Mapping the diversity and characteristics of European farm animal genetic collections: banks or museums?

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Summary

Introduction

There is a global consensus on the importance of Animal Genetic Resources (AnGR) - i.e. genetic diversity within and between livestock species and breeds - to insure our food security (CBD, 1992, FAO 2015). However despite this widely shared value of farm animal genetic diversity, there is a contraction of the livestock biodiversity, both between breeds (one third of domestic breeds are considered to be at risk of extinction, FAO 2015) and within breeds (loss of genetic variability in local breeds and mainstream breeds, see for instance Leroy et al. 2012). In order to counter act genetic erosion, there is a wide array of references on how to set up efficient conservation programs, either on farm (*in situ* conservation), with "ark farms" or "research populations" (*ex situ in vi*vo conservation) or by cryopreserving germplasm material, i.e. reproductive material such as semen or embryos (*ex situ in vitro* conservation, see for instance FAO, 2012). Besides samples of reproductive material, "genomic collections", *i.e.* collections of biological samples such as DNA, blood, tissue etc. are also set up, mostly by research teams. In this article we will refer germplasm and genomic collections as genetic collections. A specific issue for *ex situ* conservation is the lack of characterization and limited use of genetic collections.

The goal of IMAGE (Innovative Management of Animal Genetic Resources) project was to make an inventory of genetic collections in Europe. The aim of this study is to report the main results of this IMAGE survey. Information collected by the survey will be made accessible through a European portal for genetic collections, and will be used for further analysis in the IMAGE project.

Set up and results from a European survey on genetic collections

Survey set up

Data were collected through an online survey that was sent to a list of institutions or holdings managing a collection of farm animal genetic resources in Europe. The list was provided or disseminated through the IMAGE Consortium partners (www.imageh2020.eu/) and the network of European National Coordinators for animal genetic resources during the fall 2016 and answers were collected till mid-April 2017.

The survey framework was designed by IDELE with the help of partners involved in the second IMAGE work package. The 182 questions of this survey covered basic information (such as contacts, organisation involved etc.), elements about the collection itself (species, breeds, type of material stored), indications on how the collection was managed

(including security backup, sanitary requirements, database set up and existence of quality management system), conditions of access to the resources (including questions about the implementation of the Nagoya protocol on Access and Benefit Sharing).

Results of Survey
Overall results

A total of 61 organisations representing 20 countries returned the questionnaire (Figure 1). The majority of the answers (55 %) came from a single institution per country. On the other hand, as many as 29 different organisations answered the survey for Spain.

Among the 61 organisations that answered, 51 were holding a germplasm collection and 30 a genomic collection. Twenty institutions were managing both a germplasm and a genomic collection.

Collections management

Collections were mostly supervised by a public research institute or a university (61 %), but private organisations were more involved in germplasm collections (14% of the germplasm collections vs 7% of the genomic collections). At country level, 45% of the collections did not belong to a national network versus 25% which did.

FAO cryoconservation guidelines (FAO, 2012) highly recommended safety duplications. According to the survey results, this recommendation is followed by 35 % of the germplasm collections and collections with both type of materials, while this percentage drops to 11% for genomic collections. Obviously this safety rule is an issue since only 13% of collections that indicated the existence of duplicate collections were fully doing it while the rest only partially duplicate their collections.

With regard to database implementation, most germplasm collections (84%) answered this question and a slightly lower percentage of genomic collections (73%) did. Among the ones that answered, respectively 95% of the germplasm collections and 100% of the genomic collections had implemented a database. The solutions used were often rather simple since 64% of the germplasm collections and 73% of the genomic collections were using a Windows Office Excel© or Access© database. Dedicated database such as cryoweb (http://cryoweb.ch/) or in house built databases were developed for 36% of the germplasm collection. We should notice at this stage that the use of simple spreadsheet for data registration of genetic collections is not compatible with the referential NF S96-900, which is a specific quality norm set up in France for Biological Resource Centres (BRC). Interestingly, 64% of the organisations had or were considering implementing a quality management system.

