

# NEWSLETTER

MAY 2018—ISSUE 3



## *editorial*

IMAGE currently stands at the middle of its time-span and is in a very active phase. New results have been presented at the major meeting point of genetics for livestock: the World Congress of Genetics Applied to Livestock Production, which was held in Auckland, New-Zealand, Feb 11-17. A delegation of IMAGE presented 3 posters and 3 oral communications (see below) and our WP2 leader chaired the session on 'species conservation' which was considered as a 'challenge session', featuring an introduction of the main goals of IMAGE by the coordinator and one case study from the Dutch national gene bank, presented by Jack Windig (DLO). Another session, devoted to methods for population genetics, underlined the new approaches brought by large-scale genotyping, or sequencing, to manage genetic diversity, echoing the main objectives of IMAGE. This meeting was also the place where our FAO partner, Paul Boettcher, presented the Sustainable Development Goals with their translation in indicators for animal genetic resources.

***"IMAGE currently stands at the middle of its time-span and is in a very active phase"***

This is also the time of the mid-term ethical review, which appears as a bigger challenge than expected, particularly regarding the issues raised by the commission regarding the criteria to choose breeds for

cryoconservation. A large brainstorming was undertaken at our 2<sup>nd</sup> Annual meeting and it was decided to set up a communication tool to come back towards the stakeholders in order to get more feedback from them. As usual for ethical issues, an effort is needed to initiate the debate, followed by a phase where ideas are proliferating, which is the current stage for IMAGE partners. Do not hesitate to contact us if you have questions or comments !

The 2<sup>nd</sup> annual meeting was also an opportunity to work with our more distant partners from Morocco, Egypt and Argentina, this was very fruitful from both sides and we are very happy that EU gave us the possibility to fund their participation, because it is significantly enlarging the scope and the impact of IMAGE. See more about what happened at our AM2 on the following pages.

*Michèle Tixier-Boichard*



**Michèle presenting at the 2<sup>nd</sup> Annual Meeting**

# news

## IMAGE Second Annual Meeting

By Andreia Amaral

The 2<sup>nd</sup> Annual meeting of H2020 IMAGE project took place in Vienna, 21-23 March 2018. It gathered 55 participants from the various project partners, representing 15 EU countries and 3 participants from non-EU countries (Argentina, Morocco and Egypt). In addition, two members of the Advisory Board (Harvey Blackburn and Asko Maki-Tanila) also attended the meeting.

This event provided the opportunity for meetings among the various WPs and exchange of knowledge and opinions between the different partners involved in the project, in order to facilitate the implementation of IMAGE proposed workplan.

The program included the participation of two invited speakers, Christian Schlotterer from the UVM in Vienna and Marjeta Candek-Potokar from the Agricultural Institute of Slovenia and coordinator of the H2020 project TREASURE.

The contributions and achievements of IMAGE were presented by the project coordinator Michèle Tixier-Boichard and by the WP leaders:

- With the goal of engaging different stakeholders, two Dialogue Forums were held in 2016 and in 2017. These meetings were organized in coordination with the ERFP general assembly and the EAAP conference. By joining stakeholders with a wide-ranging experience

(scientists, government officials, industry, NGOs, etc.) these meetings have allowed the opportunity to increase awareness about the importance of appropriate management of genebank resources.

