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DETAILED ANALYSIS OF THE FACTORS INFLUENCING THE REPORTING OF INFORMATION IN THE DOMESTIC ANIMAL DIVERSITY INFORMATION SYSTEM

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I. INTRODUCTION

The Domestic Animal Diversity Information System (DAD-IS) was established in 1996 as the tool for the recording of information on the world's livestock breeds and is used as the primary source of data for monitoring the status of the global diversity of animal genetic resources for food and agriculture. FAO member countries are requested to regularly register in DAD-IS the sizes of their national breed populations. The breed population data in DAD-IS are used by the United Nations to monitor countries' achievement of Target 2.5¹ of the Sustainable Development Goals (SDG). The SDG Indicator 2.5.2 assesses the percentage of local livestock breeds being at risk of extinction and is monitored each year.² In addition, every two years FAO uses data in DAD-IS to prepare reports on the global status and trends of animal genetic resources, which are presented to the Commission.³ Information in DAD-IS regarding breed population size is far from complete. Considering reports at the last two sessions of the Commission, in 2016,⁴ the population size, and thus risk of extinction, was unknown for 65 percent of local livestock breeds, and this proportion increased to 67 percent in 2018⁵.

The SDG monitoring framework also includes an indicator on cryoconservation of animal genetic resources. Indicator 2.5.1b is the "number of animal genetic resources for food and agriculture secured in medium- or long-term conservation facilities",⁶ and is based on local breeds. With regard to this indicator, DAD-IS has provided the possibility for countries to report information on cryoconservation programmes since 21 November 2017. However, the information reported in DAD-IS remained quite scarce throughout 2018. At that time, data regarding storage genetic material in gene banks was reported to DAD-IS for only a very low proportion (3 percent) of local breeds. For only around 1 percent of breeds was the quantity of stored material considered to be sufficient for population reconstitution.⁷

The Commission on Genetic Resources for Food and Agriculture (Commission), at its Sixteenth Regular Session⁸ therefore requested FAO to identify possible reasons for the continuing high proportion of breeds with unknown risk status in DAD-IS, to which FAO reported that missing data for national breed population size was the main constraint.⁹ Furthermore, at its Seventeenth Regular Session in 2019, the Commission requested the FAO to develop an in-house analytical study on the factors influencing the reporting of information for breeds. This study was requested to contain, but not be limited to, factors involved in the reporting of information. The Commission requested FAO to propose solutions to reduce the proportion of breeds with unknown status for risk of extinction (i.e. breeds lacking population size data in DAD-IS).¹⁰

II. GAP ANALYSIS OF THE INFORMATION REPORTED IN DAD-IS

A. Approach used

The in-house analytical study was undertaken at the level of national breed populations, because this is the unit for which information is provided by countries, considering data entered into DAD-IS on or before 03 February 2021. Indicators based on metadata (descriptive information of breeds), population data and cryoconservation data were extracted from DAD-IS and analysed against the three following factors: region, geographical breed classification (with the classes local, regional, and international transboundary breed) and species (considering the seven species with

¹ <https://unstats.un.org/sdgs/metadata/>

² <https://unstats.un.org/sdgs/metadata?Text=&Goal=2&Target=2.5>

³ CGRFA/WG-AnGR-5/09/3.2.

⁴ <http://www.fao.org/3/a-mr792e.pdf>

⁵ <http://www.fao.org/3/CA0121EN/ca0121en.pdf>

⁶ <http://www.fao.org/sustainable-development-goals/indicators/251b/en/>

⁷ <http://www.fao.org/3/CA0121EN/ca0121en.pdf>

⁸ CGRFA-16/17/Report/Rev. 1, paragraph 46

⁹ CGRFA-17/19/11.2/Inf.3 Rev.1.

¹⁰ CGRFA-17/19/Report.; <http://www.fao.org/3/mz618en/mz618en.pdf>

more than 500 national breed populations). For the sake of simplicity only descriptive statistics were used for the analyses. For population data, the analysis focused on the number of population updates undertaken for national breed populations over the last ten years (from 2010 to 2021).

B. Gaps in metadata

To allow National Coordinators for the Management of Animal Genetic Resources (NC-AnGR) to monitor the overall completeness of data provided to DAD-IS for their national breed populations, a specific indicator and tool has been developed. This tool considers 13 categories of metadata (Population Data, In Vivo Data, Cryo Data, Distinctive Traits, Images, Name, Uses, Colour, Additional Information, Morphology, Origin and Development, Management Conditions and Performance) for which NC-AnGRs can provide descriptive information for a given national breed population. Each field category has multiple data fields. For example, the field category “Origin and Development” includes fields relative to the herdbook, including its date of establishment, the origin of the national breed population, the year of origin and so on. Based on the data provided, the tool assigns each field category a value of either 1 or 0, depending the provision of sufficient data. To derive the overall data completeness, the average of these 13 values is calculated. Therefore, for a given national breed population, the score can range from 0 (no information) to 1.0 (all 13 field categories contain a minimum level of information).

Figures 1, 2 and 3 present the data completeness for regions, geographical breed categories, and species, respectively. On average, 22.7 percent of field categories were considered as filled, with some notable differences between regions and species. The level of completeness was highest for North America (0.288) and lowest (0.177) for the Southwest Pacific. In general, completeness was greater for mammalian species (0.238) than for avian species (0.19), which were particularly less likely to have Images or information for the Colour, Morphology, Origin and Development, Management Conditions, Performance and Additional Information field categories. Among the different species, goats, cattle and sheep all had similar levels of completeness and tended to have more complete metadata, especially compared with chickens, rabbits and other species.

Figure 1. Data completeness indicator averaged over regions (number of national breed populations in parentheses, standard error provided)

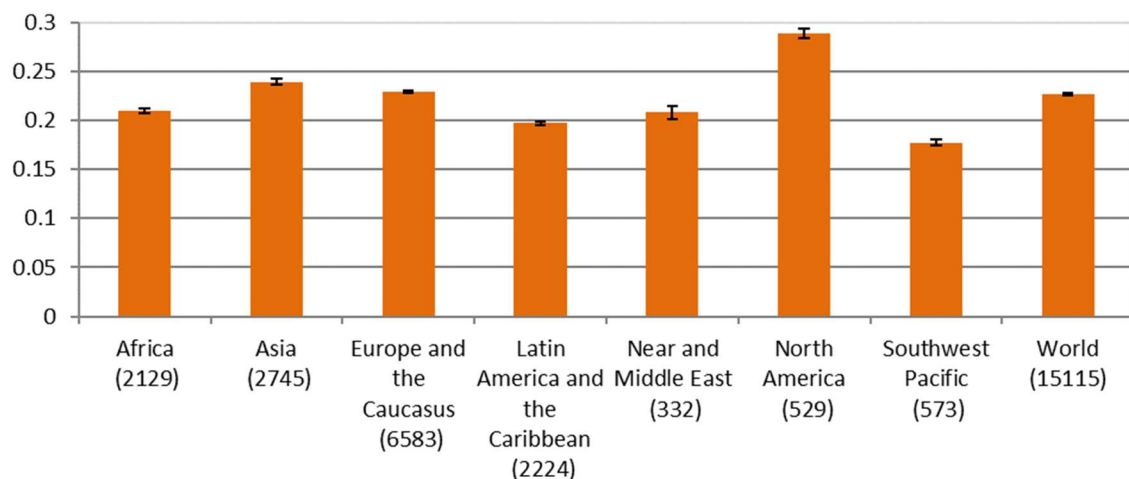


Figure 2. Data completeness indicator averaged over geographical breed status (number of national breed populations in parentheses, standard error provided)

