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منظمة  
الغذية والزراعة  
للأمم المتحدة

# COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE

## Item 3.2 of the Provisional Agenda

### INTERGOVERNMENTAL TECHNICAL WORKING GROUP ON ANIMAL GENETIC RESOURCES FOR FOOD AND AGRICULTURE

#### Tenth Session

Rome, 27 – 29 June 2018

### DETAILED ANALYSIS OF THE DOMESTIC ANIMAL DIVERSITY INFORMATION SYSTEM WITH FOCUS ON POPULATION DATA

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*<https://unstats.un.org/unsd/methodology/m49/>*

*Global Administrative Unit Layers (GAUL)*

*Food and Agriculture Organization of the United Nations (FAO)*

*<http://www.fao.org/geonetwork/srv/en/main.home?uuiid=f7e7adb0-88fd-11da-a88f-000d939bc5d8>*

*United Nations Cartographic Section, Department of Field Support*

*<http://www.un.org/Depts/Cartographic/english/htmain.htm>*



## I. INTRODUCTION

DAD-IS<sup>1</sup> is the Domestic Animal Diversity Information System hosted by FAO. It is a communication and information tool supporting the development of strategies for the management of animal genetic resources for food and agriculture (AnGR). The Commission on Genetic Resources for Food and Agriculture (Commission), at its Sixteenth Regular Session,<sup>2</sup> stressed the importance of DAD-IS as the international clearing-house mechanism for AnGR. DAD-IS provides its users with access to (*inter alia*) searchable, dynamic, multilingual databases of breed-related information. The names and contact information of all Regional and National Coordinators for the Management of Animal Genetic Resources (National Coordinators) are also available in DAD-IS.

As a result of more than three decades of work (the collection of the data stored in DAD-IS started as early as 1982), the Global Databank for Animal Genetic Resources, the backbone of DAD-IS, offers:

- information on more than 8 800 breeds of livestock (including poultry), comprising more than 15 000 national breed populations, from 182 countries and 38 species;
- information on breed characteristics, distribution and demographics;
- more than 4 000 images;
- tools for generating user-defined reports; and
- a multilingual interface and content.

DAD-IS has undergone several updates and revisions since its inception. The previous (third) version of DAD-IS (DAD-IS:3) was the centre of a global network of stand-alone information systems, also referred to as “nodes”. The global network provided links to one regional information system (EFABIS – European Farm Animal Biodiversity Information System) and from there to the subregional system for Nordic European countries (Denmark, Finland, Iceland, Sweden and Norway). EFABIS also provided direct links to the individual national information systems of 16 European countries (Austria, Bulgaria, Cyprus, Estonia, Georgia, Greece, Hungary, Ireland, Italy, the Netherlands, Poland, the Republic of Moldova, Slovakia, Slovenia, Switzerland and the United Kingdom). The European node with its subregional and national nodes is called EFABISnet.

The network of information systems treats countries as the smallest unit, and supports aggregation and synchronization at regional and worldwide levels. All information systems are accessible through the Internet using standard Web browsers.

For more than ten years, DAD-IS maintenance and development depended mostly on project funds and temporary staff, a system that came to an end in December 2014. Over the same period, demand for DAD-IS as a reference system for AnGR increased, as it is the only global system that contains the data needed for various global indicators of livestock genetic diversity. This combination of uncertain, short-term funding and increasing long-term demand posed a problem for the sustainability of the system and called for a different organizational and financial structure. Ideally, the maintenance and further development of DAD-IS should not depend on individual experts working temporarily within the framework of projects, but be maintained by a dedicated FAO team able to take care of all aspects of the application from data collection to dissemination and ensure a sustainable service.

Moreover, the original design of DAD-IS:3 and the underlying technology were outdated: data entry and dissemination tools were not user-friendly and data synchronization between the systems of the network was complex and required permanent maintenance of 19 servers (one global, one regional, one subregional and 16 national nodes). Further, the technology used constrains the implementation of necessary amendments to the system.

Because of the problems described above, the Global Focal Point for Animal Genetic Resources decided to develop a more powerful and versatile fourth version of DAD-IS (DAD-IS:4) using state-of-the-art information technology and FAO in-house expertise. This development was possible thanks to the financial support of the Government of Germany. The support from Germany, along with funds from FAO’s Regular Programme, allowed for the development of DAD-IS:4 over the course of approximately two years. DAD-IS:4 was officially launched on 21 November 2017 at the Global National Coordinator

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<sup>1</sup> <http://www.fao.org/dad-is/en/>

<sup>2</sup> CGRFA-16/17/Report/Rev.1, paragraph 46.

Workshop on DAD-IS and Sustainable Development Goal (SDG) Indicators 2.5.1 and 2.5.2, held at FAO headquarters.

This document reports in detail on developments in DAD-IS since the Ninth Session of the Intergovernmental Working Group on Animal Genetic Resources for Food and Agriculture. The document consists of two main sections. The first describes the global DAD-IS workshop, where the new system was introduced and the quality and quantity of breed population data discussed with National Coordinators. The second highlights the new features of DAD-IS:4 and presents selected results of example analyses performed on data exported from DAD-IS. (All figures presented in the document are based on the data available in DAD-IS as of the first week of March, 2018.) The document ends with a section that offers some conclusions regarding the availability of data and an outlook on the further development of DAD-IS.

## II. GLOBAL WORKSHOP AND GAP ANALYSIS

The fourth version of DAD-IS was launched on 21 November 2017 in Rome, Italy. The launch event was followed by the Global National Coordinator Workshop on DAD-IS and SDG Indicators 2.5.1 and 2.5.2, held 21–23 November 2017. The workshop agenda is given in Annex I. In total, 68 National Coordinators and government statisticians participated in the workshop, representing 46 countries and the African Union – Interafrican Bureau for Animal Resources (AU-IBAR) (see Annex II).

During the workshop, DAD-IS:4 was presented and training on data entry provided. The workshop particularly focused on the entry into DAD-IS of the data needed to calculate two indicators of livestock genetic diversity for the SDGs: SDG Indicator 2.5.1 – *Number of plant and animal genetic resources for food and agriculture secured in either medium or long-term conservation facilities*; and SDG Indicator 2.5.2 – *Proportion of local breeds, classified as being at risk, not at risk or at unknown level of risk of extinction*.

Throughout the existence of DAD-IS, population data have been lacking for many breeds, information that is critical for the calculation of SDG Indicator 2.5.2, as well as for the national management of AnGR. The Commission, at its Sixteenth Regular Session,<sup>3</sup> requested FAO to identify possible reasons for the continuing high proportion of breeds with unknown risk status in DAD-IS and potential means of addressing this issue. In this context, one objective of the workshop was to analyse reasons for the high proportion of breeds with unknown risk status. As of March 2018, if extinct breeds are excluded, 67 percent of local breeds worldwide, are classified as being of unknown status, 26 percent as being at risk, and 7 percent as being not at risk.<sup>4</sup>

The programme of the first day of the workshop focused on the demonstration of DAD-IS:4 and explanation of its links to the SDGs.

On the second day of the workshop, group work was organized on “Why do we have a data gap for SDG Indicators 2.5.1 and 2.5.2?” Participants were invited to organize themselves into regional groups and each group was requested to conduct a “problem tree” analysis to identify the reasons for gaps in the respective region’s breed population data in DAD-IS. Four groups, namely (i) Africa and the Near East and North Africa, (ii) Asia, (iii) Latin America and the Caribbean, and (iv) Europe and North America, were formed. Prior to starting the group work, each participating National Coordinator was invited to complete a short anonymous questionnaire on factors specifically constraining the entry of national breed population data into DAD-IS in their respective countries.

Before the regional groups presented their findings, FAO briefly introduced the results of the questionnaire. A basic lack of breed population data at country level was the most frequently reported constraint. In the case of Europe, several National Coordinators indicated that lack of access to existing breed data was also a constraint. Smaller numbers of respondents globally mentioned that they lacked awareness of their responsibilities as a National Coordinators to gather breed data and insert them into DAD-IS. Similar numbers indicated that they lacked knowledge on how to enter data into DAD-IS or that entering data into DAD-IS was not included in the official terms of reference for their posts of employment.

<sup>3</sup> CGRFA-16/17/Report/Rev.1, paragraph 46.

<sup>4</sup> CGRFA/WG-AnGR-9/16/Inf.3.

The following regional results were obtained:

*Africa and the Near East and North Africa*

Ms Deidre Januarie (Namibia) presented the findings of the Africa and Near East and North Africa group. Constraints identified included the following:

- lack of awareness of the importance of AnGR and data regarding their population numbers;
- lack of relevant legislative frameworks (e.g. on animal identification and recording, evaluation of local breeds and control of unregulated livestock movements);
- lack of AnGR characterization studies;
- lack of livestock and/or breed censuses and animal recording schemes;
- lack of breed associations;
- access problems caused by disasters and conflicts; and
- lack of coordination caused by a lack of an official mandate for the National Coordinator, a lack of links to relevant stakeholders and/or rigid institutional bureaucracy.

Deficiencies in funding, technical skills and suitable human resources were noted as underlying problems affecting AnGR management in general.

