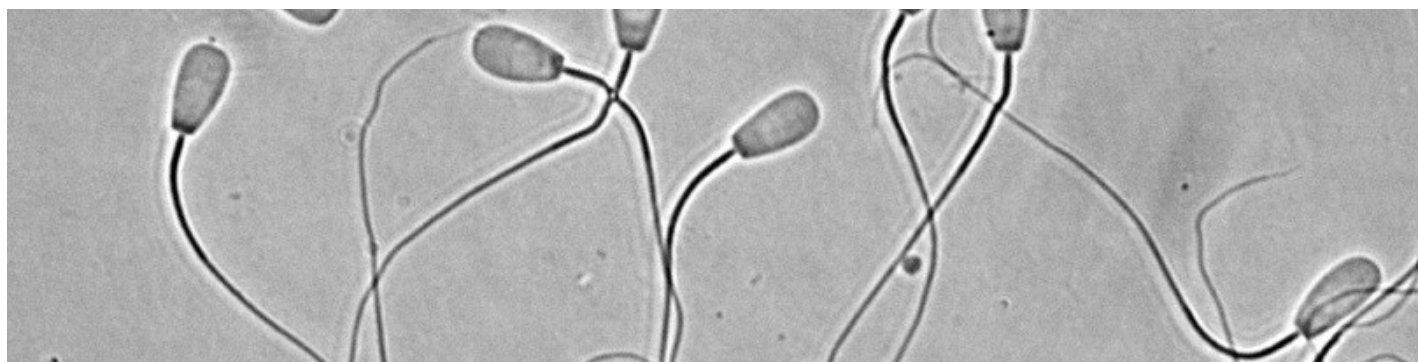


NEWSLETTER

JANUARY 2018—ISSUE 2



editorial

The reporting period 1 of IMAGE ended on August 31, 2017. A whole day presentation was organized in Brussels on November 9th with the project officer, Cristina Soriani, the policy officer, Jean-Charles Cavitte, and two scientific experts, Prof Stephen Hall and Dr Nadiya Kazachkova. The coordinator and the WP leaders presented the objectives, main achievements and next steps for the whole project. This newsletter #2 is providing you with some hot topics emerging from this review.

The coordinator underlined the rich combination of scientific approaches at play within IMAGE:

- Social sciences, interface with legal bodies (WP1)
- Management sciences, economics (WP2)

- Biology of reproduction, cryobiology, cell biology (WP3)
- Genomics, population genetics, biogeography (WP4)
- Informatics, bio-informatics (WP5)
- Mathematical modeling, quantitative and populations genetics (WP6)
- Communication, education (WP7)

The discussion with the experts showed that IMAGE occupies a unique position to make the link between commercial breeds and local breeds for a global approach of animal genetic resources. Its bottom-up approach based upon stakeholders' involvement is to be encouraged and communication towards them will be strengthened. IMAGE has furthermore joined the recent initiative of a Common Dissemination Booster which gathers 4 other EU-funded projects on livestock and is led by the GENTORE project.



news

Second IMAGE Dialogue Forum

The 2nd annual IMAGE Dialogue Forum was held on August 27th 2017 in Tallinn, Estonia. The topic was 'Sanitary regulations - Possibilities and hindrances for the exchange of gene bank material for breeding and science'. The event was designed as a four hour workshop with input presentations, group work and a conclusive discussion.

Waltraud Kugler from SAVE opened the Dialogue Forum. She outlined the legal framework in which exchange of genetic material is currently happening and the potential shortcomings. This included the Animal Health Code of the World Organisation for Animal Health (OIE), the EU Animal Health Law, as well as national regulations.



Group work— 2nd Dialogue Forum

IMAGE project leader Michèle Tixier-Boichard continued with a presentation on the objectives of IMAGE and achievements so far, regulatory issues and approaches for gene banks related to animal health, which pose fundamental challenges in collecting samples of local breeds under highly demanding regulations designed for international commercial exchange.

National gene bank manager and ERF national coordinator for Austria, Beate Berger addressed results of the IMAGE gene bank survey, the regulations in place, and presented two case studies. In conclusion, the current sanitary/veterinary regulations are not tailored for gene banking and breed conservation and action is needed to achieve derogations on a national level. She also argued that sanitary/veterinary regulations should make use of modern diagnosis methods, which would enable the inclusion of older samples.

In the second part of the Dialogue Forum, participants were split into groups according to their affiliation to 'Science', 'NGO' or 'Government' and given three topics to discuss: 1) opportunities for exchanging germinal products, 2) challenges which are present in the exchange of gene bank material, and 3) obstacles gene banks face in exchanging material. At the end of the group work, all groups suggested specific action points:

- Regarding the application of the EU Animal Health Law, identify and list exceptions of national derogations that would benefit gene bank management
- Ask for an EU implementation act specifically considering the needs of gene banks
- Start using PCR tests to guarantee safety (freedom from specific zoonosis)
- Undertake efforts to adopt clearer animal health rules and regulations as they apply to gene banks
- Promote the European gene bank network (EUGENA)
- Collect and publish success stories (e.g. countries with national derogations)
- Raise awareness for the issues of gene bank management in the European Commission, responsible national ministries, stakeholders and general public

Group work was followed by a general discussion aiming to find consensus on how to tackle sanitary regulations in favour of conservation of animal genetic resources. The two favoured actions were: 1) IMAGE should have a direct discussion with the European Commission regarding management of animal genetic resources in its sanitary regulations, and 2) IMAGE should support the respective persons responsible in European countries to push for national derogations regarding sanitary regulations which are particularly challenging for gene banks.