- An online survey targeting the needs, attitudes and preferences of stakeholders towards the management of Animal Genetic Resources (AnGR) was developed, allowing the collection of 105 answers. Results were presented at the 10th World Congress of Genetics Applied to Livestock Production.
- Also, the first survey of germplasm banks at EU level was carried-out as planned, in order to obtain an overview of the genomic and germplasm collections and sanitary regulations currently implemented. The obtained results will be available through IMAGE and the EUGENA portal (European Gene Bank Network, coordinated by the European Regional Focal Point for Animal Genetic Resources) in the near future.
- Preliminary results regarding the economic analysis of gene bank development and use, showed that the most cost-effective strategy involves storage of collections per country.
- IMAGE is characterized by the involvement of research teams with different competences, promoting multidisciplinary research and training at PhD level. In the annual meeting of IMAGE, 4 PhD candidates presented their results in the fields of: a) optimization and development of innovative methods for genebank sample collection and storage; b) genetic assessment of gene bank collections of different EU livestock populations.
- IMAGE research has resulted in the generation of several publications in important journals in their field, contributing to understand how the genetic make-up domestic animals has evolved as a result of management and genetic improvement in Europe.
- IMAGE aims to create awareness and contribute towards capacity building in "Genebank Management" in Third countries. IMAGE has successfully engaged collaborators in Argentina, Colombia, Egypt and Morocco. A training plan was developed in close collaboration with local partners in both Europe and Third countries. The first post-graduate training event focusing on Conservation of Genetic Resources took place in Balcarce, Argentina, from 5-9 March 2018.
- During the annual meeting, participants recognized the important role that IMAGE can play to enable the inclusion of several issues regarding Genebank Management into the EU policy agenda, namely those concerning animal health regulations.



IMAGE partners—2<sup>nd</sup> Annual Meeting

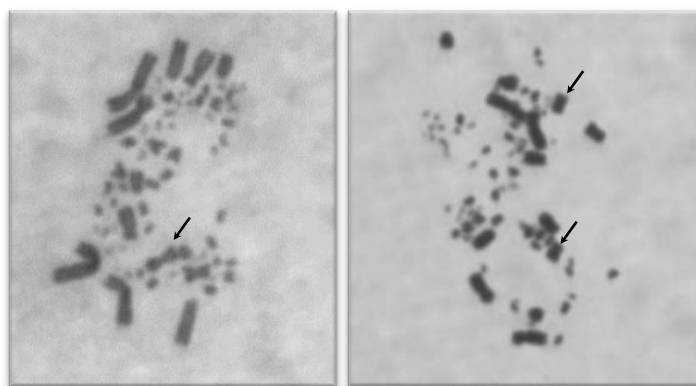
# The use of infertile interspecific hybrids for a novel model of PGC reintroduction applicable in gene preservation for poultry

By Mariann Molnár

Related to the gene preservation activities of the Research Centre for Farm Animal Gene Conservation (Gödöllő, Hungary), within the framework of the IMAGE project, female Hungarian guineafowls were crossed with Hungarian yellow roosters by artificial insemination. The aim of the research was to produce an infertile interspecific hybrid (recipient) which is able to receive primordial germ cells (PGCs) from a native poultry breed (donor). According to our expectations, this genotype will appear in the offspring of hybrids.

The hybrids hatched between the 21<sup>st</sup> and 27<sup>th</sup> day of incubation. Out of 902 incubated eggs, 31.7% were infertile, 50.9% showed either abnormal development or embryonic death (mostly before day 5), 10.8% reached full development but failed to hatch, and 6.7% hatched and were viable.

As the result of the investigation of chromosomes, 43% was female (Photo 1, left), 57% of the embryos was male (Photo 1, right). Basically, three kinds of phenotype were observed on the hatched hybrids (6.7%). A light brown, a dark brown and a white spotted phenotype was observed but none of the hybrids had helmet, crest or facial wattles (Photo 2.)



**Photo 1. Left: chromosomes of a female hybrid, right: chromosomes of a male hybrid. The black arrows show the Z chromosomes**



**Photo 2. Hybrid, dark brown phenotype**

Based on our results, the conclusion is that these interspecific hybrids may be suitable to receive primordial germ cells (PGCs). In the next steps of this research, we will first inject fluorescent labelled PG cells, and then primordial germ cells of a native chicken breed into 3 days old hybrid embryos.

A dissertation about this research was submitted to the Scientific Student Competition of Szent István University (Gödöllő, Hungary) in the Genetics and Biotechnology Section. The students could participate to this competition with a 35-50-page study and they had to make a presentation about their scientific work and results at the Scientific Student Conference. The studies and presentations were judged and ranked by scientific commission. This competition is organized every year in all disciplines at the Hungarian universities.

