and goat breeding in high-input systems and the addition of a subsection on rabbit breeding in high-input systems. The issue of breeding in the context of conservation programmes is addressed in Part 4 Section D. As indicated above, the broad context for breeding programmes (trends in the livestock sector) is addressed in Part 2.

<sup>1</sup> FAO, 2007a, Part 4 Section D (pages 381–427).

## PART 4

## 2 Scientific and technological advances

### 2.1 Quantitative genetics

Since the time the first SoW-AnGR was prepared (2005/2006), there have been few technological advances in the field of quantitative genetics. The standard method for estimating breeding values and ranking animals according to their genetic merit continues to be traditional BLUP (best linear unbiased prediction). This method uses phenotypic information on animals and their relatives to predict the genetic potential of each animal. Existing tools for controlling inbreeding in herds and populations (e.g. Meuwissen, 1997) have become more widely utilized. From a given set of selection candidates, these tools allow the selection of a group of parents in which the genetic merit is maximized while a measure of genetic variation (e.g. the average coefficient of coancestry) is constrained.

Many breeding organizations, particularly in the dairy cattle, pig and chicken industries, have long been using mate selection software to minimize the effects of inbreeding in their breeding populations (Weigel and Lin, 2000). Over recent years, the various algorithms have been made more efficient (e.g. Kinghorn, 2011) and their value in the control of genetic defects has been recognized (Van Eenennaam and Kinghorn, 2014). Not surprisingly given the increasing use of genomic information in breeding programmes (see Subsection 2.3 and Subsection 4), software for managing inbreeding in the context of increasingly available genomic data has also been developed (e.g. Schierenbeck *et al.*, 2011).

### 2.2 Molecular genetics

Knowledge of the biology of traits is being enhanced by the availability of an ever increasing amount of genetic information, much of it unavailable only a few years ago. Genotypes can now be obtained much faster and at a lower

#### Box 4C1

#### Reduction of genetic variability and its consequences in cattle breeds

Intensive selection may reduce the genetic diversity of livestock populations even if the number of animals remains high. A study of Holstein, Jersey and Angus cattle (very widely used international transboundary cattle breeds) undertaken by de Roos *et al.* (2008) used single nucleotide polymorphism (SNP) markers to investigate linkage disequilibrium (non-random association between alleles). Information on linkage disequilibrium can be used to trace the evolution of effective population size ( $N_e$ ) over past generations. Several historical episodes of reduction in  $N_e$  were identified, including one 10 000 generations ago – corresponding to the time of cattle domestication – during which  $N_e$  fell to a few thousands. Another reduction occurred over recent generations, during which time effective population sizes fell to close to 100 as a result of the introduction of new breeding techniques.

Low  $N_e$  does not yet seem to have affected the selection potential of widely used transboundary breeds. However, other effects – related to the spread of inherited disorders or to a reduction in fitness associated with inbreeding depression – have been observed. A recent study estimated that in Holstein and Jersey cattle a 1 percent increase in inbreeding, as indicated by pedigree or genomic information, was associated with a decrease of 0.4-0.6 percent of the phenotypic mean for milk, fat and protein yields and an increase of 0.02-0.05 percent for calving intervals. Inbreeding depression can be managed either by minimizing overall inbreeding within the breeding scheme or by targeting specific regions of the genome associated with inbreeding depression.

Based on de Roos *et al.* (2008) and Pryce *et al.* (2014).  
See also Part 1 Section F Table 1F1.

cost than they could just five years ago. A simple biological sample (usually blood, hair, tissue or semen) from an individual animal can be used to determine its entire DNA sequence. Of particular interest are the areas where the sequence differs, at a single point, from that of the common reference sequence for the respective species. Such differences are referred to as single nucleotide polymorphisms (SNPs). Combined with enhanced computational capacity, these developments mean that researchers can analyse the genome for more complex traits than ever previously thought possible. It is likely that genotyping costs will continue to decline and that computational capacity will continue to improve – and that therefore the use of these tools will become ever more widespread in the coming years (see Part 4 Section B).

### 2.3 Gene-based selection

As knowledge of molecular genetics and trait biology has improved, it has been possible to improve breeding programmes through the use of various types of gene-based selection. Most traits of economic importance in livestock are so-called quantitative traits, the phenotypes of which are the result of the combined small effects of many genes. In some instances, however, individual genes can have substantial effects. Molecular genetics can be used to detect the presence of these genes and this information can be used in concert with phenotypic information from animals and their relatives in a process generally referred to as marker-assisted selection (MAS), where “marker” refers to a polymorphic locus either directly responsible for the genetic differences observed or “linked” to the causative locus by being situated nearby on the same chromosome. Most commonly, MAS is applied using linked loci rather than the causative gene, although some accuracy is lost by doing this.

At the time the first SoW-AnGR was prepared (2005/2006), several countries had incorporated MAS into their national breeding programmes for dairy cattle (e.g. Liu *et al.*, 2004; Boichard *et al.*, 2006) and other species. The application of MAS

was judged to be profitable in dairy cattle even with only moderate linkage between the marker and the causative gene. However, for species lacking the complex system of artificial insemination (AI) and progeny testing that is in place for dairy cattle, MAS was considered to be a profitable strategy only in the case of highly informative markers located very close to the causative loci (Boichard *et al.*, 2006).

In recent years, the availability of genomic information has greatly increased and continues to accumulate at a rapid pace. Cost-efficient DNA sequencing methods have facilitated the development of assays that can provide genotypes for tens to hundreds of thousands of SNPs for only a few tens or hundreds of dollars per animal. Thus, nearly all genes with effects on phenotypic traits can be marked by a SNP. It has become possible to apply genome-wide approaches that are more comprehensive than simple MAS based on a few markers.

Researchers have established ways of incorporating information on the genetic make-up of individual animals into breeding programmes for complex traits influenced by many genes, a process known as genome-enabled selection. There are two general approaches to this: genome-enhanced BLUP (Garrick, 2007; VanRaden, 2007; Zhang *et al.*, 2007) and SNP-effect models.

Whereas genetic evaluations based on traditional BLUP utilize average relationships based on animals’ pedigrees, genome-enhanced BLUP utilizes the actual genomic relationship between the animals. For example, with traditional BLUP, two animals with the same sire are assumed to have exactly one-quarter of their genes in common. In reality, this proportion is not a fixed quantity, but rather ranges from zero to one-half. Genome-enhanced BLUP allows this proportion to be estimated more precisely. The approach can be extended – via a method known as single-step genome-enhanced BLUP – to incorporate phenotypes from individuals that are not genotyped (Aguilar *et al.*, 2010; Christensen and Lund, 2010).

## PART 4

Simple genome-enhanced BLUP is based on the assumption that all regions of the genome have an equal influence on the phenotype being evaluated. Although this assumption facilitates the statistical analysis and generally yields satisfactory results, our knowledge of biology tells us that this assumption is not strictly true; only certain genes have actual physiological effects on a given trait. Computational methods such as Bayesian regression allow differential weighting of specific genomic regions that have a particularly large statistical association with the trait of interest, in other words where findings are consistent with the presence of a quantitative trait locus (QTL) affecting the trait.

In SNP effect models, effects on phenotype are simultaneously estimated for all genotyped SNPs in a so-called “training population” for which full phenotypic information is available (Erbe *et al.*, 2010). The output is referred to as a “SNP-key” and can be used to predict the breeding value of animals that are genotyped, but for which no phenotypic data have been recorded. Such predicted breeding values are obtained by summing the estimated effects at each genotyped SNP. To incorporate information from individuals that have not been genotyped, the resulting genomic prediction is “blended” with an estimate of breeding value derived using traditional BLUP. This blended estimate is used as the final genetic index value for each animal.

Another distinction to note is that between high- and low-density genotyping. High-density genotyping involves analysing 50 000 to 1 million SNPs. Low-density genotyping only analyses a few hundred to a few thousand SNPs. The cost of high-density genotyping is more than twice that of low-density genotyping. Costs can be reduced via a process known as “imputation”, in which high-density genotyping is conducted only in a base population of animals that have many descendants (usually AI sires) and the information obtained is then used to develop a system for inferring or deducing the missing information for animals that have been subject only to low-density genotyping. The correlation between

low-density and high-density genotyping has been shown to be approximately 0.95 (Hickey *et al.*, 2012).

If genomic information is used alone (i.e. is based exclusively on historical phenotypic data), the genetic improvement resulting from selection may not exceed that achieved using traditional BLUP with phenotypes for selection candidates (Dekkers, 2007; Muir, 2007). Moreover, because of the effects of selection and recombination, the accuracy of genomic estimated breeding values (GEBVs) decreases as the number of generations from the training population increases. All available phenotypic and genomic information should be incorporated into GEBVs to ensure that they are as accurate as possible.

Studies have attempted to predict GEBVs for one breed based on the phenotypes of a training population belonging to another breed. The value of this approach has been found to be small or non-existent (Hayes *et al.*, 2009a; Erbe *et al.*, 2012). In numerically small breeds that have adequate phenotyping, multibreed genomic selection may, in future, prove to be an interesting option (Hozé *et al.*, 2014), especially for breeds with a shared genetic history. However, in developing countries, a lack of routinely recorded reference populations is likely to be a significant barrier for the foreseeable future (see Subsection 5.3). Development of genome-enabled selection strategies that can alleviate the constraints imposed by low population sizes and limited phenotypic data is therefore a priority.

Genome-enabled selection can be expected to improve the accuracy of EBVs, particularly for young animals for which phenotypic data are not available (Meuwissen *et al.*, 2001). Increasing EBV accuracy proportionally increases the expected rate of genetic gain. Having more accurate EBVs at a younger age allows selection decisions to be made earlier, which reduces the generation interval and increases genetic gain per unit of time.

In general, genome-enabled selection is beneficial because it can be used to increase the accuracy of the EBVs of animals without direct phenotypic measurements. This general rule applies not

only with respect to young animals, but also to sex-limited traits, traits that are difficult or impossible to measure in the live animal, traits measured at the end of an animal's productive life and as yet undetermined traits that are not currently measured but may become important in the future. In the latter instance, data collected in the future could be used to obtain EBVs for animals that are no longer living but from which cryopreserved semen or other germplasm is available. Genetic material from these animals could thus potentially be used to enhance the trait in the *in vivo* population.

Genome-enabled selection has been implemented in some animal breeding programmes, including programmes for pigs and dairy cattle. In pigs, generation intervals are already low, and hence the greatest effect of genome-enabled selection is on the accuracy of selection for traits that are difficult to measure or measured late in life, such as disease resistance (difficult to define and measure systematically), feed efficiency (expensive to measure directly) and longevity (sow longevity is a sex-limited trait that is not recorded until the animal is culled from the herd).

In addition to quantitative traits (and arguably to an even greater degree) the use of genomic information has increased our ability to manage Mendelian traits, i.e. those traits controlled by a single or small number of genes. In particular, genomic approaches have been used to identify causative mutations or genomic regions associated with deleterious recessive traits, and genetic markers have been developed to help eliminate these genetic defects or attempt to fix beneficial traits within a population.

Deleterious recessive traits are often characterized by a completely homozygous chromosomal region that includes the mutation responsible for the defect and flanking regions on either side of it. Such completely homozygous regions can be relatively simply detected by sequencing or genotyping a small group of affected animals (even as few as ten) and comparing their genotypes to those of unaffected animals (Charlier *et al.*, 2008). For example, in dairy cattle, a rare recessive genetic defect affecting cow fertility has

been identified in the Holstein breed. The defect, known as brachyspina syndrome, is caused by a 3.3 kb (kilo base pair) deletion in the so-called *FANCI* gene (Charlier *et al.*, 2012). Despite the low incidence of brachyspina syndrome (thought to be less than 1 in 100 000), the frequency of the carrier state may be greater than 7 percent. The large discrepancy between the low incidence and relatively large percentage of carriers is accounted for by the fact that almost all homozygous mutant calves die during pregnancy. Identifying this mutation would not have been possible without state of the art genomic tools. Producers can now select against animals carrying a single copy of the gene and thereby improve fertility in the Holstein breed.

Arachnomelia is a monogenic recessive defect affecting skeletal development in cattle. The causative mutation, mapped to chromosome 5, was identified using array-based sequence capture and parallel sequencing technologies (Drögemüller *et al.*, 2010), state of the art genomic tools at the time. A healthy, partially inbred cow known to be carrying one copy of the mutation was re-sequenced and a single heterozygous position was identified. As in the case of brachyspina syndrome, homozygous recessive offspring die before birth, which negatively affects fertility. Again, animals carrying the gene can be selected against in order to improve the fertility of the population.

Genomic information can also be utilized to correct pedigree errors (Seroussi *et al.*, 2013) and reconstruct pedigrees when parentage data have not been recorded (Kirkpatrick *et al.*, 2011). Using genomic information in this way not only increases the accuracy of genome-enhanced BLUP (Munoz *et al.*, 2014), but can also improve traditional BLUP EBVs. Correcting pedigree errors allows more accurate understanding of the true relationships among individuals in the herd. This is important when establishing contemporary groups to estimate breeding values.

## 2.4 Reproductive technology

The state of the art in the use of reproductive technologies has not changed greatly in recent

## PART 4

## Box 4C2

**Genetically modified animals in agriculture**

Technologies related to genetic modification (GM) have advanced significantly in recent years. Classical gene transfer techniques have been complemented by new tools such as genome editing, a technique that allows the identification and modification (small insertions or deletions) of a specific DNA sequence instead of the insertion of a foreign DNA sequence into the cell (Carlson *et al.*, 2013).

Many transgenic animals have been developed, both for biomedical purposes (production of biomolecules, xenotransplantation, medical models, etc.) and for potential use in agriculture, including in the improvement of economically important traits such as growth rate, wool growth, feed conversion, milk composition, meat quality, disease resistance and survival. One example is the development of a transgenic chicken expressing a short-hairpin RNA (an RNA sequence whose structure can be used to silence the expression of specific genes) that interferes with H5N1 propagation and thereby confers resistance to avian influenza (Lyall *et al.*, 2011).

In comparison to conventional breeding, transgenic strategies may allow faster introduction of new alleles and genes of interest. However, the production of GM animals is labour intensive and costly. Moreover, unforeseen negative pleiotropic side effects (when a

gene influences multiple unrelated phenotypes) are a possibility. It also has to be borne in mind that genetic progress often involves a multiplicity of genes and that in such cases transgenesis is of little interest.

In a large majority of cases, the development of GM animals for potential use in food production is only at the research stage. A few cases are close to final approval. As yet, no GM animals have been approved for commercial use in food production.

There are still many unresolved ethical issues related to the use and development of GM animals, including concerns related to the invasiveness of procedures and their effects on welfare and health and those related to intellectual property issues. Attitudes towards GM animals vary from country to country. In Europe, for example, the development of GM animals is subject to many restrictions. However, some developing countries have adopted a more permissive approach. For instance, Argentina and China have invested massively in the development of GM animals for food production. Such animals may play a growing role in the coming years. The extent to which this occurs is likely to depend on consumer attitudes to the use of GM technology.

For more information see Forabosco *et al.*, 2013; Jonas *et al.*, 2014.

years, at least in terms of application in the field. One area of advancement has been increased commercial use of semen sexing, predominantly in cattle and particularly in dairy cattle (see Boxes 3E6 and 3E7 in Part 3 Section E). This process involves the use of a molecular biology technology known as flow cytometry to sort X and Y sperm cells (Johnson and Welch, 1999). The obvious advantage is that sexed semen can be used to obtain offspring of the desired sex (more than 90 percent accuracy can be achieved). This allows the rate of genetic improvement to be increased, as selection intensity can be increased and the generation interval shortened. Given that

in some production systems young animals of the undesired sex often suffer from neglect, the use of sexed semen can also indirectly enhance animal welfare.

Challenges associated with the use of sexed semen include a slight decline in conception rate (a fall to 80 or 85 percent of the rate obtained using conventional semen) and the fact that sexed semen is not available from all potential sires (Van Doormaal, 2010). These challenges are likely to be overcome as more experience is gained in the use of sexed semen and as companies make sexed semen routinely available for all sires. Another challenge is that semen sexing does

not work well in all species. In cattle, for example, overall semen and sperm volumes are low and the technology works well. Pigs, however, have relatively large semen and sperm volumes, which means that a lot of time (up to a day per sample) is needed to sort a single semen collection into X and Y sperm cells. To enable widespread use of semen sexing in this species, flow cytometry technology will need to be improved so as to allow sorting to be done much more quickly, as many commercial boar studs collect semen from as many as 100 boars in a day.

Reproductive technologies targeting the female animal (multiple ovulation, embryo transfer, *in vitro* fertilization and cloning) have been available for most major livestock species for some time (all had already been developed at the time the first SoW-AnGR was prepared – 2005/2006). Active research into these technologies continues to improve their success rates and their efficiencies, hence decreasing their costs. Nevertheless, cost remains a major constraint to their more widespread use. Genomic developments could, however, help change this. As discussed above, genome-enabled BLUP and related approaches have increased the accuracies of EBVs. In particular, the EBVs of female animals, especially young females, have become more accurate. This improved accuracy has increased the monetary value of the best females (Pryce *et al.*, 2012). In theory, this increases the expected return on investments in reproductive technologies that increase the number of offspring per female.

Cloning and genetic modification (GM) have been available for many years, but have not gained widespread commercial use. This is largely for economic reasons, but there are also potential ethical concerns. Among livestock species, cloning is most frequently undertaken in horses, where individual animals can have extremely high values because of their earning potential in racing and other riding competitions. Since the first SoW-AnGR was prepared, technologies involving “genome editing” have been developed. These techniques tend to be much more efficient than more traditional GM approaches. Moreover, as genome editing does not involve

transfer of genes across species, it may also raise fewer ethical questions. Research on this technology is increasing and has the potential to have a significant effect on animal production and the management of AnGR (see Box 4C2).

### 3 The elements of a breeding programme

Genetic improvement strategies fall into three main categories: selection between breeds; selection within breeds or lines; and cross-breeding. The choice of which strategy to pursue will depend on the characteristics of the production system and of the types of animal available (i.e. already present in the local area or potentially introduced). To reduce the risk of costly failures, any options under consideration need to be thoroughly assessed. Detailed advice on planning a breeding strategy is provided in the FAO guidelines *Breeding strategies for sustainable management of animal genetic resources* (FAO, 2010).

All within-breed selection programmes (straight-breeding programmes) have a number of common elements. Setting up a breeding programme involves defining a breeding goal and the design of a scheme that is able to deliver genetic progress in line with this goal. This requires, *inter alia*, the identification of selection criteria, recording of animals’ performances and pedigrees, genetic evaluation, selection and mating, progress monitoring and dissemination of genetic improvement.

A breeding goal is a list of traits to be targeted by the breeding programme, including their relative importance, and a description of how they should be changed genetically (increased, decreased or maintained the same). Breeding goals inevitably shift over time in response to the changing requirements of livestock producers and ultimately the demands of consumers and society at large. For many years, production traits were the primary target. Later, traits affecting function such as longevity, health and reproductive ability were added, as it was observed that selection for production had led to deterioration in these



## PART 4

traits. Today, as a result of societal pressures, increasing attention is being given to behaviour, well-being and other novel traits. For example, in response to the elimination of gestation stalls in pig husbandry, the breeding industry has started to select for more docile sows, which it is hoped will be more tractable in situations where animals are housed in groups during gestation.

As breeding objectives become broader, breeders increasingly have to deal with antagonisms between different sets of traits. When the genetic correlation between two traits is favourable, selecting for one trait can bring a correlated beneficial response in the other trait. However, when traits are antagonistically correlated, selecting for one trait will lead to an undesirable response in the other. In such cases, it is common practice to include both traits in the selection objective and select animals with desirable attributes for both traits. This strategy allows all traits to be improved over time (Neeteson-van Nieuwenhoven *et al.*, 2013). Typically, the most efficient way to select for multiple traits is to combine them into a “selection index” (Phocas *et al.*, 2013). Traits are weighted according to index coefficients that consider the economic importance of traits and their genetic relationships and maximize the correlation between the selection index and the breeding goal.

The outcomes of breeding programmes, particularly in species with long generation intervals, are realized many years after selection decisions are made. Even in poultry, a genetic change implemented in a breeding nucleus will take at least three years to have a noticeable effect at commercial level. This underlines the need to anticipate future demands when defining breeding goals. Breeders and breeding organizations need to be tuned into societal pressures and how they are likely to affect future demand.

Animal identification and the recording of animals’ performance and pedigrees are the driving forces of genetic improvement. Detailed advice on the development of animal recording systems is provided in the FAO guidelines on the *Development of integrated multipurpose animal*

*recording systems* (FAO, 2015). Abundant and accurate measurements lead to efficient selection. As described above (Subsection 2), developments in the field of genome-enabled selection are creating significant new opportunities to improve animal breeding. A key prerequisite is to have sufficient phenotypic information recorded for the traits that potentially benefit the most from the use of this technology (e.g. health traits, sex-limited traits and traits that are difficult or impossible to measure in live animals).

Genetic evaluation is the process of determining which animals have a superior genotype for the traits of interest so that decisions can be taken as to which animals should be used to breed the next generation. As performance is influenced both by the animal’s genetics and by its environment, genetic evaluation involves separating environmental components from genetic components. As described above in Subsection 2, genetic evaluation methods based on information on the performance of animals and their relatives are now being supplemented by methods that involve the use of molecular genetic information. The extent to which these new methods have moved beyond the research level and into commercial production varies from species to species (see Subsection 4 and also Part 3 Section E).

Capacity to store performance and pedigree data for use in genetic evaluations is continuously increasing as more sophisticated computer hardware becomes more widely available. It is likely that technology will continue to improve and that capacity to run yet more complex genomic evaluations will not be limited by hardware availability. The greatest limitation may prove to be a lack of progress in the development of software for these types of analysis because of a lack of trained personnel in the field of animal breeding and genetics and a lack of labs working on the development of the specialized software required.

Family information in genetic evaluation increases the probability of co-selecting close relatives, which in turn leads to increased inbreeding. Various methods are used to reduce inbreeding



while maintaining high rates of genetic gain. All are based on the principle of 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 (Weigel and Lin, 2000). Other mating rules or methods for reducing the accumulation of inbreeding in a population were outlined in the first SoW-AnGR<sup>2</sup> (see also Part 4 Section D and FAO, 2013). These rules have been utilized in commercial poultry and pig breeding to maintain inbreeding at relatively low levels. Many breeding companies have moved towards using programs such as “Mate Select” to control inbreeding more systematically.

The progress achieved in a breeding programme is usually assessed by regressing average phenotypic and breeding values on year of birth. In addition, 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. Frequently, companies test their products against those of their competitors.

The impact of a breeding programme depends on the dissemination of genetic progress to customers or into the wider livestock population. Reproductive technologies, particularly AI, play an important role in many species. They allow genetic material to be transported around the world and greatly increase the number of offspring that can be obtained from a superior breeding animal. As discussed above (Subsection 2.3), recent years have not seen major technological advances in this field. However, the use of reproductive technologies is becoming more widespread in many countries (see Part 3 Section E).

Despite the ever-increasing sophistication of breeding technologies, it is important to recall

that all the elements of a breeding programme can be implemented even under very basic conditions. Success is possible without the use of elaborate data recording and genetic evaluation systems, without genomic tools and without the use of reproductive technologies (see Subsection 5 for further discussion of breeding programmes in low-input systems).

## 4 Breeding programmes in high-input systems

### 4.1 Dairy and beef cattle

The characteristics of the cattle breeding industry highlighted in the first SoW-AnGR<sup>3</sup> included:

- a relatively decentralized structure (compared to the pig and poultry sectors), with different organizations performing complementary tasks in the breeding scheme (identification, performance recording, genetic evaluation, selection and commercialization of genetics), the most distinctive feature being the role played by commercial producers in the provision of data used in genetic evaluation;
- (in the dairy sector) a historical emphasis on production traits (milk yield and components) that had led to a great increase in milk output, but also to a deterioration in so-called functional traits, i.e. those related to the animal's health and fertility; this had led breeding organizations to increase the weight of functional traits in selection indices;
- (in the beef sector) a focus on increasing growth rates that had caused an increase in calving problems associated with calf size, as well as creating potential fertility problems associated with heifers being unable to meet higher nutritional demands associated with a larger size;
- a need to improve the recording of functional traits, particularly in beef cattle;

<sup>2</sup> FAO, 2007a, page 395.

<sup>3</sup> FAO, 2007a, pages 396–400.

## PART 4

- a lack of capacity to implement direct selection for feed efficiency, resulting from a lack of capacity to obtain feed-intake data for sufficient numbers of animals;
- a lack of market mechanisms that reward producers for improved meat quality;
- (in the beef sector) a lack of well-organized cross-breeding programmes;
- a major role played by breeders' associations, along with significant input from public institutions in terms of data management and genetic evaluation; and
- a trend towards the internationalization of AI companies.

These characteristics have changed little in the years since the first SoW-AnGR was prepared (2005/2006). Decentralization remains a common theme. Ownership of individual animals remains with private livestock keepers, particularly in the case of female animals, although there is a general trend towards concentration. Breed associations continue to play a major role. The trend towards globalization continues, both in terms of the organization of AI companies and the use of breeds in a transboundary manner. Cross-breeding is a routine practice in dairy cattle as a means of increasing profitability by improving functionality and fitness. As discussed in more detail below, the adoption of genomic selection has been nothing short of revolutionary. The evaluation, acquisition and marketing of AI bulls have been transformed, with a much greater emphasis now given to younger bulls with no progeny.

The breeding objectives listed in the first SoW-AnGR<sup>4</sup> are still relevant to most selection programmes worldwide, but some changes have occurred. In many countries, selection indices for dairy cattle have been adjusted so as to reduce the emphasis given to production traits and to accentuate functional traits such as fertility, longevity and udder health. The major obstacle to including more health traits and novel traits such as feed efficiency in selection programmes is a lack

of reliable phenotypic records, either because of logistical problems or because of high costs. The automation of milking procedures has become significantly more widespread during the past decade and is generating a large volume of new records that could potentially be used to expand the portfolio of traits evaluated. The practice of breeding companies establishing contracts with the owners of large herds to collect data on novel traits is foreseen to become more common in the future and to play an increasingly important role in genetic evaluation of these traits. These practices may increase the accuracy of genetic evaluation, but perhaps only for the specific standardized environment in which they are recorded. In beef cattle, growth and carcass traits continue to be the main selection objectives, although calving and fertility traits are receiving increasing attention. Difficulties with reliable recording are even more acute in beef than in dairy operations. Assessing the sophisticated carcass classification data collected by slaughterhouses (e.g. the EUROP carcass classification system)<sup>5</sup> for genetic evaluation purposes would improve the selection process. However, it would require a consistent animal identification infrastructure, from birth to slaughter (or, perhaps, much more widespread reliance on DNA-based measures of animal identification and genetic relationships) that would allow the development of consolidated databases. Current breeding objectives in dairy and beef cattle are summarized in Tables 4C1 and 4C2.

The development of technologies that allow fast, accurate and affordable determination of SNPs has enabled the AI industry to make efficient use of genetic markers for selection purposes and represents the most significant advance in cattle breeding since the adoption of AI (see Subsection 2 for a general description of the role of genetic markers in animal breeding). The completion of the bovine genome sequence and reference assembly (Elsik *et al.*, 2009) enabled the

<sup>4</sup> FAO, 2007a, Table 99 (page 397).

<sup>5</sup> See Commission Regulation (EEC) No 2930/81 of 12 October 1981 adopting additional provisions for the application of the Community scale for the classification of carcasses of adult bovine animals (available at <http://tinyurl.com/qejooac>).

TABLE 4C1  
Selection criteria in dairy cattle

| Traits              |                     | Comments   |
|---------------------|---------------------|--|
| Production traits   | Milk quantity       | More frequently the quantity of protein and/or fat   |
|                     | Milk quality        | Concentration of protein and/or fat  |
|                     | Feed efficiency     | Rarely measured directly   |
| Reproduction traits | Conception rate     | For males, it may be calculated based on mates or daughters  |
|                     | Ease of calving     | Often used for mating, rather than selection   |
| Robustness traits   | Survival            | Measured as longevity  |
|                     | Mastitis resistance | Either directly based on incidence or indirectly based on somatic cell concentration in milk and udder conformation of daughters |
|                     | Leg soundness       | Usually based on conformation traits and observed mobility   |
|                     | Body conformation   | Decreased body size has a positive association with feed efficiency and longevity  |

Note: This table updates and expands upon information provided in Table 99 of the first SoW-AnGR (FAO, 2007a).

TABLE 4C2  
Selection criteria in beef cattle

| Traits              |                   | Comments   |
|---------------------|-------------------|--|
| Production traits   | Body size         | Ideal size depends on environment  |
|                     | Growth rate       | Weight at various ages (e.g. birth, weaning, one year of age)  |
|                     | Milking ability   | Measured indirectly based on growth, has an intermediate optimum because high milk production results in waste |
|                     | Carcass quality   | Carcass yield, loin muscle area  |
|                     | Feed efficiency   |  |
|                     | Meat quality      | Marbling (intramuscular fat), tenderness   |
| Reproduction traits | Male fertility    | Measured by using scrotal circumference  |
|                     | Mothering ability |  |
|                     | Ease of calving   | Based on scores provided by breeders   |
|                     | Calving interval  | Seasonal production requires regular yearly calving  |
| Robustness traits   | Survival          | Longevity  |
|                     | Conformation      | Leg soundness is important for function in rangeland conditions  |
|                     | Temperament       | To improve safety and increase ease of management  |

Note: This table updates and expands upon information provided in Table 99 of the first SoW-AnGR (FAO, 2007a).

identification of the several thousands of SNPs used to develop low-cost SNP chips. Genomic screening of a large proportion of the population facilitates the discovery of haplotypes associated with economically important traits such as recessive disorders, reproductive performance, coat colour and polledness. Carriers of such haplotypes

are now regularly identified among genotyped cattle (Table 4C3).