"IMAGE should have a direct discussion with the European Commission regarding management of animal genetic resources and its regulations"

The last part was a social event where participants could continue discussing these issues over drinks and Estonian culinary specialties. The organisers look back on a successful discussion event with a clear outcome and are looking forward to the next Dialogue Forum, which will be held in August 2018 in Dubrovnik, Croatia.

Primordial germ cells in chicken: what can we do with them?

Primordial germ cells (PGCs) are the reproductive diploid 'stem' cells in the embryo that will make sperm or eggs in the adult animal. They can be transplanted between embryos such that the resulting adult host animal will produce offspring with the genotype of the transplanted cells. Because it is actually impossible to store bird embryos (due to the telolecithal egg), PGC cryopreservation, followed by their reintroduction in host birds, is an alternative solution to semen preservation for genetic diversity conservation programs.

“IMAGE has successfully cryopreserved multiple genotypes from two traditional Hungarian breeds and the French ‘Noire de Berry’ breed”

PGCs are also key cells for transgenic studies in research labs. There are very few primordial germ cells in the bird embryo so it is technically difficult to biobank these cells. We have learned to culture primordial germ cells *in vitro*, and starting with ten primordial germ cells we are able to grow up to 100,000 cells within one month. These

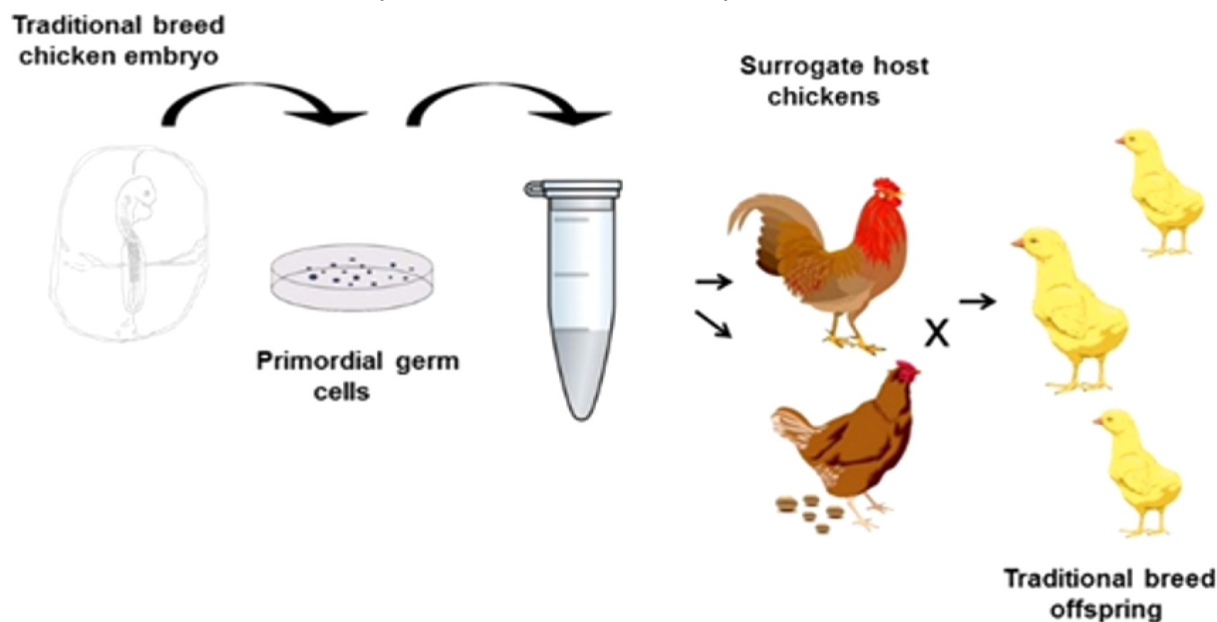


A male (left) and a female (right)

cells can then be safely cryopreserved in multiple independent cryovials, increasing greatly their capacities for use in genetic reintroduction programs.

In the IMAGE H2020 program, we have already successfully cryopreserved multiple genotypes from two traditional Hungarian breeds and the French 'Noire de Berry' breed. We have identified a commercially available cell freezing mix that is animal product free which will help our efforts to provide a sanitary biobanking procedure for primordial germ cells. In the next part of our program we will demonstrate how we can regenerate a pure breed of chicken from these frozen cells.