One of the follow up of the CBD (1992) is the Nagoya Protocol on Access and Benefit Sharing (2010). In this context, it was important to investigate if there was a formal agreement/contract to regulate the acquisition of genetic material by the germplasm collection (Material Acquisition Agreements, MAA). Only 15% of the germplasm collections stated having such an agreement and this number drops to 10% for genomic collections. Material Transfer Agreements (MTA) or equivalent agreements for distributing genetic collections were also fairly rare since respectively 26% of the germplasm collections and 33% of the genomic collections reported having such type of contracts.

What is in the European genetic collections?

Five main species are found in the European genetic collections (cf. Table 1): cattle, sheep, goat, horse/donkey and pig. The ranking for poultry seems higher for genomic collections but it is actually a combination of six different species, chicken (9 collections), turkey (4), duck (3), goose (3), guinea-fowl (2) and quail (2). Some wild species are also found, ranging from a large collection in Iberian Ibex (249 donors and 7,409 doses) to limited editions for giraffe or giant panda for instance (one donor per species only).

We have a detailed knowledge of the breeds held in the collections for 76% of the germplasm collections and 53% of the genomic collections. For germplasm, there was a total of 546 distinct breeds/populations hosted in the collections: 84% of the breeds were represented in a single collection, the most common breed being the Holstein cattle (reported by 16 germplasm collections) followed by the Brown Swiss cattle (11 collections). For both breeds, half the organisations detaining a collection were Spanish. The highest number of breeds was found for sheep (188) followed by cattle (161), chicken (112), pig (93) and rabbit (68). In chicken, pig and rabbit, numerous commercial lines (sometimes extinct) can be found in the collections. For germplasm collections still, when grouping by country, the highest average number of doses and donors per breed are found in cattle (cf. Table 2).

Regarding sampling procedures, 90% of germplasm collections followed specific guidelines to choose their donors. Two types of fairly different approaches were implemented following genetic procedures: one was to sample individuals representing the within breed genetic variability (rare breeds) and the other to sample donors according to their specific features or genetic values (larger breeds). Another main sampling approach, not related with genetics, was to sample donors according to their sanitary status. For genomic collections, about 70% of them followed specific rules to choose donors. In most cases, for genomic collections, sampling was dependent of the research project the material was stored for. On some occasions, genetic material of donors was collected in order to supplement germplasm collections, each donor having both its reproductive and genomic material stored in parallel.

What are the collections' purposes?

As one of the IMAGE goals is to enhance the use of genetic collections, we needed first to have a clear sight on why the European collections were created. For germplasm collections, 80% of them said that their purpose was long-term conservation as insurance and 91% to support *in situ* conservation of local/native breeds. Hence, requirements to access collections followed this logic since most organisations would release material for conservation purposes (such as recovery of a breed or use of original bloodlines). All the collections reported restricted access: distribution was limited to breeders' association and/or depended on the request. One of the main reasons to limit access seemed to be that these collections were meant to be for long term conservation. A limited number of available doses was also a concern. Requirements to access genomic collections was much more research oriented. In most cases, access depended on the realisation of a research project.

Discussion

Answering the questionnaire was voluntary and obviously not all countries and genetic collections returned the questionnaire. Based on previous investigations done (including the one carried out by Hiemstra et al., 2014 for the European Genebank Network - EUGENA; FAO 2015) the germplasm collections' coverage seems fairly accurate. On the other hand, no equivalent work was ever done for genomic collections. The number of genomic collections

across Europe might be expected to be much higher. One of the reason we missed data might be that scientists keeping DNA samples for their research may not consider themselves as collection managers.

A complication to access genetic collections could be that there is little formalisation of the collections acquisition and access conditions, as we saw earlier with the low percentage of existing MAAs and MTAs. A reason why it might be complicated for institutions to implement such documents is ownership rights: according to our survey, 39% of the collections were owned by at least two entities or more. Also, 37 % of the collections did not belong to the organisation managing the collection, which means that any use could be dependent of the owner's consent. It gives the impression that genetic collections were mostly in a phase of storing material while the process of distributing samples had not been thought through yet. A distinction should be made between germplasm and genomic collections: it was interesting to see that MTAs or equivalent were actually more common (in percentage) for genomic collections than for germplasm collections. The difference is probably due to the fact that genomic collections were far more project oriented (the material sampling and storage is designed with an expected use in mind) than the germplasm ones (material is stored mainly for long term conservation purposes).