Adoption of genomic selection has been extremely rapid in the dairy sector and has already replaced the progeny testing schemes that were the state of the art for several decades. Males, and a rapidly increasing number of females, are

## PART 4

TABLE 4C3

**Recessive haplotypes tracked in the genomic evaluation system in the United States of America**

| Breed       | Haplo-type | OMIA 9913 ID <sup>1</sup> | Gene name          | Condition/trait  | Frequency (%) | Chromosome | Reference  |
|-------------|------------|---------------------------|--------------------|--|---------------|------------|--|
| Ayrshire    | AH1        | 001934                    | <i>UBE3B</i>       | Conception rate  | 13.0          | 17         | Cooper <i>et al.</i> , 2014, Venhoranta <i>et al.</i> , 2014   |
| Brown Swiss | BH1        | 001825                    | —                  | Abortion   | 6.67          | 7          | VanRaden <i>et al.</i> , 2011                                  |
|             | BH2        | 001939                    | —                  | Abortion   | 7.78          | 19         | Schwarzenbacher <i>et al.</i> , 2012                           |
|             | BHD        | 001247                    | <i>SPAST</i>       | Spinal dysmyelination  | 2.19          | 11         | Hafner <i>et al.</i> , 1993, Thomsen <i>et al.</i> , 2010      |
|             | BHM        | 000939                    | <i>KDSR (FVT1)</i> | Spinal muscular atrophy  | 3.61          | 24         | El-Hamidi <i>et al.</i> , 1989, Krebs <i>et al.</i> , 2007     |
|             | BHW        | 000827                    |                    | Progressive degenerative myeloencephalopathy (Weaver syndrome) | 1.56          | 4          | McClure <i>et al.</i> , 2013                                   |
| Holstein    | HBR        | —                         | <i>MC1R (MSHR)</i> | Black/red coat colour  | 0.8           | 18         | Lawlor <i>et al.</i> , 2014                                    |
|             | HDR        | —                         |                    | Dominant red coat colour                                       | 0.04          | 3          | Lawlor <i>et al.</i> , 2014                                    |
|             | HH0        | 000151                    | <i>FANCI</i>       | Brachyspina  | 2.76          | 21         | Agerholm <i>et al.</i> , 2006, Charlier <i>et al.</i> , 2012   |
|             | HH1        | 000001                    | <i>APAF1</i>       | Abortion   | 1.92          | 5          | Adams <i>et al.</i> , 2012                                     |
|             | HH2        | 001823                    | —                  | Abortion   | 1.66          | 1          | VanRaden <i>et al.</i> , 2011, McClure <i>et al.</i> , 2014    |
|             | HH3        | 001824                    | <i>SMC2</i>        | Abortion   | 2.95          | 8          | Daetwyler <i>et al.</i> , 2014, McClure <i>et al.</i> , 2014   |
|             | HH4        | 001826                    | <i>GART</i>        | Abortion   | 0.37          | 1          | Fritz <i>et al.</i> , 2013                                     |
|             | HH5        | 001941                    | —                  | Abortion   | 2.22          | 9          | Cooper <i>et al.</i> , 2013                                    |
|             | HHB        | 000595                    | <i>ITGB2</i>       | Leukocyte adhesion deficiency, type I (BLAD)                   | 0.25          | 1          | Shuster <i>et al.</i> , 1992                                   |
|             | HHC        | 001340                    | <i>SLC35A3</i>     | Complex vertebral malformation                                 | 1.37          | 3          | Agerholm <i>et al.</i> , 2001                                  |
|             | HHD        | 000262                    | <i>UMPS</i>        | Deficiency of uridine monophosphate synthase (DUMPS)           | 0.01          | 1          | Shanks <i>et al.</i> , 1984                                    |
|             | HHM        | 000963                    | <i>LRP4</i>        | Syndactyly (mule foot)   | 0.07          | 15         | Eldridge <i>et al.</i> , 1951, Duchesne <i>et al.</i> , 2006   |
|             | HHP        | 000483                    | <i>POLLED</i>      | Polled/horns   | 0.71          | 1          | Medugorac <i>et al.</i> , 2012, Rothammer <i>et al.</i> , 2014 |
|             | HHR        | 001199                    | <i>MC1R (MSHR)</i> | Red coat colour  | 5.42          | 18         | Joerg <i>et al.</i> , 1996                                     |
| Jersey      | JH1        | 001697                    | <i>CWC15</i>       | Abortion   | 12.10         | 15         | Sonstegard <i>et al.</i> , 2013                                |
|             | JH2        | 001942                    | —                  | Abortion   | 1.3           | 26         | VanRaden <i>et al.</i> , 2014                                  |

Note: <sup>1</sup> Online Mendelian Inheritance in Animals (<http://omia.angis.org.au/>) identification number for *Bos taurus* (National Center for Biotechnology Information species code 9913).

Source: Cole *et al.*, 2015.

genotyped at very young ages and not used as breeding animals if their GEBVs do not meet the selection criteria. In combination with advances in multiple ovulation and embryo transfer (MOET), genomic selection has shortened the generation interval to such an extent that the sires of the currently active AI bulls do not yet have any recorded progeny. The replacement of progeny testing has been a revolution in dairy cattle breeding, but yet another paradigm shift is now taking hold. The relatively low reproductive capacity of cattle and the rates of involuntary culling have traditionally meant that the female offspring from all cows were needed as replacements within a given herd. Therefore, genetic improvement via the dam-of-daughters pathway has been negligible. Now, the combination of sexed-semen technologies and low-density, low-cost SNP chips has increased both the selection intensity and the selection accuracy within this pathway, thus creating a new opportunity for additional genetic improvement.

Because the accuracy of GEBVs is highly dependent on the size of reference populations (Hayes *et al.*, 2009b), even the largest cattle populations greatly benefit from international exchanges of genomic data. Exporting countries took the lead in adopting genomic technologies and formed consortia to share genotypes. Interbull, a subcommittee of the International Committee for Animal Recording (ICAR), has continually adapted its activities to account for the use of genomic information in genetic evaluation. The market has become polarized into two major blocks, the importers and the exporters of genetics. The technological gap between these two blocks has widened rapidly, both because of the investments required and because of a relative lack of expertise in the importing countries. Poor results from multibreed genomic predictions have hindered genomic applications in smaller, non-mainstream, populations and the hegemony of the Holstein has been increasing at a greater speed. The potential uses of genomics are seemingly limitless. New actors coming from sectors not directly related to dairy or beef breeding (e.g. pharmaceutical companies) have started to

take the lead and supply innovative and customized services to dairy breeders in a manner similar to that already pertaining in the poultry and pig industries. Data ownership has become a key issue and control over the genetic-improvement process may shift from breeders to corporations (Dürr, 2013).

Genomic selection has advanced more slowly in the beef sector. This is mainly because of differences in population structure (in dairy breeds, the large number of offspring produced per bull through AI improves the precision of genomic selection), the fact that major production traits such as growth rate can be measured in all animals relatively early in life and the lack of large phenotypic and animal-pedigree databases for beef cattle.

## 4.2 Sheep

The first SoW-AnGR presented an overview of the state of sheep breeding in high-input systems, noting the selection criteria utilized and describing the organization of the breeding sector in different parts of the world.<sup>6</sup> Table 4C4 summarizes the traits most commonly considered in current sheep breeding programmes. While the broad characteristics of the sheep breeding industry remain similar to those described in the first SoW-AnGR, breeding programmes for high-input systems have undergone considerable change in the past decade. Although developments in genomic prediction are exciting and have attracted considerable research investment in a number of countries, structural and economic effects are also very important.

While in general, sheep breeding programmes have typically aimed to improve production and reproduction traits, identification of molecular markers for major genes that directly affect sheep health has led to the incorporation of selection for health traits. Selection for the ARR haplotype at the *PRNP* locus and against the VRQ haplotype has been used in several countries to reduce susceptibility to scrapie (Hunter, 2007). Selection

<sup>6</sup> FAO, 2007a, pages 400–402.

## PART 4

TABLE 4C4

## Selection criteria in sheep

|                     | Traits                    | Comments  |
|---------------------|---------------------------|---|
| Production traits   | Body size                 | Ideal size depends on environment   |
|                     | Growth rate               | Weight at various ages (e.g. birth, weaning, one year of age)   |
|                     | Meat yield                | Proportion of fat in the carcass and lean distribution across carcass regions   |
|                     | Meat quality              | Marbling (intramuscular fat), tenderness  |
|                     | Wool quantity and quality | Fleece weight, fibre diameter, advanced processing characteristics (e.g. coefficient of variation of fibre diameter, staple strength) |
|                     | Milk yield and quality    |   |
| Reproduction traits | Litter size               | Twinning rate, larger numbers of offspring may be detrimental   |
|                     | Mothering ability         | Number of lambs weaned, milk yield, early growth  |
|                     | Weaning rate              | Number of lambs weaned, combining effects of litter size and lamb survival  |
| Robustness traits   | Survival                  | Longevity   |
|                     | Parasite resistance       | Helminths, blowfly strike   |
|                     | Scrapie resistance        | Based on molecular tests  |
|                     | Mastitis resistance       | Trait indirectly selected for based on somatic cell concentration in milk   |
|                     | Udder conformation        |   |

Note: This table updates and expands upon information provided in Table 99 of the first SoW-AnGR (FAO, 2007a).

against day blindness in Awassi sheep is being undertaken via the *CNGA3* locus (Reicher *et al.*, 2010) and resistance to maedi visna infection has been shown to have favourable alleles at the *TMEM154* locus (Heaton *et al.*, 2012).

In the very intensive sheep-farming systems of Europe and the Middle East, where high prolificacy is economically important, use of genetic technologies such as introgression of the *FecB* mutation with the aid of molecular genotyping (Gootwine *et al.*, 2008) and the advent of genomic selection (Larroque *et al.*, 2014) have created substantial opportunities to increase the rate of genetic progress. Breeding programmes for improving milk production traits are in place in several European countries. Most milk recording is carried out in France, Italy and Spain, where large-scale use of AI facilitates breeding work. According to an ICAR survey reported in 2013 (Astruc, 2014), there are about 2 million sheep under recording, almost exclusively in European countries.

The potential to exploit genomic selection is less in small milking ruminants than in dairy cattle breeds such as the Holstein, which have larger values per animal, longer generation intervals in progeny testing schemes, smaller effective population sizes and larger numbers of historical individuals with accurately recorded phenotypes and genotypes. However, because genomic selection simplifies the AI cooperative structure, a shift towards genomic breeding strategies is occurring, at least in some French milking sheep breeding programmes (Duchemin *et al.*, 2012; Larroque *et al.*, 2014) (see Box 4C3).

In the meat and wool sectors, programmes such as the National Sheep Improvement Program in the United States of America<sup>7</sup> and LAMBPLAN<sup>8</sup> in Australia evaluate records of on-farm performance

<sup>7</sup> [www.nsip.org](http://www.nsip.org)

<sup>8</sup> <http://www.sheepgenetics.org.au/Breeding-services/LAMBPLAN-Home>

## Box 4C3

**Adoption of genomic selection in French dairy sheep breeds**

Given the importance of ewe-milk production in France, there is growing interest in implementing genomic selection in dairy sheep breeds. The reliabilities of genomic breeding values for the Lacaune and Blond-Faced Manech sheep breeds are similar to those of the Montbéliard and Normande dairy cattle breeds, as they all have reference populations of a similar size (Duchemin, 2012; Baloché *et al.*, 2014). A simulation study of the Lacaune has indicated that genomic selection could increase annual genetic gain by 15 percent as a result of an increase in the intensity of selection of young rams (Buisson *et al.*, 2014). The simulation predicted that the increased income obtained would compensate for the extra costs of genotyping. Based on this information, Lacaune breeders decided, in 2015, to shift to a genomic breeding programme. It is assumed that genotyping costs will continue to decrease in the future, thus increasing the potential economic benefits of genomic selection. Breeders of the Blond-Faced Manech breed are planning to adopt routine genomic selection in the near future.

records and provide the industry with EBVs for many traits for elite and young rams belonging to a range of breeds. Some EBVs are combined to calculate indexes for specific breeding goals.

Breed shifts and the introduction of composite breed types have been transformational in New Zealand and Australia over recent decades. This has been driven, at least partly, by shifts in focus from wool production to meat production. Interestingly, in New Zealand, although higher performance composites rapidly took substantial market share following the introduction of novel breeds from Europe, much of this market share has since been recovered by breed types (including lower-performance composites) identified by farmers as having higher levels of robustness in breeding ewes. Sheep flocks in New Zealand are

increasingly being forced into harsher production environments due to rapid expansion of the dairy industry (Morris and Kenyon, 2014). The three test sites of the country's central progeny testing structure, widely recognized as a key facilitator of accelerating rates of genetic progress, have recently been supplemented by two additional sites, both of which are commercial farms operating in very harsh production environments.

Despite considerable investment in genomic approaches, there are still challenges to the integration of these technologies into breeding programmes. Both the Australian approach, based on a very large reference population with intensive phenotypic recording, and the New Zealand approach, based on industry sires as the training resource, have produced relatively modest improvements in selection accuracy compared, for example, to those achieved in Holstein cattle (Dodds *et al.*, 2014; Swann *et al.*, 2014). To date, adoption of genomic selection approaches in both countries has been limited to highly progressive breeders who wish to be at the forefront of technology and are content with marginal gains in the rate of genetic progress. Work on how to integrate genomic predictions into novel breeding programme structures and attempts to reduce testing costs per animal and per breeding scheme via two-stage selection strategies (Sise *et al.*, 2011) and combination with reproductive technologies (Granleese *et al.*, 2013) have been identified as keys to increased adoption. Research is also being undertaken into higher-density chips and gene sequences, although there is little evidence of practical benefits. Exploiting the ever-decreasing costs of genome sequencing remains an exciting challenge for the future.

Formal industry structures and coordinated provision of genetic improvement services such as databases and genetic evaluation systems are critical to the success of genetic evaluation systems. However, even where such systems exist, rates of adoption of new technologies may be poor and rates of penetration into the commercial sector by rams from flocks in which the latest technologies are used may be very low (Amer *et al.*, 2007). An

## PART 4

example of steps that can be taken to overcome challenges of this kind is provided in Box 4C4.

### 4.3 Goats

The first SoW-AnGR provided a short review of the state of goat-breeding programmes in high-input systems, noting that such programmes were mainly concentrated in Europe and North America and focused mainly on dairy breeds. Breeding programmes for meat goats were described as being present in a few countries with well-developed goat-meat sectors, such as Australia, South Africa and the United States of America.<sup>9</sup> This overall picture has not changed greatly in the recent years. Well-structured goat breeding programmes are generally found only in developed countries where the production, processing and commercialization of goat products are well organized. Table 4C5 lists the most important traits considered in contemporary breeding programmes for dairy and meat breeds.

All effective goat breeding programmes are based on straight-breeding. They rely on the existence of well-characterized breeds and breeders' associations that can manage herd books and performance-recording systems. As with other

#### Box 4C4

#### Improving the system of sheep breeding in Ireland

In Ireland, a new and modern support structure has been put in place to support sheep breeding. The initial challenge has been to engage with a breeding sector that historically relied on basic phenotypes and physical type traits as primary selection criteria, and to overcome the barrier of having many small breeder flocks with low levels of genetic connectedness among them. A central progeny testing scheme has been established, which originally had the goal of increasing levels of genetic connectedness. More recently, the focus has switched to identifying sires of sires that excel for a balance of maternal and carcass traits (Pabiou *et al.*, 2014). If these sires get used through AI in a large number of flocks that market rams for natural service, it will be possible to multiply the elite genetic material across a substantial proportion of the industry. This strategy is less reliant on widespread uptake of recording by all breeders, for many of whom ram production and marketing is a secondary source of income. In addition, interest is growing in Ireland in the potential of genomic selection, and also imported genetics, to accelerate genetic progress.

<sup>9</sup> FAO, 2007a, page 402.

TABLE 4C5  
Selection criteria in goats

| Traits              |                            | Comments   |
|---------------------|----------------------------|--|
| Production traits   | Body size                  |  |
|                     | Growth rate                | Weight at various ages (e.g. birth, weaning, one year of age)            |
|                     | Meat quality               | Marbling (intramuscular fat), tenderness                                 |
|                     | Milk yield and quality     |  |
|                     | Fibre quantity and quality | Fleece weight and fibre diameter (for mohair and cashmere producers)     |
| Reproduction traits | Litter size                | Twinning rate, larger numbers of offspring may be detrimental            |
|                     | Mothering ability          | Number of kids weaned, combining effects of litter size and kid survival |
| Robustness traits   | Survival                   | Longevity  |
|                     | Mastitis resistance        |  |

Note: This table updates and expands upon information provided in Table 99 of the first SoW-AnGR (FAO, 2007a).



species, goat breeds are monitored for inbreeding, and the selection and diffusion of AI bucks is modulated to minimize inbreeding (Colleau *et al.*, 2011; Palhiere *et al.*, 2014). Obtaining EBVs that are sufficiently reliable for efficient selection requires the recording of pedigree information and at least a minimum of genetic connection between herds. Schemes based on progeny testing and the collective use of sires have become somewhat more common in recent years. In addition to the French and Norwegian programmes noted in the first SoW-AnGR (the former involving the use of AI and the latter the sharing of sires among cooperating breeders), examples now include selection schemes for Spanish dairy breeds (Murciano-granadina, Malagueña, Florida and Payoya), based on progeny-tested males and the use of their semen for planned matings throughout the whole selection nucleus (Seradilla, 2014). Although some of these schemes have achieved a degree of success (Menendez-Buxadera *et al.*, 2014), several constraints to their further development remain to be resolved, particularly with regard to their economic sustainability (Serradilla, 2008).

There have also been some notable developments in Latin America. In Brazil, selection schemes for improving meat and milk production have been implemented in small selection nuclei of imported and locally adapted breeds (Lôbo *et al.*, 2010). In Mexico, a small selection nucleus has been organized by a group of breeders from the state of Guanajuato, which also progeny tests sires through AI and undertakes genetic evaluation of sires and dams (Torres Vázquez *et al.*, 2009).

The main technological innovation in recent years has been the development of tools for the exploitation of molecular genomics in advanced selection schemes. Gene-assisted selection is currently applied in France and Norway to improve milk protein content (Manfredi and Ådnøi, 2012). The International Goat Genome Consortium<sup>10</sup> has worked with a private company to develop a commercially available SNP chip for goats (Tossler-Klopp, 2012). France has investigated the

adoption of genomic selection and has established reference populations for the popular Alpine and Saanen breeds (Larroque *et al.*, 2014). Study of these populations suggests that the reliability of genomic evaluation would be less than in dairy cattle breeds with large populations, but similar to that in cattle breeds with equivalent population sizes (*ibid.*). In addition, in contrast to the findings of most studies in dairy cattle (e.g. Kemper *et al.*, 2015), joint genomic evaluation of goat breeds tends to improve the accuracy of GEBVs (Carillier *et al.*, 2014).

#### 4.4 Pigs

The basic structure of the pig breeding sector remains similar to that described in the first SoW-AnGR.<sup>11</sup> In the typical breeding programme, pedigree selection occurs only within pure-bred lines (designated as sire or dam lines) in the nucleus (i.e. the top layer of the production pyramid). Sire lines are selected for growth and carcass traits, meat quality and robustness. Dam lines are also selected for reproduction traits. New lines are regularly developed by crossing existing lines and/or by specialized selection in a particular direction. A breeding organization's final products are parent sows (two- or three-way crosses) and parent boars (pure lines or two-way crosses). These parent animals are used by producers to breed pigs for slaughter.

The pig-breeding sector is less concentrated than the poultry sector (see Subsection 4.5). There are still many breed associations and many countries have some kind of national, often semi-governmental, genetic evaluation scheme (e.g. the National Swine Registry in the United States of America, the Canadian Centre for Swine Improvement Inc. and LGPC-IFIP-INRA<sup>12</sup> in France). These schemes compete with pig-breeding companies that may be owned by cooperatives (e.g. Topigs, Danavl, Nucléus and ANAS) or by families (e.g. ACMC, Grimaud, Hendrix and JSR) or may be

<sup>11</sup> FAO, 2007a, pages 402–405.

<sup>12</sup> Livres Généalogiques Porcins Collectifs - Institut de la Filière Porcine - Institut National de la Recherche Agronomique.

<sup>10</sup> <http://www.goatgenome.org/>

## PART 4

corporations (e.g. PIC). Over the years, pig-breeding companies have tended to amalgamate into larger and more cost-efficient entities.

Pig-breeding programmes have been very successful in improving economically important traits (e.g. Chen *et al.*, 2002; Tribout *et al.*, 2010), with growth and carcass performance (growth rate, leanness and feed efficiency) having been targeted since the 1970s and greater attention given to reproductive performance (litter size, piglet survival and farrowing interval) and meat quality (water binding capacity, colour and intramuscular fat content) from the 1990s onwards. Since the 2000s, the focus has been shifting towards breeding for more robust and efficient animals to meet the needs of a more diverse range of production environments (Merks *et al.*, 2012). This has required strategies for dealing with genotype by environment interactions. One popular approach is the combined cross-bred and pure-bred selection (CCPS) scheme, which involves recording the cross-bred progeny of AI nucleus boars under commercial conditions and using the data to estimate the breeding values of

pure-bred relatives that are selection candidates in the nucleus (Wei and Van der Steen, 1991). This approach implies increasing the emphasis given to robustness traits such as survival rates, leg soundness, disease resistance, stress susceptibility and longevity. Table 4C6 presents a summary of current selection objectives in pig breeding. Recent changes have been quantitative rather than qualitative: a gradual shift towards robustness traits and efficiency. An important development for the late 2010s will be the introduction of boar taint as a breeding goal trait in the European Union, where piglet castration is likely to end in 2018.

With ongoing intensification of the production sector, pig health is becoming ever more important. This requires, in the first place, improving sanitary status and biosecurity at the breeding-farm level, so that diseases are not introduced from the breeding farms into the production pyramid. It has also triggered attempts to breed for disease resistance and against metabolic disorders. However, this work is only in its initial stages. Globally, pig

TABLE 4C6

**Selection criteria in pigs**

| Traits              |  | Comments   |
|---------------------|--|--|
| Production traits   | Growth rate                                  | At various ages  |
|                     | Carcass quality                              | Carcass yield, carcass leanness, uniformity  |
|                     | Feed efficiency                              |  |
|                     | Meat quality                                 | Water-holding capacity, colour, intramuscular fat content                            |
| Reproduction traits | Litter size                                  |  |
|                     | Piglet survival                              | Mothering ability of the sow, viability of the piglets, litter uniformity            |
|                     | Farrowing interval                           |  |
| Robustness traits   | Stress susceptibility: halothane sensitivity | Allele eradication at a single gene; still relevant in a few extreme sire lines only |
|                     | Congenital defects                           | Atresia ani, cryptorchidism, splayleg, hernias, hermaphrodites, etc.                 |
|                     | Leg soundness                                | Osteochondrosis and many other aspects   |
|                     | Disease resistance                           | Specific <i>Escherichia coli</i> strains   |
|                     | Survival                                     | Piglet viability (effect of the sire); postweaning survival rates                    |
|                     | Sow longevity                                |  |

Note: This is an updated version of Table 100 of the first SoW-AnGR (FAO, 2007a).

production is gradually shifting from temperate to warmer climatic zones and this has created requirements for animals that are resilient to hot conditions. This has led to the introduction of novel breeding-goal traits such as lactation feed intake (Renaudeau *et al.*, 2014). In Western societies, increasing attention to animal welfare is leading to the introduction of novel housing systems, which in turn is leading to the adoption of a new set of breeding-goal traits, mainly related to various aspects of animal behaviour. Growing concern about environmental efficiency (e.g. greenhouse gas emission, phosphorus retention and nitrogen excretion) is likely to increase the emphasis given to feed efficiency in genetic improvement programmes.

Because of the competitive nature of the industry and its high levels of investment, commercial breeding companies usually spearhead the use of technologies. Many use MAS in one form or another and a handful have implemented full-scale genomic selection (Van Eenennaam *et al.*, 2014). These are expensive technologies, and studies have been undertaken to evaluate their financial feasibility in various breeding systems (e.g. Abell *et al.*, 2014). Another important innovation has been the development of optimization routines that balance between genetic improvement and inbreeding in the planning of selection and mating schedules at nucleus level (see Subsections 2.1 and 3). At present, a major focus of development is accommodating genomic information in mate-selection procedures.

#### 4.5 Poultry

The first SoW-AnGR provided an overview of the poultry-breeding industry, noting its hierarchical structure, often referred to as the “breeding pyramid”, and its concentration in the hands of a small number of companies.<sup>13</sup> It also discussed the main selection criteria in poultry breeding programmes, noting a trend towards the inclusion of ever more traits in breeding objectives.

A typical poultry breeding programme includes a biosecure breeding nucleus from which genetic improvement is disseminated to the wider industry through multiplication tiers at great-grand parent, grandparent and parent levels. Improved birds are multiplied and crossed, in three or four steps, in the lower tiers of the breeding structure to produce broiler or layer birds (see Table 4C7). It is important to note, however, that the traditional portrayal of the structure of the poultry industry as a pyramid, with the breeding programme at the apex, is something of an over simplification (Laughlin, 2007). The structure can more accurately be represented by two pyramids: a small supporting pyramid at the base, representing the specialized breeding programmes, and a larger inverted pyramid above, representing the other tiers of production, with the consumer at the top (see Figure 4C1). The supporting pyramid contains all the elements needed to maintain a breeding programme: experimental lines, test lines and pure lines, along with the various support systems of modern genetics, including a strong research

<sup>13</sup> FAO, 2007a, pages 404–405.

TABLE 4C7

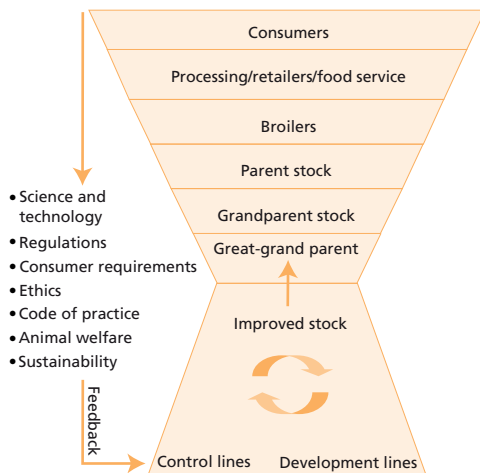
#### Cross-breeding scheme and relative numbers in a typical broiler breeding programme

| Level in breeding pyramid | Paternal lines           |                | Maternal lines        |                |
|---------------------------|--------------------------|----------------|-----------------------|----------------|
| Pedigree stock            | A♂ × A♀                  | B♂ × B♀        | C♂ × C♀               | D♂ × D♀        |
| Great grand parents       | 1 A♂ × 10 A♀             | 10 B♂ × 100 B♀ | 3 C♂ × 30 C♀          | 25 D♂ × 250 D♀ |
| Grand parents             | 250 A♂ × 2 500 B♀        |                | 1 500 C ♂ × 12 500 D♀ |                |
| Parents                   | 62 500 AB♂ × 625 000 CD♀ |                |                       |                |
| Broilers                  | 87 million ABCD          |                |                       |                |

Source: Adapted from Hiemstra and Napel, 2013.

## PART 4

FIGURE 4C1

**Structure of the poultry breeding industry**

and development base geared towards responding to feedback from every tier of the industry and from society.

The poultry-breeding industry remains concentrated in few hands. Fewer than five groups of primary breeders dominate the market for breeding stock (Fuglie and Heisey, 2011) and some of these are involved in the production of more than one poultry species. Most breeding companies are based in Europe or North America, with subsidiaries in major production regions.

The main breeding objectives and selection criteria in commercial poultry breeding are summarized in Table 4C8. Since the 1960s, breeding goals have evolved from a narrow starting point emphasizing production traits to now encompass a very broad range of considerations, including reproduction, animal health, product quality and environmental impact. This expansion has been particularly notable during the last two decades (Neeteson-van Nieuwenhoven *et al.*, 2013). The trend has been driven by the need for efficiency, including in environmental terms, as well as by the need for robustness and adaptability to varying production environments.

Poultry breeding is a global business and poultry are raised in production environments that vary substantially in terms of ambient temperature, humidity, altitude, disease exposure, feed quality and management capacity. Many regions where poultry are produced are highly vulnerable to climate change, and the development of resilient strains able to cope with climate change-affected production environments has become a focus of many breeding programmes. The high cost of recording and the need to maintain strict biosecurity mean that breeding companies typically undertake selection at a limited number of sites, rather than at many sites spread around the world. There is therefore a high potential for genotype  $\times$  environment interactions (Neeteson-van Nieuwenhoven *et al.*, 2013). To reduce the problem, poultry breeders have developed crosses that are robust to minor changes in the production environment. This is achieved by testing the siblings of selection candidates, different lines or different cross-bred progeny in multiple production facilities and field environments. The field data are then combined with data obtained in the breeding nucleus.

Increasing attention is also being paid to the need to reduce the carbon footprint of poultry production systems. This has led to an increased focus on the efficiency of production and a consequent shift in breeding objectives. Life-cycle analyses have indicated that the feed supply chain contributes a large proportion of the poultry sector's share of global greenhouse gas emissions (Pelletier *et al.*, 2014). Improving feed efficiency is thus a key factor in reducing the environmental impact of poultry production (Olori, 2010; Pelletier *et al.*, 2014). It has been estimated that an improvement in feed efficiency resulting in a saving of 15 g feed per kg body weight gained would reduce global poultry feed requirements by around 1.85 million tonnes per year, freeing up about 4 000 km<sup>2</sup> of arable land<sup>14</sup> (Neeteson-van Nieuwenhoven *et al.*, 2013). Feed intake, feed conversion ratio and residual feed intake are included in breeding objectives in

<sup>14</sup> Based on 2010 harvest yield of 466 tonnes of wheat per km<sup>2</sup>.