***"Mariann Molnár won the second prize of the Hungarian Scientific Student Competition with her IMAGE research for a novel model of PGC reintroduction"***

The best studies are proposed to participate in the Hungarian National Scientific Student Competition which is organized every two years. Mariann Molnár (MSc student at Szent István University, Gödöllő, Hungary) won the second place in the Genetics and Biotechnology Section of the University and will participate the National competition in 2019.



# Shrinking domestic chickens leads to unique and identifiable genetic diversity

By Chiara Bortoluzzi

The Netherlands has an extensive collection of traditional chicken breeds showing exceptional phenotypes. Most breeds were originally kept for egg and meat production, but since the advent of commercial poultry breeding in the 60s, they have gradually become marginalised and are nowadays kept for ornamental purposes. Over the last decades, miniature versions of large fowls have started to appear in the backyards of many hobby breeders and their extraordinary success is due to the captivating appearance and small size. These smaller-sized chickens, called “(neo-)bantams”, come in many varieties, such as booted, crested, frizzled, bearded, barred, and speckled, and in a phantasmagoria of colours, displaying a colour gradient from white to black.

The hobby breeders’ interest for bantams has started a bantamising trend that involved most traditional breeds. The surprising success of the on-going bantamising trend, however, raises important questions related to the genetic diversity, inbreeding level, and contribution to the national livestock biodiversity of the bantam breeds. In our study, recently published in [Heredity](#), we addressed these questions using genotype data of 480 individuals of 37 recognised traditional breeds, including large fowls, neo-bantams, and original bantams, sampled from 1998 to 2011.

According to our study, bantams of the same breed show an overall high inbreeding level, because of matings between highly related individuals that are pursued for selection purposes. The Eikenburger bantam was the most inbred breed. In fact, this breed is kept by a single breeder that frequently uses parent-offspring mating. Furthermore, for the crosses, the Sebright bantam, which is also a highly inbred breed, is used. On the opposite side we have the Chaam fowl and the Dutch Owl bearded that are the least inbred, because they are a mix of different breeds. We also observed that bantamisation has changed over time. In fact, if large fowls and original bantams were used at the early stages of the bantamising trend, bantams of the same and of different breeds would have started to be used in establishing more bantam breeds. By mixing different

breeds, hobby breeders create not only miniature chickens showing original characteristics, but also new breeds. These new breeding strategies were particularly evident in the Groninger Mew bantam, which shows genetic influences from the Groninger Mew and the Frisian Fowl bantam.

The results of our study indicate that hobby farming has a number of limitations. Although part of these limitations can be solved using DNA technologies, additional data need to be collected and added to the DNA information to better understand an individual’s history. Easy-to-implement conservation programmes can then be set up to preserve the extraordinary variation that hobby breeders have created over hundreds of generations and that are part of the national biodiversity. To accomplish the long-term goal of setting up improved management and conservation programmes, we will start a pilot study in which few breeders will be directly involved in the collection of data about their breeds. The pilot study will start in April and will last for 2-3 months. Data about reproductive performance, selection, health, and abnormalities will be collected. At the end of the pilot study, data will be analysed and integrated to the whole-genome sequence data generated under the IMAGE project. Depending on the success of this pilot study, more follow-up studies may start later in the year involving potentially all hobby breeders and traditional breeds. So, stay tuned for more successful stories in the next newsletter.



**An Eikenburger bantam**

# IMAGE at the WCGALP

## Genetic diversity within and relationships among Dutch horse populations

By Anouk Schurink

The historical and ongoing formation of horse breeds is driven by purpose, geographical and environmental conditions. Narrow breeding goals were defined with the emergence of studbooks in the late 19th century, resulting in fast divergence between horse populations. This is often at the expense of genetic diversity.



Investigating the genomic make-up of horse populations from varying development and background can

contribute to an understanding of breeding history and insights in how to conserve or improve horse populations in the future.

At the WCGALP, I presented a poster presenting the genetic relationships and diversity within and among 9 horse populations in the Netherlands (Friesian, Belgian draft, Harness, Gelder, Groningen, KWPN, Lipizzaner, Icelandic, and Shetland). This work showed how admixture, drift, and demography have shaped the genome-wide diversity of these horse populations.