*Asia*

Mr Yang Hongjie (China) presented the findings of the Asia group. Constraints identified included both immediate constraints related specifically to the work of National Coordinators (e.g. a lack of an appropriate mandate, a lack of resources, problems with translating data from local languages and time constraints caused by the need to undertake other duties) and constraints at a wider level (e.g. a lack of policies addressing breed monitoring and a lack of awareness of the significance of such data on the part of decision-makers).

*Europe and North America*

Ms Danijela Bojkovski (Slovenia) presented the findings of the Europe and North America group. The group had identified constraints relevant to three groups of countries: those with no data; those with some data; and those that have data but do not enter them into DAD-IS.

Constraints identified with regard to the first group included a lack of monitoring systems as a consequence of a lack of funds or a lack of human capacity, a lack of identification or registration systems for some breeds, lines or species, and a lack of willingness on the part of private organizations to release data.

Constraints identified for the second group included the availability of data only at species level (i.e. not at breed level) and the availability of data only for subsets of breed populations, such as only for animals registered in herd books.

Constraints identified with regard to the third group included concerns about entering data into DAD-IS for breeds that have a small population size within the respective country but are native to and principally present in another country. Such reporting would lead to the breed becoming recognized as transboundary and hence preclude it from being taken into account in calculating the relevant SDG Indicator, which addresses only local breeds.

*Latin America and the Caribbean*

Mr Arthur da Silva Mariante (Brazil) presented the findings of the Latin America and the Caribbean group. Constraints identified related to three main areas: surveys and censuses; breed recognition mechanisms; and resource limitations.

Constraints identified in the first main area included an unwillingness on the part of countries to upload “unofficial” data, the relative infrequency of agricultural censuses, a lack of coverage of certain species and of small population units in such censuses and a lack of collection of breed-level data (i.e. as opposed to data at species level).

Constraints identified in the second category included an unwillingness on the part of countries to record breeds in DAD-IS that have not been officially recognized and a lack of awareness at country level of the significance of AnGR, particularly of locally adapted breeds.

Activities reported to be constrained by resource limitations included the collection of breed characterization data.

Issues raised during the questions and comments session that followed the presentations included the reasons why some breeds are not recognized by national authorities. Constraints identified in this regard included a lack of relevant procedures and regulatory frameworks and a lack of financial and human resources for field characterization studies. Participants also discussed the role of DAD-IS and hence the benefits to be obtained by providing more complete breed population data. The participants noted that DAD-IS provides countries with a tool that can be used to meet their reporting commitments with respect to the SDG Indicators and the Global Plan of Action for Animal Genetic Resources.<sup>5</sup> It was also noted that DAD-IS includes early-warning tools that – provided population data are recorded and updated – can draw attention to breeds whose demographic data indicate that they are on a trajectory towards extinction.

The regional groups then were invited to reconvene and convert their “problem trees” into “solution trees” by identifying means of addressing the various constraints identified during their previous discussions. The following solutions were presented:

#### *Africa and the Near East and North Africa*

Ms Januarie presented the findings of the Africa and the Near East and North Africa group. Opportunities identified included the following:

- with regard to the lack of awareness – targeted awareness-raising for all stakeholders, revival of National Advisory Committees on AnGR (or equivalent multistakeholder bodies), and lobbying for resource allocation for advocacy and awareness raising;
- with regard to the lack of relevant legislative frameworks – advocacy for the development of relevant laws, and establishment of identification and traceability systems;
- with regard to the lack of breed characterization – creation of multistakeholder “knowledge hubs” to promote information sharing, use of existing tools (e.g. FAO’s guideline publications on characterization<sup>6,7</sup> and surveying and monitoring<sup>8</sup> and AU-IBAR’s characterization, inventory and monitoring tool) and capacity-building for relevant skills;
- with regard to the lack of functional systems – improving coordination (with National Coordinators to play a key role);
- with regard to the absence of breed-specific associations – promoting the establishment of associations of this kind, strengthening coordination among stakeholders, promoting the economic importance of specific breeds, and strengthening value chains and establishing breeding schemes for local breeds;
- with regard to the lack of coordination – revival of National Advisory Committees on AnGR (or equivalent multistakeholder bodies) and use of the FAO guidelines on institutional frameworks for the management of AnGR;<sup>9</sup> and
- with regard to the inaccessibility of data collection areas – provision of support during recovery phases following disasters and conflicts.

During the question and comments session following the presentation, participants discussed the significance of the above-listed activities to the specific problem of gaps in breed population data in DAD-IS. With regard to breed-development activities such as breeding programmes and improvements to the value chain, it was argued that these would both directly generate data and

<sup>5</sup> <http://www.fao.org/docrep/010/a1404e/a1404e00.htm>

<sup>6</sup> <http://www.fao.org/docrep/014/i2413e/i2413e00.htm>

<sup>7</sup> <http://www.fao.org/docrep/015/i2686e/i2686e00.htm>

<sup>8</sup> [www.fao.org/docrep/014/ba0055e/ba0055e00.pdf](http://www.fao.org/docrep/014/ba0055e/ba0055e00.pdf)

<sup>9</sup> [www.fao.org/docrep/014/ba0054e/ba0054e00.pdf](http://www.fao.org/docrep/014/ba0054e/ba0054e00.pdf)

stimulate greater interest in the respective breeds and hence in data concerning them. More generally, it was argued that the data gap is a result of structural issues and that these underlying causes need to be addressed. Participants reiterated the importance of phenotypic characterization studies and of establishing or reviving National Advisory Committees.

#### *Asia*

Mr Bidhan Baral (Bangladesh) introduced the findings of the Asia group. The group had noted that appropriate initiatives would vary from country to country, as some have stronger national statistics systems than others. The participants had therefore discussed general solutions. The main priorities identified were as follows:

- establishing national plans of action that identify synergies between various national and international data collection initiatives, clarify national targets and strategies, and provide a road map for minimizing the data gap on AnGR;
- forming or revitalizing National Advisory Committees on AnGR, which would be responsible for preparing the above-mentioned national plans, supporting the development of legal frameworks related to AnGR and building awareness (organization of national workshops was a specific recommendation in this regard);
- giving national SDG monitoring committees a directing role, involving, *inter alia*, organization of workshops, publicizing recommendations and provision of guidelines on how to bridge gaps between policy-makers and implementing agencies;
- increasing the role of FAO at international and regional levels, particularly with regard to capacity-building activities of various kinds;
- developing appropriate methodologies for transforming administrative data into official statistics;
- forming teams led by National Coordinators to work on improving DAD-IS data;
- establishing formal coordination between national statistical offices and departments of animal resources (or equivalent departments) as a basis for planning and implementing data collection and disseminating findings; and
- including questions relevant to the AnGR-related SDG Indicators in upcoming livestock censuses and surveys.

During the questions and comments session following the presentation, the discussion focused, in particular, on how to establish or strengthen collaboration between national statistical offices and bodies responsible for AnGR or livestock development and on mechanisms for integrating administrative data into national statistics. Participants noted the need to make the most of existing administrative data, but also the need to ensure that they are reliable and consistent.

#### *Europe and North America*

Ms Christina Ligda (Greece) presented the findings of the Europe and North America group. Potential solutions identified included standardizing data entry and terminology to promote more consistent approaches across countries, improving collaboration with breed associations and strengthening efforts to persuade such associations to make data available, and reviewing approaches taken with respect to the entry of data on transboundary breeds into DAD-IS.

During the questions and comments session that followed the presentation, participants discussed the question of how to use data on subsections of breed populations to generate national-level data.

#### *Latin America and the Caribbean*

Mr Mariante presented the findings of the Latin America and the Caribbean group. Solutions identified included the following:

- with regard to censuses and surveys – improving collaboration between institutions in the design of censuses and surveys, broadening the coverage of censuses and surveys so as to include all species and breeds and cover small populations, and strengthening connections between national information systems and DAD-IS;

- with regard to official recognition of breeds – promoting reviews of legal frameworks for breed recognition, and including a field in DAD-IS to record whether or not breeds have been officially recognized; and
- with regard to resource limitations – developing capacity through cooperation among the countries of the region, promoting the inclusion of AnGR management in university courses, facilitating data collection and entry into DAD-IS by making available printable and offline forms and allowing additional log-ins for entry of data (with a mechanism for review by the National Coordinator before definitive upload into the system).

During the questions and comments session that followed the presentation, participants further discussed the proposed mechanisms for facilitating data collection and entry. It was noted that in some cases National Coordinators lack the authority to approve national data.

### III. NEW DAD-IS FEATURES AND SELECTED RESULTS

DAD-IS:4 uses state-of-the-art technology and in-house expertise from FAO's Information Technology Division (CIO). A project financed by the Government of Germany focused on restructuring the DAD-IS:3 front-end (i.e. user interface) without affecting the database structure of DAD-IS or EFABIS. This involved ensuring smooth data synchronization between DAD-IS and EFABIS, improving the user-friendliness of established reports, developing new reports and developing a data-export tool to facilitate the merging of DAD-IS data on AnGR with other types of food and agricultural data from other sources.

The new version of DAD-IS is available at <http://www.fao.org/dad-is/en/>. The landing page is shown in Figure 1.