TABLE 4C8

**Selection criteria in poultry**

| Traits                                |   | Comments   |
|---------------------------------------|---|--|
| Egg production                        | Egg number<br>Hen house production<br>Hen-day percentage  | Chickens, ducks and geese: number of saleable eggs per bird  |
| Egg weight                            | Egg weight/size, shape index  |  |
| Egg quality – external                | Shell breaking strength<br>Shell thickness<br>Shell porosity/egg weight loss<br>Shell colour, egg shape   | Broiler and layer chickens: shell breaking strength, puncture score, dynamic stiffness, resonance frequency; egg weight loss between setting and transfer as a measure of shell porosity   |
| Egg quality – internal                | Haugh unit, albumen height, yolk percentage   |  |
| Meat production                       | Growth rate<br>Body weight at various ages<br>Breast meat percentage<br>Leg meat percentage<br>Fat percentage<br>Eviscerated yield percentage                                   | Chickens, turkeys and ducks: high emphasis on selection against fat in meat-type ducks; fat percentage assessed on live birds using multidimensional ultrasound measures as well as condition scoring  |
| Feed efficiency                       | Feed intake<br>Residual feed intake<br>Feed conversion ratio  | Feed conversion ratio is feed intake per kg weight gain in meat-type birds and per kg egg mass in layers   |
| Health, welfare and metabolic fitness | Liveability, leg health and walking<br>Gait, bone strength<br>Gut health<br>Heart and lung function<br>Feather-pecking behaviour<br>Feather cover<br>End of lay condition score | Selection for improved robustness, disease resistance and liveability traits and for decrease of (for example) tibial dyschondroplasia assessed with a lixoscope, valgus/varus, osteoporosis, toe defects, footpad dermatitis, femoral head necrosis and hockburn; heart and lung function assessed by measuring blood oxygen saturation using an oximeter |
| Reproductive efficiency               | Fertility and hatchability<br>Early and late embryo mortality<br>Chick viability (survivability beyond day of hatch)  | Broiler and layer chickens and turkeys: hatchability in terms of hatch of fertile eggs or hatch of set eggs  |
| Plumage                               | Plumage colour<br>Feather quality   |  |

Note: This is an updated version of Table 101 of the first SoW-AnGR (FAO, 2007a).

the turkey, layer and broiler sectors. To account for group dynamics in feeding, some breeding programmes have invested in feed recording systems based on transponder technology that allow continuous recording of the feed intake of individual birds in housed groups (Bley and Bessei, 2008; Howie *et al.*, 2010; Tu *et al.*, 2011). This technology also allows the genetic basis of feeding behaviour under competition to be studied (Howie *et al.*, 2009; Howie *et al.*, 2010).

One problem that has been highlighted by some authors (e.g. Dawkins and Layton, 2012) is the risk that rapid growth potential may pose to the welfare and the fertility of breeding birds. Feed management has been effective in optimizing

reproductive performance while avoiding obesity and associated welfare problems in breeding birds. However, welfare concerns about hunger have also been raised (D'Eath, 2009). Recent research has focused on behavioural and neuro-physiological measures of hunger (Dixon *et al.*, 2014; Dunn *et al.*, 2013) and the development of feeding strategies that optimise reproductive performance while avoiding both obesity and hunger (Van Emous, 2015).

Reproductive ability is not only vital to the profitability of the breeding companies' customers, it also affects the intensity of selection within the breeding nucleus. Increased longevity, egg fertility and hatchability, chick viability and persistency of

## PART 4

performance are therefore key breeding objectives. These traits are significantly affected by hen age. New methodologies based on random regression models are now used to evaluate these traits (Wolc *et al.*, 2009; 2010) and this facilitates examination of the persistency of performance over time.

Livability (survival to the end of the production cycle) and persistent performance require healthy birds that are free of physical and physiological defects. Breeding objectives therefore include traits that contribute to the health and welfare of the birds. For example, in the egg-layer sector, efforts are made to minimize cannibalism and feather pecking in group-housing systems. Traits monitored include feather coverage at various ages. Some companies select breeding stock while the birds are housed in groups, particularly in the case of broilers. A strategy based on group selection using so-called social interaction models has also been shown to be feasible (Bijma, 2010) and is being evaluated (Ellen *et al.*, 2011). However, it is generally difficult to estimate genetic parameters for such effects, especially when group sizes are large, and this may limit the use of such methods. Livability also requires reduction in the incidence of cardio-vascular problems (sudden death syndrome and ascites) and leg problems in broilers and turkeys. However, the causes of these problems are multifactorial and have been the focus of research efforts for decades. Many breeding programmes regularly select against contact dermatitis (foot pad and hock burn) (Kapell *et al.*, 2012a) and for improved clinical and subclinical leg health (Kapell *et al.*, 2012b), as well as for measures of heart rate and oxygen saturation as indicators of ascites and sudden death.

Poultry breeders have adopted genomic selection (see Subsection 2.3) as a means of increasing selection accuracy and reducing generation intervals (Avendano *et al.*, 2010; Avendano *et al.*, 2012; Sitzenstock *et al.*, 2013; Wolc *et al.*, 2014). The greatest benefit from genomic selection is expected to be seen in the improvement of traits expressed in only one sex and/or at a late age (e.g. egg production, fertility and hatchability), carcass traits that hitherto required the sacrifice of potential selection

candidates, and disease-resistance traits that could otherwise only be meaningfully selected for on the basis of challenge tests (i.e. tests involving exposure to disease). It is now clear that despite these developments traditional data recording remains important, as the accuracy of genomics-predicted breeding values relies on accurate phenotypic data. Further statistical and technological developments that reduce the cost of genotyping individual birds will be key to the widespread application of genomic selection and its contribution to poultry breeding in the coming decades.

#### 4.6 Rabbits

Intensive rabbit-meat production is based on three-way or four-way cross-breeding (Baselga and Blasco 1989; Lebas *et al.* 1997). In maternal lines, litter size remains the most common selection criterion because of its high economic value (Prayaga and Eady, 2000; Cartuche *et al.*, 2014). However, functional traits, such as doe longevity, kit survival, maternal traits and genetic resistance to bacterial disease, are emerging as criteria in breeding programmes targeting more sustainable production (Piles *et al.*, 2006; Eady *et al.*, 2007; Garreau *et al.*, 2008a; Sanchez *et al.*, 2008). Paternal lines are commonly selected for post-weaning daily gain or for weight at a point close to market age (Rochambeau *et al.*, 1989; Lukefahr *et al.*, 1996; Piles and Blasco, 2003; Larzul *et al.*, 2005). These criteria are easy to record and have a favourable genetic correlation with feed conversion index (Piles *et al.*, 2004), which is very important for efficient production, as feeding accounts for the highest proportion of total costs. In Europe, demands from slaughterhouses mean that carcass yield is becoming increasingly important. Disease resistance has also become a major issue. Thus, in addition to weight at slaughter age or average daily gain, some paternal lines are now selected for carcass traits and against susceptibility to digestive disorders (Eady *et al.*, 2007; Garreau *et al.*, 2008b). Breeding objectives in rabbits are summarized in Table 4C9.

Meat-rabbit selection schemes are found mainly in France, Spain, Italy, Hungary, Egypt and Saudi

TABLE 4C9

**Selection criteria in rabbits**

|                               | Traits  | Comments                            |
|-------------------------------|---|-------------------------------------|
| Meat production               | Growth rate or weight at slaughter                      |                                     |
|                               | Carcass yield   |                                     |
|                               | Thigh muscle volume                                     | Using computerized tomography       |
| Reproductive efficiency       | Litter size   |                                     |
|                               | Litter weight   |                                     |
|                               | Individual weaning weight                               | Direct and maternal effects         |
|                               | Number of teats   |                                     |
| Longevity                     | Length of productive life                               |                                     |
| Health and welfare            | Homogeneity of birth weight                             | Indirect criterion for kit survival |
|                               | Genetic resistance to diseases                          | Mainly digestive disorders          |
| Fibre production              | Total fleece weight at each harvest (every 80-120 days) |                                     |
| Fur size                      | Live body weight  |                                     |
| Fur density                   | Density of fibres per skin unit area                    |                                     |
| Fur structure and composition | Bristliness or guard-hair content                       |                                     |
| Fur priming                   | Scoring extent of the moult and hair follicle activity  |                                     |

Arabia. Pedigree selection occurs strictly in specialized paternal and maternal lines, mainly using the BLUP methodology. Genetic improvement is diffused from the breeding nucleus into the wider population via pyramidally structured multiplication units. Some public research organizations are deeply involved in meat-rabbit breeding, either providing scientific and logistic support to private breeding companies (e.g. the Institut National de la Recherche Agronomique in France) or directly managing breeding nuclei (e.g. the Polytechnic University of Valencia and Instituto de Investigación y Tecnología Agroalimentarias in Spain and the University of Kaposvár in Hungary).

In contrast to meat-rabbit breeding, fibre (Rafat *et al.*, 2008) and fur production in rabbits is based on pure-bred selection in specialized breeds: Angora for fibre and Rex for fur. Genetic improvement of fibre and fur production in rabbits targets:

- increasing production of fibre or fur to give greater economic return per animal and production unit; and

- improving the quality of the fibre or fur so that it can be processed into superior end-products and thus attract a higher unit value.

Functional and adaptation traits (reproduction, health, growth and maternal traits) are also taken into consideration, but to a lesser extent than in meat production. BLUP methodology is used for genetic evaluation. Programmes are mainly located in France and China and are operated by public organizations and some private companies.

The main objectives of selection in commercial rabbit lines (i.e. prolificacy and feed efficiency) have not changed in recent years. However, research has provided information on the feasibility of improving traits such as the length of does' productive lives (Sanchez *et al.*, 2008; Larzul *et al.*, 2014), homogeneity of litter weight at birth (Garreau *et al.*, 2008a), carcass dressing percentage, heat tolerance (Sanchez and Piles, 2013), resistance to pasteurellosis and diseases causing digestive disorders (Garreau

## PART 4

*et al.*, 2008b; Eady *et al.*, 2007), and efficient production of semen doses for AI (Tusell *et al.*, 2012). As a consequence, new breeding programmes targeting kit and doe survival, carcass dressing percentage and digestive health have been implemented in commercial lines, with successful results. In addition, new selection criteria for improving prolificacy (ovulation rate and litter size – Ziadi *et al.*, 2013) and feed efficiency (residual feed intake and daily weight gain under feed restriction – Drouilhet *et al.*, 2013) have also been introduced. Results from experiments on Angora rabbits have shown that selection for total fleece weight, a simple trait that is easy to measure on-farm, positively affects both quantitative and qualitative traits in wool production (Rafat *et al.*, 2007; Rafat *et al.*, 2008).

Future priorities in rabbit breeding relate to the intensification of production to cope with the expected growth in global demand for animal protein in a way that is economically, environmentally and socially sustainable and to the need to adapt to changing environmental conditions. Breeding for improved disease resistance (robustness) has become a major challenge because of the effect that some infectious diseases (e.g. epizootic rabbit enteropathy and pasteurellosis) have been having on efficiency and productivity, the safety of rabbit products, animal welfare and public perceptions of rabbit production. Research objectives are increasingly focusing on quantifying the genetic control of the host–pathogen interactions, as well as on identifying SNPs associated with resistance.

The recent development of high-throughput genomic tools and statistical methods for dealing with massive amounts of data could allow selection based on SNPs associated with resistance traits. The rabbit genome has been sequenced (Carneiro *et al.*, 2014) and the implementation of gene-based and genomic selection is an emerging area of research in rabbit breeding. Its suitability in this species is still under discussion. As with other species, the use of genomic information could also lead to better understanding of

the biological processes underlying important traits.

The design and implementation of recording systems for specific difficult-to-measure traits, such as individual feed intake, would allow consideration to be given to new breeding strategies for improving the efficiency of production. The development of advanced statistical models and procedures involving, *inter alia*, direct and indirect effects (e.g. social effects for traits recorded in animals raised in groups), genetic × environment interactions and the use of information from cross-bred animals in commercial farms is also a major issue for future research.

## 5 Breeding programmes in low-input systems

The first SoW-AnGR provided an overview of the various challenges involved in establishing breeding programmes (including those involving cross-breeding) in low-input systems.<sup>15</sup> It highlighted the importance of involving livestock keepers from the outset in the planning and implementation of such programmes and of paying attention to traits related to the efficiency of production (i.e. taking input use into account rather than simply targeting increased output). This subsection provides an updated account, beginning with a short description of the main options currently available for establishing breeding programmes in low-input systems and then addressing the specific considerations that need to be taken into account in the implementation of such programmes.

### 5.1 Breeding strategy options

As noted above (Subsection 3), a genetic improvement strategy can involve selection among breeds, cross-breeding and/or within-breed selection. In a low-input system it is particularly important to ensure that any breeds introduced

<sup>15</sup> FAO, 2007a, pages 405–419.



and any crosses produced are able to thrive in the local production environment. As in all circumstances, breeding strategies for low-input systems should be based on careful assessments of the current state of the targeted production systems, the trends affecting them and the needs and objectives of the local livestock keepers and of society more broadly (FAO, 2010).

A properly implemented cross-breeding scheme offers the opportunity to combine the positive attributes of two different breeds. In a low-input system, this will often involve an attempt to combine the adaptive qualities of a locally adapted breed with the higher production potential of an exotic breed. There are several different types of breeding schemes that can be considered:

- pure-bred or terminal crossing systems – mating of animals from separate pure-bred populations over one or two generations to produce a generation of cross-bred animals that “terminates” the system, i.e. has desirable qualities in production terms, but is not used for breeding;
- rotational crossing – producing an initial two-way cross and then, in each subsequent generation, alternating the sire breed used (can include the incorporation of additional breeds); and
- creation of a new synthetic breed – crossing two or more breeds in order to achieve a desired proportion of each, followed by *inter se* mating of these animals.

The two first options have the advantage of continuously producing a heterosis effect. However, they may present logistical difficulties, and maintaining an exotic parental line in low-input conditions may be problematic (see Serradilla, 2001 for discussion of this issue in goats). As with any other kind of breeding scheme, determining what is possible in the specific local circumstances is a key element of planning a cross-breeding strategy. It has to be emphasized that if cross-breeding efforts are not carefully planned, or if plans are not properly followed, activities of this kind may create serious problems, both in terms of producing animals that are not well suited to local conditions

and in terms of eroding the existing locally adapted animal genetic resources. Uncontrolled cross-breeding is regarded as major threat to animal genetic resources in many countries (see Part 1 Section F).

Meta-analyses of studies on dairy and beef cattle in tropical environments (Burrow, 2006; Galukende *et al.*, 2013) have shown that in most cases F1 crosses perform better than other genotypes. For instance, Galukende *et al.* (2013) showed that 50 percent *B. taurus* × *B. indicus* cross-breeds had on average 2.6, 2.4 and 2.2 times higher milk yield than local *B. indicus* in highland, tropical wet and dry and semi-arid climatic zones, respectively. However, harsher production environments can lead to increasing problems with a lack of adaptedness (including reproductive problems) in cross-bred animals and particularly in exotic parental lines. When evaluating a programme involving cross-breeding with exotics, it is therefore important to consider a multiyear time horizon, accounting both for the lifetime profitability of individual animals (i.e. considering input costs, lifespan, reproductive success, etc., in addition to product output) and the costs of maintaining the various populations needed to keep the programme operating in the long term.

Improving a breed through straight breeding is a long-term commitment. In low-input systems it generally involves either a programme based on a central nucleus or a community-based breeding programme. Central nucleus schemes involve genetic improvement in a nucleus flock or herd and subsequent dissemination of improved genetic material directly or indirectly (via a multiplier layer) into the base population. The scope of the operation is, in principle, the whole population of the respective breed. The nucleus may be “closed” (gene flow occurs in one direction only – from the nucleus to the base population) or “open” (gene flow can also occur in the opposite direction, i.e. superior animals from the base population may be used to supplement the nucleus).

## PART 4

The advantage of a programme based on a central nucleus is that it allows the use of advanced genetic evaluation methods (BLUP) and hence rapid genetic progress. Performance and pedigree recording is usually limited to the nucleus. A weakness is that such schemes depend heavily on organizational, technical and financial support (Mueller *et al.*, 2015). They also tend to be hierarchical rather than participatory in their planning and operation and hence often fail adequately to address the needs of livestock keepers in low-input systems (e.g. Gizaw *et al.*, 2013). Over the years, schemes of this type, entirely managed and controlled by governments or state operators – and with minimal, if any, participation on the part of livestock keepers – have been established in many developing countries (Wurzinger *et al.*, 2013a). A large proportion of them have failed. Such schemes have proven to be effective only when governments and other funding agencies have a long-term perspective and continue to provide technical and financial support until the programmes have achieved self-sustainability (Wurzinger *et al.*, 2011).

Community-based schemes (Mueller; 2006; Mueller *et al.*, 2015) operate at the scale of a single community rather than at the scale of the whole breed population. As well as operating at community scale, they are also community-based in the sense that livestock keepers are the main players in their design and operation, although support of various kinds may be provided by external stakeholders. A number of different types of structure are possible (Haile *et al.*, 2011; Gizaw *et al.*, 2013). Schemes may operate with or without a nucleus and, if present, the nucleus may be open or closed. The nucleus may also have a “dispersed” character, i.e. rather than being maintained as a single unit the nucleus animals are maintained in several different flocks or herds. Table 4C10 contrasts the typical characteristics of conventional and community-based breeding programmes.

The number of community-based breeding programmes implemented in low-input systems

has increased in recent years (e.g. Kosgey *et al.*, 2006; Mueller, 2006; Pastor *et al.*, 2008; Wurzinger *et al.*, 2008; Tadele *et al.*, 2010; Valle Zárate and Markemann, 2010; Wurzinger *et al.*, 2011; Abegaz *et al.*, 2013). A review prepared by Mueller *et al.* (2015) describes eight case studies of community-based programmes. An overview of the main characteristics of these programmes is provided in Table 4C11, along with some additional examples.

Experience indicates that establishing a successful community-based programme requires the involvement of a range of stakeholders (livestock keepers, local government, NGOs, universities, etc.) (Wurzinger *et al.*, 2013a). Adopting a participatory approach from the start of the planning process will help to ensure commitment and ownership and to clarify the roles and responsibilities of the various stakeholders involved.

## 5.2 Specific challenges involved in establishing and operating breeding programmes in low-input systems

The recording scheme of a community-based breeding programme needs to be cost-effective and should not be too elaborate for local conditions (Wurzinger *et al.*, 2011). Performance testing at central stations and visual appraisal in herds are commonly used in recording schemes for meat and fibre production. A milk-recording scheme is more challenging, as it requires repeated measurements. Timely feedback is needed in order to maintain livestock keepers’ interest in the recording scheme (Wurzinger *et al.*, 2011; Iñiguez *et al.*, 2013).

As most livestock keepers are interested in improving many different traits, the use of an economic selection index (see Subsection 3) to determine which animals should be used for breeding is generally recommended (e.g. Gizaw *et al.*, 2010). In the case of breeding schemes based on dispersed nuclei, livestock keepers will need to be more involved in the implementation of the animal identification and recording activities, and they will also need to agree on arrangements for sharing males to establish genetic linkages between herds/flocks.

TABLE 4C10

**Characteristics of conventional and community-based livestock breeding programmes**

| Characteristic                | Conventional breeding programme           | Community-based breeding programme    |
|-------------------------------|---|---------------------------------------|
| Geographical limit            | Regional – inter-regional                 | Communities                           |
| Market orientation            | Commercial                                | Subsistence – commercial              |
| Agent of programme            | Breeding company – breeder organization   | Livestock keeper – breeder            |
| Breeding objective            | Defined by company – breeder organization | Defined by breeder – livestock keeper |
| Breeding structure            | Large scale, pyramidal                    | Small scale, one or two tiers         |
| Genetic resources             | International                             | Local                                 |
| Infrastructure                | Available                                 | Limited                               |
| Management                    | Intensive – high input                    | Extensive – low input                 |
| Risk taker                    | Company – livestock keeper organization   | Livestock keeper                      |
| Decision on share of benefits | Variable                                  | Livestock keeper                      |

Source: Mueller *et al.*, 2015.

TABLE 4C11

**Selected community-based breeding programmes**

| Country                          | Species  | Main product | Period         | Location         | Total animal population | Breeding system           | Key references  |
|----------------------------------|----------|--------------|----------------|------------------|-------------------------|---------------------------|---|
| Argentina                        | Goats    | Mohair       | 1987 – ongoing | Dispersed        | 62 000                  | Open nucleus              | Mueller, 1995; Lanari <i>et al.</i> , 2009; Mueller, 2013b                            |
| Bolivia (Plurinational State of) | Llamas   | Fibre        | 2008 – 2012    | Villages         | 2 500                   | Open nucleus              | Wurzinger <i>et al.</i> , 2008  |
| Ethiopia                         | Sheep    | Meat         | 2009 – ongoing | Communal         | 10 000                  | All flock                 | Haile <i>et al.</i> , 2011; Duguma <i>et al.</i> , 2011; Mirkena <i>et al.</i> , 2012 |
| Iran (Islamic Republic of)       | Goats    | Cashmere     | 2009 – ongoing | Nomad            | 2 800                   | Open nucleus              | Mueller, 2013   |
| Kenya                            | Goats    | Dairy        | 1997 – ongoing | Dispersed groups | 20 000                  | Open nucleus              | Ojango <i>et al.</i> , 2010   |
| Mexico                           | Goats    | Dairy        | 2007 – ongoing | Village          | 200                     | All flock                 | Wurzinger <i>et al.</i> , 2013b   |
| Mexico                           | Goats    | Dairy        | 2000 – ongoing | Villages         | 1 500                   | Open nucleus              | Valencia-Posadas <i>et al.</i> , 2012   |
| Peru                             | Sheep    | Wool         | 1996 – ongoing | Communal         | 160 000                 | Open nucleus              | Mueller <i>et al.</i> , 2002; Mueller, 2013   |
| Uganda                           | Chickens | Eggs         | 2003 – ongoing | Dispersed groups | >120 000                | Multilevel cross-breeding | Roothaert <i>et al.</i> , 2011  |
| Viet Nam                         | Pigs     | Meat         | 2000 – ongoing | Villages         | 700                     | Open nucleus              | Valle Zárate and Markemann, 2010; Roessler <i>et al.</i> , 2012                       |

Sources: Mueller *et al.*, 2015; Valencia-Posadas *et al.*, 2012.

## PART 4

## Box 4C5

**GENECOC – the breeding programme for meat goats and sheep in Brazil**

In 2003, the Brazilian Agricultural Research Corporation (EMBRAPA) launched the Breeding Program for Meat Goats and Sheep – GENECOC\*. Up to that time, there had been no structured breeding programmes for goats and sheep in Brazil and there was a lack of recorded information on the performance of these species.

GENECOC is a genetic advisory service that aims to encourage and assist programme participants with record keeping in their flocks and the generation of reliable information that can be used in selection decisions. GENECOC targets all kinds of animals and breeders, focusing particularly on locally adapted breeds and low-input systems. Breeding strategies are matched to local production systems. However, the main feature of the scheme is the use of web-based software to record, organize, store and manage the information generated. The system includes tools for selecting animals for total genetic merit through the use of (breed specific) selection indexes and identifying the set of matings that maximizes the genetic gain of the flock, while controlling inbreeding.

One important action undertaken under the programme targets the Morada Nova sheep, a locally adapted breed that was once at risk of extinction. Participatory methodologies are used

in the implementation of a community-based programme, including in the definition of breeding objectives, performance testing in young rams and the organization of monthly planning meetings.

Today, in addition to its activities in Brazil, GENECOC also participates in projects in other countries, including Ethiopia and the United States of America.

The principal impacts of the programme have been in adding value to locally adapted sheep and goat breeds and optimizing their use while respecting environmental concerns. Experience has shown that it is important to identify and involve key stakeholders, to use a well-organized and well-trusted data-collection system backed-up by government funding and, when designing breeding objectives and selection criteria, to consider not only traits related to market trends, but also traits that livestock keepers judge to be important. Future plans include expanding activities to include additional sheep and goat breeds and expanding the system for multiplying improved animals to cover additional local production systems.

Provided by Raimundo Nonato Braga Lôbo.

For further information see Lôbo *et al.* (2010); Lôbo *et al.* (2011) and Shiotsuki *et al.* (2014).

\*<http://srvgen.cnp.embrapa.br/pagina/english/principal.php>

**Morada Nova sheep in Northeast region of Brazil**

Photo credit: Olivardo Facó.

**Weighing Morada Nova lambs**

Photo credit: Olivardo Facó.

## Box 4C6

**Establishing a cross-breeding scheme for dairy goats in the United Republic of Tanzania**

Toggenburg goats were introduced into Babati, United Republic of Tanzania, as the result of a Farm Africa project in 1990. The project originally brought in four pure-bred Toggenburg does and one Toggenburg buck and established a women's group that operated a goat-in-trust\* scheme. Because of the poor performance of the women's group, a sister project was initiated, under which commercial groups (groups of goat keepers raising animals for commercial as well as subsistence purposes) were established through a goat-in-trust scheme.

In 1997, the commercial goat raisers formed the Toggenburg Breed Association (TOBRA) as a commercial dairy goat production association. In 1998, TOBRA was registered by the Ministry of Home Affairs. At the time it had only 12 members. In 2001, TOBRA established eight dairy goat production groups. By the end of 2007,\*\* the number of groups had expanded to 52, involving 188 farmers, with an average of eight goats each. People were initially very reluctant to join the groups, but following sensitization efforts they began to join voluntarily. Association members raise pure Toggenburgs, 75 percent Toggenburg crosses and 50 percent Toggenburg crosses. The cross-bred animals are carefully evaluated by analysing their pedigrees and productive and reproductive performances.

TOBRA started with 249 000 shillings\*\*\* in the form of registration fees and other contributions. As of 2007, it had more than 12 000 000 shillings. It has employed a treasurer and manages the costs of its meetings and agricultural shows at district, region, zonal and national levels.

The main objectives in forming the association were:

- to increase milk productivity from goats through cross-breeding Toggenburg and indigenous goats, taking advantage of the high milk production of the former and the disease resistance of the latter;
- to produce pure Toggenburgs so that genetics could be exchanged with farmers from Kenya and Uganda; and
- to improve the income of the members through selling milk and live animals (pure-breeds and crosses).

\*A scheme in which the loan of a goat is paid back in the form of another goat that can be passed on to another participant.

\*\*This is the most recent date for which published figures are available. Since then the farmers have continued their goat breeding and production activities under the supervision of the local extension services.

\*\*\* Equivalent to approximately US\$400 at the time.

Provided by Yacobo Msanga, National Coordinator for the Management of Animal Genetic Resources, the United Republic of Tanzania.

For further information see Msanga and Bee (2006) and Bee *et al.* (2006).

Participatory approaches to setting breeding goals and identifying traits to be recorded have been recommended as a means of promoting the involvement of livestock keepers in the operation of community-based programmes (Gizaw *et al.*, 2010; Wurzinger *et al.*, 2011). Potential methods include individual interviews with livestock keepers, workshops with groups of livestock keepers and exercises involving the use of choice cards or the ranking of live animals (e.g. Duguma *et al.*, 2010; Haile *et al.*, 2011). More generally, a participatory approach that engages the various actors involved will help ensure their commitment and ownership,

prerequisites for the long-term sustainability of a breeding programme.

Controlling inbreeding can be a major issue in breeding schemes in low-input systems, especially in closed central nucleus schemes and in community-based schemes operating on a limited scale. Gizaw *et al.* (2009) recommend that for an acceptable rate of inbreeding, sheep breeding schemes should include at least 600 ewes and 15 rams. Rotation of males between livestock keepers' herds/flocks or between the nucleus and livestock keepers' herds/flocks can help to limit inbreeding. The use of sire-reference schemes (i.e. schemes in which each cooperating livestock keeper agrees

## PART 4

Box 4C7

**Community-driven breeding programmes for locally adapted pig breeds in Viet Nam**

Demand for pork in Viet Nam has increased substantially since the 1990s, driven by economic development and urbanization. Although large-scale private enterprises have benefited from subsidies introduced with the aim of expanding exports, smallholder farmers still represent the backbone of the Vietnamese pig sector, especially in the northern part of the country. To cope with increasing competition and quality requirements, market-oriented smallholders increasingly raise modern pig lines and hybrids, often in unsystematic cross-breeding schemes. This has reduced the population sizes of autochthonous breeds and pushed them into remote areas.

Under a pilot project implemented by German and Vietnamese research institutions in collaboration with the provincial veterinary department and private partners (funded by the German Research Foundation, DFG), a community-driven pig-breeding and marketing programme was established in the mountainous Son La province in northwestern Viet Nam. The farmers' pig-breeding cooperative involves ten villages, representing communities with different resource endowments, production objectives and consequently different requirements from their pig genetic resources.

Initially, pure-bred indigenous Mong Cai and Ban gilts were distributed among 179 cooperative members and a revolving fund was established with the aim of

enabling the smallholders to be independent in terms of supplying replacement animals and improving genetic stocks. Prolific Mong Cai gilts were distributed mainly to semi-intensive producers and robust Ban sows to less market-oriented smallholders.

Although some of the collective actions planned under the project were successfully implemented – for instance, improving the access of rural small-scale pig producers to veterinary services and establishing multipronged market outlets – the attempt to establish a community-based stratified cross-breeding scheme proved to be difficult. The organizational structures of a cross-breeding scheme must be accompanied by a well-balanced business plan that accounts for the greater burden placed upon nucleus breeders. In this example, although farmers preferred to use pure-bred dam lines, and Mong Cai breeders could therefore obtain a good price for sows, this was

**Mog Cai sow and fatteners****Ban sow and litter**

Photo credit: Kerstin Schöll.



Photo credit: Kerstin Schöll.

(Cont.)

## Box 4C7 (Cont.)

**Community-driven breeding programmes for locally adapted pig breeds in Viet Nam**

not sufficient to compensate them for the low prices obtained for pure-bred Mong Cai finishers. The market for the latter completely collapsed because of rapid shifts in customer preferences towards leaner pork. In the future, farmers will probably turn to breeding centres or commercial farms to obtain pure-bred Mong Cai sow replacements. In contrast, marketing of pure-bred Ban products via a short supply chain, avoiding a large number of intermediaries, proved to be successful in linking remote resource-poor Ban keepers to highly remunerative specialty markets in the Red River Delta. Because of the prices that can be realized

in these niche markets, farmers will probably continue pure-breeding the Ban breed and this will create a pool of sow replacements for farmers that exclusively practice cross-breeding.

In conclusion, this case illustrates how a self-sustained community-driven pig breeding and marketing programme can only sustainably contribute to rural development and breed conservation if it can be flexibly adapted to market conditions.

Note: This box updates Box 89 of the first SoW-AnGR (FAO, 2007a).  
Provided by Philipp Muth and Anne Valle Zárate.

to use sires or semen from a group of high-quality so-called “reference” sires – Simm *et al.*, 2001) in the implementation of dispersed-nucleus schemes may reduce inbreeding in the short term but increase it in the long term at herd level. Systems for regularly providing males from other herds/flocks are particularly important in situations where introducing animals (or semen or embryos) from outside is not feasible.