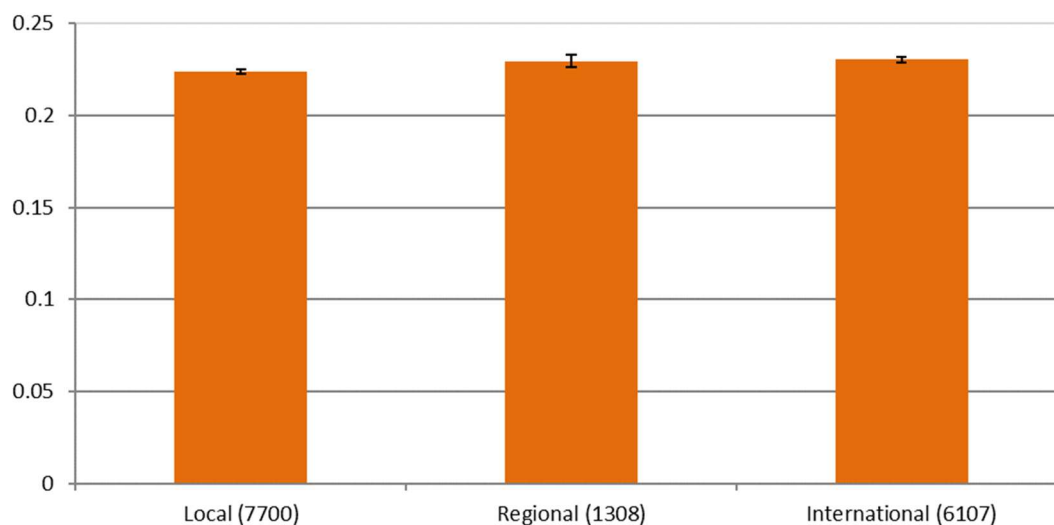
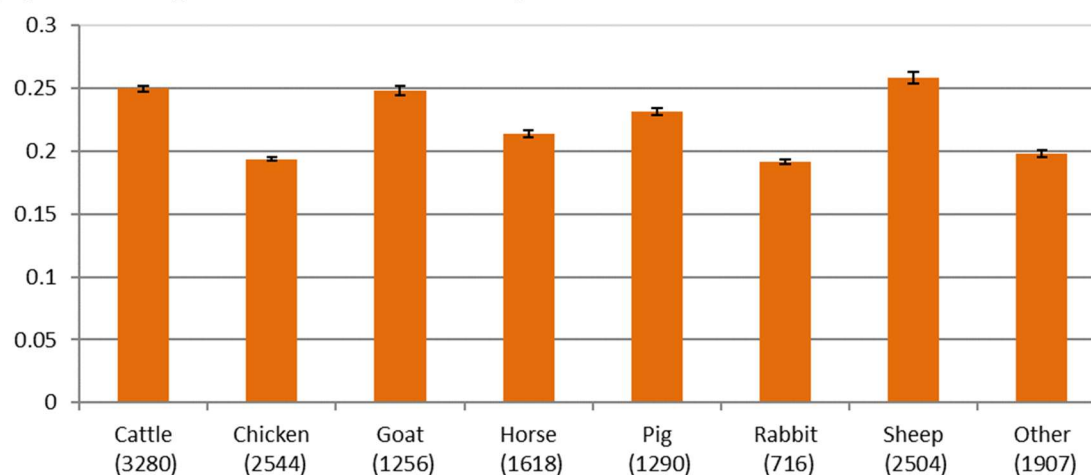


Figure 3. Data completeness indicator averaged over species (number of national breed populations in parentheses, standard error provided)



C. Gaps in population data

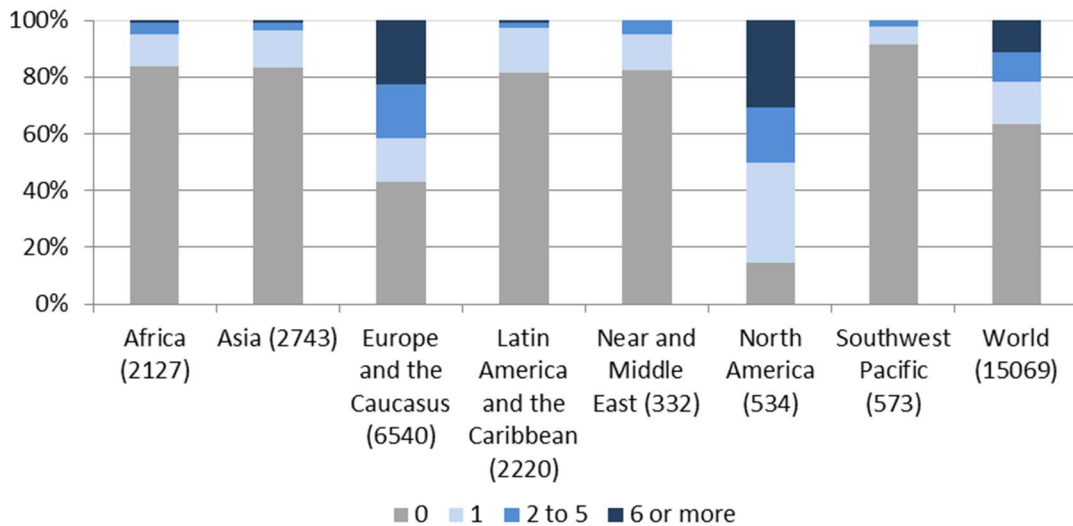
To investigate the updating activities, four classes were established related to the number of updates of national breed population data: (i) No updates, (ii) 1 update, (iii) 2 to 5 updates, and (iv) 6 or more updates over an investigation period of 10 years (2011 to 2021). Then, for each factor (region, geographical status and species) frequency distributions were determined.

Figures 4, 5 and 6 present the numbers of population updates for national breed populations according to region, geographical breed status, and species, respectively. Out of the 15 088 national breed populations considered, 64 percent have had no update over the last ten years, meaning their risk status is considered to be unknown. Approximately 15 percent of national breed populations had just a single update, 11 percent had 2 to 5 updates, and 11 percent had more than 5 updates during this period.

On average, countries with some updates reported 1.4 updates per national breed population over the period 2011-2021. Results differed substantially across regions. The percentages of national breed populations with population data updates were much higher in Europe and the Caucasus and North America than in the other regions (Figure 4). The Near and Middle East and Southwest Pacific showed particularly large gaps in population data reporting. However, as shown in Figure

7, reporting is not homogenous within regions. For instance, Thailand reported on average 6.3 updates per national breed population (compared to an average of 0.21 updates in Asia), and Niger 4.9 (compared to an average of 0.29 updates in Africa).