**Figure 1. The DAD-IS landing page**

The screenshot shows the landing page for the Domestic Animal Diversity Information System (DAD-IS). At the top, there is the FAO logo and the text 'Food and Agriculture Organization of the United Nations'. A search bar for 'Google Custom Search' is on the right. Below the logo, there is a navigation menu with links for 'About FAO', 'In Action', 'Countries', 'Themes', 'Media', 'Publications', 'Statistics', and 'Partnerships'. Language options are listed below the menu: العربية, 中文, English, Français, Русский, Español.

The main heading is 'Domestic Animal Diversity Information System (DAD-IS)'. Below this is a navigation bar with 'Data', 'In Focus', 'Publications', and 'National Coordinators'. A large image shows a herd of animals in a field. A text box on the left describes the system's purpose: 'DAD-IS is the Domestic Animal Diversity Information System maintained and developed by FAO. It provides you with access to searchable databases of breed-related information and photos and links to other online resources on livestock diversity. Furthermore, you can find the contact information of all National Coordinators for the Management of Animal Genetic Resources. It allows you to analyse the diversity of livestock breeds on national, regional and global levels including the status of breeds regarding their risk of extinction.'

Below this is a 'Key facts' section with four cards:

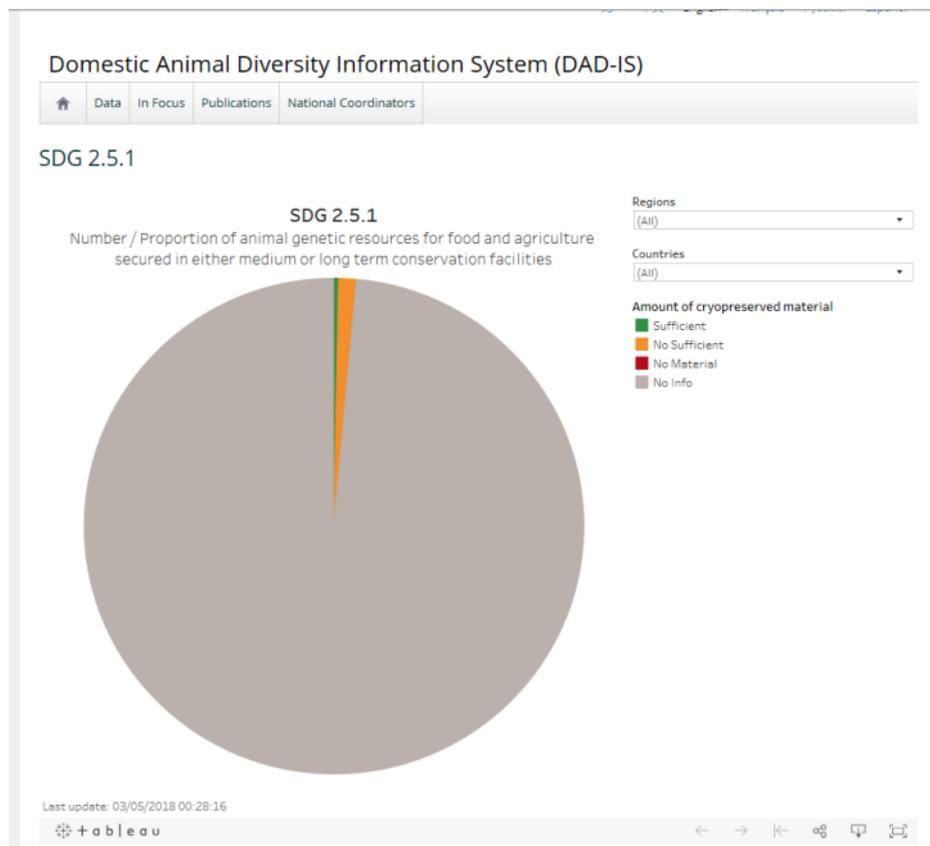
- 1. The roles and values of animal genetic resources remain diverse, particularly with regard to the livelihoods of poor people.
- 2. There are around 8800 livestock breeds of 38 different species in the world, providing a diversity of products and services.
- 3. Many breeds have unique characteristics that can contribute to meeting challenges related to climate change.
- 4. The threats to animal genetic resources need to be better identified and their potential effects better assessed, so that action can be taken.

The tools for viewing, downloading and utilizing the data in DAD-IS are publicly available. Data entry is password-protected and therefore only available to the National Coordinators. For the first time, all National Coordinators have the opportunity to report on the quantities of various types of cryoconserved

material stored for each breed.

The new features of the system include a tool for calculating SDG Indicators 2.5.1 and 2.5.2 that allows the calculation of the indicators at national, regional and global levels. Figure 2 shows an example of the result obtained when calculating SDG Indicator 2.5.1 at the global level.

**Figure 2. The DAD-IS tool for the calculation of SDG Indicator 2.5.1**



For the first time in its history, DAD-IS now includes a data export tool, a feature that allows users to perform any analysis of DAD-IS data that they wish, as well as to combine the DAD-IS data on AnGR with other types of food and agricultural data obtained from other sources. The following section presents the results of some selected analyses performed using data exported from DAD-IS.

### Categories of breeds

As indicated in the document *Status and trends of animal genetic resources – 2018*,<sup>10</sup> there are currently more than 15 000 national breed populations recorded in DAD-IS, representing 38 species. Two main breed classification systems are currently used in DAD-IS. These are based, respectively, on: (i) the geographical distribution of breed populations among countries (national breed populations being thus categorized as belonging to “local”, “regional transboundary” or “international transboundary” breeds); and (ii) the degree of adaptedness of national breed populations to their production environments (national breed populations being thus classified as either “locally adapted” or “exotic”). For both classification systems, assignment is made by the respective National Coordinator. For more detailed information on these classification systems, see the *Report of a consultation on the definition of breed categories*<sup>11</sup> and the *Report of the Fourteenth Regular Session of the Commission on Genetic Resources for Food and Agriculture*.<sup>12</sup>

There are currently 7 745 local breeds, 511 regional transboundary breeds (corresponding to 1 303

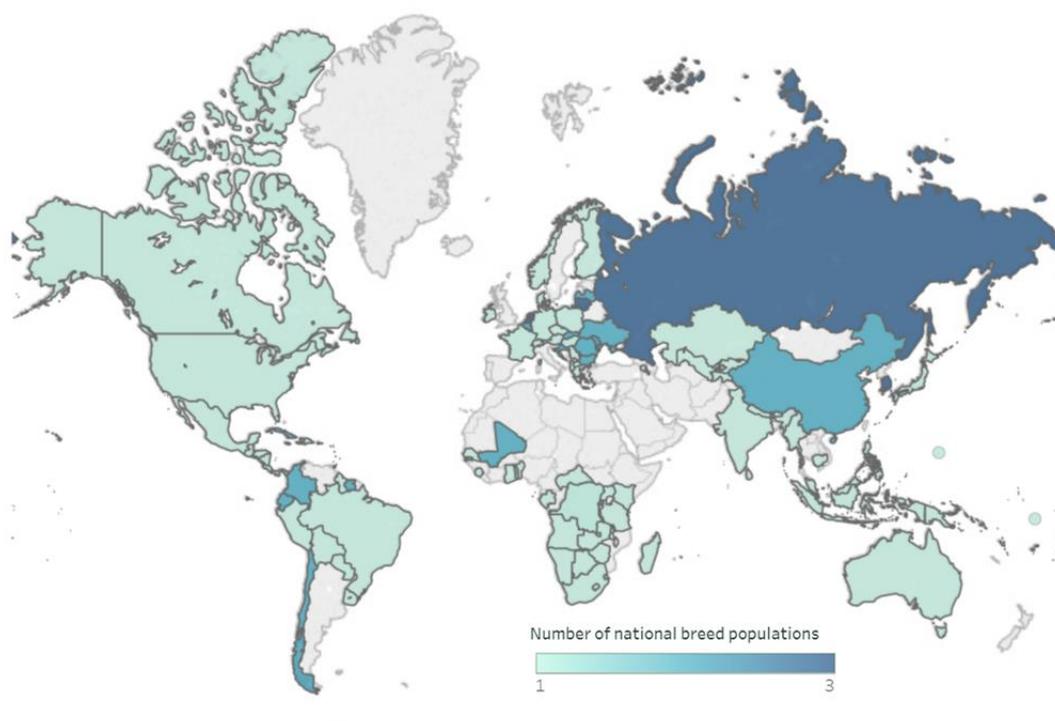
<sup>10</sup> CGRFA/WG-AnGR-10/18/ Inf.3.

<sup>11</sup> CGRFA/WG-AnGR-7/12/Inf.7.

<sup>12</sup> CGRFA-14/13/Report, paragraph 31.

national breed populations) and 547 international transboundary breeds (corresponding to 6 012 national breed populations) recorded in DAD-IS. In the case of transboundary breeds, the number of corresponding national breed populations recorded in DAD-IS ranges from one (95 of the breeds assigned transboundary status by National Coordinators are actually reported only in one country) to 163 (Holstein, Friesian and other Black and White cattle). The number of transboundary breeds reported by individual countries ranges from 1 to 132. Some countries report multiple national breed populations of the same transboundary breed. Figure 3 shows an example in detail – 115 countries report 140 national breed populations belonging to the transboundary Large White breed of pigs. The number of national breed populations of Large White pigs ranges from 1 to 3 per country.