When calculating the economic efficiency of a given breeding programme, it is important to take into account both the tangible and the intangible benefits that accrue to various different groups of stakeholders (livestock keepers, retailers, government, etc.). Advice on how to evaluate investment decisions in breeding programmes is provided in FAO’s guideline publication *Breeding strategies for sustainable management of animal genetic resources* (FAO, 2010). Computer simulation of the breeding programme can be used to predict changes in targeted traits and their sensitivity to changes in various factors affecting genetic response (e.g. Gebre *et al.*, 2014).

Finally, in addition to genetic considerations, factors related to market chains usually have a major influence on the success of breeding programmes in low-input environments. The absence of effective marketing chains will present a significant

challenge. This is true for both output and input markets (Haile *et al.*, 2011). Although a multi-trait breeding objective is likely to be optimal, such breeding programmes are usually designed so as to increase production to some degree. In theory, the increased production may be used simply to improve food security and nutrition within a subsistence system, but more commonly the programme is designed so as to generate excess product that can be marketed. Genetic improvement requires investment of human and financial capital, and these inputs will be wasted if no market channel is available. Improvements to productivity achieved by breeding programmes in low-input systems are rarely due only, or even primarily, to genetic improvement. Successful genetic improvement programmes are usually complemented by enhanced veterinary care and nutrition, so reliable access to these resources is also important. Organization of livestock keepers into associations or cooperatives to coordinate activities and increase access to input and output markets is usually beneficial. In the longer term, establishing a marketing system for superior breeding stock will also be beneficial, as it will provide breeders with another source of income and incentive for genetic improvement.



## PART 4

### 5.3 Genomics and future developments

As discussed in Subsection 2, techniques that enable the use of genomic information in animal breeding have advanced greatly in recent years, particularly in the case of cattle, pigs and poultry. While these techniques offer major potential benefits, particularly in terms of allowing the selection of animals at earlier ages and reducing generation intervals, there are several concerns regarding their use in low-input production systems. Effective use of these techniques requires more than just vague information on the phenotypes and genotypes of the breeds concerned. A reliable data-recording scheme is absolutely necessary in order to provide the basis for associating genotypes to phenotypes. Such schemes are lacking in most low-input situations. There are nevertheless steps that can begin to be taken towards the use of these new technologies in developing countries. Efforts to identify genes or genomic regions associated with adaptation or variation in production traits in harsh environments need to be stepped up in developing countries and in low-input smallholder and pastoralist production systems (Rothschild and Plastow, 2014). Once relevant genes have been characterized, livestock populations can potentially be improved through genetic introgression or gene-assisted breeding programmes. With regard to genomic selection more specifically, implementation requires the establishment of training and validation populations, in which both phenotypes and genotypes are recorded, so that the prediction model can be established. Indigenous populations with low linkage disequilibrium generally do not meet these requirements (Akanno *et al.*, 2014). The use of widely used international transboundary breeds as reference populations for genomic selection in locally adapted breeds seems to have little or no value, except perhaps in cross-bred populations, but this has not been studied. Any attempt to implement genomic improvement programmes needs to take into account the need for adequate infrastructure, technical skills, policies and communication

strategies, and the need for a long-term perspective in planning and implementation (Rothschild and Plastow, 2014).

## 6 Conclusions and research priorities

The main advances in breeding programmes and related technologies over recent years have been in the application of genomic information, particularly in high-input production systems. Genotyping costs have dropped precipitously and for some species nearly all of the important selection candidates are genotyped, as have been the major ancestors from which genetic material is available. Genomic selection increases the accuracy of EBVs, particularly for those animals for which no phenotypic data are yet available. The impact on the commercial dairy breeding industry has been revolutionary. Progeny testing now plays a minor role. Breeding goals have seen various adjustments. In particular, greater emphasis is now being placed on profit, rather than output, and therefore on health, survival and other traits that influence production costs.

The genomic revolution has yet to affect developing countries to a significant degree. Accurate genomic selection depends on the availability of phenotypic data, which are usually lacking in the low-input production systems typically found in developing countries. Nevertheless, the situation in these countries has not remained static. Formal breeding programmes, usually community-based, have become more common and are improving the productivity of animals and livelihoods of their keepers. However, significant work is still required. Animal identification and pedigree and performance recording need to be expanded. This is necessary even to take advantage of traditional approaches to breeding, let alone genomic selection.

Little if any direct progress has occurred since the first SoW-AnGR was prepared in terms of determining the underlying genetics of phenotypic adaptation to the environment. However, the



tools with which to do this are in place. Genomic analysis should allow breeders to determine actual genetic by environment interactions, although a tremendous amount of work remains to be done in order to obtain the phenotypic information needed to accurately predict such interactions.

Future research will need to address the need for new modes of production that can help meet the expected growth in global demand for animal protein in ways that are economically, environmentally and socially sustainable and address the need to adapt livestock production to changing environmental conditions. In other words, efficiency of production will be an increasingly important consideration. This will include a wide range of efficiencies and involve not only increasing product yield per unit of input, but also addressing negative effects such as environmental damage (see Box 4C8 for an example). Improvement in the use of feed resources, reproductive efficacy and prolificacy, and animal health will be key topics for research, both in developed and in developing countries.

The following list of research priorities draws on the Strategic Research Agenda of the Sustainable Farm Animal Breeding and Reproduction Technology Platform, an extensive review of research priorities in livestock breeding in Europe (FABRE TP, 2011).

#### ***Selection to balance functionality and production***

- improving knowledge of the genetics of:
  - disease resistance, resilience and immune response;
  - host–pathogen interactions;
  - gut functionality and its relationship with gut microbiota in different environments;
  - emission of methane and production of other greenhouse gases;
  - variation in digestion of specific amino acids and phosphorus – along with improving knowledge of nutrient (e.g. amino acid) requirements under different production conditions; and
  - uniformity;

- developing economically viable means of including traits of increasing consumer concern in breeding goals, including traits with uncertain economic value;
- developing strategies for improving disease resistance without compromising production;
- developing phenotype definitions for novel traits;
- establishing standard phenotypic trait ontologies encompassing production traits, disease traits and other welfare traits and environmental sensitivity;
- developing tools to estimate and exploit non-additive genetic variation;
- developing social-interaction models including, male–female interactions, to facilitate the improvement of reproductive, health and welfare traits;

#### ***Genomics and other “-omics”***

- characterizing the genome sequences (and variation therein, including epigenetic transmissible variants) of species, populations and individuals;
- developing methods for optimal incorporation of genomic information in breeding-value estimation;
- developing proteomic and immunological metabolomic technologies for high-throughput analyses;
- developing schemes incorporating large-scale genotyping at embryo level;
- metagenomic sequencing of gastro-intestinal microbial communities;

#### ***Bioinformatics and biostatistics***

- developing statistical programming tools relevant to new traits and new phenotypes;
- supporting continued annotation and maintenance of public genome databases;
- developing scalable bioinformatics tools to handle high-throughput data (e.g. genomic selection procedures or inference of genome-wide diversity parameters);

## PART 4

Box 4C8

**Genetic selection for reduced methane production – a future tool for climate change mitigation**

The expanding world human population will require greater food production within the constraints of increasing societal pressure to minimize impact on the environment. Animal breeding has in the past achieved substantial reductions in environmental load per unit of product, despite no explicit inclusion of environmental load in breeding goals. Higher gains can be expected if breeding goals focus more specifically on environmental objectives. One important objective is to reduce the amount of enteric methane – a greenhouse gas with a warming potential 25 times that of carbon dioxide – produced by ruminants. However, a successful breeding strategy requires measurements on a large population of animals. To facilitate genetic selection for reduced methane production, it would therefore be highly desirable to combine individual national datasets to produce a multicountry database. However, data are collected using different protocols, and combining them requires intensive consultation among contributing scientists across a range of disciplines. More importantly, however, scientists planning to undertake future studies on methane production have not yet agreed protocols for how to proceed with the collection of data.

The networks of METHAGENE ([www.methagene.eu](http://www.methagene.eu)) and ASGGN ([www.asggn.org](http://www.asggn.org)) have joined

forces with the International Committee for Animal Recording ([www.icar.org](http://www.icar.org)) to develop consensus on protocols for the collection of methane production data, with the aim of facilitating the harmonization and combination of existing and future data obtained from different countries and with different collection methods. The project will also facilitate discussions among experts aiming to identify possible predictor traits for methane production (e.g. biomarkers in milk) that could be easily exploited. Methane production is currently not directly included in any national cattle breeding objective anywhere in the world. This is not only because of a lack of sufficient data with which to make selection decisions, but also because of a lack of consensus on how to optimally include methane production in a breeding objective. The project will develop standards for expressing methane production, taking into account the advantages and disadvantages of expressing methane per unit (digestible) feed and per unit of consumable product (i.e. milk and/or meat) and also the need to consider the time horizon of emissions via a life-cycle assessment and to ensure that selection for low emissions does not compromise production efficiency.

Provided by Yvette de Haas.

- developing means of exploiting distributed computing technologies (GRID, Cloud) for more effective data storage, sharing, integration and analysis;
- improving the use of genomic sequences for predicting genetic values and detection of *de novo* mutations;
- developing transcriptomic tools (arrays and RNA-seq);

***Breeding strategies in low-input production systems***

- improving methods for planning and implementing breeding strategies in production systems where there is little or no organizational infrastructure, including means of determining where breeding programmes are feasible and appropriate and how they can be adapted to local circumstances;
- exploiting the use of telecommunications and informatics technologies to improve data collection;

- improving strategies for the establishment of stable cross-breeding systems; and
- developing simulation tools to predict the consequences of introducing exotic breeds into local populations (as part of genetic impact assessment).

### Improving research cooperation

Research in the field of animal breeding could be strengthened by promoting greater cooperation among the various stakeholders involved. Relevant measures include:

- promoting even greater collaboration between the breeding industry, academia and the public sector;
- exploring the feasibility of capturing and using production data from commercial producers (e.g. encouraging the use of commercial populations for high-resolution genetic analyses); and
- developing data-sharing policies that allow the value extracted from complex datasets to be maximized without compromising legitimate commercial interests.

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## PART 4

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## Section D

## Conservation

## 1 Introduction

A substantial proportion of the world's live-stock breeds are at risk of extinction (see Part 1 Section B). The need for action to protect them is recognized in the Global Plan of Action for Animal Genetic Resources (FAO, 2007a), whose Strategic Priority Area 3 is devoted to conservation. The state of implementation of conservation programmes (comprehensiveness of coverage, extent of use of different conservation methods, extent of involvement of different stakeholder groups, etc.) is described in Part 3 Section D. The present section describes the "state of the art" in the field, i.e. the methods, tools and approaches that can be drawn upon in order to design and implement effective conservation programmes and strategies. It serves as an update of the equivalent section of the first report on *The State of the World's Animal Genetic Resources for Food and Agriculture* (first SoW-AnGR) (FAO, 2007b). It draws heavily on two guideline publications on conservation prepared by FAO since 2007 – *Cryo-conservation of animal genetic resources* (FAO, 2012) and *In vivo conservation of animal genetic resources* (FAO, 2013) – and focuses in particular on recent developments.

Various methods can be used to conserve animal genetic resources (AnGR). Conservation activities can be categorized according to whether they involve the maintenance of genetic material *in vivo* or *in vitro* (see Box 4D1). *In vivo* conservation can, in turn, be classified according to whether it takes place *in situ* or *ex situ*. *In situ* conservation is undertaken in the traditional production system of the conserved AnGR. *Ex situ* conservation is undertaken elsewhere (clearly, all *in vitro* conservation is *ex situ*). *In situ* and *ex situ* conservation are usually

regarded as complementary (FAO, 2012; 2013)<sup>1</sup> and in combination they can form the basis of a powerful conservation strategy.

The first part of the section focuses on themes common to all conservation methods: planning tools; methods for identifying breeds at risk of extinction (including a description of the updated risk classification system developed by FAO since the first SoW-AnGR was published); and methodologies for determining the conservation value

<sup>1</sup> See also the "rationale" of Strategic Priority 9 of the Global Plan of Action for Animal Genetic Resources (FAO, 2007a).

## Box 4D1

Glossary: *in vivo* and *in vitro* conservation

***In vivo* conservation** is conservation through the maintenance of live animal populations. It encompasses both *in situ* conservation and *ex situ in vivo* conservation.

***In situ* conservation** is conservation through continued use of live animal populations by livestock keepers in the production system in which the respective populations evolved or are now normally found and bred.

***Ex situ in vivo* conservation** is conservation through the maintenance of live animal populations not kept under normal management conditions (e.g. in a zoological park or a governmental farm) and/or outside the area where they evolved or are now normally found and bred.

***Ex situ in vitro* conservation** is conservation through the maintenance, under cryogenic conditions, of cells or tissues that have the potential to be used to reconstitute live animals and populations at a later date.

## PART 4

of a breed as a basis for priority setting. This is followed by in-depth discussions of the two major categories of conservation: first *in vivo* conservation methods and then *in vitro* methods (otherwise referred to as cryoconservation). The subsection on *in vivo* conservation includes a look at institutional arrangements, methods for maintaining genetic variability in small populations, and strategies and methods for increasing demand for at-risk breeds. The subsection on *in vitro* conservation discusses the infrastructure and institutional frameworks for the operation of a gene bank, strategies for the development and assessment of gene bank collections, developments in cryobiology and reproductive physiology, developments in information systems and documentation of gene banked material, and legal aspects of gene banking.

A number of different arguments have been put forward as to why efforts should be made to conserve AnGR (see the first SoW-AnGR<sup>2</sup> for more detailed discussion). Conservation programmes for AnGR usually address one or more of the following objectives:

- economic – maintaining the livestock sector's capacity to respond to ecological changes (e.g. those caused by climate change), changing market demands, changing regulatory frameworks, changes in the availability of inputs, and so on;
- social and cultural – maintaining the roles of livestock in the cultural and historical identities of the communities that developed them (and for the social and cultural benefit of society more broadly);
- environmental – AnGR make an intrinsic contribution to biodiversity and they also contribute to maintaining capacity to utilize livestock in the provision of ecosystem services and to reduce the negative environmental effects of livestock production; and
- research and training – maintaining resources that are valuable for research or educational purposes (e.g. in the fields of immunology,

nutrition, reproduction, genetics, genomics and adaptation to climatic and other environmental changes).

As well as considering arguments for conservation, the discussion presented in the first SoW-AnGR also addressed differences between genetic resources conservation in the plant and animal sectors.<sup>3</sup> A number of biological (e.g. reproductive rates, generation intervals and level of diversity within breeds/varieties), operational (e.g. feasibility and costs of activities such as *in vitro* conservation, germplasm collection and clonal propagation) and institutional (e.g. patterns of ownership and use of genetic resources and the state of development of gene banks) differences between the two sectors were identified. The combined effect of these differences is that AnGR conservation programmes are generally more complicated to organize than those for plant genetic resources. A particular difference is the primary role of the private sector in managing AnGR. Individual animals are usually owned by individuals or groups of individuals, which can make implementation of organized conservation programmes more complex. Owner prerogative as to the direction of selection and mating strategies adds a unique and dynamic nature to conservation actions in this sector.

The various types of conservation programme each have advantages and disadvantages with respect to addressing particular conservation objectives. These advantages and disadvantages are summarized in Table 4D1. This summary refers to situations in which only one of the types of conservation is used. For example, if only *in vitro* conservation is used and no *in vivo* population is present, the conserved AnGR will be making no ongoing contribution to rural development.

*In situ* conservation is considered to have a number of advantages, including:

- allowing the conserved breed to continue adapting to its production environment as it changes over time;

<sup>2</sup> FAO, 2007b, pages 444–488.

<sup>3</sup> FAO, 2007b, pages 449–451.



- facilitating the maintenance of local knowledge regarding the breed and its management; and
- providing opportunities for the development of strategies that enable the breed to become self-supporting (i.e. that remove the need for external support).

However, *in situ* conservation is not without risks. For example, a population maintained *in situ* may be struck by a disease outbreak or other disaster or may be affected by inbreeding, genetic drift or introgression from another breed. *Ex situ* conservation decreases these risks by providing a backup that can be drawn upon if required. *Ex situ* conservation as a stand-alone strategy does not allow for adaptation. However, if the population is also maintained *in situ*, regularly collecting and conserving new samples *in vitro* can help to maintain the potential for future adaptation.

As described above, *ex situ* conservation can be undertaken either *in vivo* or *in vitro*. While in many circumstances maintaining a live *ex situ* population adds little to a conservation strategy that already includes *in situ* and *in vitro* components, it can have some advantages. For example, *ex situ in vivo* programmes are usually under centralized control,

which can facilitate management actions such as the control of mating. In cases where the population size is very small and no facilities are available for cryopreservation, *ex situ in vivo* conservation may be the only viable option. One weakness of *ex situ in vivo* conservation is that, because the populations are usually small (and thus highly subject to genetic drift) and animals are often kept in a single location that may not replicate their original production environments, the conserved population will usually not maintain the complete genetic diversity of the original founder population.

Table 4D1 helps demonstrate the benefits of using complementary approaches to conservation. If an *in vivo* population is maintained along with an *in vitro* collection, then the living population can be periodically sampled to enrich the *in vitro* collection and account for changes in gene frequency that occur via the adaptive process. Likewise, although in the absence of an *in vivo* population an *in vitro* collection cannot contribute to the ongoing development of rural areas, if both types of programme are in place then material from the *in vitro* collection can be actively used in the management of genetic variation in the *in vivo* population.

TABLE 4D1

#### Conservation methods and their potential to contribute to various objectives

| Objective   | Type of conservation (if implemented as a stand-alone measure) |                        |                  |
|---|--|------------------------|------------------|
|   | <i>In situ</i>   | <i>Ex situ in vivo</i> | Cryoconservation |
| <b>Maintaining flexibility for the future</b>     |  |                        |                  |
| Insuring against changes in production conditions | Yes  | Yes                    | Yes              |
| Safeguarding against diseases, disasters, etc. *  | No   | No                     | Yes              |
| Providing opportunities for research              | Yes  | Yes                    | Yes              |
| <b>Genetic factors</b>                            |  |                        |                  |
| Allowing continued evolution/genetic adaptation   | Yes  | Limited                | No               |
| Increasing knowledge of breed characteristics     | Yes  | Limited                | Limited          |
| Limiting exposure to genetic drift**              | Yes  | No                     | Yes              |
| <b>Sustainable management of rural areas</b>      |  |                        |                  |
| Providing opportunities for rural development     | Yes  | Limited                | No               |
| Maintaining agro-ecosystem diversity              | Yes  | Limited                | No               |
| Maintaining rural cultural diversity              | Yes  | Limited                | No               |

Note: \*Risk from disease in *in vivo* programmes can be decreased by maintaining animals in geographically dispersed locations.

\*\*The extent of genetic drift will depend on the population size *in situ* and the number of animals sampled for cryoconservation.

Genetic drift cannot be eliminated in *in vivo* populations, but proper management can limit drift to an acceptable level.

Source: FAO, 2013.



## PART 4

## Box 4D2

**Analysis of strengths, weaknesses, opportunities and threats (SWOT analysis) of Groningen White Headed cattle in the Netherlands**

The Groningen White Headed is a native Dutch cattle breed. The first description of the breed dates from the fourteenth century. Pictures of red and of black White Headed cows were painted during the Middle Ages. A herdbook was founded at the end of the nineteenth century. Around that time, 90 percent of all cattle in the Province of Groningen (in the northern part of the Netherlands) were White Headed cattle. They were dual-purpose animals used for milk and beef production. Animals belonging to the breed were also found near the cities of Utrecht and Leiden (in the southwest), where their milk was used for cheese production. Around 1970, the breed had 20 000 milk-recorded females, but due to cross-breeding with Holstein-Friesians, the number of milk-recorded pure-bred females had fallen to approximately 600 in 2014.

A number of national and regional groups of farmers and breeders are interested in the breed. One of them, the "Blaarkop Stichting", is very active in promoting it.

A SWOT analysis undertaken for this breed produced the following results:

**Strengths:** good performance in terms of functional traits and milk quality; distinctive appearance.

**Weaknesses:** relatively low milk yield; risk of genetic drift and loss of genetic variation.

**Opportunities:** renewed interest in functional traits is increasing the use of pure-bred Groningen White

Headed sires for cross-breeding with Holstein-Friesians; increasing use of the breed for beef production and as suckler cows.

**Threats:** the abolition of milk quotas in the European Union will increase the emphasis given to the efficiency of milk production.

Based on the results of the SWOT analysis, the breed interest groups decided to initiate three strategic actions:

1. stimulating farmers to keep the breed or to use pure-bred sires for cross-breeding with Holstein Friesians (some 20 sires are marketed by artificial insemination studs), thus taking advantage of the breed's strength of having good functional traits;
2. making Groningen White Headed semen from the National Gene bank (CGN) available to breeders when its use will increase the genetic variability in the population of pure-bred females (CGN has collected semen from 70 sires since 1973), thus addressing the weakness related to genetic variation; and
3. producing cheese and beef for niche markets and using the breed in the provision of ecological services, thus addressing the threat posed by the abolition of milk quotas by providing alternative sources of income.

Source: Adapted from Hiemstra et al., 2010.



Photo credit: Veeteelt.



Photo credit: Zwanet Faber.

## 2 Planning a conservation strategy

The planning process for a conservation strategy for a region or a country should start with a review of the status of each breed or breeding population potentially targeted for conservation activities. If inventories of breeds and populations are incomplete, effort should be made to improve them (see Part 4 Section A), as unrecorded breeds will clearly not be included in the planning process and not accounted for in the conservation strategy (although they may benefit indirectly from measures that support the sustainability of the production systems in which they are kept).

The characteristics of each breed should be described, along with its production environment and its uses, roles and values. It is also important to evaluate drivers of change and how they are affecting production systems and the breed's roles within them. Data on the size and structure of the breed population and how these are changing over time are also essential. See Part 4 Section A for a discussion of data collection methods. The estimation of risk status is discussed in greater detail below in Subsection 3. Specific threats – whether associated with production system trends, weaknesses in management or exposure to risks such as disease outbreaks or climatic disasters – should, as far as possible, be identified and evaluated (see Part 1 Section F). The overall objectives of the conservation strategy also need to be considered, i.e. which of the objectives described above in Subsection 1 are to be prioritized?

Once the relevant information has been assembled, priorities can be set (see Subsections 3 and 4) and management strategies for individual breeds can be developed. One approach to planning a conservation strategy for an individual breed is to undertake a SWOT (strengths, weaknesses, opportunities and threats) analysis of the breed and its production system (Martin-Collado *et al.*, 2013) (see Box 4D2 for an example). Threats or opportunities can be identified by analysing trends and drivers of change in the production system. Strengths

and weaknesses can be determined by considering the characteristics of the breed in relation to the requirements of production systems and national objectives for conservation and livestock development. Also relevant are population-level factors that affect risk of extinction (e.g. the size, structure and distribution of the breed population, the demographics of the livestock-keeping population) or affect capacity to implement conservation and other management activities (e.g. the presence or absence of breeders' organizations).

## 3 Identifying breeds at risk

Population size and rate of change in population size are the most important criteria for determining a breed's risk of extinction and should be recorded regularly. The two aspects of breed extinction – loss of animals and loss of gene variants – are deeply interconnected. The loss of breeding animals and consequently a low number of parents available to breed the next generation increases the average relationship between parents and may lead to a higher occurrence of genetic defects and inbreeding depression.

Species differ greatly in terms of their reproductive capacity, and this influences the ability of populations to recover after a decline. For example, a small population size creates a higher risk of extinction in horses than in pigs. In order to account for differences of this kind, FAO's amended risk categorization system (FAO, 2013) distinguishes between species with low and high reproductive capacities and includes different risk-status thresholds for each group (see Tables 4D2 and 4D3; note also that a new category – "vulnerable" – has been added to the classification system).

Once a breed's risk category has been assessed, different objectives for the management of its population can be considered. Four (non-mutually exclusive) means of strengthening the position of the breed can be distinguished:

- enlarging the population;
- managing diversity;

## PART 4

- selecting for improved productivity; and
- establishing a store of cryoconserved genetic material.

The relevance of each of these objectives for breeds in the various risk-status categories is indicated in Table 4D4.

In addition to population size and trends, other demographic factors can influence risk status. Concentration of the population in a restricted area or in a limited number of herds may place it at greater risk of extinction (Carson *et al.*, 2009). Another factor to consider is the possible presence

TABLE 4D2

**Risk categories for species with high reproductive capacity**

| Population trend and pure-breeding proportion <sup>1</sup> | Population size <sup>2</sup> (n) |     |          |           |             |               |               |         |
|--|----------------------------------|-----|----------|-----------|-------------|---------------|---------------|---------|
|  | Males (n)                        | ≤80 | 81 – 120 | 121 – 800 | 801 – 1 200 | 1 201 – 1 600 | 1 601 – 2 400 | > 2 400 |
| Increasing trend and >80% pure-breeding                    | ≤5                               |     |          |           |             |               |               |         |
|  | 6 – 20                           |     |          |           |             |               |               |         |
|  | 21 – 35                          |     |          |           |             |               |               |         |
|  | >35                              |     |          |           |             |               |               |         |
| Stable or decreasing trend or ≤80% pure-breeding           | ≤5                               |     |          |           |             |               |               |         |
|  | 6 – 20                           |     |          |           |             |               |               |         |
|  | 21 – 35                          |     |          |           |             |               |               |         |
|  | >35                              |     |          |           |             |               |               |         |

■ = Critical ■ = Endangered ■ = Vulnerable ■ = Not at risk

Note: High reproductive capacity species = pigs, rabbits, guinea pigs, dogs and all avian species.

<sup>1</sup> Many countries do not have historical data with which to determine population trends or do not regularly monitor the proportion of pure-breeding. When this information is not available, the lower part of the table should be used.

<sup>2</sup> Some combinations with large numbers of females relative to males are not realistic, especially in the absences of artificial insemination. However, they illustrate that increasing numbers of one gender may not compensate for small numbers of the other.

Source: FAO, 2013.

TABLE 4D3

**Risk categories for species with low reproductive capacity**

| Population trend and pure-breeding proportion <sup>1</sup> | Population size <sup>2</sup> (n) |      |           |             |               |               |               |        |
|--|----------------------------------|------|-----------|-------------|---------------|---------------|---------------|--------|
|  | Males (n)                        | ≤240 | 241 – 360 | 361 – 2 400 | 2 401 – 3 600 | 3 601 – 4 800 | 4 801 – 7 200 | >7 200 |
| Increasing trend and >80% pure-breeding                    | ≤5                               |      |           |             |               |               |               |        |
|  | 6 – 20                           |      |           |             |               |               |               |        |
|  | 21 – 35                          |      |           |             |               |               |               |        |
|  | >35                              |      |           |             |               |               |               |        |
| Stable or decreasing trend or ≤80% pure-breeding           | ≤5                               |      |           |             |               |               |               |        |
|  | 6 – 20                           |      |           |             |               |               |               |        |
|  | 21 – 35                          |      |           |             |               |               |               |        |
|  | >35                              |      |           |             |               |               |               |        |

■ = Critical ■ = Endangered ■ = Vulnerable ■ = Not at risk

Note: Low reproductive capacity species = horses, donkeys, cattle, yaks, buffaloes, deer, sheep, goats and camelids.

<sup>1</sup> Many countries do not have historical data with which to determine population trends or do not regularly monitor the proportion of pure-breeding. When this information is not available, the lower part of the table should be used.

<sup>2</sup> Some combinations with large numbers of females relative to males are not realistic, especially in the absences of artificial insemination. However, they illustrate that increasing numbers of one gender may not compensate for small numbers of the other.

Source: FAO, 2013.

TABLE 4D4

**Relative importance of population management objectives according to risk status**

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

Note: The larger the number of plus (+) signs, the more important the objective. Minus (-) signs indicate that the objective should not be pursued. Absence of a sign means that the objective can or should be pursued, but the decision as to whether to do so should take other factors (e.g. the cost) into account.

Source: FAO, 2013.

of controlled or uncontrolled cross-breeding. The average age of breeders, their plans to continue livestock-keeping activities and their “exit strategies” and “legacy plans”, if any, can also be significant. In many developed countries, significant proportions of livestock keepers are quite advanced in years and sufficiently financially secure to keep relatively unprofitable breeds because of tradition or as a hobby. When these breeders retire from active livestock keeping, the breeds they raise may be lost if younger breeders are not willing to take their place.

## 4 Determining the conservation value of a breed

All breeds or breeding populations categorized as being at risk of extinction can be considered candidates for inclusion in a conservation programme. However, it may be necessary to set priorities among these candidates. Risk status is often considered the most important criterion in setting conservation priorities. However, the value of conserving a given breed will be affected by a range of factors. Potentially relevant criteria include genetic uniqueness, within-breed genetic variation, traits of economic importance, unique traits and traits related to adaptation to a specific environment. The sociocultural value of the breed or its role in maintaining a unique ecosystem may also be reasons for assigning it a high priority.

When multiple factors need to be taken into account in establishing conservation priorities, one approach is to develop a “conservation priority index” that assigns different weights to the various factors (FAO, 2013). Once breeds have been prioritized, the costs of potential conservation programmes, along with their probability of success, need to be taken into account. Breed-ranking methods that include non-market values along with genetic variation and market values continue to be developed (e.g. Martin-Collado *et al.*, 2014; Zander *et al.*, 2013). However, to date such methods have mainly been limited to research. They are not widely used by countries when prioritizing breeds for conservation. Developments in this field are discussed in greater detail in Part 4 Section E.

In the case of transboundary breeds (see Part 1 Section B), prioritization may be complicated by the need to consider risk status not just at national level, but also across several countries. Collaboration at regional or global levels in the prioritization and planning of conservation activities should help ensure that transboundary breeds are not neglected because stakeholders at national level assume that they will be conserved elsewhere.

Molecular genetic data can contribute to the setting of conservation priorities (e.g. Tadano *et al.*, 2013). The panel of 30 species-specific microsatellite markers recommended by ISAG-FAO Advisory Group (FAO, 2011) still has some utility, especially for minor species, but is quickly being superseded

## PART 4

by more advanced approaches. Genomic techniques, such as detecting large numbers of single nucleotide polymorphisms (SNPs) or whole genome sequencing, allow the variety of alleles, haplotypes and genotypes within the genome to be established and the presence of rare alleles and unique genome sequences to be verified. The state of the art in the use of molecular tools is discussed in Part 4 Section B.