Figure 4. Proportions of national breed populations with varying numbers of population updates over the last 10 years, according to regions (number of national breed populations in parentheses)



As illustrated in Figure 5 only small differences are observed in the numbers of population data updates among the three geographical breed categories. National breed populations of local breeds are not more frequently updated compared to transboundary ones, or vice versa. In particular, the proportions of national breed populations with no updates in the last 10 years (thus considered to have unknown risk status) were similar across geographical breed categories.

Figure 5. Proportions of national breed populations with varying numbers of population updates over the last 10 years, according to geographic breed category (number of national breed populations in parentheses)

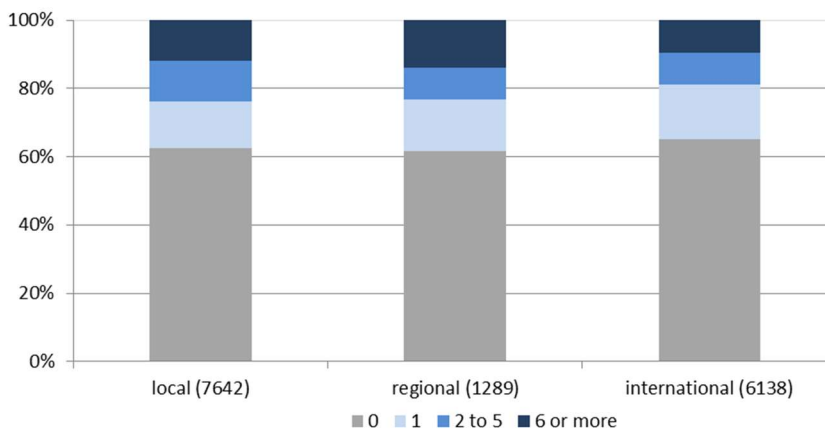


Figure 6 shows the differences in numbers of population data updates for the “Big 5” livestock species (cattle, chicken, goats, pigs and sheep) plus rabbits and horses, and all other species grouped into a single category “others”. Among the Big 5 species, pigs showed the lowest proportion of updates, with 76 percent of national breed populations having no new information over the last ten years. By contrast, for rabbits, this proportion is less than 50 percent. The large number of populations with updates in rabbit might be partially related to the project “Rabbit Genome Biology Network” (RGBnet),¹¹ funded by the European Union, in which FAO participated. One of the activities of RGBnet was the compilation of DAD-IS breed data sheets, which were then shared

¹¹ <http://www.biocomp.unibo.it/rabbit>

with the respective NC-AnGRs. This project does not entirely explain the active reporting for rabbits, as the RGBnet participants provided data for a single population update only, whereas many rabbit populations have been updated multiple times in the last decade. Large gaps were found for the “other” species, which showed the highest proportion of national breed populations with no population updates (75 percent).

Figure 6. Proportions of national breed populations with varying numbers of population updates over the last 10 years, according to species (number of national breed populations in parentheses)

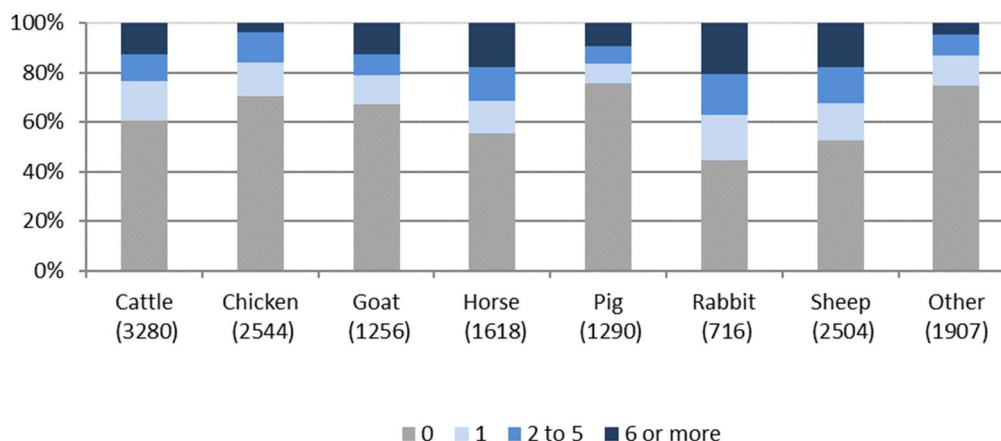


Figure 7. Average number of population updates over the last 10 years per national breed population according to countries

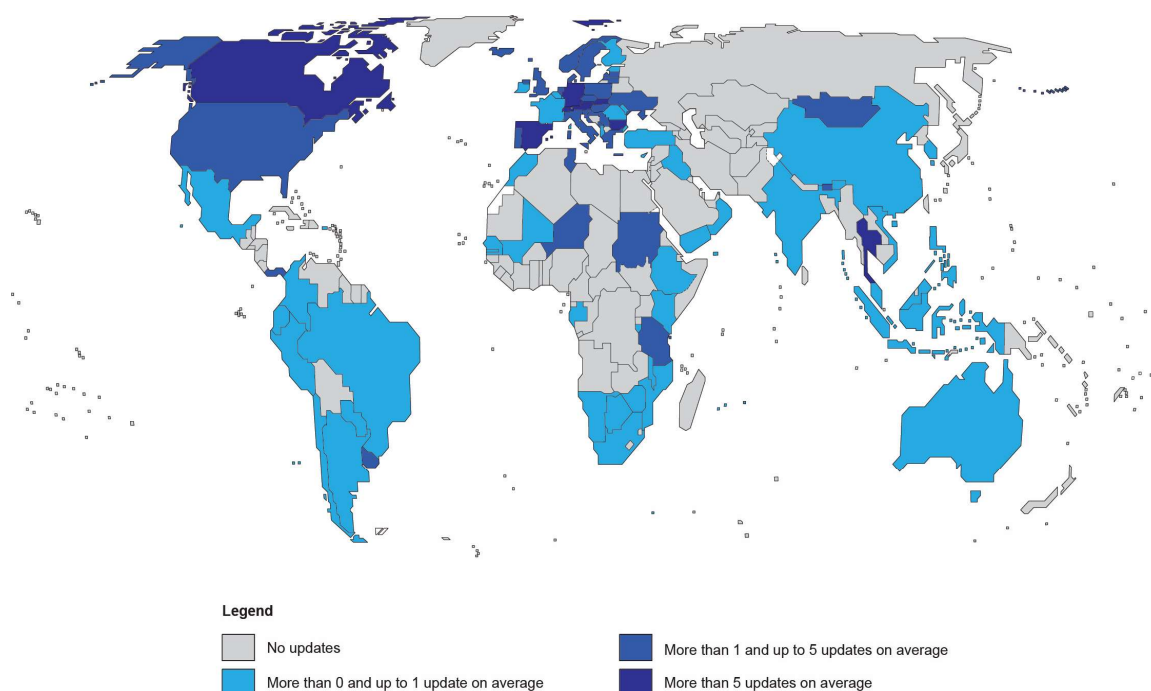
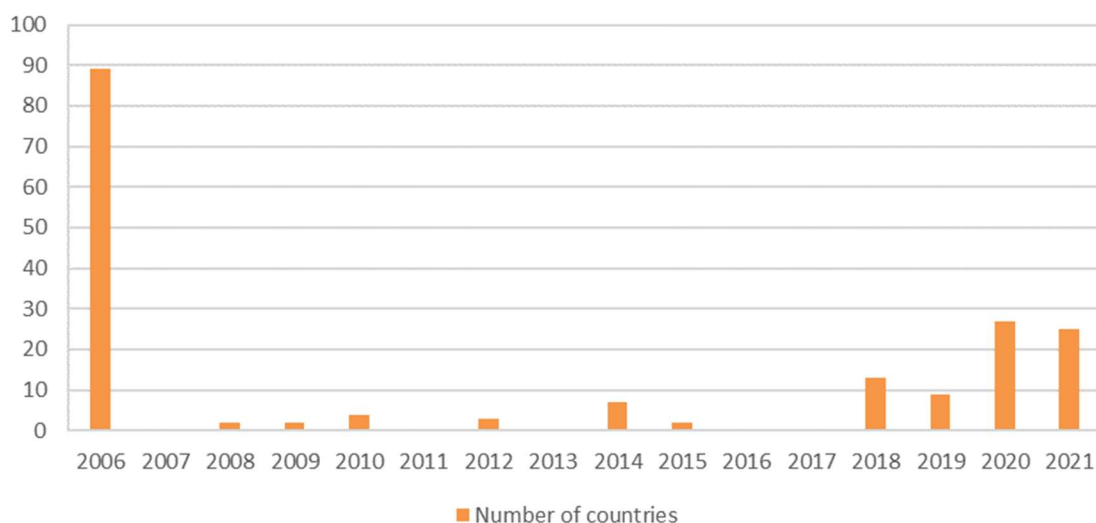