Estimated diversity within and most of the quantified relationships among the populations were in agreement with their history and classifications. Runs of Homozygosity aided in understanding breeding history as it enabled us to differentiate between more recent and past inbreeding. Future research will determine which populations comprise unique alleles and contribute significantly to the genetic diversity that is present to ultimately be able to make well-informed decisions in genetic conservation.



Aim	Results																																												
Investigate the genetic make-up of nine horse populations in the Netherlands → Increase our understanding of their evolutionary history → provide valuable information on how to best conserve or improve these populations	<ul style="list-style-type: none"> <li>Distinct clusters except for four Dutch warmblood populations</li> <li>Largest differentiation from other populations for Shetland ponies and Friesian horses</li> </ul>																																												
<b>Conclusions</b> <ul style="list-style-type: none"> <li>Genetic diversity and most quantified relationships were in agreement with their history and classifications</li> <li>Runs of homozygosity (ROHs) aid in understanding breeding history</li> <li>Future research to identify populations with unique genes and significant contribution to genetic diversity</li> </ul>	 <p>Figure 1 – Relationships within and between populations</p> <ul style="list-style-type: none"> <li>Limited inbreeding in open populations e.g. Gelder horses</li> <li>Many long ROHs within a population represents inbreeding of recent origin in e.g. Shetland ponies</li> <li>Short ROHs and limited inbreeding in Icelandic horses, an ancient population with past inbreeding</li> </ul>																																												
 <p>Gelder horse – one of the investigated Dutch warmblood horse populations</p>	<p>Table 1 – Mean ROH characteristics per population (SE in superscript)</p> <table border="1"> <thead> <tr> <th>population</th> <th>inbreeding</th> <th>number</th> <th>length, Mb</th> </tr> </thead> <tbody> <tr> <td>Belgian draft horse</td> <td>10.1<sup>1</sup></td> <td>34.3<sup>1</sup></td> <td>6.2<sup>1</sup></td> </tr> <tr> <td>Friesian horse</td> <td>22.3<sup>1</sup></td> <td>74.3<sup>1</sup></td> <td>6.7<sup>1</sup></td> </tr> <tr> <td>Gelder horse</td> <td>5.9<sup>1</sup></td> <td>22.2<sup>1</sup></td> <td>6.0<sup>1</sup></td> </tr> <tr> <td>Groningen horse</td> <td>6.2<sup>1</sup></td> <td>25.5<sup>1</sup></td> <td>5.5<sup>1</sup></td> </tr> <tr> <td>Harness horse</td> <td>9.7<sup>1</sup></td> <td>28.0<sup>1</sup></td> <td>7.2<sup>1</sup></td> </tr> <tr> <td>Icelandic horse</td> <td>4.1<sup>1</sup></td> <td>15.1<sup>1</sup></td> <td>6.1<sup>1</sup></td> </tr> <tr> <td>KWPN sport horse</td> <td>5.3<sup>1</sup></td> <td>22.2<sup>1</sup></td> <td>5.4<sup>1</sup></td> </tr> <tr> <td>Lipizzaner horse</td> <td>9.0<sup>1</sup></td> <td>31.7<sup>1</sup></td> <td>6.4<sup>1</sup></td> </tr> <tr> <td>Shetland pony</td> <td>14.4<sup>1</sup></td> <td>45.3<sup>1</sup></td> <td>7.5<sup>1</sup></td> </tr> <tr> <td>Mean ROHs</td> <td>9.7<sup>1</sup></td> <td>33.5<sup>1</sup></td> <td>6.5<sup>1</sup></td> </tr> </tbody> </table> <p>ROHs were segments of at least 50 consecutive homozygous SNPs; inbreeding being the proportion of the genome that was homozygous based on ROHs</p>	population	inbreeding	number	length, Mb	Belgian draft horse	10.1 <sup>1</sup>	34.3 <sup>1</sup>	6.2 <sup>1</sup>	Friesian horse	22.3 <sup>1</sup>	74.3 <sup>1</sup>	6.7 <sup>1</sup>	Gelder horse	5.9 <sup>1</sup>	22.2 <sup>1</sup>	6.0 <sup>1</sup>	Groningen horse	6.2 <sup>1</sup>	25.5 <sup>1</sup>	5.5 <sup>1</sup>	Harness horse	9.7 <sup>1</sup>	28.0 <sup>1</sup>	7.2 <sup>1</sup>	Icelandic horse	4.1 <sup>1</sup>	15.1 <sup>1</sup>	6.1 <sup>1</sup>	KWPN sport horse	5.3 <sup>1</sup>	22.2 <sup>1</sup>	5.4 <sup>1</sup>	Lipizzaner horse	9.0 <sup>1</sup>	31.7 <sup>1</sup>	6.4 <sup>1</sup>	Shetland pony	14.4 <sup>1</sup>	45.3 <sup>1</sup>	7.5 <sup>1</sup>	Mean ROHs	9.7 <sup>1</sup>	33.5 <sup>1</sup>	6.5 <sup>1</sup>
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<b>Materials and methods</b> <ul style="list-style-type: none"> <li>50k genotype data from nine populations with about 20 horses per population (n = 184)</li> <li>Parameters estimated using PLINK software v1.9 (Purcell, 2007)</li> </ul>																																													