## 5 *In vivo* conservation

*In vivo* conservation programmes can involve a range of different types of action. In the case of *in situ* conservation, the general objectives are to support livestock keepers that raise at-risk breeds, to promote the sustainability of production systems in which at-risk breeds are kept and to promote developments that enable at-risk breeds to become more self-sustaining. More specifically, *in situ* programmes can involve (*inter alia*):

- breeding programmes that focus on increasing the productivity of at-risk breeds while managing their genetic diversity;
- efforts to promote the marketing of products from at-risk breeds;
- efforts to promote alternative uses for at-risk breeds;
- efforts to promote community-level initiatives to improve the management of at-risk breeds;
- the provision of advice on the management of at-risk breeds; and
- the provision of support payments to the keepers of at-risk breeds.

The range of activities that can be undertaken at an *ex situ in vivo* conservation site is more limited. Direct support payments are generally considered to be feasible only on a short-term basis.

The success of an *in vivo* conservation programme is likely to depend on the presence of an appropriate institutional framework. The tasks involved in organizing such a framework are discussed below in Subsection 5.1. Specific tools and approaches are discussed in Subsections 5.2 and 5.3.

### 5.1 Institutional arrangements

The context for *in vivo* conservation programmes will vary greatly between countries and between species. However, sustainable and realistic plans and appropriate mechanisms for involvement of livestock keepers and other stakeholders will always be required. An *in vivo* conservation programme, particularly an *in situ* programme, is likely to involve a wide array of stakeholders. Depending on the circumstances, these may include livestock keepers and breeders, government institutions, breeders' associations, breeding companies, research and education institutes, NGOs, consumers and marketers. Livestock keepers and breeders are the cornerstones of any *in situ* conservation programme and ensuring their commitment to the goals of the programme is essential.

In some countries, mechanisms for livestock-keeper participation in conservation programmes are well developed, particularly via the activities of breeders' associations. Elsewhere, involving livestock keepers in organized conservation activities often remains very challenging. Initiatives to promote so-called community-based conservation programmes have been taken in various countries (FAO, 2003). Establishing a programme of this kind is normally a multi-faceted task and requires careful assessment of the current and potential future roles of the targeted breed(s) in the livelihoods of local people. A top-down approach is unlikely to be successful. In other words, the livestock keepers potentially involved in the conservation activities will need to participate, from the start, in assessing the feasibility of the scheme and its relevance to their livelihoods and future objectives. New measures introduced to support the maintenance of the targeted breeds (e.g. breeding or marketing activities) will need to be planned in close collaboration with livestock keepers and other relevant stakeholders.

The long-term success of a community-based scheme is likely to depend on its being able to operate effectively with relatively little outside support (e.g. from government agencies).

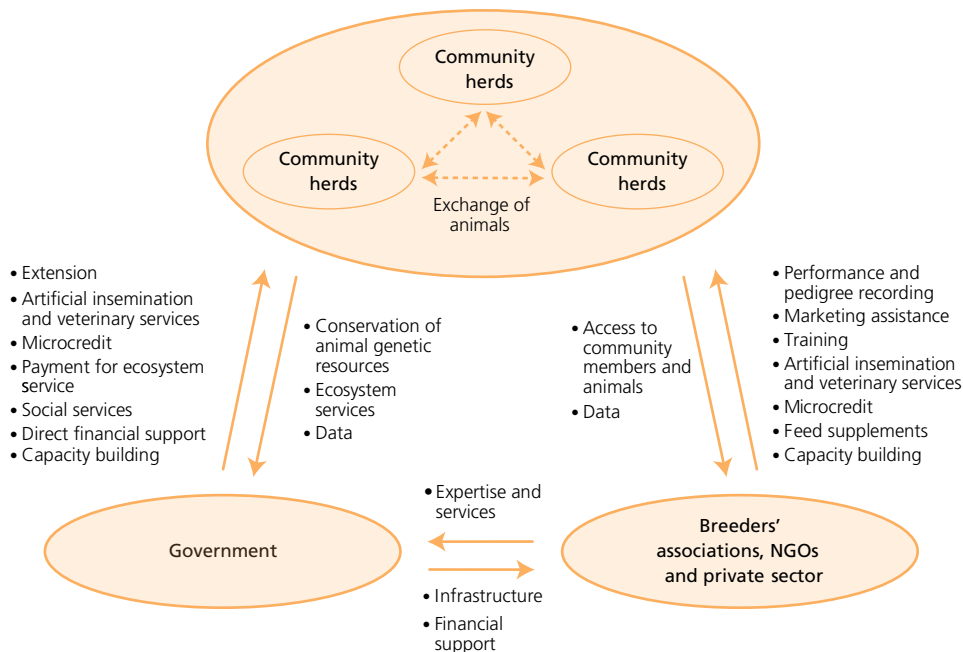
Establishing or strengthening organizations within the community that are able to undertake the various tasks involved in implementing the programme (breeders' associations, marketing cooperatives, etc.) will therefore be essential. Nevertheless, as illustrated in Figure 4D1, some outside support from government or NGOs is likely to be necessary, particularly during the early phases of the programme. For example, at the start of a programme it may be necessary to create infrastructure such as new facilities for processing livestock products. Capacity-building to strengthen livestock keepers' abilities to undertake any new activities introduced as part of the programme is likely to be essential.

In many instances, particularly in developing countries, a livestock-keeping community that is a potential player in a conservation programme

will have a very strong cultural tie to their breed and strong interactions are likely to exist between the community, the breed and the production environment. In such cases, the survival of the breed *in situ* will depend on the sustainability of these interactions. The community will often have indigenous knowledge on how to co-manage the animals and the local environment and have clear goals and ideas about selection. Documenting a community's role in the maintenance of AnGR diversity (and biodiversity more broadly) may encourage the development of policies that are favourable to the continued existence of the community and thus to the conservation of the breeds they keep. One approach that has been attracting increasing interest in recent years is to record such information in

FIGURE 4D1

#### Interactions among the potential stakeholders of a community-based conservation programme



Note: The ellipses indicate the major stakeholders. The bulleted lists indicate the goods and services exchanged between each pair of stakeholders, with the solid arrows indicating the flow of these goods and services.

## PART 4

the form of a biocultural community protocol, a formal document prepared on the basis of consultations between community members, lawyers and experts in indigenous knowledge (see Box 4D3).

Breeders' associations can contribute in many ways to conservation activities, as well as to other aspects of AnGR management. Promoting the establishment of well-organized and well-functioning breeders' associations, where they do

## Box 4D3

**Biocultural community protocols**

Biocultural community protocols (BCPs) are a tool developed in response to the Nagoya Protocol on Access and Benefit-Sharing. The Protocol mandates governments to support indigenous and local communities, including women within these communities, to develop "community protocols in relation to access to traditional knowledge associated with genetic resources and the fair and equitable sharing of benefits arising out of the utilization of such knowledge."

BCPs are established through a facilitated process in which a community or group of livestock keepers reflect about the meaning and importance of their breeds and their production system, their own role in maintaining these resources and their vision and concerns for and about the future. The facilitators help the community to put these reflections down on paper, and provide information and advice about existing national rules and international legal frameworks that support the role of communities in *in situ* conservation and provision of ecological services.

BCPs make visible the linkages between breeds and the communities that have developed them. They establish breeds as the "prior art" of communities and therefore represent community claims over animal genetic resources. With regard to the implementation of the Nagoya Protocol, BCPs are potential tools in the process of establishing prior informed consent and mutually agreed terms when animal genetic resources sourced from indigenous and local communities are either utilized for research within the country or moved across international borders for that purpose.

BCPs also document community assets, including genetic resources, customary rights and traditional knowledge, and raise awareness about the value and

potential of local production systems. They may also be important when public-private partnerships that involve livestock keepers are set up, and could be a first step towards payment for environmental services.

The process itself is extremely empowering for communities, as a means of self-reflection and understanding their existing rights. In addition, having at hand a written document that details their rights puts communities in a much better negotiating position with outside actors.

By October 2014, about eight livestock-keeping communities in India, Kenya and Pakistan had established BCPs. Interest in and demand for this approach are also increasing in other countries, especially in Africa and Latin America. A programme to develop more BCPs in India is ongoing.

Communities that have benefitted from the BCP process include the Brela pastoralists of Pakistan, who are nomadic and keep chickens and camels. The Brela camel breed is highly valued by the camel dairy industry in oil-rich countries because of its exceptional dairy potential. After going through the BCP process and becoming aware of the value of their genetic resource, the Brela pastoralists were able to double, triple and even quintuple the prices obtained for their female camels – increases of such a magnitude that sale of even one camel will provide sellers with enough income for the rest of their lives (Abdul Raziq Kakar and Rao Qadeer, personal communication).

Provided by Ilse Köhler-Rollefson and Evelyn Mathias.  
For further information see UNEP and Natural Justice (2009) and the  
"Community Protocols" website maintained by Natural Justice (<http://www.community-protocols.org/>).

not already exist, is therefore an important objective. However, this can again be a challenging task. For example, potential members may lack the relevant organizational skills or there may be a lack of agreement over objectives for the management of the targeted breed. Elements that need to be considered in the establishment of a breeders' association include rules on eligibility for membership, procedures for registering animals and validating pedigrees, by-laws for the operation of the association (election procedures, composition of the board of directors, etc.), procedures for communication among the membership, procedures for conflict resolution and procedures for evaluating the performance of the association.

Where a range of different stakeholders are involved in conservation activities (e.g. both commercial farmers and hobbyists) and the animals are kept for a variety of purposes (e.g. for food production and for the management of landscapes and wildlife habitats) different objectives may result in different views about what breeding goals are appropriate (Lauvie *et al.*, 2011). However, the populations concerned will often be too small to allow the simultaneous operation of several different conservation and/or selection programmes.

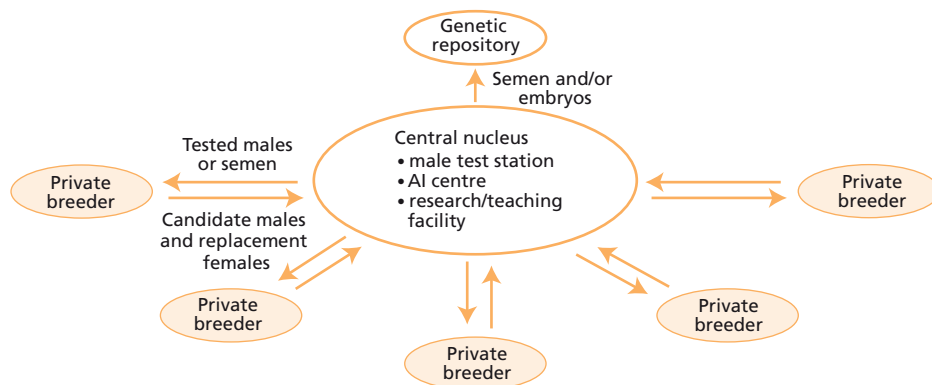
In these circumstances, it is important to ensure effective communication among stakeholders and discussion of any tensions that may arise.

Breeding goals may change over time and this will affect the genetic variability of a breed population conserved *in vivo*. For example, as noted by Martyniuk *et al.* (2014), many dual-purpose (milk and beef) cattle breeds in Europe are no longer used primarily for mainstream food production and their numbers have decreased sharply. Animals belonging to these breeds are now used for a variety of purposes, mainly in suckler cow systems, where improving beef production from the offspring is an important objective. This has meant that the breeding goal (in the past a balance between milk and beef production) has shifted more towards beef production. This, in turn, means that genetic diversity in the populations maintained *in situ* will come to differ from that present in the original dual-purpose populations. This phenomenon calls for storage of genetic material from the original populations in a gene bank.

The maintenance of *ex situ in vivo* populations can also play an important role in conservation strategies. For example, they may provide a means of sustaining a breed whose population

FIGURE 4D2

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



Source: FAO, 2013.



## PART 4

has declined to such an extent that it is difficult to maintain *in situ* or a breed for which there are few current options for promoting profitable production *in situ*. Establishing and operating an *ex situ in vivo* facility involves a substantial investment and provides little return in the short term. Programmes of this type are typically operated by governments, research institutes or NGOs and their long-term existence may be threatened by financial shortfalls.

One potential means of overcoming the constraints imposed by the cost of operating a centralized institutional farm is through the use of a dispersed model in which a breeding nucleus is linked to herds kept by NGOs and by private individuals who are willing to raise animals on a commercial or hobby basis. A network of several herds can provide a basis for an integrated conservation programme and systematic genetic improvement. The basic design of this type of model is illustrated in Figure 4D2. This approach is promoted in India as a means of conserving several of its indigenous cattle breeds.

## 5.2 Conserving genetic variability in small populations

The probability that a breed will survive depends greatly on the amount of genetic diversity it harbours. A high level of genetic diversity allows the population to adapt to changes in the production environment. It prevents the rise of inbreeding and its detrimental effects. In very small populations, i.e. breeds whose risk status is critical or endangered, the management of genetic diversity is crucial to survival, and breeding programmes should focus on this task (see Subsection 3 for an explanation of the risk-status categories). In populations that are somewhat larger, i.e. breeds whose risk status is vulnerable, there is more opportunity to implement programmes aimed at genetic improvement. However, maintaining genetic variation remains essential.

A strategy aimed at maintaining a breed's genetic variability needs to focus on managing the relationships among the breeding animals. Measures that can be taken include:

- involving as many animals as possible in the programme from the start in order to minimize genetic drift;
- increasing the number of males used for breeding;
- lengthening the generation interval;
- optimizing the contribution of each individual to the next generation;
- banking genetic material at the start of the programme and then at regular intervals, so that it can be used in subsequent generations; and
- in species with low reproductive rates, using embryo transfer to increase the population size.

It is also possible to adopt a mating strategy aimed at reducing inbreeding. This can involve:

- setting a limit to the degree of relationship between mates;
- using algorithms and software that determine the ideal set of matings for the entire population; and
- simple strategies that can be implemented even if no pedigree information is available (e.g. fixed rotation of males between herds).

Determining molecular coancestry using SNP-chip technology is a very effective tool in the management of genetic diversity within a population (Gómez-Romano, 2013). Several strategies for maintaining molecular genetic diversity in conserved populations have been developed (Fernandez *et al.*, 2011; Toro *et al.*, 2014). In general, molecular coancestry is a better descriptor of genetic relationships in a population than pedigree coancestry and is a better indicator of inbreeding and inbreeding effects. Pedigrees only indicate expected genetic relationships, whereas molecular coancestry provides information about the actual transmission of genes from parents to offspring. Moreover, pedigree registration occasionally includes errors (e.g. Kugonza *et al.*, 2012). Errors occur in genotyping as well, and these errors can affect the accuracy of estimates of genetic parameters (Hinrichs and Suarez, 2005). However, they tend to be less serious than incorrect assignments of parentage in pedigrees.

It is, however, important to pay particular attention to determining whether genetic similarity between animals at molecular level indicates identity by state or identity by descent (Powell *et al.*, 2010; Stevens *et al.*, 2011). Where maintaining diversity in a conserved population is concerned, identity by descent is of primary interest (Toro *et al.*, 2011).

Use of genomic technology in small conserved populations is very informative and highly recommended where possible (e.g. Pertoldi *et al.*, 2014). Clearly, however, costs and requirements for technical expertise will limit such applications, especially in developing countries. Accuracy of inference depends on the amount of genomic information available (e.g. the number animals genotyped and the number of SNPs per animal) (Toro *et al.*, 2011).

Further information on the various tools and approaches discussed in this subsection can be found in FAO's guidelines on *in vivo* conservation (FAO, 2013).

### 5.3 Potential strategies for increasing demand for at-risk breeds

Breeds may face the risk of extinction because their productivity is low and therefore keeping them provides inadequate economic returns. Breeding strategies can be a means of addressing this problem. Options include within-breed selection programmes (balancing between genetic progress in terms of increasing production and avoiding an increase in inbreeding) and strategies based on cross-breeding. The optimal approach will depend on the situation. As in all circumstances, any breeding strategy adopted must be well-matched to the production system (FAO, 2010). The size of the population is also an important consideration. If populations are too small, within-breed selection may not be a viable option. Genetic drift is likely to negate any potential for progress through selection.

Cross-breeding may not, at first sight, appear to be a good means of promoting the conservation of an at-risk population. However, there are situations where cross-breeding can be extremely

useful. For example, if a breed population has become so small that it is non-viable, limited crossing with a genetically similar breed to increase the population size and increase genetic variability may be an option to consider. Moreover, cross-breeding strategies that involve ongoing maintenance of pure-bred populations (e.g. terminal crossing systems) may create a profitable means of utilizing breeds that in their pure-bred form are not sufficiently competitive to encourage livestock keepers to maintain them.

Aside from breeding strategies, a number of other methods can potentially be used to increase the value of at-risk breeds to livestock keepers (or other potential users) and hence promote their continued use. Techniques such as SWOT analysis (see Subsection 2) can help in the identification of appropriate strategies for specific breeds.

One potential, and relatively straightforward, approach is to provide practical support to livestock keepers that raise at-risk breeds. This can both increase the likelihood that the livestock keepers will be willing and able continue raising the targeted breeds and help ensure that they are appropriately managed in genetic terms. The type of support needed will clearly vary depending on the circumstances. Where an organized community-based conservation programme (see Subsection 5.1) is being implemented, the aim should be to tailor advice and support to the specific conservation activities being undertaken. More broadly, the provision of appropriate services that support the sustainability of diverse livestock-keeping communities – particularly smallholder and pastoralist communities – is likely to promote the continued use of the locally adapted breeds associated with these communities. In many circumstances there will be potential for increasing the profitability of livestock keeping by improving management at farm (or herd/flock) level (improving feeding, housing, disease control, etc.). Where “hobby farmers” (largely a developed-country phenomenon) are concerned, enthusiasm for keeping locally adapted breeds may not be matched by sufficient experience in breeding and in other aspects of animal husbandry. Advice on these matters may

## PART 4

therefore be needed. One option for disseminating breed-specific knowledge is to implement a “role model breeders” programme that enables the experience accumulated by long-standing and successful breeders to be passed on to others (see FAO, 2013 for further discussion of schemes of this kind).

Another means of increasing the profitability of keeping an at-risk breed is to increase the marketability of its products (see Box 4D4). This may enable lower production levels to be compensated for by higher per-unit prices. Particularly in developed countries, a lot of attention has been paid in recent years to the development of niche markets for the products of “non-mainstream” breeds (e.g. Ligda

and Casabianca, 2013). In some cases, this involves marketing on the basis of some unique and desirable characteristic of the product itself (e.g. superior taste). In others, it involves some desirable aspect of the breed’s production system (e.g. the appeal of buying a locally grown product). Initiatives of this kind can be facilitated by the existence of labelling schemes that increase consumer confidence in the provenance of the products (see Part 3 Section F Subsection 4.4 for a discussion of legal frameworks for schemes of this type).

As well as providing marketable goods and services, livestock also have the potential to deliver various other kinds of benefits within the

## Box 4D4

**Identifying keys to success in breed conservation and development in France: the VARAPE project**

About 30 percent of French local breeds are considered to be endangered according to thresholds set by national legislation (fewer than 5 000 breeding females for cattle, 8 000 for sheep and goats, 1 000 for pigs). Most of these breeds declined until the 1970s, at which time the introduction of national conservation policies and programmes helped to stabilise or increase their population sizes.

The VARAPE project (valorization of rare breeds with short supply chains), which ran from 2012 to 2014 and targeted 13 breeds, was coordinated by France’s Institut de l’Élevage, working in association with seven technical partners. Based on 13 breed surveys (involving inventories of production and marketing, and meetings with local committees) and 16 case studies, the project aimed to assess factors influencing the success of collective projects targeting the development of short supply chains for breed products.

One output was a diagnostic tool that can be used to formalize breed valorization projects and choose optimal organizational structures. Eight keys to success were identified:

- building a network involving all relevant stakeholders (farmers, processors, retailers, etc.);
- ensuring long-term coordination of the network;

- sharing a common vision and common objectives;
- highlighting links to history and culture;
- developing products and markets in a way that is consistent with the production capacity of the livestock keepers involved;
- establishing adequate quality indicators or labels;
- identifying relevant economic and technical indicators; and
- maintaining links with partners.

The results of the study showed that breed associations generally wanted to improve marketing structures, with the aim of increasing the number of livestock keepers raising the breed and improving the protection of their products from unfair competition (misleading labelling, etc.). They also showed that quality indicators (individual brands or schemes such as the European Union’s Protected Designation of Origin or Traditional Specialities Guaranteed) need to be chosen according to the specific context of the breed, considering factors such as the size of the breed population and the type of product involved.

Provided by Lucie Markey and Christèle Couzy.  
For further information on the VARAPE project (in French)  
see [www.varape.idel.fr](http://www.varape.idel.fr)

ecosystems in which they are kept, for example by maintaining landscapes and wildlife habitats (see Part 1 Section D and Part 4 Section E for further discussion). Given that these benefits tend to be public goods, they generally cannot be marketed (i.e. directly sold to consumers) to provide additional income for livestock keepers. However, governments may be willing to pay for services of this kind. For example, so-called “conservation grazing” has become a significant tool in the management of wild biodiversity in a number of countries, mainly in developed regions. This trend has created opportunities to keep locally adapted breeds of grazing animals such as cattle, sheep, goats and horses in use and hence to promote their conservation. Locally adapted breeds are often the best suited to this role because of their ability to cope with the harsh environments (mountains, heaths, wetlands, etc.) where such services are often required.

Touristic value is another attribute that can potentially be exploited to promote conservation. This is more likely to be the case where the breed has some kind of distinctive appearance or is closely linked to local products or cultural traditions. Some communities hold festivals celebrating traditional customs associated with raising local breeds of livestock. Such events, although they may not provide direct economic support to livestock keepers, may improve the economic status of the communities in general (e.g. by promoting tourism) and can provide marketing opportunities for the breeds’ products.

When possible, combining a number of different conservation activities is a logical approach. Box 4D5 describes a proposed programme to conserve Pantaneiro dairy cattle in Brazil. The programme aims to combine practical support for breeding with the marketing of a breed-specific product. In addition, opportunities have been identified to exploit specific genes from the Pantaneiro in breeding programmes for other breeds, as well as to leverage the ecosystem services provided by the breed in its traditional production environment.

## 6 Cryoconservation

As described in Part 3 Section D, recent years have seen an increase in the number of national gene banks and in the sizes of their collections (see also Boettcher and Akin, 2010; Pizzi *et al.*, 2010). National gene banks are a relatively new element of AnGR management and there have been ongoing efforts to develop the protocols and facilities needed to increase their operational efficiency.

All the available scientific evidence indicates that cryopreserved biological material can be stored without deterioration for several thousand years (Mazur, 1985). The possibility of long-term storage opens opportunities to conserve and utilize animal genetic diversity in ways that were impossible in the past when *in vivo* conservation was the only option available. Cryoconservation programmes can serve a number of purposes. FAO (2012) identified the following major objectives:

- One common reason for gene banking is to provide the possibility of recreating breeds or breeding lines if they are lost as the result of a catastrophic event or deliberately allowed to go extinct for financial reasons (e.g. the discontinuation of a specialized research line). In such cases, having sufficiently large and genetically diverse collections of germplasm from the affected breeds can allow them to be reconstituted.
- Cryoconserved material can be used to introduce genetic diversity into *in vivo* populations for the purposes of reducing inbreeding levels and broadening diversity. It can also be used to provide flexibility to the livestock industry when selection goals are found not to be as desirable as initially thought.
- Gene bank collections are invaluable if breeds are threatened with extinction because of an extreme genetic condition such as high frequency of a genetic defect resulting from selection or genetic drift. Stored material

## PART 4

Box 4D5

**Indigenous people and scientists team up to conserve Pantaneiro cattle in Brazil**

Pantaneiro cattle have lived in Brazil's Pantanal Biome since their introduction by the Portuguese some 400 years ago. They are believed to be resistant to trypanosomosis, myiasis, worms and ticks. They are able to survive under the challenging ecological conditions of the Pantanal, which include both floods and droughts, as well as coarse native pastures and jaguar predation.

At the beginning of the twentieth century there were several thousand Pantaneiro cattle. However, the breed's population has since fallen to a few hundred. Interbreeding with commercial breeds is the main threat to its survival. Today, only 500 pure-bred animals, split between two herds, are left. This small population size and the accompanying loss of genetic variation threaten to erode the breed's capacity to adapt and survive.

Commercial breeds have lost some alleles associated with fitness and survival in harsh environments. One example is the G1 allele of the bovine growth hormone gene, dubbed the "thrifty gene", which has become essentially extinct in commercial breeds, but can be found in some traditional cattle (Dani *et al.*, 2010), including the Pantaneiro.

As part of efforts to protect the Pantaneiro breed and the ecosystem to which it is adapted, as well as

their own livelihoods and culture, indigenous people from the Pantanal region have teamed up with scientists from several Brazilian research institutes to develop the Pantanal Biome Cheese Project. As the true "Nicola cheese", a traditional local product of the Pantanal, is prepared with the milk of Pantaneiro cows, it is threatened with extinction along with the breed. However, it may also hold the key to the breed's conservation. The production and commercialization of Pantaneiro cattle and Nicola cheese may provide the Pantaneiro people with regular income, while also helping them conserve the local ecosystem.

One of the activities undertaken by the scientists working on the Pantanal Biome Cheese Project is to screen the Pantaneiro cattle for genetic polymorphisms associated with milk protein and fat composition, as well with the "thrifty" phenotype of these cattle. This molecular characterization will not only help identify valuable genetic resources for breeding, but will also serve as the basis for marker-assisted certification to ensure accurate identification of the genetic material of Pantaneiro animals and the breed's products. The scientists believe that a conservation programme that includes marker-assisted selection, distribution of genetic material such as semen and embryos, and marker-assisted certification of origin may help save the Pantaneiro cattle from extinction and also contribute to the conservation of the Pantanal Biome and the life and traditions of its people.

The Pantanal Biome Cheese Project capitalizes on the fact that the Pantanal Biome is a Biosphere Reserve included in UNESCO's World Heritage and the MAB-Man and Biosphere programme of the United Nations.



Photo credit: José Medeiros.

Provided by Sergio Ulhoa Dani and Marcus Vinicius Morais de Oliveira.  
For further information see Dani and Oliveira (2013) and  
<http://biomacheese.blogspot.it/>

from animals not carrying the deleterious allele can be used to decrease the frequency of the defect to a manageable level.

- Gene bank collections can be used to develop new lines or breeds, introgress desired characteristics from one breed into another or quickly reorient the evolution or selection of a population.
- Gene banks serve as a ready source of genetically diverse and specialized DNA for genetic diversity studies, genome-wide association studies, exploration of gene function and other types of research. Importantly, gene banks can, over time, provide multigenerational samples that contribute to increasing the accuracy of genomic selection. These latter benefits will be more easily realized if information on animals' phenotypes is maintained along with their genetic material (see Subsection 6.4).

### 6.1 Gene bank operations, infrastructure and institutional frameworks

A national gene bank should be designed in accordance with the needs and capacities of the country. Staffing a gene bank requires, in particular, expertise in genetics, cryobiology/reproduction and data management. The necessary physical infrastructure also needs to be developed. Figures presented by FAO (2012) illustrated that, in the case of small repositories, the cryopreservation component of a gene bank could potentially be established for less than US\$50 000 in equipment costs. Greater access to commercial genotyping and potentially to large amounts of genomic data implies that a gene bank needs either to develop within-house capacity to conduct statistical analysis and interpret genetic and genomic data or contract out the analysis phase of genetic diversity studies. Hardware costs associated with the development of information systems are relatively minor. The largest recurrent costs in the operation of a gene bank are usually those associated with human resources.

A cryoconservation programme can involve the collection of various types of genetic material. Semen is the most commonly banked material. Embryos are more complicated and expensive to collect and store (Gandini *et al.*, 2007). However, if a breed needs to be reconstituted, embryos have an advantage over semen in that they provide the full genetic complement of the reconstituted breed in a single generation. Reconstitution with semen requires several generations of backcrossing and will never achieve 100 percent reconstitution of the original genome. Moreover, the mitochondrial genome of the original breed is totally lost if only semen is stored. As well as semen and embryos, gene bank collections can include oocytes and various gonadal and non-gonadal tissues.

Because of the role of the private sector in maintaining breeds *in situ*, it is essential that gene banks have close links to individual breeders and to breed organizations or live-stock-keeping communities. This allows stakeholders to communicate their needs and helps establish working relationships that facilitate the collection of samples.

Gene bank collections should be viewed dynamically, with samples entering and exiting the gene bank as a matter of routine and being used for a variety of purposes. This type of approach is relatively new in the livestock sector. Each gene bank should have a set of protocols and procedures for assessing requests for germplasm. One option is to establish an advisory committee (e.g. consisting of industry and public-sector representatives) to review and make recommendations concerning requests. Issues for consideration when reviewing such requests can include the availability of the respective genetic resource *in situ*, whether the gene pool needs to be expanded, current and projected inbreeding levels, selection options available to the breeders and the way in which the progeny obtained using the gene bank material are to be utilized. Depending on the policies or regulations of the country, the advisory committee may also be interested in knowing whether,

## PART 4

and if so how, germplasm from the progeny will eventually be made available to help replenish the gene bank.

Choice of breeds for inclusion in a gene bank collection can be politically sensitive. Gene bank managers should recall that while breeds do not need to be treated equally they should be treated equitably and reasonably.

Because of the increasing number of national gene banks (see Part 3 Section D) the question of potential international cooperation in gene banking is becoming increasingly prominent. Potential cooperative activities need to be evaluated on the basis of the needs and capabilities of the potential partners and the potential benefits that might be gained. Establishing linkages between gene banks is likely to be easiest at regional level, as there are likely to be shared interests, similar breed types and similarities in collection protocols. For example, groups of countries in the Americas and in Europe have identified common goals and interests. These are generally based on broad initiatives such as the development of shared databases (or at least some level of commonality among databases) and the exchange of experiences and technical know-how. Protocols used to cryopreserve samples or to genetically evaluate collections are another area of collaboration.

In the plant genetic resources sector, pairs or groups of countries have agreed to back up each other's gene banks by holding a complementary collection of some or all samples. However, for several reasons this approach has rarely been employed in the AnGR sector. Sanitary regulations restricting germplasm movement across national boundaries are a major limitation. It may, however, be possible to overcome constraints of this kind by classifying material "for gene bank storage only" (i.e. not for use within the importing country). If the material is not used in the importing country, then the risk of disease transmission will be low. Administratively, the most direct and effective means for a country to back up samples from another country is via a bilateral agreement. Such an approach also facilitates the

identification of the specific needs of the cooperating countries and their rights, limitations and obligations with respect to storing and using the material.