Figure 8 shows the most recent year when updates have been provided on population data. Out of 183 countries that have made at least one population update since DAD-IS was established in 1996, 89 have not provided any new information since 2006 (the year when information was collected for the first report on *The State of the World's Animal Genetic Resources for Food and Agriculture*¹²). Twenty countries provided most recent updates between 2008 and 2015, with seven countries updating in 2014 during the process of *The Second Report on the State of the World's*

¹² <http://www.fao.org/3/a-a1250e.pdf>

Animal Genetic Resources for Food and Agriculture.¹³ but not since then. Over the past four years, 74 countries have provided updates.

Figure 8. Distribution of countries according to the most recent year when updates have been provided on population data



D. Gaps in cryoconservation data

Since the release of its latest version in November 2017, DAD-IS has included a group of data fields that allow countries to report on the extent to which genetic material has been collected from national breed populations and stored within gene banks. The fields in DAD-IS also allow NC-AnGRs to specifically indicate national breed populations for which no material is cryoconserved and to indicate whether they consider that the material collected is sufficient to reconstitute the breed in case of extinction *in vivo*. Figures 8, 9 and 10 present the cryopreservation status of national breed populations according to regions, geographical status, and species; respectively. Among the 15 115 national breed populations considered, 52 percent had some information of cryoconserved material.

Countries that operate a national gene bank should have well-documented information on the material stored.¹⁴ NC-AnGRs should regularly communicate with managers of national gene banks to obtain the required data. DAD-IS also allows countries to report an absence of cryoconserved material for their national breed populations, as this yields relevant information for SDG indicator 2.5.1b (as lacking material sufficient to reconstitute the breed in case of extinction) and for management of animal genetic diversity in general. Breeds with no cryoconserved material stored are at increased risk of extinction.

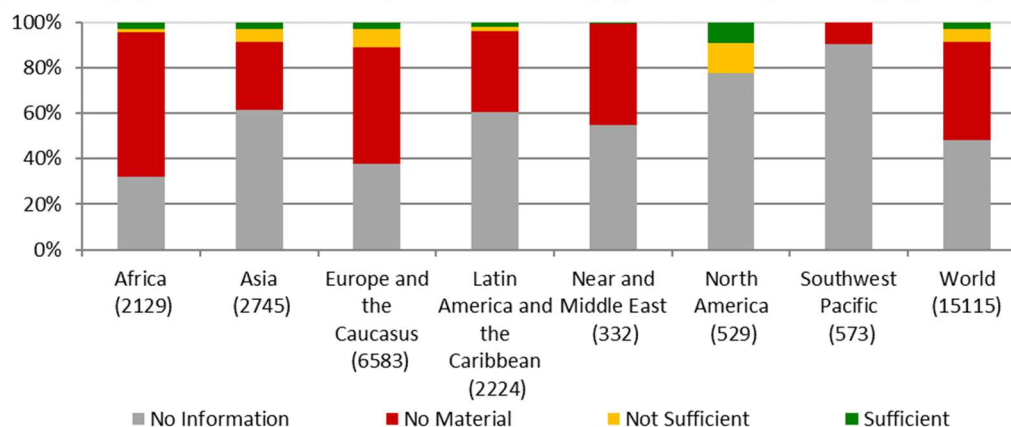
As of February 2021, at the global level, 52 percent of national breed populations were reported with information on cryoconserved material. 3.0 percent were considered to have sufficient material to reconstitute the breeds, and 5.5 percent with some, but non-sufficient material, and 43 percent were reported to have no material collected. The latter value is almost certain to be underestimated. Results differed substantially across regions. The highest proportions of national breed populations with information on cryoconserved material were observed in Africa and Europe and the Caucasus, 68 percent and 62 percent respectively (Figure 9). Limited feedback was received from Southwest Pacific, as information was provided for less than 10 percent of national breed populations. North American countries reported a substantially higher proportion of national breed populations with material (sufficient or not), even compared to Europe and the Caucasus (23 percent and 11 percent, respectively). While the differences in reporting according to countries

¹³ <http://www.fao.org/3/a-i4787e.pdf>

¹⁴ <http://www.fao.org/3/i3017e/i3017e00.pdf>

is somewhat linked to the reporting process initiated in 2020 (see Section IV), the differences in material collection are more generally associated with the presence of national gene banks.¹⁵ A greater proportion of countries have gene banks in Europe and the Caucasus and North America than other regions and thus have more complete reporting on stored material.

Figure 9. Cryopreservation status of national breed populations in percentage per region



As illustrated by Figure 10, the gaps in cryomaterial reporting do not show much variation according to the geographical classification of national breed populations, even if it can be noted that there is a slightly higher proportion of national breed populations belonging to international transboundary breeds with sufficient material collected (3.6 percent), compared to regional (2.6 percent) and local breeds (2.7 percent). Because transboundary breeds are present in several countries, the relative proportions of transboundary populations with material and sufficient material collected increases when reporting information according to breeds rather than national breed populations.¹⁶

Figure 11 shows the differences in reporting of cryomaterial according to species. Included are the five main species, plus rabbits and horses, with the remaining species being merged into a single “other” category. The proportion of national breed populations with information did not differ much across species, ranging from 45 percent to 56 percent. Cattle (55 percent) and chicken (56 percent) showed the highest proportions. Cattle, goat and sheep were the species with the highest proportion of stored cryomaterial with 16, 10 and 9 percent, respectively. For rabbits, the percentage of populations with stored material was close to zero. This variation among species is related to differences in the status of development of reproductive biotechnologies. Methods for collection and storage of cryomaterial differ across species, resulting in differences in reporting to DAD-IS. Because of their economic importance, reproductive biotechnologies and gamete cryoconservation methods tend to be more advanced for ruminants, which consequently have a greater proportion of breeds with material in gene banks than do other species.