**Figure 3. Repartition of Large White Pig national breed populations across the world**



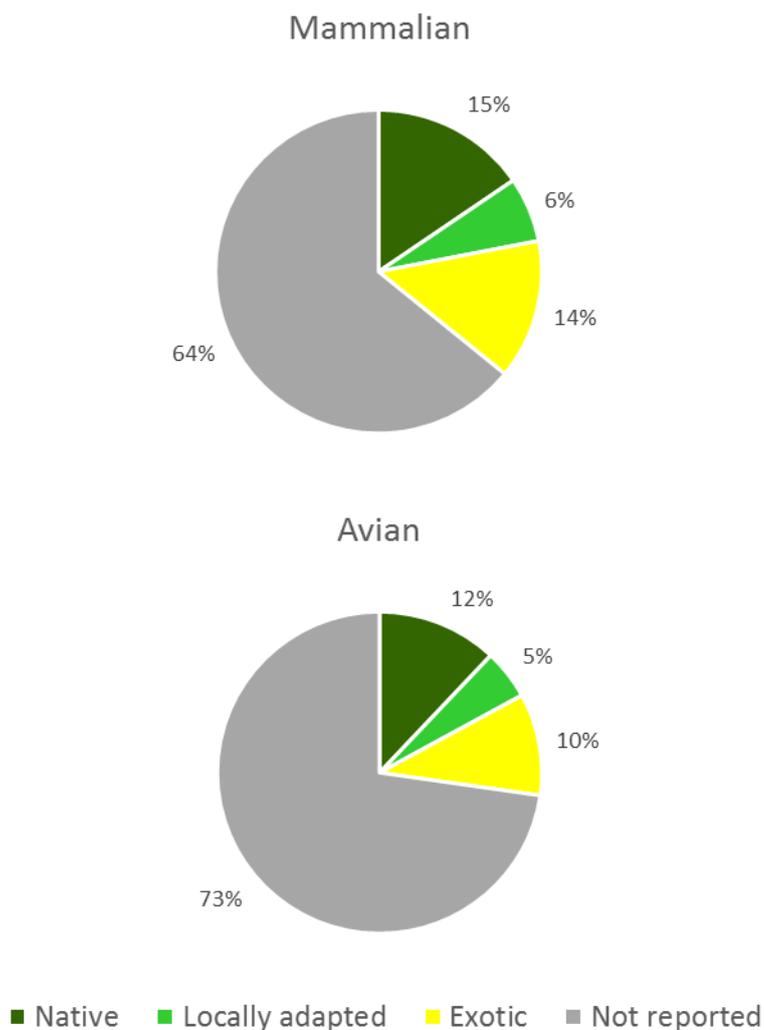
Since 2012, all National Coordinators have been regularly reminded to classify their national breed populations according to their adaptedness. Within this categorization system, National Coordinators have the further option of indicating whether a given locally adapted breed is “native” to the respective country. Currently, slightly more than one-third (5 090) of national breed populations have been classified for adaptedness. Among these populations, 3 124 are classified as locally adapted (of which 2 200 are considered native) and 1 966 as exotic. A greater proportion of mammalian populations has been classified for adaptedness than avian populations (36 percent versus 27 percent). Figure 4 shows the results of this classification according to species group (i.e. mammalian and avian). Among the classified populations, proportions of locally adapted, native and exotic populations are similar in the two species groups.

Figure 5 shows the distribution of national breed populations across adaptedness categories for the five main livestock species (i.e. chicken, cattle, goat, pig and sheep). Sheep are the species for which the largest proportion of national breed populations have been classified according to adaptedness (41 percent) and pigs are the species with the smallest proportion (23 percent). The highest proportions of locally adapted breed populations are reported for sheep and goats (28 percent and 22 percent, respectively).

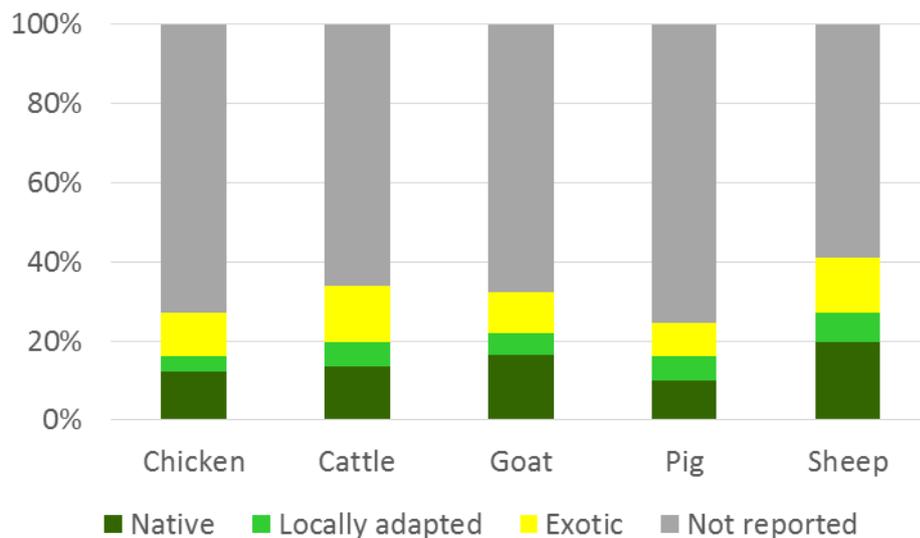
Results show substantial differences among regions in both completeness of reporting and distribution of national populations across the adaptedness categories (Figure 6). At regional level, the proportion of national breed populations classified according to their adaptedness status ranges from 0 (Southwest

Pacific) to 79 percent (North America). Among national breed populations with adaptedness status reported, the proportion classified as exotic ranges from 0.2 percent (North America) to 83 percent (Latin America and the Caribbean).

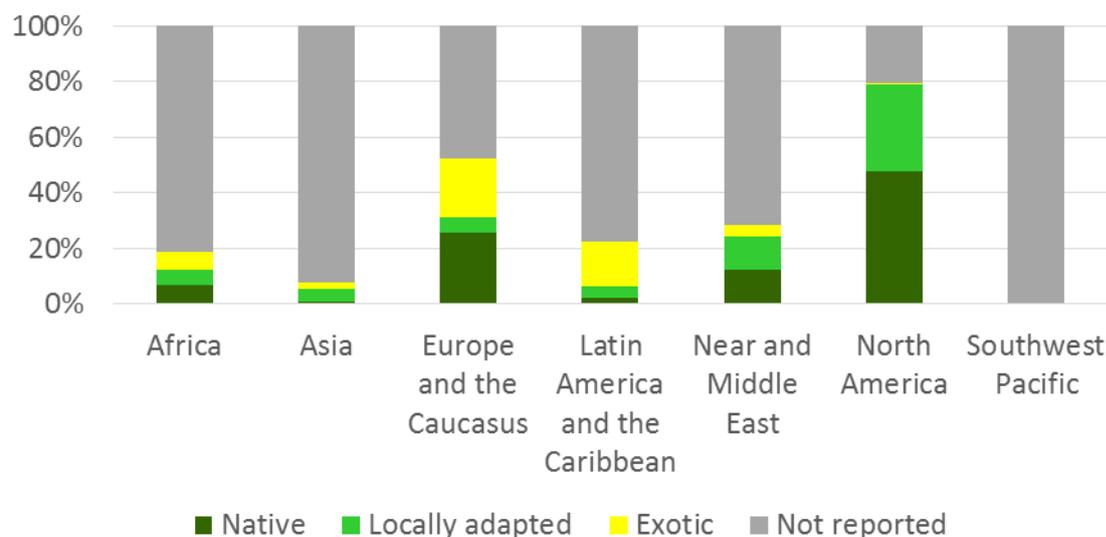
**Figure 4. Proportions of the world's national breed populations by adaptedness category**



**Figure 5. Proportions of the world's national breed populations by adaptedness category for chicken, cattle, goat, pig and sheep**

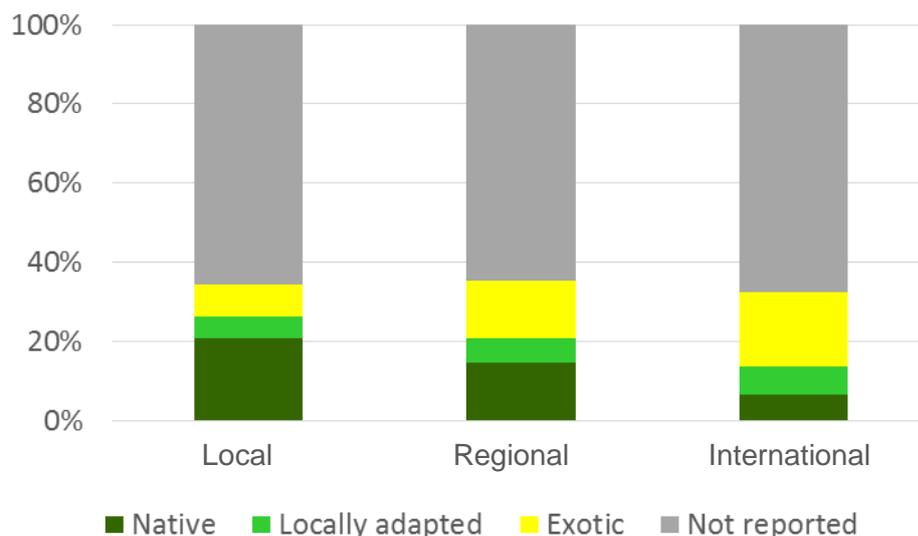


**Figure 6. Proportions of the world's national breed populations by adaptedness category and by region**



As shown in Figure 7, the proportion of national breed populations with adaptedness status reported does not differ much across the local (34 percent), regional transboundary (35 percent) and international transboundary (33 percent) breed categories. However, among those breed populations whose adaptedness status is recorded, the proportion of native national breed populations is greater among local breeds (61 percent) than among regional (41 percent) and international transboundary breed populations (20 percent). This finding is logical, because if a breed exists only in a single country (and is thus a local breed), that country is likely to be its country of origin (and hence the breed is also native). The proportion of local breeds classified as exotic (8 percent) is surprisingly high, however, and may be, to some extent, related to misclassification, such as the failure by a country to properly declare a given exotic national breed population as transboundary.