## Genomic selection and inbreeding in Dutch-Flemish Holstein Friesian dairy cattle

By Harmen Doekes

The implementation of genomic selection has been accompanied by a strong increase in the rate of inbreeding in Dutch-Flemish Holstein-Friesian dairy cattle. How to manage inbreeding under genomic selection efficiently, is still a matter of debate .

As a second-year PhD-candidate from Wageningen University & Research Animal Breeding and Genomics, I was honoured to present my work at the World Congress on Genetics Applied to Livestock Production (WCGALP 2018). The session in which I presented, "Theory to Application 2", took place in the large theatre room and was well attended (guestimate: 300-400 people). My presentation was well received, with a lively discussion that continued on Twitter .

Since 2009, genomic selection (GS) has been widely applied in Holstein Friesian (HF) breeding programs. We evaluated how the introduction of GS has affected inbreeding trends in the Dutch-Flemish HF population.

\*Corresponding author: [anouk.schurink@wur.nl](mailto:anouk.schurink@wur.nl)  
 1Wageningen University & Research, Animal Breeding and Genomics, the Netherlands  
 2Wageningen University & Research, Centre for Genetic Resources, the Netherlands  
 3Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Sweden  
 4Department of Equine Science, Faculty of Veterinary Medicine, Utrecht University, the Netherlands  
 5Department of Surgery and Anaesthesiology of Domestic Animals, Ghent University, Belgium



Harmen presenting at the WCGALP

Two groups were considered separately: 1) the breeding program, represented by AI-bulls, and 2) the cow population. Both pedigree-based and genomic measures of inbreeding were used. We found that rates of inbreeding increased with the introduction of GS, especially in the breeding program (up to 1.6-2.5% per generation in 2009-2017). We also found specific regions of the genome that displayed higher levels of inbreeding since the implementation of GS. These trends were also present in the cow population, although less pronounced than in AI-bulls.

But how to efficiently manage inbreeding with genomic selection? This question was addressed at the world congress by several speakers, including prof. Theo Meuwissen (NMBU, Norway) and Dr. Mark Henryon (SEGES, Denmark). While both speakers focused on the use of optimal contribution selection (OCS) for maximising genetic gain while restricting the rate of inbreeding, their conclusions were rather contradictory. Prof. Meuwissen underlined that pedigree-based control of inbreeding (POCS) is not suitable with GS, because it allows the true inbreeding rate to keep on increasing over time. Dr. Henryon, in contrast, showed that POCS may result in more genetic gain at a specific true inbreeding rate than genomic control of inbreeding. Clearly, the question on how to best manage inbreeding with GS remains a matter of debate.

