

250. Genebank collections in relation to risk status in livestock species

G. Leroy¹, H. Blackburn², C. Danchin-Burge³, F. Tejerina Ampudia⁴, S.J. Hiemstra⁵, C. Ligda⁶, P. Boettcher¹ and R. Baumung¹

¹Food and Agriculture Organization, viale delle Terme de Caracalla, 00153 Roma, Italy; ²United States Department of Agriculture, 1111 South Mason St., 80521 Fort Collins, USA; ³IDELE, 149 rue de Bercy, 75012 Paris, France; ⁴MAPA, C-Almagro 33, 28010 Madrid, Spain; ⁵Centre for Genetic Resources, the Netherlands (CGN), Wageningen University & Research, P.O. Box 338, 6700 AH Wageningen, the Netherlands; ⁶Hellenic Agricultural Organization, VRI, P.O. Box 60 272, 57001 Thessaloniki, Greece; gregoire.leroy@fao.org

Abstract

This study investigated national genebanking priorities based on information reported in the Domestic Animal Diversity Information System (DAD-IS) and feedback provided by gene bank managers. Only 3.2% of national breed populations are reported to have enough material collected to allow breed reconstitution in case of extinction. Depending on species, region and demographic risk status, there are substantial differences in quantities of germplasm collected when comparing breeds with a high risk status vs demographically important breeds. Most genebanks have small budgets and use pragmatic approaches for collecting germplasm by partnering with breeding organisations and/or artificial insemination companies. They also work with a variety of breed associations to implement collection strategies to ensure that the breadth of genetic diversity is captured. Future collection growth within countries will be driven by national programs that incorporate stakeholder participation, collection use, the scope of diversity captured; and will depend upon levels of public and private funding.

Introduction

Ex situ conservation by genebanks is an approach that provides insurance against losses of animal genetic resources in the field, caused by breed replacement, genetic erosion and/or emergencies (Smith, 1984; Paiva *et al.*, 2016). Currently, two indicators of the Sustainable Development Goals (namely 2.5.2 and 2.5.1b) consider *in situ* and *ex situ* conservation of animal genetic resources, respectively. Indicator 2.5.2 is defined as the proportion of local breeds (i.e. being reported to exist only in one country) classified as being at risk of extinction. Indicator 2.5.1b considers the number of local breeds stored within a genebank collection with an amount of genetic material (semen, embryos, oocytes, etc.) stored sufficient to reconstitute the breed in case of extinction (FAO, 2012; Leroy *et al.* 2019). Those indicators are based on official data provided by countries to the Domestic Animal Diversity Information System (DAD-IS).

The aim of this study was to assess to what extent genebank collection strategies in livestock consider risks related to genetic diversity, both at species and breed level. To investigate this, DAD-IS data from 197 countries and territories were analysed and augmented with feedback provided by some countries in Europe and North America.

Materials & methods

Data from 15,121 national breed populations belonging to 37 species and species crosses, reported by 197 countries and territories, were extracted from DAD-IS in December 2021. Depending on the information provided, the cryoconservation status of a national breed population can fall into four categories: (1) no information (no information provided on cryomaterial); (2) no material (no material collected, according to the country); (3) not sufficient (material collected, but with an amount insufficient to allow breed reconstitution in case of extinction); and (4) sufficient. Countries can indicate whether they consider the quantities of material stored to be 'sufficient', based on their own conservation objectives and their local

capacity in reproductive biotechnologies, as these factors can vary substantially across breeds, species and countries. Otherwise, sufficiency is determined by default, based on internationally agreed criteria considering species, numbers of samples and donors and type of material stored (frozen semen, embryos, oocytes; FAO, 2012).

The cryoconservation status of national breed populations were analysed as the dependent variable in a multinomial logistic regression model (R multinom function) with the following explanatory categorical variables: (1) species (Cattle, Chicken, Goat, Horse, Pig, Rabbit, Sheep, Other avians, Other mammals); (2) region (Africa, Asia, Europe and the Caucasus, Latin America and the Caribbean, Near and Middle East, North America); (3) the breed's geographical classification (Local, Regional transboundary, International transboundary); and (4) the breed's risk classification (Unknown, Not at risk, Vulnerable, Endangered, Critical, Extinct). The risk classification is defined based on demographic thresholds endorsed by the FAO Commission on Genetic Resources for Food and Agriculture (FAO, 2013).

Data from 11 European countries collected through the ERF (European Regional Focal Point) Ad Hoc Action were used to assess the challenges on developing national strategies for cryoconservation. In addition, five countries from Europe and North America also provided open comments on the question of genetic risk in relation to topics such as the criteria used for selecting breeds sampled for cryoconservation, the amount of material requested, and the sampling strategy at breed level.

Results

On the 15,121 national breed populations reported in DAD-IS, 47.8% are reported without information regarding their cryoconservation status, 43.5% are reported to not have any cryo-material collected, 5.5% are reported to have material collected, but with insufficient amount, and only 3.2% have enough material collected to allow breed reconstitution in case of extinction. Among species, mammals and especially cattle (9.5% of national breed populations with not sufficient and 6.7% with sufficient material), showed larger genebank collections compared to avian species ($P < 0.001$). When compared to other regions, Asia, Europe and the Caucasus and North America, showed larger proportions of national breed populations with material stored, either not sufficient (1.4 vs 5.1, 8.2 and 13.4%, respectively) or sufficient (2.2 vs 3.8, 3.2 and 9.2%, respectively) ($P < 0.001$). By contrast, cryoconservation status did not vary substantially by geographic status of the breed (local, regional transboundary, or international transboundary breeds) with proportion being 5.9, 4.4 and 5.2% for not sufficient, respectively, and 2.8, 3.1 and 3.6% for sufficient respectively ($P < 0.01$). When considering risk status (Figure 1), national breed populations with unknown risk status (i.e. no information provided on their population over the last past years), were the most likely to not have information reported on their cryoconservation status (55.4%) ($P < 0.001$). Risk status (population size) seemed to be both a driver (increased need) and an obstacle (greater difficulty in accessing donors) for material collection in small populations. The proportion of national breed populations with material collected was greatest for 'Vulnerable' populations. Among larger (i.e. 'Not at risk') populations, a smaller