¹⁵, The Second Report on the State of the World’s Animal Genetic Resources for Food and Agriculture, page 296, <http://www.fao.org/3/a-i4787e.pdf>

¹⁶, Leroy, G., Boettcher, P., Besbes, B., Danchin-Burge, C., Baumung, R., & Hiemstra, S. J. (2019). Cryoconservation of animal genetic resources in Europe and two African countries: A gap analysis. *Diversity*, 11(12), 240. <https://www.mdpi.com/1424-2818/11/12/240>

Figure 10 Cryopreservation status of national breed populations in percentage according to geographical breed category (number of national breed populations in parentheses)

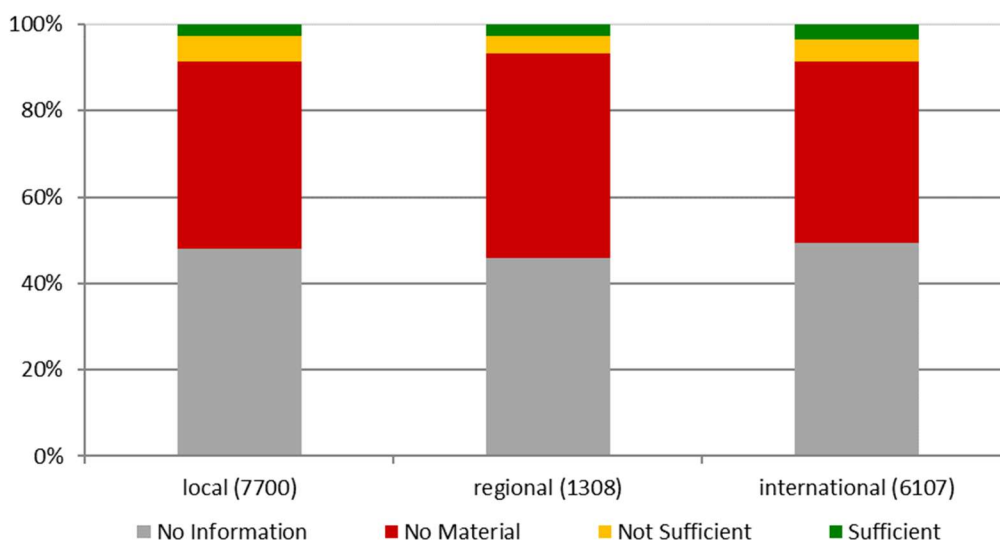
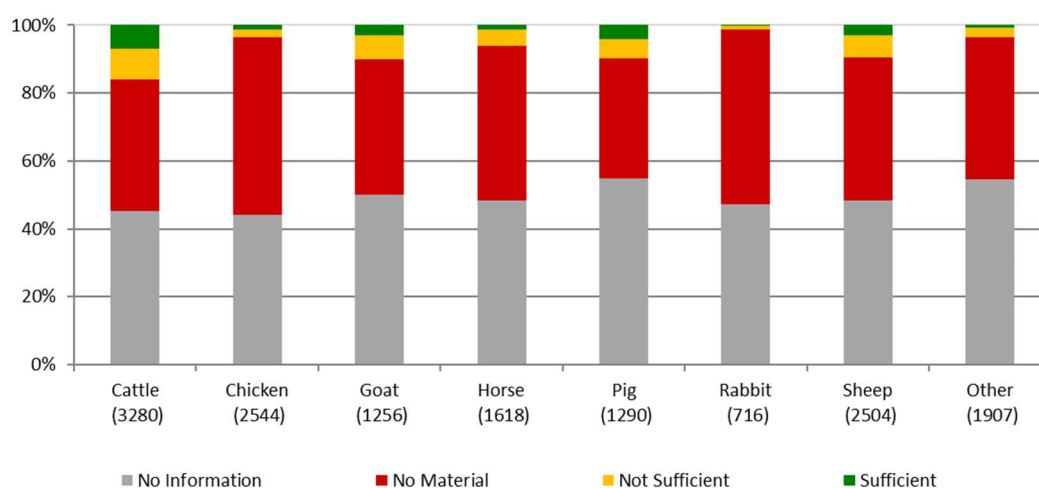


Figure 11 Cryopreservation status of national breed populations in percentage per species (number of national breed populations in parentheses)



E. Gaps regarding Sustainable Development Goal indicators

As noted in the introduction section of this document, the population size information in DAD-IS is used to calculate SDG Indicator 2.5.2 on the proportion of local breeds at risk of extinction. In addition, the cryoconservation data in DAD-IS data are used to calculate SDG Indicator 2.5.1b, which is the “the number of local breeds stored within a gene bank collection with an amount of genetic material stored which is required to reconstitute the breed in case of extinction”.¹⁷

To assess the situation of regions regarding the SDG Indicators 2.5.1b and 2.5.2, which are used to monitor the cryoconservation and risk status of local breeds, respectively, the number and proportion of countries having provided at least one update for a local breed over the 2011-2020 period were calculated. Table 1 illustrates that for SDG Indicator 2.5.1b, almost half of the countries and territories have provided recent updates. This proportion is lower for SDG indicator 2.5.2 with only 38 percent of countries and territories having provided data. Only Europe and the Caucasus for SDG 2.5.1b and 2.5.2 and Africa for SDG 2.5.1b, provided updates for more than half of their countries. The proportions of countries with updates was particularly low for the Southwest Pacific region.

¹⁷ <https://unstats.un.org/sdgs/metadata?Text=&Goal=2&Target=2.5>

Table 1. Numbers and proportions of countries (dependent territories excluded) within each region having provided data for at least one local breed in DADIS between 2011 and 2020

Region	SDG 2.5.1b	SDG 2.5.2	Total number of countries/territories
Africa	33 (66%)	15 (30%)	50
Asia	12 (43%)	10 (36%)	28
Europe and the Caucasus	31 (53%)	35 (60%)	58
Latin America and the Caribbean	12 (36%)	10 (30%)	33
Near and Middle East	5 (42%)	4 (33%)	12
North America	1 (17%)	2 (33%)	6
Southwest Pacific	3 (25%)	0 (0%)	12
World	97 (49%)	76 (38%)	199

III. ACTIVITIES TO FILL THE GAPS IN DAD-IS

At its Sixteenth Regular Session,¹⁸ in addition to requesting FAO to identify possible reasons for the continuing high proportion of breeds with unknown risk status in DAD-IS, the Commission requested FAO also to identify potential means of addressing this issue.