In addition to all the interesting presentations, WCGALP 2018 was a great opportunity to expand my professional network. My PhD is part of the consortium Innovative Management of Animal Genetic Resources (IMAGE) and I am very grateful for their contribution to this valuable experience. In addition, I would like to acknowledge my co-authors, the Dutch-Flemish cattle improvement co-operative (CRV) and the LEB-foundation for their contributions.

## A survey of stakeholder attitudes towards bio bank management in Europe

By Michael Klaffenböck

Conservation of animal genetic resources is highly relevant to ensure adaptability of livestock production systems. New technologies create novel opportunities in this field. An online survey with 29 questions was conducted, covering needs, attitudes, and preferences of different stakeholders in animal genetic resources in Europe. Results of this survey were presented at the WCGALP. Stakeholders considered the conservation of animal genetic resources to be very important and were concerned about the loss of genetic resources. Tools/technologies that should be used more frequently are bio banks, genomic selection, and in-situ conservation. Also, bio banks should prioritize endangered breeds over most profitable animals. Regarding access to material, stakeholders leaned towards free access for breed societies and public research institutions, as well as access at a fee for private research organizations and commercial companies. Breeding societies and public

### A survey of stakeholder attitudes towards bio bank management in Europe

M. Klaffenböck<sup>1</sup>, G. Mazzoni<sup>2</sup>, M. Menger<sup>3</sup>, W. Wernemant<sup>4</sup>, A. Dore<sup>5</sup>, J. Solner<sup>6</sup> & M. Wurzenig<sup>1</sup>

<sup>1</sup> University of Natural Resources and Life Sciences, Vienna, Division of Livestock Breeding

<sup>2</sup> ICRP (Research) Department, Institute of Organic Farming and Biotechnology of Paris Lodron, 8021

Thalheim, Karlsruhe 70, Austria

<sup>3</sup> University of Applied Sciences (FH OÖ), Peter Wotter Building, Kapslberg, 3400 Wels, Austria

<sup>4</sup> BOKU (University of Applied Sciences) Graz, Austria

<sup>5</sup> BOKU (University of Applied Sciences) Graz, Austria

<sup>6</sup> BOKU (University of Applied Sciences) Graz, Austria

#### Aim

Identification of needs, attitudes and preferences of different stakeholders regarding animal genetic resources (AnGR) in Europe.

#### Background

- Livestock bio banks are not well-established globally, despite their potential impact on human health and food production systems (Gronewald, 2016) and livestock diversity facilitates the adaptation of production systems (FAO, 2015).
- There is a need to strengthen institutional frameworks for the management of AnGR and the emergence of new technologies.
- EU funded project IMAGE aims to enhance the use of genetic collections, to upgrade bio bank management and to demonstrate its benefits.
- Next to this sociological research, IMAGE organises annual stakeholder meetings and dialogues which facilitate communication and cooperation among a variety of parties.

#### Material and methods

Online survey with N=105 after QC

Main professions of participants:

- Breeders/Breeding organisation
- Science
- Extension service provider

29 questions on the following topics:

- Importance of AnGR management
- Concern about loss
- Attitudes towards new technologies,
- Opinions about bio bank access & funding,
- Bio bank decision making,
- Ownership
- General satisfaction with the status quo

#### Results

- A majority of participants are at least somewhat concerned about loss of rare breeds (85%) and considered the importance of management of animal genetic resources as (very) high (75%). Strongly favoured management strategies were bio banks (52%) and genomic selection (52%).
- Regarding collection strategies, endangered breeds/diverse animals should be prioritised over profitable animals.
- Breed societies and public research institutions should have free access to material, while private entities should pay a nominal fee (>50% agreed).
- Most authority in bio bank decision making should lay with breed societies and public researchers.
- Regarding funding, there was a clear preference for public funding for bio banks.
- The work of bio banks in animal genetic resource management was found to be somewhat, mostly or fully adequate at the moment by 70% of stakeholders in this survey.

#### Conclusions

This study found a generally positive attitude of stakeholders of animal genetic resources in Europe towards an increased use of bio banks to conserve genetic diversity in the livestock sector, funded and controlled by public (research) institutions and breed societies, which hold much trust from stakeholders.