## 6.2 Establishment and assessment of gene bank collections

### *Collection strategy*

The establishment and ongoing operation of a gene bank collection require strategic decisions regarding what material to collect. Consideration needs to be given to the intended scope of the collection. For example, some countries have focused gene bank collections on at-risk breeds (Mariane *et al.*, 2009; Paiva *et al.*, 2014), while others are developing collections that include both at-risk and mainstream breeds (e.g. Pizzi *et al.*, 2010; Blackburn, 2009; Woelders and Hiemstra, 2011). While it is possible to argue that widely used transboundary breeds are not priorities for inclusion in conservation programmes, there are several reasons why countries may wish to include such breeds in their collections. For example:

- widely used transboundary breeds are likely to be important for the future of commercial agriculture and therefore need to be included in the gene bank to ensure a backup that can be drawn upon in case of need;
- large collections of material from such breeds have been shown to be invaluable in providing specific alleles or allelic combinations for use in industry or research; and
- collecting samples from such breeds will ensure that changes in allelic frequencies that may confer adaptation to environmental variables are captured and available for use as needed.

Regardless of what types of breed a country chooses to target, there will be a need to assess the genetic diversity captured and the quantity of germplasm accumulated and to optimize the collection in accordance with associated costs. Theoretical methods for prioritizing breeds (e.g. Boettcher *et al.*, 2010; Martin-Collado *et al.*, 2013) and animals



(e.g. Blackburn, 2009; Engelsma *et al.*, 2011) have been developed. Blackburn (2009 and 2012) discusses practical approaches to building collections at both within-breed and between-breed levels. In practice, effective development of a collection requires flexibility in the selection of animals within a population and the capacity to adjust and adapt cryopreservation protocols to the given situation. For example, theoretical approaches to selecting the optimal set of gene bank donors typically lack the flexibility needed to account for real-life circumstances such as the death or poor fertility of an animal targeted for collection or the refusal of its owner to allow access.

In developing a collection there is need to determine the minimum quantities of germplasm and genetic variation needed to meet the objectives of the gene bank. In general, the primary objective will be to store enough germplasm to reconstitute a breed that is extinct (*in vivo*) to create a new population with an effective population size of 50 animals. Population reconstitution is generally the objective that requires the greatest quantity of germplasm. The quantity required will depend on a number of factors, including the type of germplasm stored, the species involved and the reproductive efficiency achieved (see FAO, 2012 for further information). In general, breed reconstruction requires fewer embryos than units of semen. Species with multiple offspring per pregnancy, such as chickens, rabbits and pigs, will require fewer doses of semen than species, such as cattle, horses and small ruminants, that produce one or few offspring. The higher the expected pregnancy and survival rates, the less germplasm is needed.

Once minimum quantities for a given cryoconservation objective have been achieved (i.e. sufficient numbers of donors and quantities of germplasm per donor have been acquired), gene banks can consider various approaches to the management of their collections. For example, the national gene bank in the United States of America has developed an index that gives equal weight to quantities of germplasm and number of donors and uses this index to monitor the

inventories of breeds with material in the bank (Blackburn, 2012). The index provides a simple means of identifying breeds for which additional collection would be beneficial. Closer examination of the data contributing to the index can then determine whether a given breed simply requires collection of additional material (i.e. from the same animals or their close relatives) or whether genetically diverse material from new, unrelated donors is needed.

While meeting targets is a first objective in the development of a gene bank collection, gene bank managers may choose to expand the scope of their collections for a variety of reasons. Smith (in FAO, 1984) showed that the probability of capturing an allele in 10 or more units of semen is equal to  $1 - (1 - P)^{2N}$ , where P is the allelic frequency and N is the number of males sampled (equation modified by Blackburn, 2004). As this equation demonstrates, increasing the number of males collected raises the probability of capturing an allele, but with a trend of diminishing returns. For example, with an allele frequency of 0.005, sampling 100 males will result in a 63 percent probability of capturing the allele. With 300 males, this value jumps to 95 percent. However, increasing the number of males sampled to 500 will raise the probability only another 4 percentage points, to 99 percent. This suggests that big collections may be necessary in order to capture and preserve extremely rare alleles. For example, the United States of America's gene bank has a large collection of samples from Holstein cattle. This has allowed the cryoconservation of semen from bulls that carry rare Y chromosomes that are no longer present in the *in situ* population (Yue *et al.*, 2015).

### **Assessing and ensuring genetic diversity**

There are several approaches that gene bank managers can use to assess the genetic diversity of the collection and to identify the animals in the *in vivo* population that they wish to sample to broaden the diversity of the collection. These approaches may use pedigrees, molecular markers and/or geographic location as indicators of diversity. In addition to genetic variability, there is a



## PART 4

need to consider variability in phenotypic or genetic measurements (e.g. breeding values) for economically important characteristics.

A broad array of analyses can be applied to pedigree information to estimate genetic parameters and compare the diversity of animals in the collection and in the *in situ* population. For example, Danchin-Burge *et al.* (2011) used the parameter “effective number of founders” to demonstrate that both the French and the Dutch gene banks have fully captured the level of genetic diversity present in the *in situ* Holstein population. They also showed that the effective number of Holstein-Friesian founders stored in the United States of America’s gene bank substantially exceeds that of the current *in situ* population. With pedigree information available, the genetic coefficient of relationship between animals in the collection and the *in situ* population can be computed. This information can be extended, through various clustering routines, to determine the status of germplasm already in the collection (in terms of influential founders and their descendants) and identify groups of animals that might be targeted for procurement to increase the genetic variability in the collection (Blackburn, 2009; FAO, 2012; Blackburn, 2012).

The development of collection strategies can also be supported by the use of DNA markers (either microsatellites or SNPs) to assess differences among and within populations. For example, a comprehensive assessment of microsatellite genotypes among sheep breeds in the United States of America determined that the Warhill population should be classified as a strain of Rambouillet and not as a separate breed (Blackburn *et al.*, 2011). As a result, collection strategies were adjusted. Numerous characterization studies have evaluated breed similarities and differences at the molecular level, both within and across countries (for a review, see Groeneweld *et al.*, 2010). Countries should consider such results and consult with each other when developing gene banking strategies, particularly for transboundary breeds. As the functional role of genes marked by particular SNPs is determined, it

will become possible to incorporate such information into strategies for the assessment and acquisition of gene bank collections.

Geographic approaches to planning and evaluating collections have been used for wild animal species and plant genetic resources (e.g. Hijmans *et al.*, 2000). However, in the case of AnGR, the utility of developing or evaluating collections solely on the basis of geographic location seems to vary from situation to situation. At the breed level, pedigree or molecular data suggest that in some instances there are only slight to modest differences between geographically distant populations. For example, Maswashie and Blackburn (2004) found no evidence of substantial subpopulations of Navajo Churro sheep across the United States of America. Based on SNP data on African goat breeds, Huson *et al.* (2014) suggest that there is little genetic differentiation among goat breeds found in the various countries of East Africa.

Comparing average phenotypes or estimated breeding values (EBV) of animals with material stored in gene bank collections to those of *in situ* populations serves to gauge the completeness of the collection in terms of diversity and its utility for various functions. Whenever possible, highest and lowest values for animals in the bank should, respectively, be superior and inferior to the mean by at least one standard deviation. “Bounding” the breed’s mean in this way helps ensure that two important goals are met: first, the choice of animals with both high and low values ensures that genetic variability is captured; second, the choice of animals with high (i.e. favourable) EBVs means that samples in the collection are likely to have industry relevance for two to five decades. If this approach is followed, taking a large number of traits into account and with periodic resampling, there is no reason for gene bank collections to become obsolete.

### 6.3 Cryobiology and reproductive physiology

At one time, the advice was that gametes for cryoconservation should be collected only at artificial insemination centres (FAO, 1998). However,

the experiences of the last decade show that this is not necessary, particularly for material to be utilized at country level (i.e. that is not going to be exported). Assuming the sanitary restrictions of the respective country allow (and if proper collection, cryopreservation and health procedures are followed), germplasm and tissue from nearly all livestock species can be acquired in the field with little to no negative consequences in terms of viability or veterinary hygiene. This provides additional opportunities to capture genetic diversity and reduce collection costs. Once germplasm has been collected, it can generally be stored for 24 to 36 hours while being transferred to a cryopreservation laboratory. Fresh semen from various species has been routinely moved from place to place prior to being used successfully for insemination, suggesting that semen transported in this way can also be cryopreserved and banked. For example, Purdy *et al.* (2010) found that ram semen could be held for 24 hours before cryopreservation and still achieve acceptable fertility and prolificacy levels when subsequently used for artificial insemination.

If traditional semen collection and processing are not feasible because of a lack of facilities or expertise near the area where the targeted animals are raised, or if genetically valuable animals die before collection is possible, collecting epididymal sperm from deceased or castrated animals may be a useful means of enhancing gene bank collections (Silvia *et al.*, 2014). Testes collected from such animals are quite robust, and sperm remain viable after several hours of storage at body temperature or even longer if properly cooled. This allows collection on the farm or at the slaughterhouse and transport to a laboratory. Recent studies on the cryobiology of epididymal sperm from ibex (Pradiet *et al.*, 2014) and goats (Turri *et al.*, 2014) suggest that storing such material in gene banks is feasible.

Direct freezing of samples in the field may be an option, depending on the type of biological material involved. For example, Groeneveld *et al.* (2008) detailed a method used for collecting pig tissue from the field in Viet Nam. The equipment

needed for field collections is relatively inexpensive. For example, samples can be cryopreserved in a simple Styrofoam box and then placed in a portable liquid nitrogen tank.

Cryopreservation involves freezing cells and tissues to  $-140^{\circ}\text{C}$  (the vapour phase of liquid nitrogen) or  $-196^{\circ}\text{C}$  (the liquid phase of liquid nitrogen). The process places cells into a suspended state of animation where most biological processes cease to function. Cells that have been successfully cryopreserved remain suspended until revived by thawing. The type of cell (e.g. whether sperm, embryo or blood), particularly cell size and cell membrane composition, affects the way cells need to be prepared for freezing and the freezing rates that need to be applied. For example, the cooling rate for bovine sperm ( $-19^{\circ}\text{C}$  to  $-25^{\circ}\text{C}/\text{minute}$ ) is very different from that for embryos ( $-0.5^{\circ}\text{C}/\text{minute}$ ) (FAO, 2012) and freezing protocols for semen differ among species.

Cells to be cryopreserved are suspended in a medium containing various sugars, lipids and – most importantly – cryoprotectant compounds such as glycerol. Glycerol was the first cryoprotectant agent identified (Polge *et al.*, 1949) and is still the primary cryoprotectant used across species. The cryoprotectant compound reduces the formation of ice crystals, which can damage cells of all types. In recent years (i.e. since 2005/2006 when the first SoW-AnGR was prepared), cryopreservation research has continued to advance (e.g. Okazaki and Shimada, 2012; Woelders *et al.*, 2012), particularly with regard to the preservation of oocytes and other non-traditional types of germplasm (Pereira and Marques, 2008; Mullen and Fahy, 2012) and the analysis of changes in the cell membrane before and after cryopreservation. As a result of this and other work, new media for cryopreservation are continually being evaluated and improved upon.

Genetic material from all livestock species can be cryopreserved and stored in a gene bank. However, the efficacy of the cryopreservation process and the ease with which germplasm or tissue can be used to generate animals varies substantially across species. Protocols for cryopreservation and

## PART 4

regeneration using either semen or embryos are well established for cattle. Cryopreservation of pig germplasm is also relatively straightforward. However, for sheep and goats, both cryopreservation protocols and regeneration procedures need to be improved. For both these species, infrastructure limitations impede the widespread use of cryopreserved material. Moreover, these species have smaller commercial industries, which means there is less investment in research.

The use of cryopreserved chicken semen has been particularly problematic: not because the sperm do not freeze well, but because the cryoprotectant glycerol is a contraceptive in the hen. Several means of addressing this problem – alternative cryoprotectants such as dimethyl sulfoxide (commonly known by the abbreviation DMSO) or intramaginal inseminations – have been developed and have sometimes been used (e.g. Long *et al.*, 2014). However, results have not always been totally satisfactory for a number of reasons. The ground-breaking approach developed by Song and Silversides (2006; 2007a; 2007b) – involving the harvesting of gonads from day-old chicks, cryopreserving them and then transplanting the thawed tissue into chicks of three to seven days of age – represents a quantum step forward in the cryoconservation of avian genetic resources. Using this approach, entire breeds or lines can be reconstituted and ready for mating in approximately one year (see Box 4D6).

Lack of a stable, long-term and financially affordable source of liquid nitrogen can be a severe constraint to gene banking. Freeze-drying sperm does not require liquid nitrogen and allows sperm to be stored at 4 °C and transported at room temperature. Offspring have been obtained from oocytes fertilized with freeze-dried rat epididymal sperm stored at 4 °C for five years (Kaneko and Serikawa, 2012). However, further development is needed in order to make this approach viable in livestock species. Other innovative approaches to biobanking are being developed (see Box 4D7). For example, studies are being undertaken on the maintenance of nuclear and cellular viability in somatic cells and female

gametes following freeze-drying. The development of dry biobanks of cells and gametes, which rely on protocols that are less costly and more environmentally friendly than current methods, could become a reality in the future (for a review see Loi *et al.*, 2013).

## 6.4 Information systems and documentation

Another important aspect of gene banking is the development and management of a database and the provision of information on the collection to stakeholders. A gene bank information system needs to handle two major categories of data:

- information on the quantities and types of germplasm and tissue maintained in the collection; and
- information on the animals whose genetic material is stored – phenotypic and genetic measures and information on the production systems and environmental conditions in which the animals were raised (FAO, 2012).

If information on a gene bank's holdings is made publicly available on the internet stakeholders will be able to view the collection and make a request for samples or determine what germplasm they might like to contribute to the gene bank. Establishing a comprehensive database takes substantial effort and time. Pooling efforts internationally may be helpful. For example, Brazil and the United States of America have collaborated in the development of the Animal-Genetic Resources Information Network (Animal-GRIN),<sup>4</sup> a database used to manage their respective AnGR programmes.

Web software for the documentation of cryoconserved material in animal gene banks is widely used in Europe. The CryoWEB software (Duchev *et al.*, 2010) can record basic information on donor animals, storage facilities, and stored samples and their sites of storage within a gene bank. In order to integrate information from national gene bank collections, the European Regional Focal Point for the Management

<sup>4</sup> [http://nrrc.ars.usda.gov/A-GRIN/database\\_collaboration\\_page](http://nrrc.ars.usda.gov/A-GRIN/database_collaboration_page)

## Box 4D6

**A study of the comparative costs of *in vivo* and cryoconservation programmes for chickens**

A study estimated and compared the costs, over a 20 year period, of three different approaches to chicken conservation:

1. maintaining live populations;
2. semen cryopreservation followed by reconstitution of the population via backcrossing; and
3. ovary and semen cryopreservation followed by reconstitution of the population via ovarian transplantation and subsequent insemination.

The costs of keeping live populations vary greatly, but for the purposes of the study they were approximated on the basis of typical costs of maintaining a population at an institution in North America. It was assumed that no revenue was derived from the live populations. Costs of cryopreservation and population reconstitution were based on biological parameters derived from the literature. The costs for all three programmes were subdivided into the cost of preservation, the annual cost and the cost of recovering the population.

For populations maintained in living form, there are no costs for preservation and reconstitution. However, the annual costs are high and cumulative: the longer the live population is maintained, the higher the total costs. The costs of cryopreservation are low, and the annual costs of maintaining cryopreserved material are

extremely low. The largest cost of a cryoconservation programme relates to recovery of the population.

In this example, keeping live populations was found to be the most cost-effective strategy for periods of up to three years. However, if the population was not going to be used within five years, cryoconservation was the most cost-effective strategy. The least expensive cryoconservation strategy was found to be the one based on storing both ovaries and semen. Over an extended period of time, the estimated savings relative to the costs of maintaining live populations were found to be more than 90 percent (see table). The low cost of cryoconservation suggests that avian genetic material should be cryoconserved, with individual populations reconstituted when needed.

This study focused on chickens and used parameters particular to that species and a particular institutional situation, so the results and conclusions are not universally applicable. However, the principal of estimating and comparing the costs of various conservation programmes by dividing the costs into costs of preservation, yearly maintenance costs and costs of recovery can be used for any mammalian or avian species in any situation.

Provided by Frederick G. Silversides.  
For further information, see Silversides et al. (2012).

**Estimated costs (US\$) of different conservation programmes**

| Conservation method  | Years of storage | Number of populations stored/recovered |           |
|--|------------------|--|-----------|
|  |                  | 10/1                                   | 10/10     |
| Maintaining living birds   | 1                | 179 000                                | 179 000   |
|  | 5                | 957 000                                | 957 000   |
|  | 20               | 5 306 000                              | 5 306 000 |
| Storing semen followed by backcrossing                                       | 1                | 288 000                                | 758 000   |
|  | 5                | 298 000                                | 769 000   |
|  | 20               | 354 000                                | 825 000   |
| Storing semen and ovaries followed by ovary transplantation and insemination | 1                | 109 000                                | 218 000   |
|  | 5                | 118 000                                | 228 000   |
|  | 20               | 172 000                                | 281 000   |

## PART 4

## Box 4D7

**Use of induced pluripotent stem cells in *in vitro* conservation**

Somatic reprogramming (Takahasi and Yamanaka, 2006) has brought about a revolution in the field of stem cell research. Pluripotent stem cells whose developmental potential includes germline colonization can now be obtained via a simple non-invasive biopsy. In other words, it is now possible to transmit the diploid genetic patrimony of an individual (male or female) directly from a somatic cell. While this has so far been demonstrated only in rodents, it is hoped and expected that further research will make it possible in many species. Considerable advances have already been made, particularly in the delivery of the molecular factors able to reprogramme somatic cells without affecting the stability and integrity of the genome, i.e. without generating genetically modified cells. Importantly, the prospect of using induced pluripotent stem cells in regenerative human medicine has greatly stimulated the development of methods for obtaining safe and high-quality cells.

One of the most interesting potential roles of induced pluripotent stem cells in *in vitro* conservation is in preserving, and eventually amplifying, the diploid gene pools of individual animals with extreme phenotypes. Somatic reprogramming would allow a large and diverse group of genetically different individuals to be sampled without killing the donors and without having to produce embryos that contain

only half the interesting genetic patrimony. Moreover, the methodology is not limited to males (as is the case with the storage of semen), as female cells can also be stored and reprogrammed.

Further work will undoubtedly reveal differences between species, both in terms of the efficiency of reprogramming and the ease of germline colonization and contribution. Because of their phylogenetic proximity to the model species, the first livestock species in which these techniques can be used will probably be mammalian. The commercial and genetic value of exceptional phenotypes and individuals will help to stimulate the development of innovative methodologies.

It is impossible to know how long it will be before these techniques can be used routinely, as progress will depend on the level of research in each species. Nonetheless, collection of tissues and other sources of somatic cells in anticipation of further development may be a prudent strategy. Collection of such materials is usually simple and inexpensive, and can complement or replace the collection of semen and embryos. Once cryopreserved, the tissues and cells will remain viable indefinitely and can thus be kept until the technology needed to utilize them is well established.

Provided by Bertrand Pain.

of Animal Genetic Resources (ERFP) decided to develop the European Register of Cryomaterial as part of EFABISnet, a regional network of national AnGR information systems linked to FAO's worldwide system, DAD-IS (Hiemstra *et al.*, 2014) (see also Part 4 Section A). Information about national gene bank collections can be automatically uploaded from national databases (CryoWEB) to the European Farm Animal Diversity Information System (EFABIS). ERFP members have also recently established the European Gene Bank Network for Animal Genetic Resources (EUGENA – Hiemstra *et al.*,

2014), which allows for sharing of cryoconservation information at all levels (i.e. not only the content of national gene banks), thus allowing the optimization of conservation efforts at regional level (see Box 3D8).

Information systems for gene banks can be made even more powerful if they are integrated with systems used in *in vivo* conservation. The benefits of integrated databases increase in systems where stored materials are regularly used in the management of the *in vivo* populations.

## Box 4D8

**Bilateral agreement on sanitary issues in germplasm exchange – an example**

Health regulations are a major issue confronting regional gene bank development. As national gene banks may collect germplasm without the intention of distributing it to other countries, collections may include material collected and cryopreserved without the rigorous testing that would be needed to allow it to be exported. Thus, if countries wish to set up a regional gene bank, there may be a need to develop alternative protocols for exporting genetic material.

Arrangements for transboundary exchange of genetic material were required when Jersey cattle breeders from the Island of Jersey wanted the United States of America's gene bank to back up their breed population. In this instance, the breeders had been collecting and storing semen from their cattle since the 1960s. While health tests were performed on the cattle at the time of collection, there were no veterinary certificates that could be used to acquire permits to import samples into the United States of America.

Another complicating issue was that Jersey and the United States of America had no agreements in place to verify the health status of each other's livestock populations (similar to those existing between the United States of America and the European Union). The solution was for the relevant agency in the United States of America to issue a special permit allowing the samples to enter the country but not to be used for breeding purposes. This solution was acceptable to all parties as the intention of the transfer was to provide a mechanism for keeping the samples safely so that in the event of need the genetics could be reintroduced to Jersey. Transmission of disease into American livestock populations was considered to be practically impossible given that no live animals would be produced in the territory of the United States of America.

Provided by Harvey Blackburn, National Coordinator for the Management of Animal Genetic Resources, United States of America.

## 6.5 Legal aspects of gene banking

Gene banks need to establish policies that ensure they comply with national laws. The two primary areas that need to be considered are interactions with the owners of the livestock from which samples are obtained and compliance with relevant national or international health standards. In the former case, the main issue is normally the question of private property rights over the material as it is collected, stored and distributed. National animal-health regulations may determine which animals can be used as sources of germplasm and how the collected germplasm can be used. Where international transfers are concerned, the country's overall health status will determine the type of testing needed before, during and after collection in order to allow the movement of samples through the normal protocols of international animal germplasm transfer. If countries wish to develop bilateral backup collections of germplasm (e.g. Box 4D8), they will

need to evaluate whether current World Organisation for Animal Health (OIE) regulations will allow the required exchanges to take place or whether waivers will be needed (Blackburn and Boettcher, 2010).

In 2010, member countries of the Convention on Biological Diversity adopted the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization (see Part 3 Section F). The protocol, which entered into force in October 2014, may influence the way that livestock germplasm is exchanged internationally and could potentially impede the exchange of AnGR between the national gene banks of countries that are signatories to the agreement.

## PART 4

## 7 Conclusions and research priorities

Conservation of livestock breeds can have many objectives, and various types of activity can be employed to address them. Comprehensive planning is required in order to identify the breeds with the greatest priority for conservation and to identify the most appropriate strategies for their management. Over recent years, substantial strides have been made in the development and improvement of conservation methods. Both *in vivo* and *in vitro* conservation have their advantages and shortcomings as standalone activities, so a strategy that employs both methods is usually optimal.

In the field of *in vivo* conservation, new methods allow more effective incorporation of economic and social factors into national conservation strategies. A desire to decrease direct public subsidies and make breeds more financially self-sustainable has led to a greater focus on the development of niche markets for breed-related products and spurred interest in methods of capturing other values of locally adapted breeds, such as their contributions to landscape maintenance and agricultural tourism. These approaches based on promoting financial self-sustainability both allow and oblige individual livestock keepers to play the major role in breed management. However, while developments of this kind are providing new opportunities, it should be borne in mind that they do not necessarily provide a strong guarantee that the targeted breeds will survive. For example, niche markets can often be unstable.

An unprecedented number of national gene banks have now been established and more are planned. Effectively building gene bank collections requires countries to improve their capabilities in cryopreservation, reproductive physiology, quantitative and molecular genetics and – above all – effective and openly accessible information systems. With the explosion in the availability of genomic information, there will be a greater need for gene banks to expand their collections to assist

in conservation efforts and to serve as a reference of genomic information for various populations. Increasing the efficacy of cryopreservation protocols will facilitate cryoconservation and genetic utilization of stored material in *in situ* populations.

Effective decision-making in conservation strategies requires access to a range of data on breeds and their production environments, as well as appropriate methods for integrating these data into decision-making processes. For example, detailed DNA analysis may reveal the genetic uniqueness of a breed through the presence of rare alleles and rare haplotypes. This will improve estimates of breeds' conservation values and may indicate opportunities for sustainable use in pure- or cross-breeding programmes. New molecular approaches can facilitate the operation of such breeding programmes. Collecting data of this type is the task of characterization studies and inventory and monitoring programmes. Research priorities in these fields are discussed in Part 4 Sections A and B and needs for capacity development in Part 3 Section B.

With regard to decision-support tools in the field of conservation, research priorities include:

- improving methods for estimating breeds' extinction probabilities;
- developing user-friendly methods for prioritizing AnGR for inclusion in conservation programmes, and decision tools to guide resource allocation in conservation programmes, including methods that can effectively combine information of varying degrees of uncertainty; and
- further developing methods for incorporating genomic information into conservation planning.

Research is also required into the socio-economic, infrastructural, technical and policy factors that influence success in establishing and sustaining conservation programmes.

With regard to *in situ* conservation, research priorities include:

- developing strategies through which conservation activities can be implemented in ways that maximize livestock keepers' livelihoods,



including through value-addition methods such as niche marketing and agritourism;

- developing strategies through which genomics and other advanced tools and methods can be efficiently used to improve the genetic merit of conserved breeds while maintaining sufficient genetic variability;
- developing strategies through which breed conservation can be combined with efforts to promote the provision of services such as the maintenance of landscapes and wild-life habitats, as well as developing methods to estimate the value of these services and identify the beneficiaries; and
- determining how organizational structures can be improved so as to allow better integration and coordination among actors involved in conservation.

In the field of *ex situ in vivo* conservation, priorities include:

- identifying approaches that can enable programmes, particularly those in developing countries, to become more self-sustaining and hence less vulnerable to collapse if state support is withdrawn.

In the field of *in vitro* conservation, research priorities include:

- further developing strategies to increase and improve the utilization of stored material in *in situ* populations;
- developing information management systems that allow better monitoring and assessment of gene bank collections;
- designing comprehensive database structures and portals that are dynamic and thereby allow a broad range of users to access gene bank holdings and make requests for material;
- refining cryopreservation and freeze-drying protocols to increase the efficacy of collecting and storing germplasm;
- enhancing reproductive biotechnologies to improve the efficiency and reduce the costs of regenerating live animals from stored germplasm and cell lines;

- developing approaches for quantifying genetic differences among animals within the collection and comparing the status of the collection to *in situ* populations;
- improving methods for optimizing ongoing sampling and storage of genetic material in systems where the primary objective is to provide a backup to ongoing genetic improvement programmes;
- increasing the efficiency of reproductive technologies (in terms of the number of live animals produced per unit of material stored) in order to improve the cost-effectiveness of *in vitro* conservation programmes; and
- identifying policy, legislative and zoosanitary frameworks (and strategies for their implementation) that will facilitate the storage of germplasm in gene banks and access to such material.

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## PART 4

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## Section E

# Economics of animal genetic resources use and conservation

## 1 Introduction

Economic analysis can play an important role in the sustainable management of animal genetic resources (AnGR). The first report on *The State of the World's Animal Genetic Resources for Food and Agriculture* (first SoW-AnGR) (FAO, 2007a) included a section on methods for economic evaluation<sup>1</sup> that provided an overview of the various types of value that can be distinguished (direct and indirect use values, option values, bequest values and existence values) and described potential methods and tools for assessing them. It also presented some examples of the use of these methods and tools and the findings obtained. This updated section provides an overview of recent developments in the economics of AnGR use and conservation. The revised title reflects the way in which this field of work has moved beyond just the development and testing of methods.<sup>2</sup>

Significant research on AnGR-focused economic valuation methods largely began following an FAO/International Livestock Research Institute (ILRI) workshop (Rege, 1999) that identified relevant methodologies (see also Drucker *et al.*, 2001). Work on the testing of these methods was subsequently undertaken by ILRI (Economics of AnGR Conservation and Sustainable Use Programme) and its partners. The discussion presented in the first SoW-AnGR drew on the findings generated by the ILRI programme, many of which were reported in a special issue of the journal

*Ecological Economics* (Drucker and Scarpa, 2003) and in a CGIAR System-wide Genetic Resources Programme (SGRP) report that reviewed the applied economics literature related to the valuation and sustainable management of crop and livestock biodiversity (Drucker *et al.*, 2005, subsequently published as Smale and Drucker, 2007).

The first SoW-AnGR concluded that research in this area had led to the development of a range of methods that could be used to value livestock-keepers' breed or trait preferences and support the design of policies to counter trends towards the marginalization of locally adapted breeds. It noted that, despite the easing of some methodological/analytical constraints as a result of this body of work, data constraints remained critical. Challenges identified included the need to raise awareness regarding the important role of economic analysis in improving the sustainable use and conservation of AnGR, the need to strengthen national capacities so that relevant methods and decision-support tools could be applied and the need to integrate such tools and methods into wider national livestock development processes, including through the design of appropriate incentive mechanisms. The report also noted that there had been little practical application of such tools and methods in contexts that could influence policy-making and livestock keepers' livelihoods.

A subsequent analysis (Drucker, 2010) of the country reports prepared for the first SoW-AnGR supported the view that the field of AnGR economics had had relatively little influence on "real-life" design and implementation of conservation policy. It indicated that, at best, there was a patchy

<sup>1</sup> FAO, 2007a, pages 429–440.

<sup>2</sup> The title of the equivalent section in the first SoW-AnGR was "Methods for economic valuation".