In 2017, FAO organized the Global National Coordinators' Workshop, which was held in Rome from 21 to 23 November.¹⁹ The workshop focused on determining the reasons for the high proportion of breeds in DAD-IS with unknown status for population size and thus risk of extinction. NC-AnGRs and government statisticians were invited to attend the workshop and were requested to report and discuss the reasons for such gaps in their countries. The lack of breed population data at country level was identified as the most common constraint to reporting breed population sizes in DAD-IS. Problems with access to existing breed population data were also reported, particularly by respondents from Europe. Smaller numbers of respondents mentioned that (i) they lacked awareness of their duty to perform this task as part of their role as NC-AnGR; (ii) that they lacked knowledge on how to enter data into DAD-IS; or (iii) that entering data into DAD-IS was not included in the official terms of reference of their position of employment..

To address the gap in knowledge regarding data entry into DAD-IS, FAO developed an e-learning tool that demonstrates the process. The tool is available in English,²⁰ French²¹ and Spanish.²² FAO also developed a DAD-IS user manual available in English²³ and Spanish²⁴ and a quick guide on data entry for NC-AnGRs available in English²⁵, French²⁶ and Spanish²⁷. FAO continued to provide direct training upon request and maintains a virtual helpdesk, answering all individual questions sent to the dedicated DAD-IS mailbox (DAD-IS@fao.org). FAO staff also availed themselves to interested NC-AnGRs who voluntarily visited FAO Headquarters for any other reason.

A. Activities addressing gaps in population data

To help address the specific problem of the lack of breed population data, FAO developed a methodology to collect and/or estimate breed population data. The methodology employs a

¹⁸ CGRFA-16/17/Report Rev.1, paragraph 46.

¹⁹ CGRFA/WG-AnGR-10/18/Inf.6

²⁰ <https://360.articulate.com/review/content/95908ec3-199a-4e93-8811-1340d673f97a/review>

²¹ <https://360.articulate.com/review/content/ceaeab8d-1628-4dcb-828d-0729f7ba7acc/review>

²² <https://360.articulate.com/review/content/35e42cdd-e11c-4bce-aa87-627b1350dd79/review>

²³ <http://www.fao.org/3/cb0697en/cb0697en.pdf>

²⁴ <http://www.fao.org/3/cb0697es/cb0697es.pdf>

²⁵ <http://www.fao.org/3/cb0698en/cb0698en.pdf>

²⁶ <http://www.fao.org/3/cb0698fr/cb0698fr.pdf>

²⁷ <http://www.fao.org/3/cb0698es/cb0698es.pdf>

stratified sampling approach, which allows NC-AnGRs and other stakeholders to estimate population sizes. FAO implemented several pilot projects to assist countries in accessing existing data, estimating population sizes and entering data into DAD-IS. In Latin America and the Caribbean, the approach has been successfully implemented. Three countries²⁸ involved in these projects have used the methodology to update their data and the approach is currently being extended to a fifth country.²⁹ Figure 12 shows the impact of FAO's assistance in 2017 for three countries where the stratified sampling methodology was applied to estimate population sizes. Not only were the numbers of populations with data increased, the process also resulted in the insertion of new breeds into DAD-IS. With extra-budgetary support from the Government of Germany, FAO attempted to transfer the technology to several countries in Southern Africa. Unfortunately, the approach encountered less success due to inability to reach an agreements by regional and national actors. FAO is currently supporting several countries in Northern Africa in adoption of the methodology³⁰ using FAO regular budget resources.

In 2019, specific and targeted DAD-IS training was provided to China and Mongolia, where relevant data were already available and accessible. Vietnam was supported in collection and reporting in DAD-IS the information for five pig breeds. The breeds had been targeted with a small conservation project designed to protect them against extinction associated with the outbreaks of African Swine Fever in Asia.

Various countries have their own national data bases for monitoring of national breed populations. The Commission, at its Sixteenth Regular Session,³¹ requested FAO to develop options for improving the linkages between DAD-IS and other databases. At its Seventeenth Regular Session the Commission requested FAO and to continue to collaborate with managers of national and regional systems and other stakeholders to develop and refine procedures for exchange of data.³² To respond to these requests and assist countries having their own independent data information systems containing data similar to those in DAD-IS, FAO developed an application-programming interface (API) in close collaboration with the United States of America, Canada and Brazil. This application allows these countries to upload data directly from their system (A-GRIN)³³ into DAD-IS. The United States of America used this opportunity to update its DAD-IS data.

In addition to these initiatives, it is worth reiterating how the collaboration with the RGBnet project contributed to improve the data available for that species. National and international research projects targeting a specific species may represent a good opportunity to increase the data available for DAD-IS. NC-AnGRs are often themselves not involved directly in research (and thus may not have direct access to data from such projects.) Therefore, it's important for NC-AnGRs to network closely with the national research community studying animal genetic resources for food and agriculture and to raise awareness among researchers on the need for information on population sizes and information about other key breed characteristics.

²⁸ Colombia, Ecuador, Panama

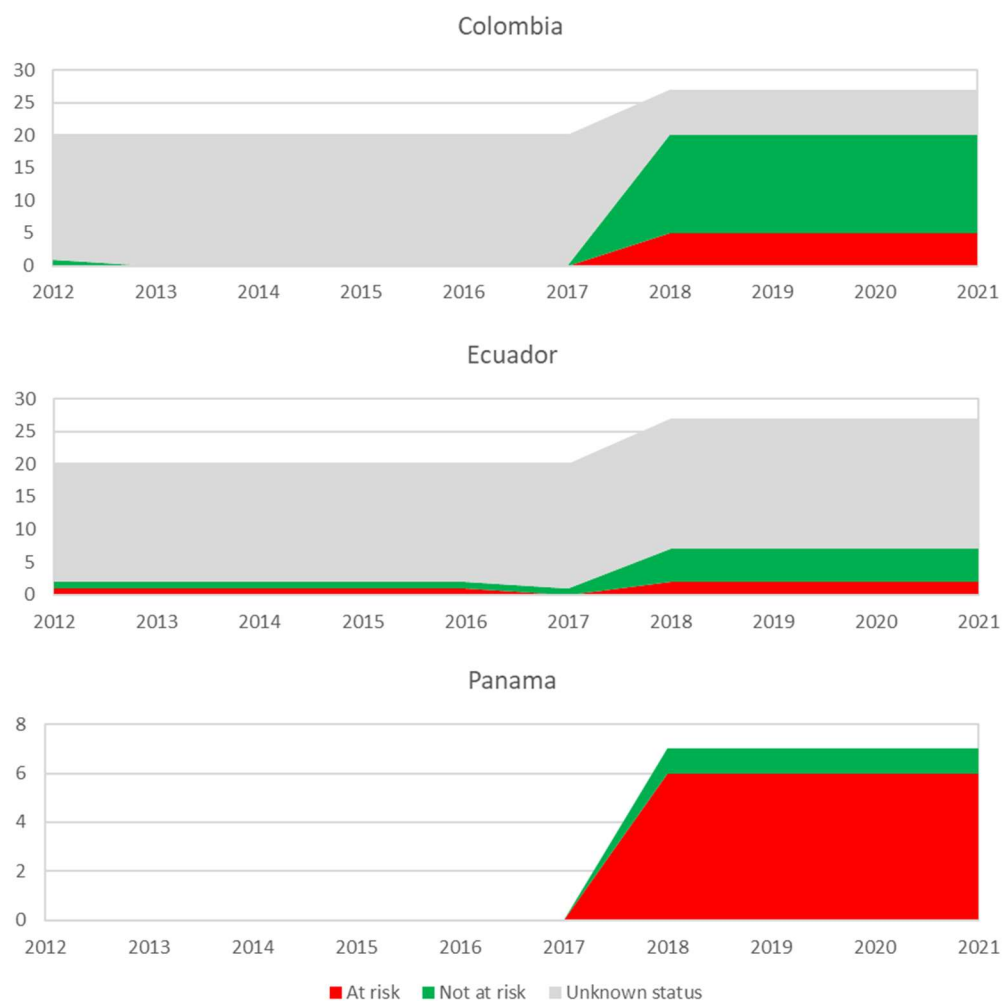
²⁹ Argentina.