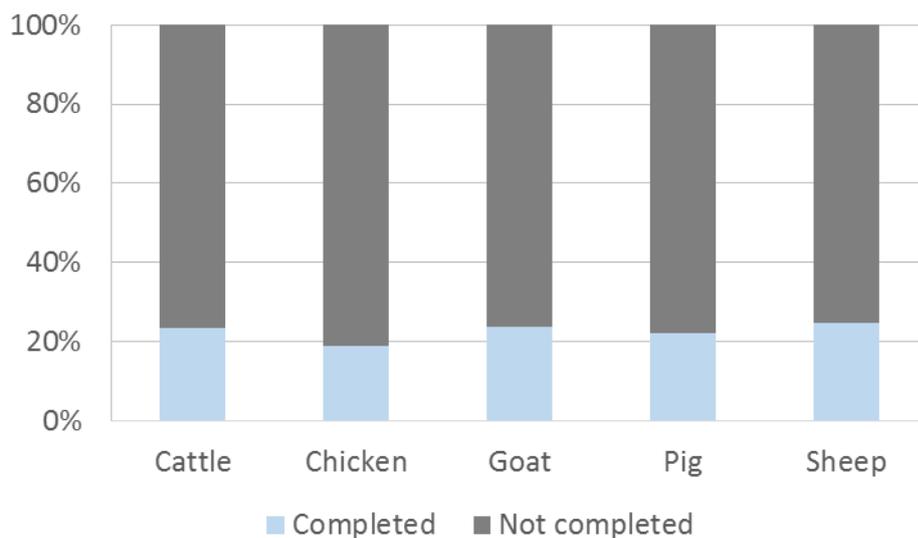
**Figure 7. Proportions of the world's local, regional and international transboundary national breed populations by adaptedness category**



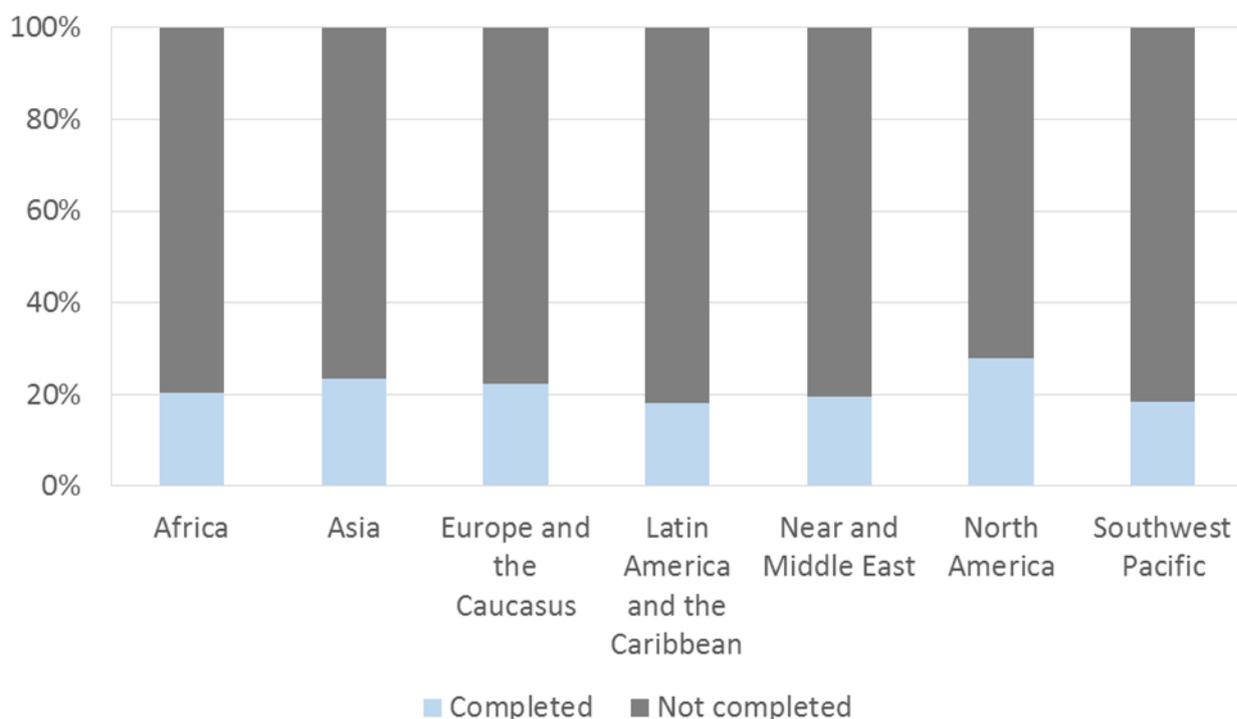
### Data completeness

To assess the level of completeness of breed data, a new tool was developed and provided to National Coordinators on their data-entry homepage. This tool sums up, over all national breed populations, the completeness of data fields falling under the following 13 groups: (a) Breed name; (b) Uses; (c) Images; (d) Origin and development; (e) Morphology; (f) Colours; (g) Additional information; (h) Distinctive traits; (i) Performance; (j) Population data; (k) Management conditions; (l) *In vivo* programmes; and (m) Cryo programmes. With the exception of the last three groups, where completeness is related to regular updates of population numbers or the existence or absence of conservation programmes, a group of data fields is considered to be complete if all fields have values. For European countries, the number of fields for a given category in EFABIS may differ from the number of fields in global DAD-IS due to the presence of fields specifically requested by the members of the European Regional Focal Point. The level of completeness for individual countries ranges from 8 percent to 45 percent, with an average around 21 percent. Despite substantial differences among countries, the average level of completeness does not differ greatly across the five main livestock species (Figure 8) or regions (Figure 9). Among species, average data completeness ranges from 19 percent (chicken) to 25 percent (sheep). For regions, the range is from 18 percent (Latin America and the Caribbean) to 28 percent (North America).

**Figure 8. Average data completeness for chicken, cattle, goat, pig and sheep national breed populations**



**Figure 9. Average data completeness by region**



### Analysis and utilization of DAD-IS data

#### *DAD-IS metadata*

The term “metadata” in DAD-IS refers to the descriptive information for each breed. These types of data can be exported separately from DAD-IS. To illustrate potential uses of the metadata, an analysis was performed on information provided by National Coordinators on the uses of national breed populations. The analysis is described and results reported in the subsequent paragraphs.

When entering data on the characteristics and utility of a given breed into DAD-IS, National Coordinators can choose from among 47 different uses. DAD-IS applies no restriction to the number of uses that can be entered per breed. To date, information on use has been provided on 7 878 national

breed populations (52 percent), for which a minority of breeds (1 241, i.e. 16 percent) have multiple uses indicated. For this example analysis, only the uses indicated for more than 50 national breed populations were considered and they were grouped into the following nine categories: (i) meat (including meat and lard); (ii) milk; (iii) eggs; (iv) cross-breeding (including general cross-breeding and sire lines); (v) wool, pelts and skins (including wool, pelts/fur, skin/hides); (vi) hobby (including sport, hobbies and riding for sport); (vii) work (including draught power, riding for work purposes and transport); (viii) research; and (ix) vegetation management.

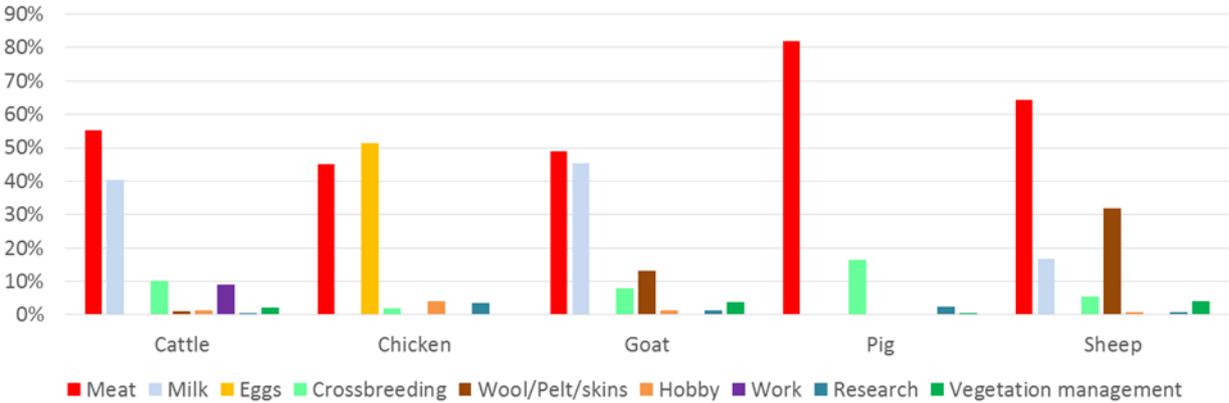
Meat is the use category reported for (by far) the largest proportion of national breed populations (54 percent; 4 266 national breed populations), followed by milk (18 percent; 1 455 national breed populations) and eggs (10 percent; 751 national breed populations). Other uses such as hobby (8 percent; 658 national breed populations), wool/pelts/skins (8 percent; 530 national breed populations), cross-breeding (7 percent; 530 national breed populations) and work (6 percent; 471 national breed populations) are also relatively commonly reported. Uses such as vegetation management (2 percent, 159 national breed populations) and research (2 percent; 135 national breed populations) are less frequently indicated.