## PART 4

recognition of the importance of valuation and the potential role of economics in the design of cost-effective conservation programmes. In addition to challenges related to a lack of awareness regarding the existence of appropriate methods and tools, a lack of capacity to collect the necessary economic characterization and valuation data through participatory mechanisms and to carry out subsequent analysis was also identified as a constraint. A further conclusion was that economic characterization and valuation was also constrained by deficiencies in the broader characterization of AnGR (for example related to genetic analysis, performance recording and the monitoring of breed status and trends). Thus, while the importance of economics is recognized in the Global Plan of Action for Animal Genetic Resources (FAO, 2007b) (e.g. with regard to the development of standards and protocols,<sup>3</sup> strengthening of policies,<sup>4</sup> provision of support to indigenous and local production systems<sup>5</sup> and establishment of national conservation policies)<sup>6</sup> translating economic valuation into a mainstream activity in AnGR management would require significant awareness-raising and capacity-building. In this context, it should also be noted that calls for biodiversity valuation work and for the design of positive incentive mechanisms have been made by the Conference of the Parties to the Convention on Biological Diversity (CBD) (Decision VIII/25) and that the CBD's Strategic Plan for 2011–2020 (CBD, 2011) calls for the removal of subsidies harmful to biodiversity. As a basis for the preparation of this section, a review of AnGR economics literature published after the first SoW-AnGR was drafted (covering the period 2006<sup>7</sup> to mid-2014) was undertaken by consulting bibliographic databases<sup>8</sup> and key AnGR experts, including through the Domestic Animal Diversity Network (DAD-Net)<sup>9</sup> a discussion

group with 2 100 members (as of December 2014), the latter with a view to identifying literature not included in bibliographic databases, including grey literature and academic theses.

In order to ensure a focus on the economics of AnGR *per se*, rather than the broader field of livestock economics, the scope of the literature review was limited to studies involving economic assessments focused either on the valuation (direct or indirect) of locally adapted breeds by livestock keepers or on production inputs and outputs for different breeds. Broader livestock economics studies, including a substantial body of literature based on productivity assessments (e.g. feed conversion efficiency), as well as those comparing breed performances in research-station settings, were considered beyond the scope of the review.

The literature review revealed that a significant body of work has been generated in recent years. Thirty-nine publications (including five theses) broadly related to the economic valuation of breeds were identified, covering a number of species and geographical areas and making use of a range of valuation methods; a further 35 publications related more broadly to AnGR economics and conservation policy were also identified. A large literature (65 publications identified) addressing the broader field of the economics of agrobiodiversity (i.e. covering, *inter alia*, concepts, ecosystem service frameworks and models related to agrobiodiversity and biodiversity in general) can also be considered relevant.

The literature identified can be grouped into the following categories:

- the economic conceptual framework for AnGR and the link between the range of AnGR economic values and specific ecosystem services;
- analytical tools used for economic valuation of breeds;
- valuation of traits to inform breeding decisions;
- public willingness to pay for conservation services; and
- incentive mechanisms for conservation services.

The following subsection provides an overview of this literature based on these categories.

<sup>3</sup> FAO, 2007b, Strategic Priority 2, Actions 1 and 2.

<sup>4</sup> FAO, 2007b, Strategic Priority 3, Action 2.

<sup>5</sup> FAO, 2007b, Strategic Priority 6, Action 1.

<sup>6</sup> FAO, 2007b, Strategic Priority 7.

<sup>7</sup> The first SoW-AnGR covered references up to 2005.

<sup>8</sup> Web of Science, Google Scholar, ResearchGate, open thesis, JURN, etc.

<sup>9</sup> <https://dgroups.org/fao/dad-net>



## 2 Developments in animal genetic resources economics

Since 2006, a body of literature has emerged that provides a more formal economic conceptual framework within which to understand the erosion of AnGR as part of a replacement or conversion process that is amplified by a divergence between the private- and public-good values associated with the maintenance of biodiversity. These effects had previously been described in the context of biodiversity in general by Swanson (1997) (conversion process) and Pearce and Moran (1994) (value divergence), among others. The latter authors also note that recognition of the broader total economic values (TEV) associated with biodiversity can be instrumental in altering decisions about resource use.<sup>10</sup> While evidence-based policy-making has its limitations (Sumburg *et al.*, 2013) and biodiversity valuation is not a panacea, it may help to “recalibrate faulty economic compasses that have led to poorly informed decision-making” (TEEB, 2010).

The economic conceptual framework has provided the basis for improved understanding of the incentive mechanisms required to help reduce AnGR erosion by better aligning private- and public-good values, including through the application of payments for ecosystem services concepts to AnGR (Narloch *et al.*, 2011a; Silvestri *et al.*, 2012; Bojkovski, forthcoming). Such frameworks have also been used to support analysis of the economics of agrobiodiversity conservation (both animal and plant genetic resources) for food security under climate change (Pascual *et al.*, 2011). Most of this body of literature refers to *in situ*/on-farm use and conservation, with only limited references (e.g. McClintock *et al.*, 2007) to *ex situ* conservation.

Finally, in recent literature, the links between nature (encompassing AnGR) and the economy have increasingly tended to be described using

the concept of ecosystem services or flows of value to human societies as a result of the state and quantity of natural capital (Jackson *et al.*, 2007; TEEB, 2010). As a result, there are increasing opportunities to consider the ecosystem services concept in the context of AnGR management and the role that economic valuation of AnGR can play within such a framework. Zander *et al.* (2013) and Martin-Collado *et al.* (2014) have demonstrated how the quantification of the different components of TEV and the underlying ecosystem services with which they may be associated can provide a useful guide to the design of policies for the sustainable use and conservation of AnGR.

### 2.1 Economic conceptual framework and ecosystem services

Narloch *et al.* (2011a) – drawing on Drucker and Rodriguez (2009), Steinfeld (2000) and Swanson (1997) – note that the erosion of agrobiodiversity can be understood in terms of the replacement of the diverse existing pool of locally adapted animal and plant genetic resources with a smaller range of specialized improved ones. Given that the latter are likely to have a higher responsiveness to external inputs, agricultural intensification (where this is possible) may make breed substitution and cross-breeding increasingly profitable (see Figure 4E1) and hence lead to a reduction in locally adapted breed numbers (Drucker and Rodriguez, 2009; Marshall, 2014).

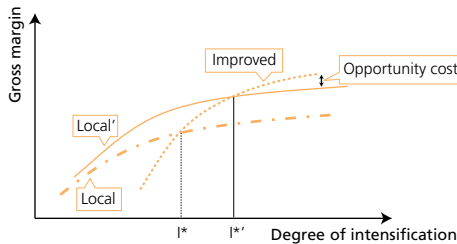
There are a number of reasons to suppose that the replacement process is resulting in less than socially desirable levels of AnGR being maintained. In particular, it is likely that significant non-market and/or public-good values associated with the various ecosystem services provided by genetic resources (see Box 4E1) are not reflected in market prices and that this creates a bias against their maintenance. Another set of values that are often not reflected in market prices and conventional economic analyses are private-good values not directly related to production outputs, but instead associated with the role of agrobiodiversity in minimizing farm-level risks related

<sup>10</sup> See FAO, 2007a, Box 93 (page 430) for a discussion of TEV in the context of AnGR.



## PART 4

FIGURE 4E1

**Breed production functions, public-good values and replacement opportunity costs**

Note: "Local" AnGR (market profitability function represented by the dash-dot line [---]) outperform "improved" AnGR (market profitability function represented by the dotted line [····]) up to a given level of production system intensity ( $I^*$ ). The term "intensity" is used here in a broad sense and includes, *inter alia*, factors related to access to markets and extension services. Once the degree of intensification passes  $I^*$ , livestock keepers face increasing financial incentives to replace the local AnGR with the improved ones. Accounting for public-good values not reflected in market prices would lead to an upward shift in the "Local" curve (to the position indicated by the solid line [—]), and a shift in the replacement point to  $I^{*'}$ .

Source: Adapted from Drucker and Rodriguez, 2009, and Zander *et al.*, 2013.

to external shocks such as extreme climatic events and disease outbreaks (e.g. Rege and Gibson, 2003).<sup>11</sup>

The framework illustrated in Figure 4E1 suggests that in certain contexts livestock-keepers will need to be compensated for the financial opportunity costs of continuing to maintain socially desirable levels of locally adapted AnGR. Incentive mechanisms that permit fuller "capture" of the economic values arising from the maintenance of genetic resources would have the effect of shifting the curve for the locally adapted AnGR upwards to the left (as shown by the solid line).

<sup>11</sup> Narloch *et al.* (2011) also identify market failures (e.g. externalization of environmental impacts) leading to an overestimation of the performance of improved AnGR, as well as important intervention failures (e.g. subsidies and support prices) that increase the financial profitability of improved AnGR. Accounting for such factors would result in a downward shift (not shown) of the "Improved" curve in Figure 4E1, resulting in the socially optimal replacement point being even further to the right than indicated by  $I^{*'}$ .

Such mechanisms could involve direct support payments, such as those provided under the European Rural Development Programmes, as well as payments for ecosystem services. In addition, private values could be enhanced through niche marketing and value-chain development for products and services (including agritourism initiatives) associated with AnGR (see further discussion below and in Part 4 Section D).

It is within this conceptual context that it becomes apparent that an understanding of non-market and public-good values is important from a conservation policy perspective (Zander *et al.*, 2013). Accounting for TEVs can be used to determine, *inter alia*, whether the benefits of intervention outweigh the costs, as well as to determine appropriate intervention strategies, including for situations in which specific AnGR have little or no current market-development potential. Where conservation funds are limited, understanding the "true" (i.e. total) economic value of different breeds and their contribution to the public good can be an important tool in prioritization and fund allocation (Fadlaoui *et al.*, 2006).

An understanding of the relative values of the different components of TEV can also be used to provide insight into the viability of different use and conservation strategies. It is possible to identify the relevance of different types of economic value and associated ecosystems services to different types of stakeholder and their willingness to pay for the services provided by the maintenance of breeds (Zander *et al.*, 2013). For example, indirect use values, such as cultural and landscape maintenance values, are likely to be of more relevance to local residents and visitors to a local area, while option values are likely to be of relevance to a much broader range of stakeholders. Given the importance of the public-good values associated with breed maintenance, Martin-Collado *et al.* (2014) argue that, in order to maximize societal welfare, *in situ/on-farm* conservation interventions and strategies need to be designed with a view to maintaining the ongoing provision of the public-good breed-related functions that people value most.

## Box 4E1

**Biodiversity valuation, ecosystem services and animal genetic resources**

Agriculture can be understood as a multifunctional activity that not only produces food, but also sustains rural landscapes, protects biodiversity, generates employment and contributes to the viability of rural areas. The benefits that humans derive from the functioning of the world's ecosystems, including agricultural ecosystems, are increasingly being discussed in terms of "ecosystem services". All these services are underpinned by biodiversity, and livestock and livestock-keeper custodianship/stewardship make an important contribution to the maintenance of many of them (WRI, 2005; Hodges *et al.*, 2014; FAO, 2014). Biodiversity-related ecosystem services are considered to be particularly significant in rural areas, where up to 75 percent of the world's poor people derive their livelihoods under continuous exposure to ecological and economic risks.

The Economics of Ecosystems and Biodiversity initiative (TEEB, 2010) defined the following four categories of ecosystem services that contribute to human well-being:

- provisioning services;
- regulatory services;
- habitat services; and
- cultural services.

The contributions of animal genetic resources (AnGR) to **provisioning services** (the supply of products and services such as food, fibre, manure, hides, transport, traction, savings and insurance) can often be quantified and evaluated using mainstream economic tools such as cost-benefit analysis, farm-simulation models and breeding-programme evaluations. These tools tend to

rely on revealed preference methods that depend on the existence of market data on prices and volumes.

In contrast, accounting for AnGR's contributions to the non-market, indirect use values associated with the **regulatory services** (processes such as nutrient cycling, soil fertility improvement, water and soil conservation and agro-ecosystem resilience – including pest and disease resistance, control of weeds and invasive species, stress buffering and adaptation to change) and **habitat services** (creation and maintenance of habitats for wild biodiversity) frequently requires the use of stated preference methods (see Box 4E2). Valuation of these contributions is further complicated by the fact that the ecological mechanisms that define many of them are not well understood (Jackson *et al.*, 2007).

AnGR-related **cultural services** include those associated with recreation, aesthetics (both of landscapes and the animals themselves) and the maintenance of traditional knowledge and sociocultural practices. Once again, non-market dimensions can complicate valuation and require the use of stated preference methods. Cultural services have been shown to play an important role in breed maintenance. For example, Widi *et al.* (2014) show that the unique cultural roles and values associated with Indonesian Madura cattle facilitate the maintenance of the breed despite the fact that crossing it with exotic breeds results in bigger animals with better body condition scores. The cultural role and value of the Javanese Pelung chicken breed, known for its singing capabilities, has similarly been found to play a positive role in ensuring its continued maintenance (Asmara, 2014).

## 2.3 Breed valuation studies

Given the existence of a range of economic values, many of which are non-market values, it is perhaps unsurprising that most of the 39 publications related to breed valuation identified in the literature review (see Subsection 1 for details) use survey-based preference-eliciting approaches. In other words, these studies determine the economic values

of AnGR by assessing people's preferences (often the preferences of livestock keepers). The use of stated preference methods is the dominant approach, with 20 studies using choice experiments or contingent valuation (see Box 4E2 for explanations of these terms). Hedonic pricing, a revealed preference method, is used in two studies. Eleven studies present results from preference-ranking techniques

## PART 4

## Box 4E2

**Environmental valuation methods**

There are many different approaches to, and views regarding, the valuation, pricing and costing of environmental and public goods and services. On the demand side, economists differentiate between **stated and revealed preference methods**, the choice of method often depending on the degree of availability of market data.

**Stated preference methods** are survey-based techniques that seek to elicit people's maximum willingness-to-pay (WTP) for an environmental good/service or their minimum willingness-to-accept (WTA) compensation to forgo such a good or service. This is done by creating a hypothetical market in which people are then asked to state, either directly or indirectly, their WTP/WTA for changes in the quality or quantity of the good/service. Hypothetical markets of this kind can be used to assess non-market (non-use) aspects of environmental goods and services and also to assess hypothetical goods and services that do not yet exist but could do in the future.

**Contingent valuation** studies, one of the most widely applied non-market valuation methods, directly ask people about their WTP/WTA for an environmental good or service *per se*. Indirect approaches include **choice experiments/choice modelling**, **choice**

**ranking** and **contingent rating**. **Conjoint analysis**, a term often used in marketing, is considered a form of choice experiment, often without a monetary attribute to trade-off. **Preference ranking** is similar. In all cases, surveys present people with a range of hypothetical options. People are then asked to choose their preferred option or to rank or rate them. By trading off the various characteristics of the presented options, which include the price/costs of the option, people indirectly indicate their WTP/WTA for the characteristics. **Hedonic pricing**, a **revealed preference method** that relies on the existence of market information, works in a similar way; implicit prices for socio-environmental attributes are estimated through people's actual demand for market goods that incorporate such attributes (e.g. different product characteristics such as taste or organic production status). **Production function** approaches use information regarding input costs (such as feed, veterinary and labour costs) and the benefits associated with different yield effects (e.g. on meat, milk and/or egg production) in order to compare the gross margins of different breeds.

Source: Adapted from Madureira *et al.*, 2007.

without explicit monetary valuation and six studies use methods based on the use of production functions of different breeds to approximate values.

Twenty-five (64 percent) of the 39 studies assess cattle, five poultry, five small ruminants and four pigs. Most of the studies from 2006 onwards relate to the economic valuation of traditional breeds in developing countries, where the livelihood functions of such breeds are particularly important. In fact, only eight of the 39 studies (21 percent: six in Asia and two in Europe) were not conducted in Africa.

The studies in Africa cover a range of breeds, including Ankole, Borana, Nguni and Zebu cattle (Table 4E1). While many studies focus on a single

breed, Duguma *et al.* (2011) assessed the importance of traits in four sheep breeds (Afar, Bonga, Horro and Menz) in Ethiopia. In Europe, Zander *et al.* (2013) assessed the TEV of two Italian cattle breeds (Modicana and Maremmana), while Martin-Collado *et al.* (2014) assessed the TEV of the Spanish Alistana-Sanabresa cattle breed. The majority of studies, however, do not refer to any particular breed, but instead seek to assess the value of specific traits (such as disease resistance) that can then be linked to locally adapted breeds. Interestingly, no Latin American studies were identifiable, although Marshall (2014) (see below) cites two breeding-related studies from the region.

TABLE 4E1

**Overview of livestock breed and trait valuation studies by region (2006 to 2014)**

| Method  | Region/Country                                       | Species  | Locally adapted breed(s)    | Reference  |
|---|--|----------|-----------------------------|--|
| <b>Africa</b>                                 |  |          |                             |  |
| Choice experiment                             | Benin  | Chickens | No specific breed           | Faustin <i>et al.</i> , 2010   |
|   | Ethiopia, Kenya                                      | Cattle   | Borana                      | Zander, 2006<br>Zander and Holm-Müller, 2007<br>Zander and Drucker, 2008<br>Zander <i>et al.</i> , 2009a |
|   | Ethiopia   | Cattle   | No specific breed           | Kassie <i>et al.</i> , 2009; 2010  |
|   | Ethiopia   | Goats    | No specific breed           | Amanu Abetu, 2013  |
|   | Kenya  | Cattle   | Zebu                        | Ruto <i>et al.</i> , 2008<br>Ruto <i>et al.</i> , 2010   |
|   | Kenya  | Cattle   | No specific breed           | Ouma <i>et al.</i> , 2007  |
|   | Kenya  | Goats    | No specific breed           | Omondi <i>et al.</i> , 2008a   |
|   | Kenya  | Sheep    | No specific breed           | Omondi <i>et al.</i> , 2008b   |
|   | South Africa   | Pigs     | No specific breed           | Madzimure, 2011  |
| Conjoint analysis                             | Ethiopia   | Sheep    | Afar, Bonga, Horro and Menz | Duguma <i>et al.</i> , 2011  |
|   | Kenya  | Chickens | No specific breed           | Bett <i>et al.</i> , 2011  |
| Contingent valuation                          | United Republic of Tanzania                          | Cattle   | Tarime Zebu                 | Ngowi <i>et al.</i> , 2008   |
| Hedonic pricing                               | Ethiopia   | Cattle   | No specific breed           | Kassie <i>et al.</i> , 2011  |
|   | Ethiopia   | Sheep    | No specific breed           | Terfa <i>et al.</i> , 2013   |
| Preference ranking                            | Burundi, Rwanda, Uganda, United Republic of Tanzania | Cattle   | Ankole                      | Wurzinger <i>et al.</i> , 2006   |
|   | Ethiopia   | Poultry  | No specific breed           | Dana <i>et al.</i> , 2010  |
|   | Ethiopia   | Cattle   | No specific breed           | Desta <i>et al.</i> , 2011   |
|   | South Africa   | Cattle   | Nguni                       | Tada <i>et al.</i> , 2012; 2013  |
|   | Uganda   | Cattle   | Ankole                      | Ndumu <i>et al.</i> , 2008   |
|   | Zimbabwe   | Chickens | No specific breed           | Muchadeyi <i>et al.</i> , 2009   |
| Production function/<br>gross margin analysis | Ethiopia   | Cattle   | No specific breed           | Dayanandan, 2011   |
|   | Kenya  | Cattle   | Orma and Sahiwal Zebu       | Maichomo <i>et al.</i> , 2009  |
| <b>Asia</b>                                   |  |          |                             |  |
| Choice experiment                             | Viet Nam   | Pigs     | No specific breed           | Roessler <i>et al.</i> , 2008  |
| Contingent valuation                          | Indonesia  | Chickens | No specific breed           | Asmara, 2014   |
| Preference ranking                            | Indonesia  | Cattle   | No specific breed           | Widi <i>et al.</i> , 2014  |
| Production function/<br>gross margin analysis | Bangladesh   | Cattle   | No specific breed           | Islam <i>et al.</i> , 2010   |
|   | Bangladesh   | Cattle   | No specific breed           | Mondal <i>et al.</i> , 2010  |
|   | India  | Cattle   | No specific breed           | Islam <i>et al.</i> , 2008   |
|   | Viet Nam   | Pigs     | Ban                         | Lemke <i>et al.</i> , 2006   |
| <b>Europe</b>                                 |  |          |                             |  |
| Choice experiment                             | Italy  | Cattle   | Modicana and Maremmana      | Zander <i>et al.</i> , 2013  |
|   | Spain  | Cattle   | Alistana-Sanabresa          | Martin-Collado <i>et al.</i> , 2014  |

## PART 4

### 2.3 Valuation of traits to inform breeding decisions

In the context of the economic valuation of AnGR, the term “breeding” refers to directing deliberate and lasting changes in the genetic constitutions of livestock populations so as to improve their utilization. In the conventional practices of breeding programmes in developed countries, economic weights of key traits are combined with estimated breeding values to derive selection indices in order to evaluate the effect of the directional genetic changes on overall profit. These tools enable livestock keepers to select, maintain and reproduce animals with the aim of maximizing overall profitability. Conceptually similar, but more loosely articulated breeding objectives, are applied in traditional production systems in developing countries, although these typically consider more diverse and often complex traits, including adaptation or resilience to biotic and abiotic stresses, multiple indirect service functions and the socio-cultural values of the animals.

In this context, it is worth noting Marshall's (2014) overview of studies that have compared performance from the socio-economic or economic viewpoint of the livestock keeper (and of other actors in the value chain). The authors identified 11 studies from Asia and Africa (the focus of their study) that fall within the scope of the current review. These studies took what may be broadly categorized as a production function approach in order to compare the gross margins of different breeds (including cross-breeds) from the point of view of the livestock keeper. They used field, rather than research-station, data related to input costs and yield effects. Six of the studies (undertaken in Ethiopia, India and Bangladesh) focused on dairy cattle (Sayeed *et al.*, 1994; Ali *et al.*, 2000; Islam *et al.*, 2008; 2010; Mondal *et al.*, 2010; Dayanandan 2011), one on dual-purpose cattle in Kenya (Maichomo *et al.*, 2009), one on chickens in Bangladesh (Rahman *et al.*, 1997), one on goats in Ethiopia (Ayalew *et al.*, 2003), and two on pigs in Viet Nam and Zimbabwe (van Eckert, 1993; Lemke *et al.*, 2006). Two additional studies from Latin-America were also

mentioned, although neither of these fall within the scope of this review, as they fail to meet the economic analysis (Madalena *et al.*, 2012) or date (Blake, 2004) criteria.

Despite the slow progress in the uptake of the results of policy decision-support tools based on the economics of AnGR (Drucker, 2010), some analytical techniques for systematically estimating relative economic values of complex traits and attributes of AnGR have recently been adopted in mainstream animal breeding. In situations where only limited production and market data are available, the relative economic importance of key traits and attributes can be estimated using stated preference techniques (Tano *et al.*, 2003). For example, Nielson and Amer (2007) used choice experiments to define economic weights for use in animal breeding selection indices where traditional bio-economic models for estimating profits are not practical. Other types of stated preference techniques, such as conjoint analysis and preference ranking, have also been used to identify and prioritize traits, and indeed breeds, for particular production scenarios (Desta *et al.*, 2011; 2012; Duguma *et al.*, 2011). These techniques can be used to capture the preferences and choices of livestock keepers for traits/attributes that are not marketed (non-market use values) and are often ignored or only given secondary consideration in the process of deriving breeding objectives and economic weights for different traits. However, further work needs to be done in order to demonstrate how the results of such stated preference methods can be applied in the development of (long-term) breeding programmes for at-risk breeds, not only in developed countries, but also in developing countries – especially for breeds found in marginal production environments (e.g. Hodges *et al.*, 2014).

Apart from allowing the valuation of indirect use values of AnGR, economic valuation methods complement and provide relevant socio-economic context to the results of global and breed-specific molecular genetic studies. For instance, a global study into the genetic structure of cattle breeds (Bovine HapMap Consortium, 2009) has

revealed significant hybridization of the rare taurine and trypanotolerant Sheko breed with indicine breeds, which is consistent with earlier molecular genetic evidence of an alarming male-mediated introgression of zebu genes (Hanotte *et al.*, 2000). Related trait and breed preference studies in the Sheko's native production environments in Ethiopia showed that despite its recognized adaptedness to endemic trypanosomosis and tsetse fly challenge, as well as its superior dairy attributes (compared to other local cattle breeds) in these stressful production environments (Lemecha *et al.*, 2006), the breed remains under sustained pressure from deliberate cross-breeding as livestock keepers choose smaller and more docile zebu bulls from adjacent highlands (Stein *et al.*, 2009; Desta *et al.*, 2011; 2012). This is in line with the earlier findings of Jabbar and Diedhiou (2003) from southwest Nigeria, which revealed a gradual shift of breed preferences away from trypanotolerant breeds towards cross-bred and zebu cattle. In addition to shedding light on breed preferences, such studies can also provide the evidence-base for defining breeding objectives for breeding programmes that are capable of meeting the current needs of livestock keepers.

## 2.4 Public willingness to pay for conservation services

As discussed above, a range of studies have investigated the values of the traits of traditional livestock breeds from livestock-keeper and breeder perspectives. In contrast, Zander *et al.* (2013) and Martin-Collado *et al.* (2014) focused on the full range of TEVs arising from the maintenance of locally adapted breeds, with a view to identifying the broader public's willingness to pay for the breed-related ecosystem services that arise from their maintenance.

Zander *et al.* (2013) show that in the case of two threatened Italian cattle breeds (Modicana and Maremmana), most (85 percent) survey respondents (members of the general public interviewed either in areas where the breeds are kept or in the nearest provincial capital city) supported breed conservation, with their stated willingness-to-pay

easily justifying existing European Union support. The high landscape-maintenance, existence<sup>12</sup> and future-option values of both breeds (around 80 percent of their TEVs) suggest that incentive mechanisms are indeed needed in order to allow livestock keepers to capture some of these public-good values and hence motivate them to undertake conservation-related activities. The positive direct use values of both breeds (around 20 percent of their TEVs) imply that niche product markets aimed at enhancing the private-good values associated with the breeds could form an (albeit secondary) element of a use and conservation strategy.

The Spanish Alistana-Sanabresa breed was also shown to be associated with significant non-market values. The value that respondents placed on each specific public-good function was shown to vary significantly. For example, functions related to indirect use cultural values and existence values were much more highly valued than landscape maintenance values. These high cultural and existence values (again totalling approximately 80 percent of TEV) suggest that an *in situ* conservation strategy, as opposed to a purely *ex situ* cryoconservation strategy, would be required and that such a strategy would need to involve livestock-keeper incentive mechanisms (Martin-Collado *et al.*, 2014).

## 2.5 Incentive mechanisms for conservation services

Given the presence of such significant non-market and public-good values associated with AnGR, it is clear that the development of positive incentives (and indeed the removal of damaging subsidies), as called for under the CBD's 2011–2020 Strategic Framework (CBD, 2011) in the context of biodiversity in general, will often be required in order to ensure that socially desirable levels of livestock diversity are maintained.

One type of positive incentive mechanism that can potentially be used is payment for ecosystem

<sup>12</sup> Existence value is the value that arises from the satisfaction of knowing that something (e.g. a particular breed) exists.

## PART 4

services. Silvestri *et al.* (2012) note that increased demand for, and scarcity of, some of the ecosystem services generated by livestock production systems (see Box 4E1) has created opportunities for implementing approaches of this kind. Examples of emerging and operational payments for ecosystem services in livestock production systems include those related to climate regulation, watershed management and hydrological services and conservation of non-domesticated biodiversity (ADB, 2014).

Of particular relevance to domesticated plant and animal biodiversity is the emerging concept of payments for agrobiodiversity conservation services (PACS),<sup>13</sup> an approach that draws on existing concepts of payments for ecosystem services and can be defined as follows:

*“an economic instrument to tackle market, intervention, and global appropriation failures associated with the public good characteristics of agrobiodiversity conservation services through the use of (monetary or in-kind) reward mechanisms in order to increase the private benefits from local plant and animal genetic resources, so as to sustain their on-farm utilization”* (Narloch *et al.*, 2011a).

PACS can be combined with prioritization protocols (such as the Weitzman approach – see earlier studies by Simianer *et al.*, 2003; Reist-Marti *et al.*, 2003; and Zander *et al.*, 2009b), the application of safe minimum standards approaches (Drucker, 2006; Zander *et al.*, 2013) and the use of competitive tenders that permit the identification of least-cost conservation service providers and transparent accounting for any efficiency–equity trade-offs that may exist in the selection of service providers (Narloch *et al.*, 2011b; see also Bojkovski [forthcoming] for an emerging livestock application in Slovenia).

In the European context, the use of PACS approaches in the field of AnGR management is in part driven by the need for improved

understanding of the type of support that needs to be provided to livestock keepers in order to permit at-risk breeds to reach population targets set under European Union legislation. Incentive payment schemes for livestock-keepers rearing traditional breeds at risk are in place in the European Union (see Part 3 Section F). However, such payment schemes have often proved to be insufficient to cover the true financial opportunity costs faced by the keepers of such breeds (Signorello and Pappalardo, 2003).

The challenges associated with ensuring the sustainable management of AnGR are compounded by the fact that agricultural production does not take place on a level playing field; large amounts of subsidy are directed (mostly) towards specialized agricultural production systems. For example, in 2012 agricultural subsidies totalled an estimated US\$486 billion in the top 21 food-producing countries in the world (Worldwatch Institute, 2014). Developing-country studies of subsidies for “improved” breeds include Drucker *et al.* (2006), which estimated the total subsidy for imported pig breeds and their crosses in Viet Nam to be in the region of 19 to 70 percent of the gross margin typically associated with sow production. These were found to be similar to OECD-country subsidy levels (reaching 60 percent of farm receipts in some cases). Although designed with specific social goals in mind, such subsidies are “harmful” in the sense that they affect the competitiveness of locally adapted versus improved breed production systems and thereby affect the extent to which AnGR diversity is used and conserved.

In addition to the direct livestock-keeper payments that could be provided by PACS, attention is also increasingly being given to the potential of existing agricultural market channels to promote the use of at-risk genetic resources (among others, see the “Adding Value” special issue of the journal *Animal Genetic Resources* [FAO, 2013a]; Tienhaara *et al.*, 2013; Lauvie *et al.*, 2011; LPP *et al.*, 2010; Mathias *et al.*, 2010). Niche-marketing mechanisms, such as eco-labelling, certification and denomination of origin schemes (see Part 3 Sections D and F

<sup>13</sup> See [www.biodiversityinternational/pacs](http://www.biodiversityinternational/pacs) for more information on PACS.



and Part 4 Section D), may allow products from locally adapted breeds to attract higher market prices and thus help to keep the breeds in use. The Schwäbisch-Hällische pig in Germany, for example, is a locally adapted breed that was revived from close to extinction to become the foundation for a regional speciality niche-market (LPP *et al.*, 2010). The population of the Bresse chicken in France has remained stable for decades as a result of similar niche market-based management (Verrier *et al.*, 2005). Niche-market development is, however, often challenging, and not all breeds have the potential to supply products that closely match consumers' current tastes and preferences. Such mechanisms alone are therefore unlikely to be able to correct fully for market failures related to the public-goods characteristics of many of the services associated with the maintenance of agrobiodiversity. Niche-market development and PACS can thus be viewed as complementary approaches (Narloch *et al.*, 2011a). A conceptual basis for PACS financing strategies, through private- and public-sector service beneficiary and purchaser identification/mapping and dialogue, has recently been developed (Drucker *et al.*, 2013).