Another reason why it is difficult to access material from the collections might be that most organisations are not ready for routine uses A mere 25% of the organisations have implemented a fee policy and only 53% recorded detailed information about costs related to the setting and operating of the genetic collection. When a fee policy existed, in most cases it seems to cover mainly storage expenses or handling costs. Some organisations have distinct fares depending on the breed (a rare breed's association will not pay for storage while a main stream breed will) or the user (researchers belonging to the organisation will benefit of a lower fare than outsiders).

Last but not least, in the case of germplasm collections, sanitary issues might limit the collections' use. In order to preserve rare breeds, some countries such as the Netherlands (personal communication, S.J. Hiemstra, Centre for Genetic Resources, the Netherlands) have set up specific rules that allow them to collect, store and use semen of males of rare breeds but does not comply with EU sanitary regulations.

It is sometimes thought that an inventory of the European collections could be a way to rationalize collections by identifying duplicates between organisations. As stated earlier we did not have access to all the details of the collections surveyed, however limited overlap in breeds was found between collections. This result leads us to think that most germplasm collections do detain a rather unique material.

Still for germplasm collections, we might wonder if the collections stored were sufficient to be able to re-establish a breed. This also relates to the agreed Sustainable Development Goal Indicators (SDG) 2.5.1 "Number of plant and animal genetic resources for food and agriculture secured in medium or long term conservation facilities" (FAO, 2016). According to FAO (2012), the goal to reach when restoring a breed is to create a population with an effective population size of 50. Table 2 shows that for cattle only the average number of donors per breeds is higher than 50, indicating that for many breeds the collection stored would not be sufficient to re-establish the breed. Furthermore, details from the survey shows that the situation is worse for rare breeds compared to the larger breeds. This outcome is quite logical since it is easier to find donors in a large population than in a small one. Also, main stream breeds usually comply better with the sanitary requirements needed to enter an AI station than rare breeds do.

Genomic collections' main targets for storage were quite different from germplasm

collections since it most cases there were devoted to the storage of material for specific research projects. Sampling procedures were often quite complex and might involve quite a lot of task force and material. Once the project is over, it appears that there was actually few thoughts on the project's collection value and the possibility of future uses.

Conclusion

Our survey showed that many European countries are hosting genetic collections, but they differ a lot in organisation, rules and development phases. Our results are fairly representative of the overall situation for germplasm collections, however for genomic collections our sampling is probably limited and may not be representative for Europe as a whole. As far as species representation, the main livestock species are well represented. There is an extreme wide array of breeds in the collections, from rare breeds to main stream breeds, but the amount of material per breed differs also greatly and generally it is actually the endangered breeds which have the least amount of material in the collections. All these results showed a strong need of formalizing the position of gene banks in Europe, harmonizing practices and stimulating exchanges of knowledge and information between gene banks. The EUGENA initiative (Hiemstra et al. 2014; ERFP 2017) is a step forward this direction which is supported by the IMAGE project.

Our survey also showed that genetic collections were mostly in the phase of storing unique genetic material whereas use was limited. The IMAGE project is a great opportunity to shift the genetic collections from a static perspective ("museum collections" with almost no flow out) to dynamic ones ("bank collections", where material flows in and out). The whole research community needs to be more aware of the relevance of this material for their projects. Also, while it is quite clear that no collections could be ever self-sustainable, economic models – including government subsidies – need to be set up to insure the future of our genetic collections The objectives is neither to deplete the collections nor to shift their objectives to a sole economic purpose, but, on the contrary to find the best way to characterize and safeguard them.

Table 1. Number of gene collections by species.