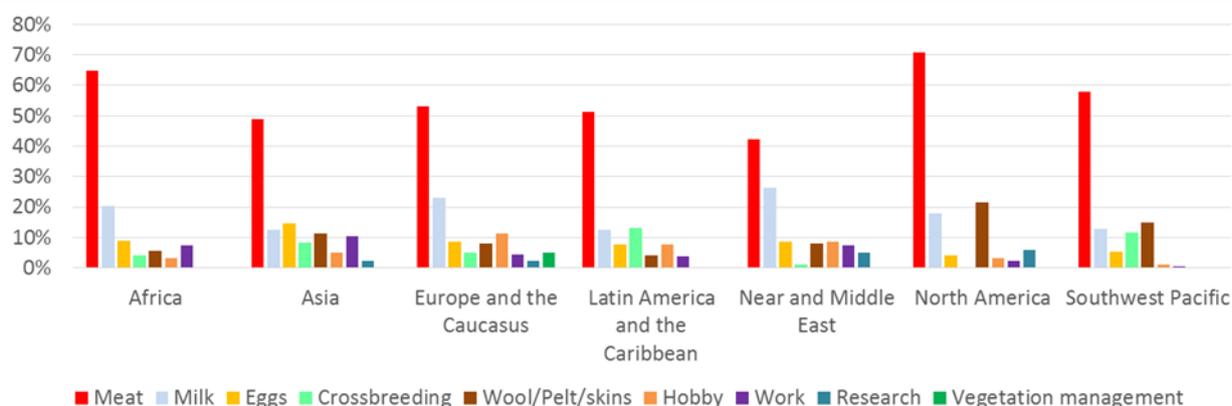
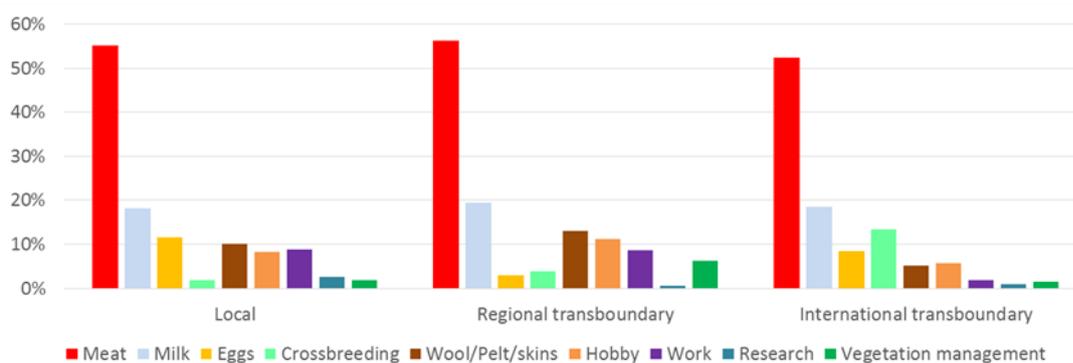
Meat is reported as the main use for all the five major livestock species except for chickens, for which meat is outranked by eggs (Figure 10). Meat production is particularly commonly reported for pigs (> 80 percent of national breed populations). The other uses indicated vary substantially across species. As might be expected, use for egg production is reported only for avian species, including for 51 percent of the chicken national breed populations for which at least one use is indicated. Among the five major species, milk and vegetation management are reported only for ruminant species, while wool/pelts/skins are reported almost exclusively for sheep and goat breeds. Among the five major species, work is reported only for cattle breeds. However, among the less common species (not shown), work is also frequently indicated for horses (30 percent; 189 national breed populations). Hobby activity is the main use reported for national breed populations of horses (64 percent; 409 national breed populations).

Figure 11 shows the distribution of the main uses of national breed populations according to region. Meat is the most commonly reported use in all the regions of the world, although there are differences in the relative frequency and importance of other uses. For instance, the use of livestock for wool/pelt/skins is more frequently reported for national breed populations from North America (18 percent; 48 national breed populations) and the Southwest Pacific (13 percent; 40 national breed populations) than for those from other regions. The use of specific breeds for vegetation management is reported almost exclusively in Europe and the Caucasus (5 percent; 158 national breed populations).

With regard to differences in the uses of national breed populations as a function of their geographical distribution classification (Figure 12), the frequency with which use for meat and for milk is reported is quite similar across categories. However, local breeds are more frequently than other categories reported to be used for eggs (12 percent, 463 national breed populations), while international transboundary breed populations are relatively frequently reported to be used for cross-breeding (13 percent, 429 national breed populations).

**Figure 10. Reported uses of national breed populations by species (cattle, chicken, goat, pig and sheep)**



**Figure 11. Reported uses of national breed populations by region****Figure 12. Reported uses of national breed populations by geographical distribution category (local, regional and international transboundary)**

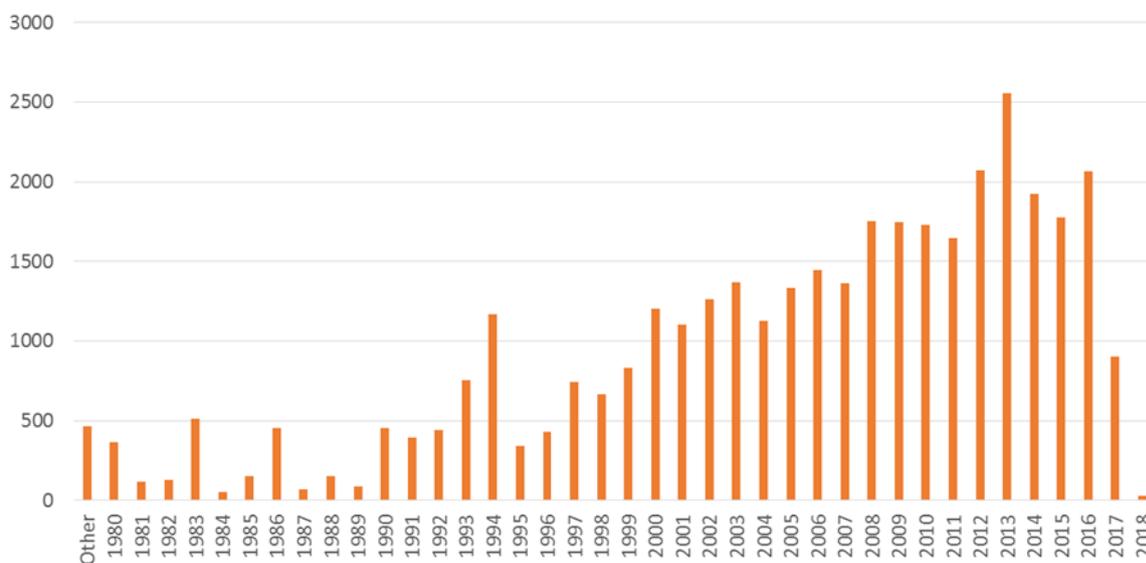
### Population size data

Fields describing the size of national breed populations are key fields in DAD-IS, inasmuch as they provide information on the past and current status of the diversity of AnGR. Population-size data for a given breed can be updated on a continual basis, although only the most recent information is stored for a given year. Currently, DAD-IS contains 38 096 data entries for population size (i.e. national breed population × year combinations) covering 9 223 national breed populations, 38 species and 185 countries and dependent territories: 23 percent of the entries relate to cattle populations, 22 percent to sheep populations and 15 percent to horse populations. Among countries, 20 percent of the entries are for national breed populations in Germany, 6 percent for those in Italy, 5 percent for those in Spain and 5 percent for those in the United Kingdom.

Several measures of the size of a breed population can be entered into DAD-IS: (i) the total population size in the form of a range with minimum and maximum values; (ii) the number of breeding males and females; (iii) the number of females registered in a herd book; (iv) the number of females mated with males of the same breed; (v) the number of herds; and (vi) the average herd size. The trend in population size (increasing, decreasing or stable), the origin of data (census or survey) and the reliability of the data can also be recorded. Minimum population size is the item of information most frequently recorded (available for 97 percent of national breed populations with recorded population data), followed by maximum population size (87 percent), number of breeding females (72 percent), number of breeding males (63 percent), reliability of population size data (61 percent), trend in population size (60 percent) and origin of data (57 percent). The other data fields have been filled for fewer than half of the entries.