³⁰ Algeria, Lybia, Mauritania, Morroco, Tunisia

³¹ CGRFA-16/17/Report Rev.1, paragraph 46.

³² CGRFA-17/19/Report, paragraph 88.

³³ https://agrin.ars.usda.gov/main_webpage_dev/ars

Figure 12: Trends of risk status of local breeds in Colombia, Ecuador and Panama

Finally, the specific inclusion of animal genetic resources in the Target and Indicator framework of the 2030 Agenda for Sustainable Development³⁴ and its Sustainable Development Goals (SDG) implies their importance in ending global hunger and achieving food security and improved nutrition. When monitoring SDG Indicator 2.5.2³⁵ on the proportion of local breeds at risk of extinction, any reasonably accurate information is far superior to a lack of information, even if the precision of the data is not high. Reporting for SDG Indicator 2.5.2 requires only a country to assess whether a breed is at risk of extinction or not at risk. Determining whether a breed is at risk requires simply knowing whether the population size is greater (or less) than 2 400 animals for highly-reproductive species (multiple-offspring species such as pigs, rabbits and most birds) and 7 200 animals for lowly-reproductive species (animals with typically single or twin births such as cattle, sheep, goats and horses).³⁶ For most national breed populations, the knowledge necessary to make such a basic assessment is almost certainly available to NC-AnGRs or other staff of the National Focal Point, or obtainable from local experts.

Furthermore, DAD-IS is programmed and formatted to facilitate reporting of such data. NC-AnGRs may report sizes of national breed populations as minimum and maximum values with no constraints on the range between the two values. In fact, reporting of only a minimum population size is acceptable, as the minimum value is used to determine risk status. DAD-IS furthermore allows NC-AnGRs to provide an indication of the precision of the data, by specifying the source upon which the data are based (such as a survey or census) and their reliability.

³⁴ <https://sustainabledevelopment.un.org>

³⁵ <http://www.fao.org/sustainable-development-goals/indicators/252/en/>

³⁶ <http://www.fao.org/3/a-i3327e.pdf>

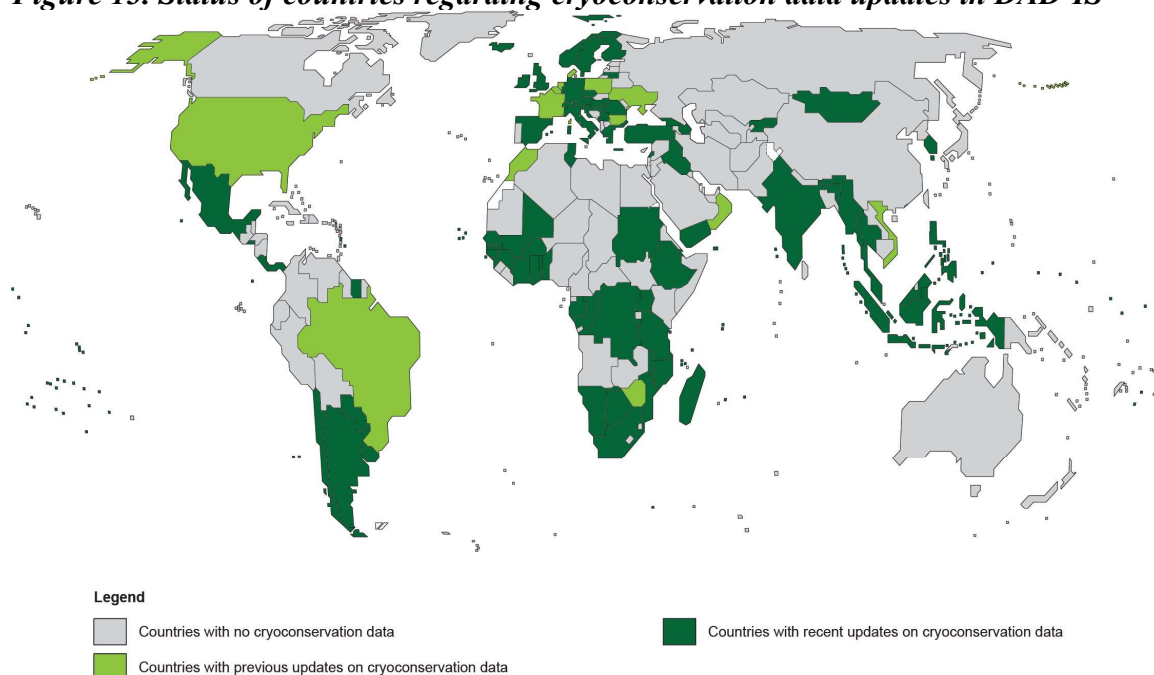
B. Activities addressing gaps in cryoconservation data

As indicated above, specific fields for cryoconservation programmes have been included in DAD-IS only in 2017. Those fields had previously been only integrated in the European Farm Animal Biodiversity Information System network (EFABIS-net) of DAD-IS. Because this development was relatively recent, and perhaps because some NC-AnGRs may have considered the absence of cryomaterial as non-relevant information for DAD-IS, As of February 2020, only 5 percent of national breed populations had information in DAD-IS for cryoconservation status.

The main reason for the large number of breeds with unknown cryoconservation status in DAD-IS thus seemed to be under-reporting in general, independent from the actual presence of material for gene banking. As mentioned previously, countries have the opportunity to explicitly indicate that no material is stored for a given national breed population, so a species totally lacking in development of reproductive biotechnologies could still have 100 percent reporting of its cryoconservation status, that is “no material” should be reported as the status for all of the national breed populations of such species.

To fill the gaps above mentioned in a cost-effective manner, a request was sent to all NC-AnGRs in June 2020, asking them to update the cryoconservation status of their national breed populations, by filling-in an attached document listing all their specific national breed populations. The request established a deadline of September 2020 for NC-AnGRs to compile and return the updated list. A total of 81 countries responded, which increased the number of countries with information on cryoconservation (for at least one breed) from 35 to 93. A majority of the responding countries were from Africa (31) followed by Europe and the Caucasus (23) (Figure 13).