	Germplasm	Genomic
Cattle	34	18
Goat	29	14
Horse/donkey	26	13
Other species	10	16
Pig	23	10
Poultry (chicken, duck etc.)	14	24
Sheep	31	17

Table 2: Number of donors (average, maximum) and straws (average, minimum, maximum) per breed and species – farm species and germplasm semen collections only.

	Donors		Straws		
	Average	Max	Average	Min	Max
Cattle	182	12,286	156,215	6	21,833,564
Goat	22	477	2,774	51	44,061
Horse/donkey	8	74	1,628	3	17,920
Pig	18	82	2,429	26	14,066
Poultry (chicken, duck etc.)	23	110	670	31	3,989
Sheep	41	2,433	5,310	9	221,352

Figure 1. Map of the countries that filled the IMAGE questionnaire.

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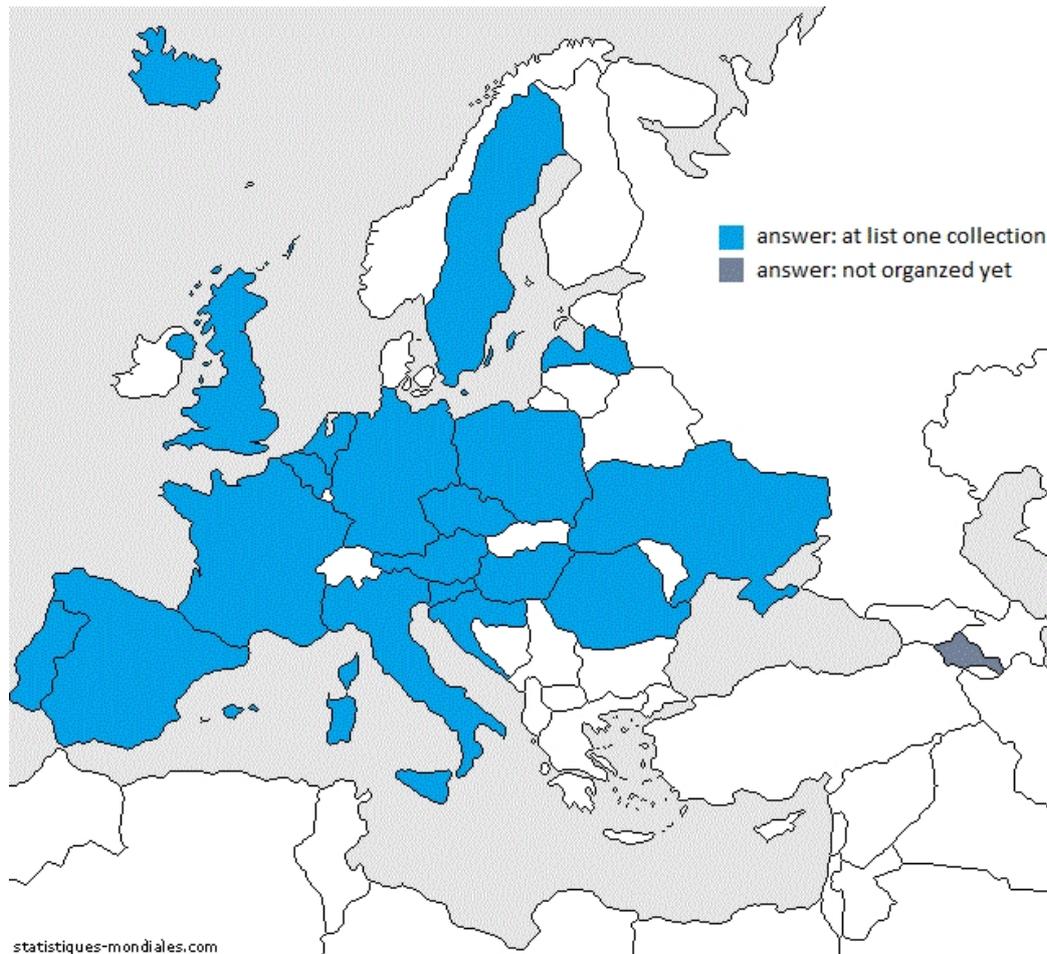
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