Population data were used to provide another example of the potential uses of the information recorded in DAD-IS. Population size, calculated as the arithmetic mean between minimum and maximum population sizes, was estimated for all cases for which the relevant data are recorded (n = 37 224). Figure 13 shows the numbers of breed populations for which mean population sizes can be calculated based on DAD-IS data for each year from 1980 to 2018. The number of such populations generally increases over the period. For every year from 2000 to 2016 population size estimates can be calculated for at least 1 000 national breed populations. This number drops to below 1 000 (n = 901) for 2017, but this decrease may simply be due to the fact that a lag occurs between the time population data are obtained and the time they are entered into DAD-IS. The population size estimates range from 0 (many breed populations) to 150 000 000 (Arbor Acres AA broiler and Lohmann Meat chickens in Indonesia in 2002 – although these latter populations are likely to represent commercial animals, rather than breeding stock), with an average of around 168 000 and a median of around 1 165 individuals. As shown in Figure 14, about half (48 percent) of the population estimates are below 1 000; 90 percent are below 100 000.

**Figure 13. Numbers of new breed population estimates available in DAD-IS, according to year**



**Figure 14. Distribution of estimates of population sizes**

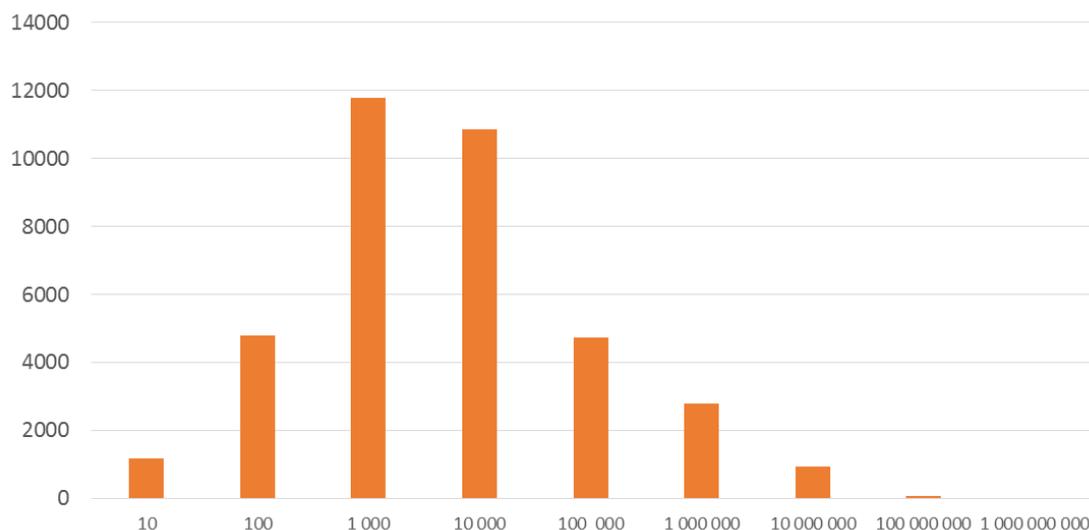


Table 1 gives information on population sizes by species (the five main species) and region. Among species, the largest number of population size data entries are for cattle and sheep (Table 1). Population size data for chicken populations are extremely skewed: the species has the largest mean population size but the smallest median. This pattern can be explained by the fact that different regions tend to report on different categories of breeds. While African, Asian and Latin American countries tend to report on commercial hybrids, some European countries report mainly on “fancy” breeds with small population sizes. Overall, the region with the largest number of data entries is Europe and the Caucasus (29 621 entries; 80 percent of the total). Average and median population size estimates are smaller in Europe and the Caucasus, North America and the Southwest Pacific than in other regions.

**Table 1. Number of data entries, arithmetic mean and median population size according to species and regions**

Species	Data entries (Count)	Population size	
		Mean	Median
Cattle	8 678	160 583	2 816
Chicken	3 702	489 699	700
Goat	3 017	287 710	1 947
Pig	3 073	75 607	1 499
Sheep	8 218	168 256	2 116
Region	Count	Mean	Median
Africa	1 583	1 042 778	134 205
Asia	2 597	990 409	70 000
Europe and the Caucasus	29 621	39 777	837
Latin America and the Caribbean	789	740 676	15 000
Near and Middle East	195	1 061 299	160 000
North America	1 826	28 489	1 367
Southwest Pacific	619	20 872	706

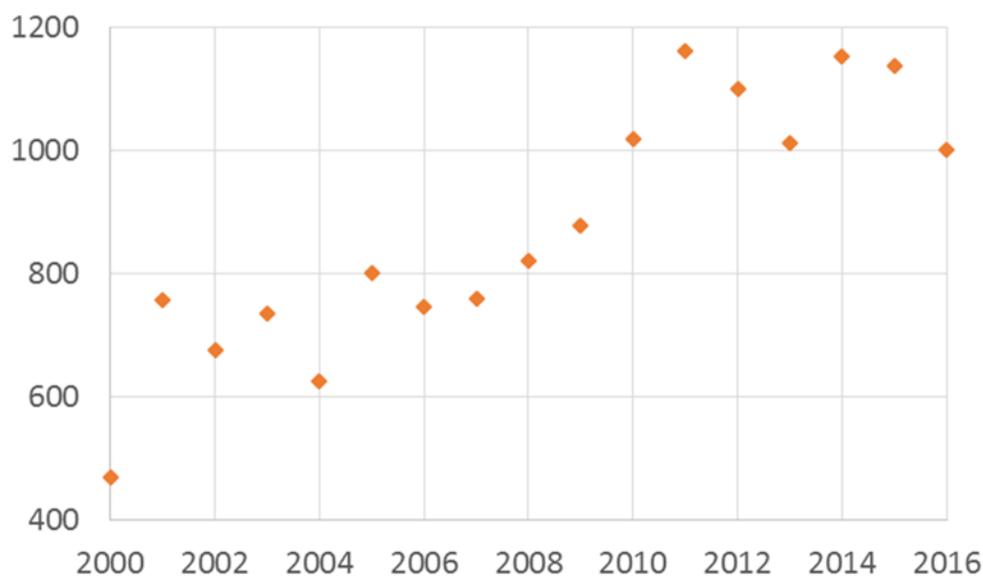
Table 2 shows the results of an in-depth analyses of the availability of population data for the period from 2000 to 2016. A total of 27 396 population size entries, referring to 6 401 national breed populations, are recorded in DAD-IS for this period. The period comprises 17 years, meaning that the number of entries stored for any one national breed population could range from 0 (no information) to 17 (data for every year). Table 2 shows the numbers of national breed populations for which population size data are recorded for given numbers of years during this period, as well as cumulative results. The findings indicate that 8 666 national breed populations (58 percent) have no population-size data recorded in DAD-IS for any year between 2000 and 2016, 2 816 (18 percent) have only one entry and 3 585 (24 percent) have two or more entries. A total of 1 928 national breed populations (13 percent) have at least six data entries for the period, corresponding to an average interval of less than three years.

**Table 2. Frequency of population size data updates for individual national breed populations for the period 2000 to 2016**

Number of population size entries	Average interval (in years) between population size entries	Number of national breed populations	Proportion of national breed populations with at least the indicated number of entries
0	...	8 666	100
1	17.0	2 816	42
2	8.5	713	24
3	5.7	415	19
4	4.3	257	16
5	3.4	272	15
6	2.8	412	13
7	2.4	223	10
8	2.1	207	9
9	1.9	140	7
10	1.7	123	6
11	1.5	115	5
12	1.4	183	5
13	1.3	143	3
14	1.2	107	3
15	1.1	40	2
16	1.1	71	2
17	1.0	164	1

To assess how individual breed population sizes have evolved over recent years, the 1 928 national breed populations with at least six population data entries for the period between 2000 and 2016 were examined more closely (Figure 15). Average median population size increased from 469 in 2000 to 1 000 in the 2016, a favourable result in terms of decreasing risk of extinction. However, this is a selected sample of data. Of the breed populations considered, 1 124 are local breeds from Europe and the Caucasus, a region where substantial financial support has been provided with the aim of increasing the population sizes of local livestock breeds. The results suggest that these investments have generally been successful, assuming that increasing population sizes was a primary objective.