### 3 Challenges and opportunities

Recent years have seen a number of significant developments in the field of AnGR-focused economics. An economic conceptual framework within which the erosion of genetic diversity can be analysed has been elaborated and the links between the different types of value associated with AnGR and potential contributions to different kinds of ecosystem services have been better articulated. A wide range of breed-valuation studies have been undertaken, the majority relating to developing-country breeds and livestock-keeper preferences. In line with the importance of AnGR values that are not reflected in the marketplace, these studies have focused particularly on stated preference and ranking methods. A range of AnGR economic studies have also been realized with a specific view

to supporting the development of breeding programmes.

While many of the recent valuation studies have drawn on livestock-keeper and breeder preferences, methods for assessing public willingness to pay for breed conservation have also been developed, drawing on both total economic value and ecosystem service frameworks. European case studies based on these approaches have confirmed the existence of very significant non-market values, a number of which can only be secured through the implementation of *in situ* conservation strategies. Such strategies may also be dependent on the development of incentive mechanisms that ensure livestock keepers can capture a sufficient proportion of the non-market public good values to cover the costs they incur in providing public-good conservation services. In this context, the emergence of agrobiodiversity-focused payments for ecosystem services, so-called PACS, is of particular interest, especially as a complementary incentive mechanism alongside niche-product and market/value-chain development.

Despite the positive developments, a range of challenges and opportunities for future work in this subfield of economics remain.

**Awareness raising:** There is a need to promote awareness and facilitate interaction among both animal and plant genetic resources researchers and development practitioners regarding developments in the economics of genetic resources use and conservation. The development of the economic conceptual framework described above, which originated from the AnGR-focused work of Drucker and Rodriguez (2009) and Steinfeld (2000), has been used to inform analysis related to agrobiodiversity more broadly (e.g. Narloch *et al.*, 2011a; Pascual *et al.* 2011; Krishna *et al.* 2013). Such work has also drawn on the conceptual framework to inform approaches based on agrobiodiversity-focused payments for ecosystem services, which while having been originally applied in a plant genetic resources context are now also beginning to be applied in AnGR contexts (e.g. Bojkovski, forthcoming). The somewhat different conceptual



## PART 4

model developed by Krishna *et al.* (2013) for the application of PACS in a plant genetic resources context could also be adapted to an AnGR context.

Another example of a method developed for use on one component of agrobiodiversity and later used to inform the management of another component is the Weitzman prioritization approach. Originally applied by Weitzman (1993) to non-domesticated animals (wild species of crane), this method was later adapted for application to AnGR by Simianer *et al.* (2003), Reist-Marti *et al.* (2003) and Zander *et al.* (2009). It has recently been usefully applied to a plant genetic resource (cacao) case study (Samuel *et al.*, 2013). While there continues to be relatively limited interaction between animal and plant genetic resources researchers/development practitioners, it is clear that at least in the field of the economics of genetic resources use and conservation, there is high potential for mutual learning and collaboration – and that should be further encouraged.

**Assigning breed types:** In situations where genotypic information may be absent, as in most developing countries, identifying and verifying the breed type of a given AnGR can prove difficult. Livestock keepers tend to keep multiple genotypes to derive multiple benefits, and breeds tend to be defined in more subjective and less quantitative ways (Marshall, 2014). Under such circumstances, breed and trait valuation tools may be used to facilitate breed characterization through improved understanding of breeds and their values. In such contexts, greater collaboration between geneticists and economists may prove to be particularly valuable.

**Research focus:** The valuation studies discussed above mainly focused on developing countries and on-farm/*in situ* use and conservation strategies. While further work in these areas is still very much needed (including in Latin America, where relatively little work of this type has been undertaken so far), an increasing number of developed-country studies and studies considering the costs and benefits of *ex situ* conservation would also be welcome.

**Costing conservation efforts:** A number of studies, including Drucker (2006) for livestock

and Narloch *et al.* (2011a) for plants, have suggested that given modest conservation goals (the recently updated FAO [2013b] “not at risk” status category requires 2 000 breeding females in species with high reproductive capacity and 6 000 in species with low reproductive capacity), the costs of conserving a priority portfolio of at-risk breeds may also be quite modest. The assessment of public willingness to pay for conservation by Zander *et al.* (2013) and estimates of the support payments that would be required to achieve stated conservation goals suggest that such conservation costs may well be both economically justifiable (benefits outweighing costs) and relatively low cost. In this context, it is also interesting to note the findings of a plant genetic resources case study conducted by Krishna *et al.* (2013), which suggest that farmer willingness to participate in genetic resources conservation activities for the public good may be more closely related to the consumption values of the genetic resources in question than to their production opportunity costs (which generally do not take into account the existence of farmers’ many non-market preferences and values). Hence, conservation costs may be overestimated if based only on conventional economic opportunity cost estimates.

Such considerations are important, as national and global level efforts to cost the resources required in order to secure priority portfolios of AnGR could help to inform policy development. Such costing exercises could address both *in situ* conservation strategies and complementary *ex situ* interventions. It should, however, be noted that the different *in situ* risk-status thresholds adopted by different countries imply different implicit conservation costs.<sup>14</sup>

<sup>14</sup> Alderson (2009) notes differences between the breed status criteria adopted by the FAO and widely applied in AnGR valuation studies, and those independently developed by the European Union (EU), Rare Breeds International (RBI), the European Federation of Animal Science (EAAP) and the Rare Breeds Survival Trust (RBST). The choice of breed risk status criteria can have strong implications for overall conservation costs, insofar as such costs may be proportional to total herd size (Zander *et al.*, 2013).

**Linking conservation goals and values to the provision of ecosystem services:** The articulation of the link between conservation goals, values and ecosystem services is another area where plant genetic resources and AnGR work could be mutually supportive. CGIAR research<sup>15</sup> on the development of agrobiodiversity-focused ecosystem service indicators/metrics and on PACS includes work that is currently oriented towards plant genetic resources but also has potential AnGR applications. This work also includes consideration of the degree to which private- and public-good values and associated ecosystem services may, in certain contexts, need to be traded-off and the degree to which this can be done transparently and in a socially equitable manner.

A related area of interest for future research addresses conservation goal setting and levels of ecosystem-service provision. There is a need to overcome the current relative lack of knowledge of how different conservation goals and risk-status thresholds actually relate to the provision of specific ecosystem services. For example, one livestock-keeper with 2 000 breeding females of a particular breed maintained in a single herd/location would have quite different implications for ecosystem services related to the maintenance of landscape-level resilience, evolutionary processes/future option values and traditional knowledge and cultural practices than would 200 livestock keepers spread across the countryside, each with a herd of 10 breeding females. Once again, the existing plant genetic resources-focused CGIAR Research Programme work on ecosystem services and indicators could potentially also contribute to work in the AnGR field.

**Impact assessment:** Finally, in the context of impact assessment, Marshall (2014) identifies the need to provide decision-support information, both to livestock keepers and to policy-makers, through increased evaluation of the impact of different livestock breed types in developing-country livestock production systems. Such

assessments (which could draw on the indicator/metric development mentioned above) might address, *inter alia*, food and nutrition security and environmental sustainability. It is important that gender and intrahousehold dimensions are also considered, given that the benefits derived from interventions that affect breed and genotype choices can vary both between and within households, especially in low-input production environments, where both direct and indirect use values of livestock are likely to be important.

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<sup>15</sup> Water, Land and Ecosystems and Policies, Markets and Institutions Research Programmes.

<sup>16</sup> An annotated bibliography of AnGR economics-related literature associated with the SGRP report and updated in 2007 can be found on the IFPRI website at <http://tinyurl.com/AnGR-Economics-lit-to-2007>. A further update to mid-2011 prepared by Bioversity International can be found at <http://tinyurl.com/AnGR-Economics-lit-to-mid-2011>. A link to the full list of literature consulted for this section can be found at <http://www.fao.org/3/a-i4787e/i4787e196.pdf>.

## PART 4

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## Part 5

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# NEEDS AND CHALLENGES





# Introduction

The major global challenge for the twenty-first century is to sustainably feed a growing population that is expected to reach 9 billion by 2050: the so-called “2050 challenge to our global food system”.<sup>1</sup> Further increase in production is needed. At the same time, the ecological footprint of food production needs to be reduced and the quantity and quality of natural resources, including biodiversity, need to be sustained. There is a need to reduce waste, increase efficiency in the use of water, feed and energy and reduce greenhouse gas emissions and the pollution of land, air and water. Ecological and economic challenges are increasingly interconnected and global. Collaboration and cooperation across national boundaries have never been more important.

Since 2007, when the first report on *The State of the World's Animal Genetic Resources for Food and Agriculture* (FAO, 2007a)<sup>2</sup> was published and the international community adopted the Global Plan of Action for Animal Genetic Resources (FAO, 2007b),<sup>3</sup> the importance of genetic resources for food and agriculture, including animal genetic resources (AnGR), has been highlighted in several major international initiatives and agreements. In 2010, the Conference of the Parties to the Convention on Biological Diversity (CBD) agreed on the Strategic Plan for Biodiversity 2011–2020, including the Aichi Biodiversity Targets.<sup>4</sup> The following two targets are particularly relevant to AnGR management:

*“Target 7: By 2020 areas under agriculture, aquaculture and forestry are managed sustainably, ensuring conservation of biodiversity.”*

*“Target 13: By 2020, the genetic diversity of cultivated plants and farmed and domesticated animals and of wild relatives, including other socio-economically as well as culturally valuable species, is maintained, and strategies have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity.”*

In 2012, the Rio+20 International Environmental Summit of Nations agreed to set new multiyear global objectives to succeed the Millennium Development Goals (2000–2015). Biodiversity featured prominently in the outcome document, *The future we want*:

*“111. We reaffirm the necessity to promote, enhance and support more sustainable agriculture, including crops, livestock, forestry, fisheries and aquaculture, that improves food security, eradicates hunger, and is economically viable, while conserving land, water, plant and animal genetic resources, biodiversity and ecosystems, and enhancing resilience to climate change and natural disasters ...*

*112. We stress the need to enhance sustainable livestock production systems, including through improving pasture land and irrigation schemes in line with*

<sup>1</sup> <http://www.iatp.org/documents/the-2050-challenge-to-our-global-food-system>

<sup>2</sup> FAO. 2007a. *The State of the World's Animal Genetic Resources for Food and Agriculture*, edited by B. Rischkowsky & D. Pilling. Rome (available at [www.fao.org/3/a-a1250e.pdf](http://www.fao.org/3/a-a1250e.pdf)).

<sup>3</sup> FAO. 2007b. *The Global Plan of Action for Animal Genetic Resources and the Interlaken Declaration*. Rome (available at <http://www.fao.org/docrep/010/a1404e/a1404e00.htm>).

<sup>4</sup> <http://www.cbd.int/sp/default.shtml>

## PART 5

*national policies, legislation, rules and regulations, enhanced sustainable water management systems, and efforts to eradicate and prevent the spread of animal diseases, recognizing that the livelihoods of farmers including pastoralists and the health of livestock are intertwined.”<sup>5</sup>*

and subsequently in the post-2015 Sustainable Development Goals:

*“Goal 2. End hunger, achieve food security and improved nutrition and promote sustainable agriculture”*

*“2.5 By 2020 maintain the genetic diversity of seeds, cultivated plants and farmed and domesticated animals and their related wild species, including through soundly managed and diversified seed and plant banks at national, regional and international levels, and ensure access to and fair and equitable sharing of benefits arising from the utilization of genetic resources and associated traditional knowledge as internationally agreed”*

*“2.a Increase investment, including through enhanced international cooperation, in rural infrastructure, agricultural research and extension services, technology development and plant and livestock gene banks in order to enhance agricultural productive capacity in developing countries, in particular in least developed countries”*

*“Goal 15. Protect, restore and promote sustainable use of terrestrial ecosystems, sustainably manage forests, combat desertification, and halt and reverse land degradation and halt biodiversity loss”*

*“15.6 Ensure fair and equitable sharing of the benefits arising from the utilization of genetic resources, and promote appropriate access to such resources”*

*“15.9 By 2020, integrate ecosystems and biodiversity values into national and local planning, development processes and poverty reduction strategies, and accounts”*

*“15.a Mobilize and significantly increase financial resources from all sources to conserve and sustainably use biodiversity and ecosystems”<sup>6</sup>*

The Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization<sup>7</sup> entered into force in October 2014. It provides a legal framework for the implementation of one of the three objectives of the CBD: the fair and equitable sharing of benefits arising out of the utilization of genetic resources.

In order to monitor progress in the implementation of the Global Plan of Action for Animal Genetic Resources, the Commission on Genetic Resources for Food and Agriculture has adopted indicators for measuring both the state of implementation of the various elements of the plan itself (so-called process indicators) and outcomes in terms of AnGR diversity (so-called resource indicators).<sup>8</sup> The process indicators were calculated in 2012<sup>9</sup> and 2014,<sup>10</sup> based on country reporting, and the resource indicators are calculated biennially,<sup>11</sup> based on data entered by countries into the Domestic Animal Diversity Information System (DAD-IS)<sup>12</sup>.

<sup>5</sup> <http://tinyurl.com/czenz9g>

<sup>6</sup> <http://sustainabledevelopment.un.org/focussdgs.html>

<sup>7</sup> <https://www.cbd.int/abs/>

<sup>8</sup> [http://www.fao.org/Ag/AGAInfo/programmes/en/genetics/Targets\\_and\\_indicators.html](http://www.fao.org/Ag/AGAInfo/programmes/en/genetics/Targets_and_indicators.html)

<sup>9</sup> <http://www.fao.org/docrep/meeting/027/mg044e.pdf>

<sup>10</sup> <http://www.fao.org/3/a-at136e.pdf>

<sup>11</sup> <http://www.fao.org/3/a-at135e.pdf>

<sup>12</sup> <http://fao.org/dad-is>

## Section A

# Challenges posed by livestock sector trends

Economic, social and environmental trends in the livestock sector continue to pose many challenges to the sustainable management of AnGR. Rapid growth in demand for animal products has been a major driver of change in the livestock sector in recent decades, particularly in some developing regions, and the associated changes in livestock production systems have had a major effect on AnGR management and often posed a threat to diversity. Traditional production systems that harbour diverse genetic resources have been marginalized and a narrow range of international transboundary breeds have become more widely used. In some circumstances, these breeds have been indiscriminately crossed with locally adapted breeds, a development that is regarded as a major threat to AnGR diversity in many countries. Growth in global demand for animal-source foods is expected to continue over the coming decades, although at a slower pace overall. Africa and South Asia are predicted to be major centres of growth in demand. Both are resource-constrained regions where smallholder and pastoral production is still widely practised and where smallholder milk production has historically been strong. Both are also home to a wealth of locally adapted AnGR.

Economic and market-related factors are frequently highlighted by stakeholders as threats to AnGR. Shifts in market demand or increasing competition may mean that particular breeds can no longer be raised profitably. Shifts of this kind are part of social and economic change, and there are always likely to be some breeds that are at risk of falling out of use and declining towards extinction. However, there may be measures that can be taken to reduce economic threats, either by

“valorizing” individual at-risk breeds via marketing initiatives, genetic improvement or the identification of new roles, or by more general policy measures such as eliminating support measures that create favourable economic conditions for breed replacement.

Climate change is placing increasing pressure on the livestock sector, especially on production systems that depend heavily on the state of the local ecosystems. Livestock are recognized as contributors to climate change, but also as an entry point for climate change mitigation. Grazing systems in arid and semi-arid areas are likely to be particularly severely affected, but mixed farming systems will also need to adapt. Grazing and small-scale mixed farming systems harbour many locally adapted livestock breeds that possess characteristics that enable them to thrive in harsh conditions. These breeds, and other AnGR, increase the options available for adapting production systems to the effects of climate change. However, climate change also poses threats to AnGR diversity: for example, because of the increased risk of breed loss as a result of natural disasters. It remains difficult to predict how climate change will affect the future of livestock production and what the consequences will be for AnGR diversity. The uncertainty of climatic projections is a major constraint, but there is also frequently a lack of data on breeds’ characteristics, distributions and production environments. Information on the level of threat posed to AnGR by extreme climatic events and other disasters and emergencies remains limited.

Given the major roles of small-scale livestock keepers and pastoralists in maintaining AnGR

## PART 5

diversity, factors that undermine the sustainability of smallholder and pastoralist production systems constitute significant threats to AnGR. These threats may include both market-related factors (e.g. competition from large-scale producers or exclusion from markets because of difficulties in meeting the specific requirements of retailers and consumers) and problems related to the degradation of (or lack of access to) natural resources. The importance of livestock-keeping to the livelihoods of many of the world's poorest people and the major significance of livestock-keeping areas (e.g. grasslands) in the provision of ecosystem services (carbon sequestration, water cycling, provision of wildlife habitats, etc.) imply that the sustainable use and development of livestock populations in pastoralist and smallholder production systems is a challenge that extends well beyond the immediate field of AnGR management. Balancing different objectives is unlikely to be easy. However, there may be scope for synergies in efforts to promote AnGR-management, livelihood and environmental objectives.

One trend affecting the livestock sector in many parts of the world is a movement of people out of livestock keeping and into alternative employment. In most countries, small-scale livestock keeping is unlikely to disappear in the short or medium term. However, where trends of this type are strong, AnGR associated with particular traditional types of livestock keeping or particular communities may be threatened.

International gene flows have continued to expand over recent years. Exchanges are still

dominated by North–North and North–South exchanges, with importers taking advantage of the genetic improvements achieved in the world's most advanced breeding programmes. The share of global imports accounted for by imports into developing countries has increased in some sub-sectors. This represents a large increase in gene flows of high-output international transboundary breeds from the North to the South. For many developing countries, South–South gene flows are also significant.

Gene flows clearly have the potential to increase the options available to livestock keepers and breeders as they seek to improve the productivity of their animals and adapt to change. However, countries are increasingly concerned about the effects of international gene flows on the diversity of their livestock populations and recognize that the establishment of exotic breeds and the production systems needed to maintain them can be challenging in terms of the additional resources and management skills required and the vulnerability of the animals to diseases, feed shortages and climatic hazards. Effective management of gene flow and effective use of imported genetics involve all the main elements of AnGR management: characterization of breeds and production environments to ensure that they are well matched; well-planned breeding strategies; monitoring of outcomes in terms of productivity and genetic diversity; measures to promote the sustainable use and conservation of breeds that may be put at risk of extinction; and appropriate policies and legal frameworks.

## Section B

# Characterization and monitoring

Characterization and monitoring are the foundations of sustainable AnGR management. However, in most regions of the world, there are still major gaps in the coverage of characterization activities and hence major gaps in knowledge about the characteristics of AnGR. There are also major gaps in programmes for monitoring trends in breed populations and hence the current risk status of many breeds is unknown. These gaps in knowledge inevitably hamper the sustainable use, development and conservation of AnGR.

In many countries, the basic task of establishing a complete inventory of national breeds across the full range of mammalian and avian livestock species has not been completed. For many recognized breeds, phenotypic characteristics – morphology, performance in specific production environments, degree of adaptation to specific diseases or climatic challenges, and so on – have been inadequately studied. Gaps are particularly prominent in developing countries, which means that the characteristics of the locally adapted breeds of these countries have been poorly described and that the comparative performance of different breeds in the production conditions prevailing in these countries has been inadequately assessed. Detailed description of typical production environments has been undertaken only for a limited number of breeds, precluding even the application of basic intuitive or heuristic approaches to breed comparison. At within-breed level, advanced technologies such as those related to the prediction of breeding values for individual animals and genomic selection have huge potential, but require phenotypic data. If developing countries lack characterization and performance data, they will be unable to take

advantage of new technologies of this kind.

Reporting on AnGR has improved over recent years. The number of national breed populations recorded in the Domestic Animal Diversity Information System (DAD-IS) has increased. However, breed-related information remains far from complete. For almost two-thirds of all reported breeds, risk status is unknown because of a lack of recent population data. Trends in the global state of AnGR diversity cannot therefore be monitored precisely. However, the available data indicate that genetic erosion is ongoing. Missing population data remains the biggest weakness of the current system for monitoring the global state of AnGR diversity. Another concern is the non-coverage of cross-bred and non-descript populations, which make up a large part of livestock populations worldwide. To obtain a more comprehensive picture, all livestock populations, regardless of their level of cross-breeding, need to be included in the monitoring system.

Breed effect is one of the many factors that influence the composition and quality of animal-source foods. Interest in the relationship between breed diversity and human nutrition has increased to some extent in recent years. Some comparative studies that assess the effect of breed *per se* and identify nutritional differences by controlling for other factors have been undertaken. However, high-quality studies that disentangle genetic and environmental factors are lacking, particularly for locally adapted breeds.

## Section C

# Sustainable use and development

While the majority of countries report that they have at least some livestock breeding programmes in place, the information provided in the country reports suggest that these programmes are often in a rudimentary state – or in some cases non-existent in the sense of organized programmes involving the establishment of breeding goals, recording of performance and subsequent selection of superior animals for mating. Efficient mechanisms for appropriately distributing improved genetic material are also often lacking.

Recent advances in the field of genomic selection have created opportunities to increase the rate of genetic progress for some traits (particularly those that are difficult to measure in all animals at a young age). However, use of genomic selection has, for the most part, been restricted to particular circumstances that favour its application (extremely large reference populations with extensive phenotypic data, high values of individual animals and established systems for distributing improved germplasm). This has further increased the gap between the most technically advanced breeding programmes and the rest of the sector – for example, Holstein breeding programmes relative to programmes for other breeds of dairy cattle.

Policies aimed at improving the state of livestock breeding are widespread, but in many countries these policies focus mainly on the introduction of exotic breeds for use in cross-breeding, sometimes paying little attention to the establishment of breeding programmes at national level. Introducing exotic AnGR can help countries boost their output of livestock products. However, great

care is needed to ensure that these resources are managed appropriately. Exotic breeds are sometimes introduced into production environments where they fail to flourish or prove to be risky investments. Moreover, indiscriminate cross-breeding – often with exotic genetic material – is one of the most widely reported threats to the survival of locally adapted genetic resources. Developing a national breeding strategy can be very challenging, particularly given that the information needed to assess the relative costs and benefits of different approaches is often unavailable. The existence of these knowledge gaps underlines the importance of strengthening efforts to characterize breeds and their production environments and the need to keep track of trends and drivers of change in the livestock sector.

While interest in expanding the use of exotic breeds is practically universal in developing countries, a number have also recognized the need to take greater advantage of the characteristics of their locally adapted breeds, particularly given the challenges associated with climate change and the ongoing need for livestock that are suitable for use by small-scale producers and in low-input production systems. In this context, breeding programmes for locally adapted breeds offer a potential means both of supporting rural livelihoods and of helping to keep a diverse range of breeds in use and hence available as resources for the future. In many countries, however, the underlying preconditions for the establishment of breeding programmes remain weak, particularly the organizational structures needed to facilitate the involvement of livestock keepers and breeders and the relatively high levels of knowledge



## PART 5

and technical skills needed to plan and implement programmes successfully. Experience indicates that while breeding programmes can be initiated by governments and research organizations, the involvement of breeders' associations and/or commercial companies increases the likelihood that they will be sustainable in the longer term.

One significant development in recent years has been a growing interest among developing countries in establishing animal identification schemes. These programmes are introduced primarily with the aim of improving animal health and product traceability, often driven by the incentive of gaining access to export markets that have high animal-health and product-safety standards. However, they may serve as the basis for more comprehensive programmes that include performance and pedigree recording.

Much of the potential of AnGR diversity remains untapped. For example, the inclusion of genetic elements in disease-control strategies has achieved some successes, but knowledge of the genetics of resistance and tolerance remains inadequate. The urgency of adopting more holistic alternative strategies is increasing as greater numbers of microbicides are losing their efficacy. A sign of the commercial recognition of health and other functional traits is that measures of health, robustness and other traits not directly related to performance have acquired an increas-

ing share in selection indices used in breeding programmes in developed countries.

A range of different activities can both help to increase the ongoing benefits derived from AnGR and to maintain genetic diversity for future use. Many breeds that are not at present valued in mainstream livestock production have characteristics that make them potentially valuable in the supply of products valued by a subsection of the market (niche products) or in the provision of public goods, including cultural services. Niche marketing of products from locally adapted breeds is quite widespread in developed regions such as Europe and contributes both to sustaining diversity and to rural livelihoods. Well-managed livestock can contribute to the provision of a number of ecosystem services, including those related to landscape management and the maintenance of wildlife habitats. Because of their ability to thrive in the relevant ecosystems, locally adapted breeds are often effective providers of services of this kind. However, harnessing these roles to promote the use of locally adapted breeds is not straightforward, as the benefits provided are not valued by the market. In this context, the emergence of the concept of payments for ecosystem services is an interesting development. Approaches of this kind potentially have a role in the sustainable management of AnGR.

## Section D

# Conservation

Conservation activities have become more widespread over the last ten years. Few countries report that they have no conservation measures of any kind in place. However, major gaps remain, both in *in situ* and in *ex situ* conservation programmes. Many breeds remain untargeted or inadequately covered by conservation programmes.

Information on threats to AnGR diversity remains far from complete. The risk status of the majority of breeds is classified as “unknown”. Even where population trends are monitored, detailed assessments of threats to specific breeds are not common. This clearly constrains the development of effective conservation programmes and the prioritization of breeds for inclusion in such programmes. Given the complexity of the drivers of change affecting the livestock sector and the potential for rapid shifts in the management of AnGR, there is a need for national early-warning and response systems that can rapidly identify threatened breeds and allow quick and well-defined action to be taken.

*In situ* conservation programmes can involve a diverse range of activities, including those that aim to create demand for the products and services provided by at-risk breeds, those that support and incentivize livestock keepers and breeders who raise at-risk breeds, those related to breeding programmes, and those that involve promoting participation and empowerment at community level. Careful assessment of livestock-sector trends and the characteristics of particular breeds and production systems will help countries and other stakeholders to identify appropriate *in situ* strategies for particular circumstances.

An increasing number of countries have set up AnGR gene banks. However, inadequate funding, infrastructure and technical skills often remain significant obstacles to the establishment or further development of such facilities. Establishing gene banks at subregional or regional level is a potential option. However, this would require agreements on rules for the transfer of genetic material and the identification of locations considered “safe” by all parties.

## Section E

# Policies, institutions and capacity-building

Without effective institutions, it is difficult to strengthen AnGR management programmes. Many countries report major gaps and weakness in their institutional frameworks for AnGR management. There have, nonetheless, been several positive developments in recent years, including the more widespread establishment of specifically AnGR-focused institutional structures and policy instruments – in particular the appointment of more National Coordinators for the Management of AnGR and the development of national strategies and action plans for AnGR. The establishment of several additional regional and sub-regional focal points for AnGR over recent years has strengthened cooperation and capacity to undertake AnGR management actions at supranational level.

Legal and policy frameworks relevant to AnGR management have been supplemented by a substantial number of new instruments over recent years. However, effective implementation remains a problem for many countries. In many cases, the basic prerequisites for effective implementation remain weak or absent. Physical and organizational infrastructure, stakeholder participation, and knowledge and awareness of AnGR-related issues are often inadequate. Financial shortfalls and a lack of well-trained personnel are widely reported to be serious constraints in all areas of AnGR management. Communication and coordination among stakeholders involved in AnGR management and with those in the wider agricultural, rural-development and environmental sectors often need to be improved. Smallholders and pastoralists are often neglected by the private sector, but are also poorly served

by public policies and programmes and have little voice in policy development.

There is a big gap between the state of the art in the use, development and conservation of AnGR and the current level of management capacity in many countries. Better education and training of development professionals, livestock keepers and other stakeholders, in animal breeding and all aspects of AnGR management, is needed. Integrating education and research across disciplines and across national boundaries and establishing partnerships spanning academic institutions, ministries and private industry – particularly between developed and developing countries – will help to decrease the gap in capacity.

In 2007, by adopting the Global Plan of Action and the Interlaken Declaration, governments *“confirmed their common and individual responsibilities for the conservation, sustainable use and development of animal genetic resources for food and agriculture; for world food security; for improving human nutritional status; and for rural development.”*<sup>1</sup>

Governments recognized the need both for “substantial and additional financial resources” and for predictable allocation of these resources. While awareness has increased and some countries have allocated additional resources, the evidence provided in the country reports indicates that sufficient funding has not yet been mobilized,

<sup>1</sup> FAO. 2007. *The Global Plan of Action for Animal Genetic Resources and the Interlaken Declaration*. Rome (available at <http://www.fao.org/docrep/010/a1404e/a1404e00.htm>).

**PART 5**

particularly at national level. Governments must demonstrate the sustained political will needed to ensure the successful implementation of the Global Plan of Action, including through the provision of adequate financial resources. If this does

not happen, genetic erosion is likely to continue and world's livestock biodiversity will remain underutilized and underdeveloped. Much of its potential to contribute to sustainably increasing food production will remain unrealized.

**A**nimal genetic resource diversity underpins the supply livestock products and services across a wide range of production environments. It promotes resilience and serves as a basis for adapting livestock management to changing conditions. It is vital to livelihoods of many of the world's poor people. It can contribute to the delivery of ecosystem services such as landscape management and the maintenance of wildlife habitats. However, it is often undervalued, underused and under threat.

This report updates the global assessment provided in the first report on *The State of the World's Animal Genetic Resources for Food and Agriculture*, published in 2007. It focuses particularly on changes that have occurred during the period since the first report was published. It serves as a basis for a review, and potential update, of the Global Plan of Action for Animal Genetic Resources, which since 2007 has provided an agreed international framework for the management of livestock biodiversity. Drawing on 129 country reports, it presents an analysis of the state of livestock diversity, the influence of livestock-sector trends on the management of animal genetic resources, the state of capacity to manage animal genetic resources, including legal and policy frameworks, and the state of the art in tools and methods for characterization, valuation, use, development and conservation.



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