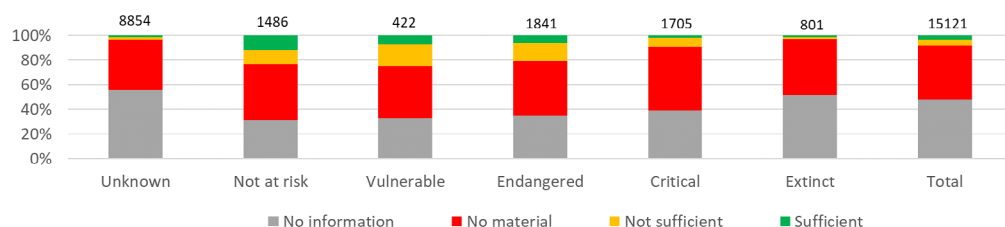


Figure 1. Collection status of national breed populations by risk status.

proportion of breeds had material collected, but the material was sufficient for a greater proportion of these populations, in part due to the economic importance of these populations and the ability to more effectively acquire germplasm. ‘Endangered’ populations were collected at a rate similar to those ‘Not at risk’, but the proportion with sufficient material was much less. Practical factors seemed to strongly limit collection of material from ‘Critical’ populations.

From the ERFIP dataset, obstacles related with funding and policy issues were considered as the main drawbacks in development national genebank collections (Table 1). Among them, lack of funding, lack of infrastructures, low interest of breeders’ societies and low priorities in governmental policies were ranked as the main ones. Technical issues link to specific species and genetic diversity aspects (low number of males in certain breeds) were ranked as medium obstacles (8.8 and 8.5 on 0-20 scale, respectively). When providing open input, national coordinators indicated that genetic and demographic risk status is only one among many factors for the selection of breeds to be collected. They reported that national genebanks use opportunities to collect material already available in AI centers (i.e. often from mainstream breeds) or through research projects, while trying at the same time to encourage and support breeding associations from local breeds to implement collection strategies. At the breed level, depending on information available (geographic distribution, pedigree and/or genomic information), donor animals are sampled to display a high genetic variability, using for instance optimal contribution selection (the Netherlands) or Ward’s Minimum Variance method (USA), but often a more pragmatic approach.

Table 1. Obstacles reported by European countries for the development of ex-situ conservation strategies ranked from 1 (less important) to 20 (most important).¹

	Obstacles	Rank (s.e.)	Obstacles	Rank (s.e.)	
Funding	Lack of public funding for ex situ conservation	16.9 (1.1)	Private companies/AI centers not involved	9.5 (1.8)	Organizational
	Unexploited funding opportunities	9.7 (1.5)	Low level of public awareness, in the farmer’s community	9 (2.1)	
	No stable funding source	9.4 (2.5)	No integration of ex situ and in situ conservation activities	8.7 (1.6)	
			Weak structure of breeders associations / poorly developed breeding programs	8.2 (2.6)	
Policies	Low interest of breeder societies in ex situ conservation activities	12.5 (1.6)	Lack of infrastructure and technical capacity	13.3 (1.5)	Technical
	Ex situ conservation of animal genetic resources is low priority in governmental policies	11.5 (2)	Gaps in methods for freezing semen and insufficient fertility in some species	8.8 (2.3)	
	Poor/lack of coordination among actors	10 (2.5)	Extremely small number of males in the population intended to be preserved	8.5 (1.7)	
	Absence of regulations on ex situ conservation	8.9 (2.6)	Lack of awareness on EUGENA activities	6.8 (1.9)	
	Bureaucratic burdens in financial planning and agreements	6.6 (1.8)	Lack of capacities at sub-country level	6.7 (2.2)	
	Low coordination among countries in case of transboundary breeds	6.2 (1.9)	Difficulties in the development of new biotechnologies	5.5 (1.3)	
	Legal restrictions in collections on the field or use of old material.	5.5 (1.8)	Problems with storage of duplicate collection	4.5 (1.6)	

¹ In bold the 5 most important obstacles.

Discussion & conclusions

Analysis of DAD-IS data shows that breeds not at risk are well represented in national genebank collections and that breeds at risk on average have limited amounts of genetic material stored in genebanks. Feedback provided by national coordinators indicate that national genebanks take into consideration more than genetic risk based upon a breed's threat level (e.g. socio-economic importance of a breed, or unique phenotypes). Although it is important for any breed and breeding program to develop *ex situ* collections, countries have different priorities and opportunities to support that. In practice, the level of development of genebank collections depends on national priorities, funding, stakeholder participation and the available infrastructure, institutions and capacities. When viewed globally, substantial germplasm collections have been developed in Europe and North America (Paiva *et al.*, 2016) and these resources present interesting research opportunities in the area of genomics and reestablishing lost genotypes (Dechow *et al.*, 2020). But national genetic resource programs must strive to increase the utilization of these collections to the research community and industry, as public and private goods. By increasing utilization of these resources, the genebank raises awareness of the collection's utility, which in turn can justify and facilitate the expansion of the collection.

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