**Figure 15. Average median population sizes from 2000 to 2016 of national breed populations with more than six population size entries in DAD-IS for this period**

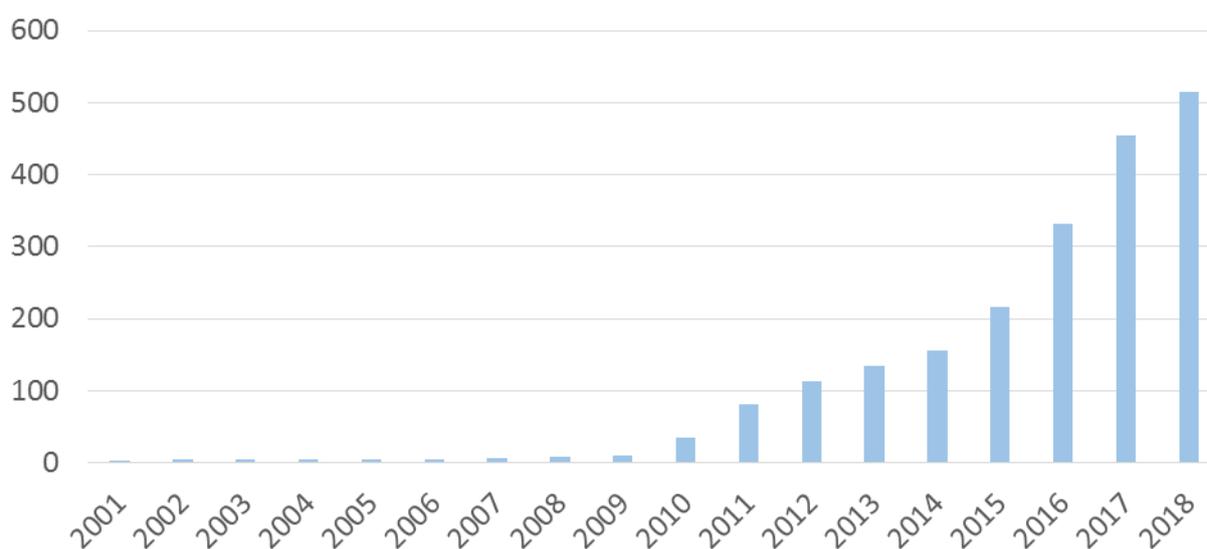


### Conservation data

As reported in the document *Status and trends of animal genetic resources – 2018*<sup>13</sup>, the number of national breed populations and breeds with cryopreserved material reported in DAD-IS is still very low. This section describes, and summarizes the results of, an analysis of this information undertaken using the cryoconservation data export tool developed for DAD-IS:4.

DAD-IS currently contains 2 889 data entries (combinations of national breed populations × year) covering 520 national breed populations, 12 species (37 percent from cattle, 18 percent from sheep and 13 percent from chicken) and 27 countries (45 percent from the Netherlands, 19 percent from Austria and 18 percent from Spain). The data suggest that semen samples are by far the most commonly stored type of material in national gene banks. Semen samples are reported for 88 percent of the national breed populations for which cryoconservation data are recorded in DAD-IS. Embryos are reported to be stored for 14 percent of these populations, followed by DNA (9 percent), somatic cells (4 percent) and oocytes (1 percent). Although the data are still very scant, the number of national breed populations reported to have cryopreserved material stored has increased greatly since 2000, particularly over the last ten years (Figure 16). The amount of material stored is, however, often still limited. For example the median number of semen donors per national breed population with reported data is about 12, less than half the number recommended in the FAO guidelines on *Cryoconservation of animal genetic resources*.<sup>14</sup> The small amount of data on cryoconservation recorded in DAD-IS is the result both of incomplete coverage of AnGR gene banks globally and of the newness of the tools in DAD-IS:4 for reporting cryoconservation-related information.

**Figure 16. Accumulated number of national breed populations reported to have cryopreserved material stored**



<sup>13</sup> CGRFA/WG-AnGR-9/16/Inf.3

<sup>14</sup> [www.fao.org/docrep/016/i3017e/i3017e00.htm](http://www.fao.org/docrep/016/i3017e/i3017e00.htm)

## VI. CONCLUSIONS AND OUTLOOK

DAD-IS:4, the new version of DAD-IS, has been operational since November 2017 and provides National Coordinators and governments with greater possibilities to monitor the status of diversity of their respective country's AnGR than ever before. For example, the tools for calculating SDG Indicators 2.5.1 and 2.5.2 are a new and easy-to-use service provided to countries. The export tools allow the production of virtually limitless numbers of datasets and thus create opportunities for manifold analyses, which will make DAD-IS data more useful and attractive for research institutions and universities.

Alas, the data gaps in DAD-IS are still large, a problem that calls for action by countries. The Commission, at its Sixteenth Regular Session,<sup>15</sup> stressed the need for countries to regularly update their national data in DAD-IS or FABIS-net, including information on animal genetic resources both *in situ* and *ex situ*, and to provide information on breed classifications. Nearly 60 percent of national breed populations have not been updated since the turn of the century and many have never had estimates of population size entered into DAD-IS. A lack of breed population data at country level is reportedly the most frequent constraint to data entry. Raising awareness on the importance of such data, along with the development of tools and methodologies for obtaining reliable estimates of population sizes in a cost-efficient way will be key in closing the gap. The SDGs may be an opportunity to spur new or renewed efforts to estimate breed population sizes, given that the calculation of SDG Indicator 2.5.2 relies on the availability of such information.

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<sup>15</sup> CGRFA-16/17/Report/Rev.1, paragraph 46.

**Annex I: Agenda of the Global National Coordinator Workshop on DAD-IS and SDG Indicators 2.5.1 and 2.5.2**

**Workshop Agenda:  
DAD-IS and SDG Indicators 2.5.1 and 2.5.2**

Day	Time	Topic
<b>21.11</b>	14:00 - 17:00	Demonstration of DAD-IS version 4 SDG Indicators and DAD-IS
<b>22.11</b>	9:00-10:00	Introduction to the group work “Why do we have a data gap for SDG Indicators 2.5.1 and 2.5.2?”
	10:15 -13:00	<b>Group work</b> “Why do we have a data gap for SDG Indicators 2.5.1 and 2.5.2?”
	14:00 – 15:30	Presentation of the group work and discussion of the regional results
	15:30-16:00	Introduction to the group work “How to fill the data gap?”
	16:00 -17:00	<b>Group work</b> “How to fill the data gap?”
<b>23.11</b>	10:00 – 12:30	Presentation and general discussion of the group work “How to fill the data gap?”
	14:00 – 16:00	Training on the new DAD-IS
	16:00 – 16:30	Closure of the workshop

**Annex II. Participants list**

Name	Family name	Country
Carlos Aden	REISING	Argentina
Bidhan	BARAL	Bangladesh
Md. Azharul Islam	TALUKDER	Bangladesh
Arthur	DA SILVA MARIANTE	Brazil
Samuel	REZENDE PAIVA	Brazil
Jean Marie	BATIEBO	Burkina Faso
David Telesphore	OUEDRAOGO	Burkina Faso
Chepnda Vitalis	RINGMUH MOLEBUIN	Cameroon
Pamela	HIND	Canada
Teresa Doris	AGUERO TEARE	Chile
Jorge Andres	URRUTIA SEPULVEDA	Chile
Hongjie	YANG	China
Leon	TATI	Congo
Xinia Maria	ANDRADE RUIZ	Costa Rica
Argerie	CRUZ MENDEZ	Costa Rica
Tomas	NEMECEK	Czechia
Malene Kamp	PALNE	Denmark
Ghada	ELZONOKOLY	Egypt
Christine	BERTRAND	France
Samba	BARROW	Gambia
Momodu	JENG	Gambia
Vasil	TSAKADZE	Georgia
Holger	GOEDERZ	Germany
Jan Hendrik	SCHNEIDER	Germany
Margaret Marie	SUMAH	Ghana
Elissavet	ILIOPOULOU	Greece
Christina	LIGDA	Greece
Sandra Elizabeth	GOMAR OROZCO	Guatemala
Peter	TOTH	Hungary
Ahmed Abdulhussein	AL-BAYATTI SAHAR	Iraq
Luca	BUTTAZZONI	Italy
Gennaro	CATILLO	Italy
Colomba	SERMONETA	Italy
Saed	ALSAWAWREH	Jordan

Name	Family name	Country
Khaleel Ibrahim	JAWASREH	Jordan
John Gitau	MBURU	Kenya
Cleopas	OKORE	Kenya
Mohamad	SOUKARIE	Lebanon
Molapo	HLASOA	Lesotho
Mathato Mantho	MASEMENE	Lesotho
Simone	RAVAOARIMANANA	Madagascar
Terbish	JAMBALDORJ	Mongolia
Dusica	RADONJIC	Montenegro
Adriano Atanasio	MATSIMBE	Mozambique
Maria Da Gloria	TAELA	Mozambique
Deidre Arntrud	JANUARIE	Namibia
Isak	NEEMA	Namibia
Sipke Joost	HIEMSTRA	Netherlands
Rita	HOVING	Netherlands
Abdelmuhsen	ALALAMI	Palestine
Borhan	ISSA	Palestine
Blas Marino	COUSIRAT SANABRIA	Paraguay
Jose Luis	HIJERTAS CHUMBES	Peru
Eudosiso Amancio	VELI RIVERA	Peru
Jocelyn V.	BOREJON	Philippines
Elizabeth	CABRERA	Philippines
Grazyna	POLAK	Poland
Anna	TYLKOWSCA-SIEK	Poland
Hamad	ALSHAMARI	Qatar
Danijela	BOJKCOVSKI	Slovenia
Tlou Caswell.	CHOKOE	South Africa
Francisco Javier	NAVAS GONZALEZ	Spain
Wimaladharma Wijesekara	AB EYGUNAWARDHANA	Sri Lanka
Gemunu Sujith	UDUWANA	Sri Lanka
Hassan	MRUTTU	United Republic of Tanzania
Mnaouar Sassi	JAMALI	Tunisia
Cue	NGO THI KIM	Viet Nam
Name	Family name	Organization
Mary Ndila	MBOLE-KARIUKI	AU-IBAR