

Part 4

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 encompassed by the phrase “management of AnGR”. However, it can be taken to encompass 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 2007. 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.”¹

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.²

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”.*³

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 breed⁴ 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

³ FAO, 2007b, page 347.

⁴ 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.

¹ FAO, 2007a, Paragraph 23, Introduction to Strategic Priority Area 1.

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

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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).⁵

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

⁵ 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).

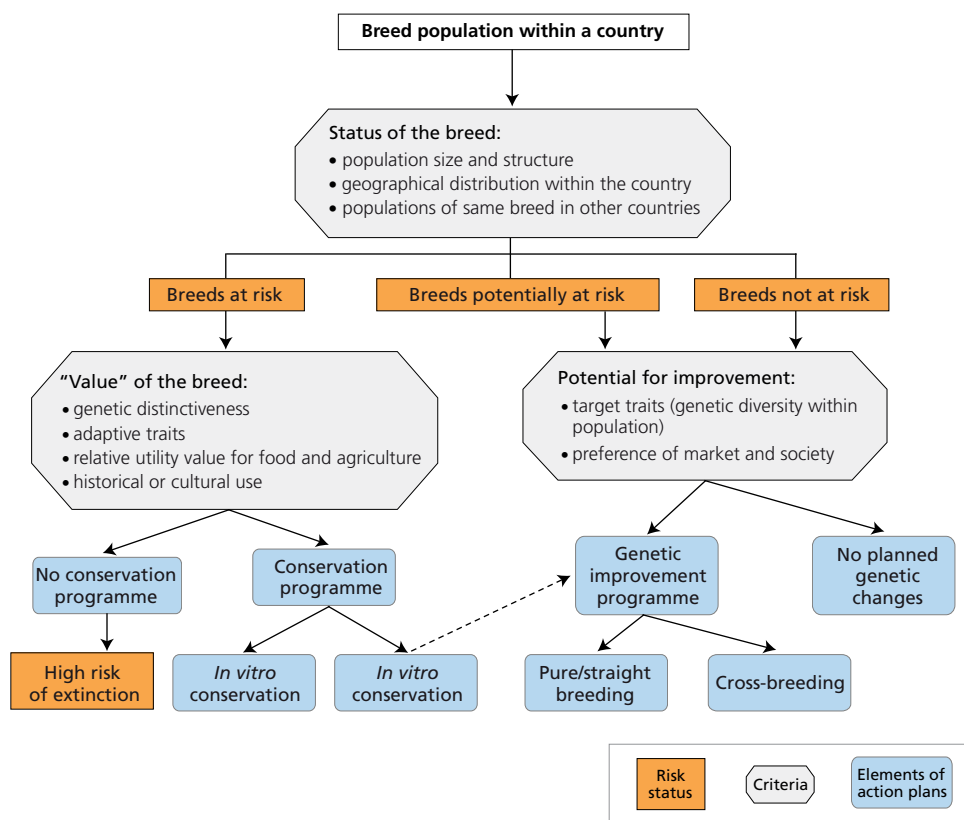
Analysis of data from molecular characterization studies allows inferences to be drawn not only on the present genetic structure of a breed population, but also on the breed's history (see Part 1 Section A). Molecular characterization can also be used to refine knowledge about transboundary populations 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

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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

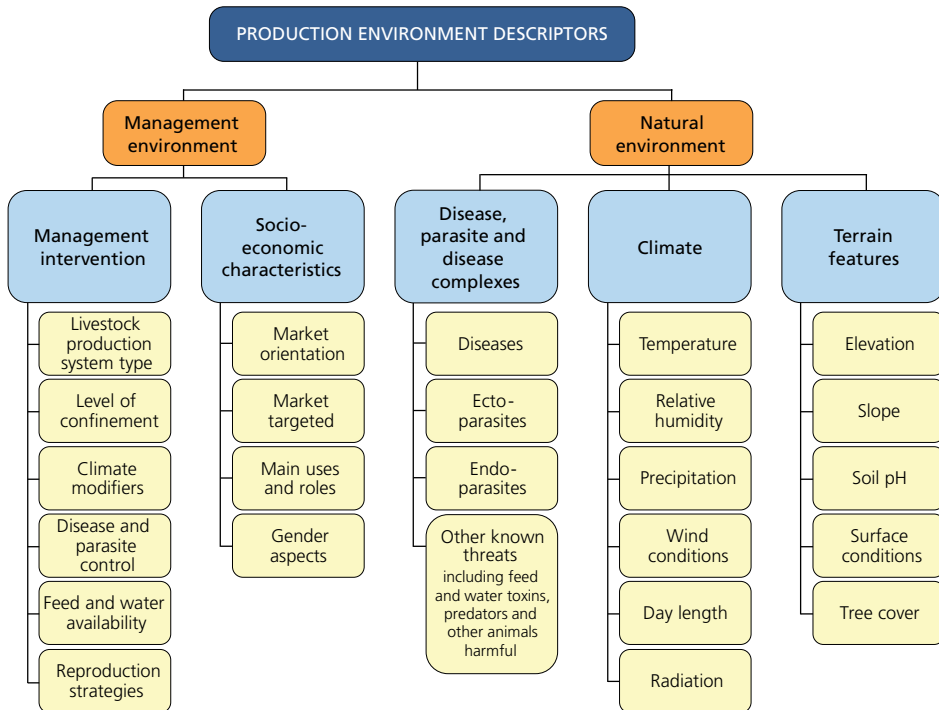
to be drawn regarding a breed's potential for improvement, particularly whether or not its genetic potential is being constrained by the environment (natural conditions or management capacity). Describing the production environment in which a breed has been raised for many years can also serve as an 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.

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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.)

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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 ¹ | Aerial survey | Rapid appraisal | Household survey | Census |
|--|--------------------|-------------------|-----------------------|---------------|-----------------|------------------|--------|
| Identification and characterization | | | | | | | |
| 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? | * | ** | ** | * | ***** | ***** | * |
| Monitoring | | | | | | | |
| 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.

¹ 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)⁶ and the European Farm Animal Biodiversity Information System (EFABIS)⁷

⁶ <http://fao.org/DAD-IS>

⁷ <http://efabis.tzv.fal.de/>

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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 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)⁸. Countries are able to set up their own national information systems (“nodes”) linked to EFABIS. Seventeen countries⁹ (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),¹⁰ 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 Livestock¹¹ 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)¹² as a common platform for the management of AnGR-related data.¹³ Wikipedia, the online

⁸ <http://efabis.net>

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

¹⁰ <http://dagris.ilri.cgiar.org/>

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

¹² http://nrcc.ars.usda.gov/A-GRIN/main_webpage/ars?record_source=US

¹³ http://nrcc.ars.usda.gov/A-GRIN/database_collaboration_page#

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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,¹⁴ 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.

¹⁴ 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) 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). 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), 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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