Figure 13. Status of countries regarding cryoconservation data updates in DAD-IS

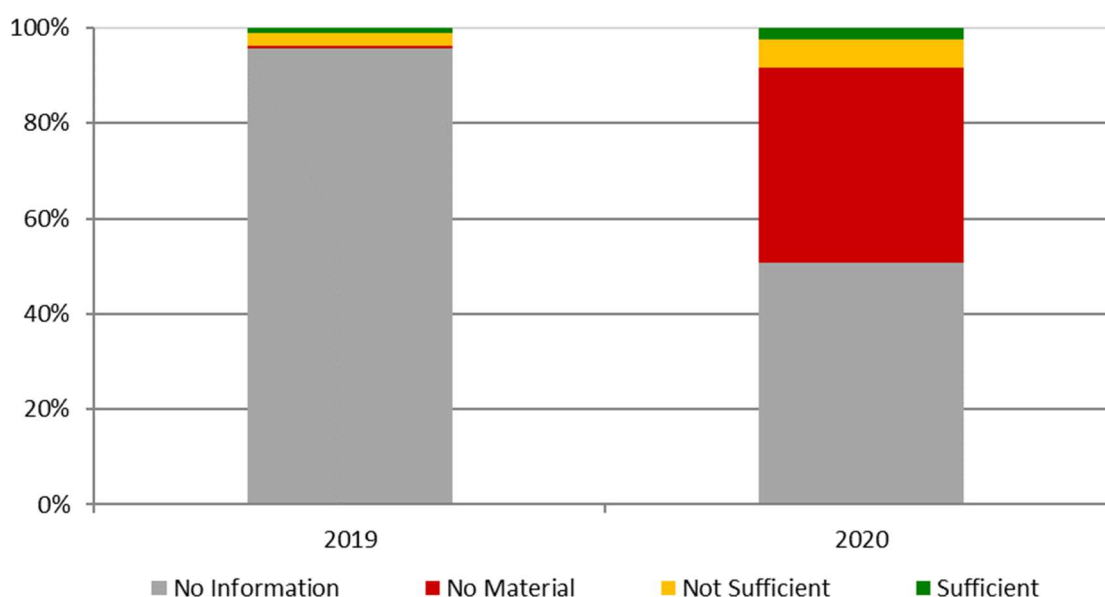


The process increased the proportion of national breed populations with information on their cryopreservation status from around 5 percent to around 50 percent. As illustrated by Figure 14 focusing on local breeds, most of the updated information related to breeds with no material collected. Nevertheless, between February 2020 and February 2021, the proportions of local breeds with non-sufficient or sufficient material collected also increased, from 1.0 to 2.6 percent and from 2.8 to 6.2 percent respectively.

The success of the initiative was largely linked to the fact that, especially compared with population risk status, the cryoconservation status of a given breed population is relatively easy to collect. As explained earlier in this document, for a large majority of national breed populations, no material is collected because no gene bank exists in the country. NC-AnGRs should be aware of whether or not an animal gene bank exists in their country. For breeds for which collected material is stored in a gene bank, NC-AnGRs can presumably obtain such information directly from (the generally limited number of) gene banks active in the country.

The abundant response to the request from FAO to provide cryoconservation information demonstrated the great interest of NC-AnGRs to provide information for DAD-IS even for cases where no cryoconserved material was present in their respective countries.

Figure 14. Change in cryoconservation status for local breeds from February to October 2020 (SDG 2.5.1b)



IV. CONCLUSIONS

As requested by the Commission, FAO has consulted with NC-AnGRs to identify reasons for the continuing high proportion of breeds with unknown status regarding risk of extinction. Further, FAO undertook an in-house analytical study on the factors influencing the reporting of information for national breed populations. The interaction with NC-AnGRs allowed the identification of a lack of breed population data and/or access to those data as primary reasons for the high proportion of breeds with unknown risk status. The in-house study revealed geographic region to be the factor with the strongest association with the proportion of breeds with unknown status for risk of extinction. Although more specific hypotheses were not tested, this relationship is likely the results of regional socio-economic factors, rather than other geographical factors such as temperature, rainfall and altitude. In general, reporting of population sizes, breed descriptive metadata and quantities of cryoconserved genetic material was more complete in regions such as North America and Europe and the Caucasus that have a greater median income and level of agricultural development. The countries in these regions tend to have invested more capital in developing breeding and conservation programmes, are more likely to have established policy related to management of animal genetic resources for food and agriculture and have more extensive research, education and extension programmes.³⁷ All of these factors facilitate the availability of

³⁷ *The Second Report on the State of the World's Animal Genetic Resources*; <http://www.fao.org/publications/sowangr/en/>

data on breeds and their risk status. Within the other regions, some countries have been similarly active in reporting information to DAD-IS and many of them share some of these features.

Differences regarding the quantities of data available in DAD-IS were also observed in association with species. In general, more data are available for mammalian species than for avian species. Within these major species groups, differences among individual species were not always consistent across the classes of information. For example, among mammals, rabbits tended to have low metadata completeness, but their population size data have been updated more frequently. Cattle, sheep and goats are generally similar for all measures of data completion,

No strong general trend was observed regarding the geographical classification of national breed populations as either local or transboundary (regional or international).

FAO has launched various initiatives to help address the reasons for the large proportion of breeds with unknown risk status. FAO has supported the development of a stratified sampling method for estimating population sizes and has successfully tested the method in several countries. Further application is underway in several other countries. FAO has developed several training materials on DAD-IS data entry and has supported several countries directly with training. FAO staff are available for support via email and other forms of electronic communication.

Countries can take advantage of opportunities to report any information in DAD-IS, even if highly precise population census data are not available. Aiming to have comprehensive animal identification and breed monitoring systems is a reasonable long-term goal, but countries should avoid “allowing perfection to be the enemy of good”. DAD-IS provides the opportunity for countries to express population data as a range between minimum and maximum values and does not restrict the precision of these ranges. The thresholds for identifying breeds at risk are far less than 10 000 animals for all livestock species. Many breeds with “unknown” risk status can be reasonably considered to have population sizes that far exceed the thresholds.

Substantial gaps are also present in breed metadata and data regarding cryoconservation. Metadata do not require population monitoring systems. For cryoconservation, countries without a national gene bank can report that all their breeds have no material.

Finally, greater collaboration between NC-AnGRs, the National Focal Point and local stakeholders can improve data availability and quality for DAD-IS. Breeders, especially formal or informal breeders’ associations, can assist in estimation of population sizes and provision of metadata. Researchers often produce metadata that are reported in the informal or scientific literature, but are not documented in DAD-IS. Scientists may also be able to assist in developing new methods for estimating population sizes. When gene banks exist within a country, they will likely have an accurate system for documenting the amounts and types of material that they have stored.

In conclusion, several different reasons and factors have been identified that contribute to the large amounts of missing information in DAD-IS. The multiple number of reasons can be viewed by countries and NC-AnGRs as a wide choice of opportunities to improve their reporting in DAD-IS. FAO staff are available to offer technical support upon request.