The research leading to these results has been conducted as part of the IMAGE project which received funding from the European Union's Horizon 2020 Research and Innovation Programme under the grant agreement n° 677253



research institutions should have the most authority in decision making, according to stakeholders, also indicating that funding should come from public sources. This was also supported by the higher level of stakeholder trust in public organizations. This study found a generally positive attitude of stakeholders towards an increased use of bio banks to conserve genetic diversity in the livestock sector, funded, and controlled by public institutions and breed societies.

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

By Coralie Danchin

Setting up germplasm collections (frozen reproductive material) is of crucial importance for long term conservation of Animal Genetic Resources as recommended by FAO. Research teams and private laboratories have a wide array of genomic collections which are of great interest to characterize Animal Genetic Resources. The IMAGE project aims to enhance the use of genetic collections and to upgrade animal gene bank management by further developing genomic methodologies, biotechnologies and bioinformatics for a better knowledge and exploitation of animal genetic resources. One of its first goals was to obtain detailed information about the diversity of germplasm and genomic collections across Europe.

### ***“IMAGE obtained detailed information about the diversity of germplasm and genomic collections across Europe”***

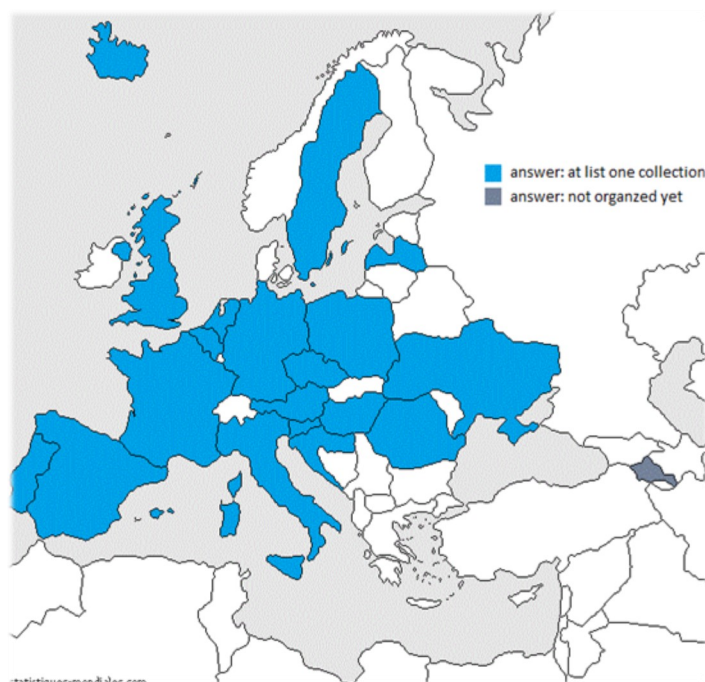
Data were collected through an online survey that was sent to a list of institutions holding or managing a collection of farm animal genetic resources in Europe. For this survey, two types of genetic collections were distinguished: 1) Germplasm collection, which stores biological samples of reproductive material (semen, embryo, etc.) and 2) Genomic collection, which includes other biological material (DNA, blood, tissue etc.).

A total of 61 organizations representing 20 different countries answered the survey (cf. figure 1), of which 51

are holding a germplasm collection, 30 a genomic collection, 20 are managing both. Collections are mostly supervised by a public research institute or a university (61 %). Despite FAO safety recommendations, only 35% of the germplasm collections have backup site.

Key information from this research:

- Many European countries are hosting germplasm and genomic collections preserving farm animal breed diversity, but they differ a lot in organization, rules and development phases.
- The main livestock species are well represented in the collections; there is an extreme wide array of breeds.
- The endangered breeds are the ones with the least amount of material.
- Genetic collections are mostly in the phase of storing unique genetic material whereas use is limited so far.
- 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 such as breed characterization, management of the breeds’ genetic variability.
- No collections could ever be self-sustainable, however economic models need to be set up to insure the future of our genetic collections.



**Map of the countries which filled the IMAGE questionnaire.**

## profiles



### **Dr. Hendrik-Jan Megens , Wageningen University** **WP4 Leader—Innovative genomic characterization for better evaluation of genetic collections**

[hendrik-jan.megens@wur.nl](mailto:hendrik-jan.megens@wur.nl)

Hendrik-Jan Megens is Assistant Professor at Animal Breeding & Genetics, Wageningen University. Hendrik-Jan's primary research interests revolve around understanding how variation in genomes and populations of wild and domesticated animals is shaped by selection and demography. His main areas of expertise are functional genomics, population genomics, and bioinformatics. Over the past 14 years, working first as post-doc and later as staff scientist at ABG, he has been at the forefront of implementing the latest genotyping and sequencing techniques for characterization of variation in animal genomes, from SNP arrays to 2nd and 3rd generation sequencing. Hendrik-Jan strongly believes in application of whole-genome information as 'natural archives' to compare managed and unmanaged populations and to uncover relevant information to aid future management and breeding.



### **Prof. Henner Simianer, University of Goettingen** **WP6 Leader— Sustainable and innovative use of genetic collections**

[hsimian@gwdg.de](mailto:hsimian@gwdg.de)

Henner Simianer is Professor of animal breeding and genetics at the department of animal sciences of the University of Goettingen since 2001. He has a strong background in quantitative and population genetics and his research group has a focus on the integration of genomic methods into livestock breeding programs. Recently, he initiated the formation of the 'Center for integrated plant and animal breeding' and is now the founding director. His research interests comprise a better understanding of the genetic basis of inheritance of quantitative traits, improved prediction of breeding values and phenotypes, and assessment and efficient maintenance of genetic diversity in breeding populations. For this, his group works with large scale genomic data across different livestock and crop species. He was involved in a number of (inter-)national research co-operations and the president of the Genetics Commission of the EAAP from 2010-2015.

## publications

An overview of all IMAGE publications can be found on the website: [www.imageh2020.eu](http://www.imageh2020.eu). The newest publications are listed below:

[C. Bortoluzzi, R.P.M.A. Crooijmans, M. Bosse, S.J. Hiemstra, M.A.M. Groenen, H.-J. Megens. "The effects of recent changes in breeding preferences on maintaining traditional Dutch chicken genomic diversity." \*Heredity\*. 2018.](#)

[M.F.L. Derks, H.-J. Megens, M. Bosse, J. Visscher, K. Peeters, M.C.A.M. Bink, A. Vereijken, C Gross, D. de Ridder, M.J.T. Reinders, and M.A.M. Groenen. "A survey of functional genomic variation in domestic chickens." \*Genet. Sel. Evol.\* 2018.](#)



## videos

IMAGE has its own [YouTube channel](#). Every now and then we will publish a video from a IMAGE partner, explaining the impact of their contributions to the IMAGE project. We use this videos for informing a wide range of individuals — from lay people to animal breeders or gene bank managers.

The IMAGE project coordinator, Michèle Tixier-Boichard was the first to be interviewed. She briefly summarizes the project. Click the picture below to see the video.



Michèle Tixier-Boichard  
IMAGE Coordinator

Waltraud Kugler, SAVE Foundation is the Task Leader of "Dialogue Forum". She is summarizing the importance of IMAGE for the whole society. Click the picture below to see the video.



Waltraud Kugler, SAVE Foundation  
IMAGE "Dialogue Forum" Task Leader



In the next issue, Elisabeth Blesbois, INRA, WP3 Leader will explain why it is important to improve reproductive technologies for gene banking. Moreover, Sipke Joost Hiemstra, CGN, WP2 leader will explain the importance to improve the quality and access transparency of gene banks.

## contact



WP7 Outreach

Prof. Luís Telo Gama

[ltgama@fmv.ulisboa.pt](mailto:ltgama@fmv.ulisboa.pt)



IMAGE Newsletter

Tessa Brinker MSc.

[tessa.brinker@effab.info](mailto:tessa.brinker@effab.info)



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