PGCs treatment for reintroduction of donor genetic material



The PGCs of a donor embryo are cultured *in vitro* and then frozen. They can later be thawed and reintroduced in host eggs for further transmission of the donor genome in the host animal and transmission to the progeny.

When less can be more: optimizing the cost of *ex situ* genetic collections

Global challenges and threatening factors for *in situ* conservation of animal genetic resources are well-documented. While *ex situ* collections may have some limitations they nevertheless offer the potential to reduce risk of extinction, affording so-called option value to society in terms of maintaining future breeding opportunities that might otherwise be foreclosed. But how much should we be seeking to collect and conserve *ex situ* collections and where? A basic aim might be to harmonize collections to avoid costly overlaps in material. In other words, assuming an overall societal perspective, what is the most diverse collection that can be planned at a reasonable cost?

“We developed a mathematical model to find the best way to select breeds, gene banks, and collection strategies”

Ex situ collections are still potentially expensive and, as resources are often limited, candidate breeds have to be selected to maximize a variety of possible future eventualities. The scale of this managerial challenge involves choosing among nearly 2000 candidate breeds from various species and locations across Europe, while facing various budgetary constraints and limitations such as storage capacity, capital and specialized labor availability. Therefore, the use of optimization techniques to address these challenges is justified.

To address this problem in the IMAGE project, we developed a mathematical model to find the best way to select breeds, gene banks and collection strategies. The model maximizes breed diversity, measured as the number of preserved breeds, subject to a series of constraints. The model allowed us to construct ‘efficiency curves’ showing the supply of breed diversity potentially available for a given budget. This model will enable policy makers to perform efficient decisions regarding the selection of strategies for *ex situ* conservation. We also hope it will help animal scientists to define conservation objectives to manage genetic collections according to specific conservation objectives and to guide genetic and reproductive material collections.

Characterization of animal genetic resources – mining vital information from DNA sequence data

Much has been done in the past decades to enhance awareness for maintaining genetic diversity in domestic animal species. The continued consolidation of commercial breeding companies is potentially leading to an ever narrower genetic basis for future breeding and food security. There is continued interest in preserving or restoring local breeds, and to preserve at least part of the commercial diversity that is being lost. Preserving diversity is in part done by maintaining local breeds *in situ* – often by enthusiasts that have no direct commercial interest. And, in part, preservation of genetic diversity is done by Genebanks that keep genetic-collections *ex situ*, usually as frozen semen.

Invariably, what is preserved by keeping *in situ* or *ex situ* collections is poorly understood. Even pedigree data is often lacking, and phenotype data is almost always scarce or absent. For *in situ* collections in particular, absence of information on the demographic background of founding populations can be problematic, further exacerbated by the lack of pedigree-informed breeding. Without information on relatedness, avoiding inbreeding is hard, especially in breeds that are kept in low numbers.

For Genebanks, the absence of information on animals to sample for their collections is equally problematic. Which of the available animals would be good to preserve if resources do not allow to sample them all? Once stored in the gene bank, the question regarding the value of the collected material arises. Does it have unique characteristics, e.g. a desirable phenotype, that was not recorded? Or, equally relevant, did the collected material contain variation that could lead to genetic defects.

“DNA as a ‘universal archive’ for demographic and functional information has many applications throughout the IMAGE project”

Many questions regarding the origin of collections, the genetic diversity and kinship, and even phenotypic

traits, could be mined from the DNA. DNA data contains signatures of demography, such as effective population size, or geographic origin, that could be valuable to know for conservation of genetic diversity. It also can be used to estimate genetic relatedness between animals, and therefore can be used to guide breeding, e.g. to control inbreeding rates. Moreover, whole-genome DNA sequence information in particular should contain the genetic blueprint for what makes an animal different from others of the same species. Although predicting the animals phenotype directly from sequence data is still far into the future, there are some things that we currently can start to predict.

DNA data can be derived from any tissue or semen collection as long as the quality of the DNA is still sufficient. In addition, DNA sequence data is the same in nature for any cellular organism and therefore is a 'natural' information source that can be readily databased, and, increasingly, interpreted. The IMAGE project is also aiming to generate new data from a number of collections, to demonstrate the use of enhanced 'interpretation' methods. For instance, methods for inferring demographic parameters and signatures of artificial ('breeding') selection are being applied to genetic collections to establish their origin. This allows researchers and gene bank managers to quantify the contributions of collections to local and global biodiversity. Other activities are aiming to infer the existence of genetic defects in genetic collections – for instance in in-situ collections for which little other sources of information are present. This information can then be used to guide breeding programs to avoid inbreeding depression.

Activities in the past 18 months have focused primarily on aggregating existing data sources. Currently, new data sources for chicken, cattle, sheep, and pigs are being completed and in-depth analyses on these genetic resources have started.

DNA as a 'universal archive' for demographic and functional information has many applications throughout the IMAGE project. Interestingly, as new data is becoming available, it is also becoming apparent that DNA data can be the basis for stakeholder involvement. Providing answers to such previously unknowns such as 'what is the origin of my breed', or 'how related are my animals' is recognized by many breeders as a leap forward.

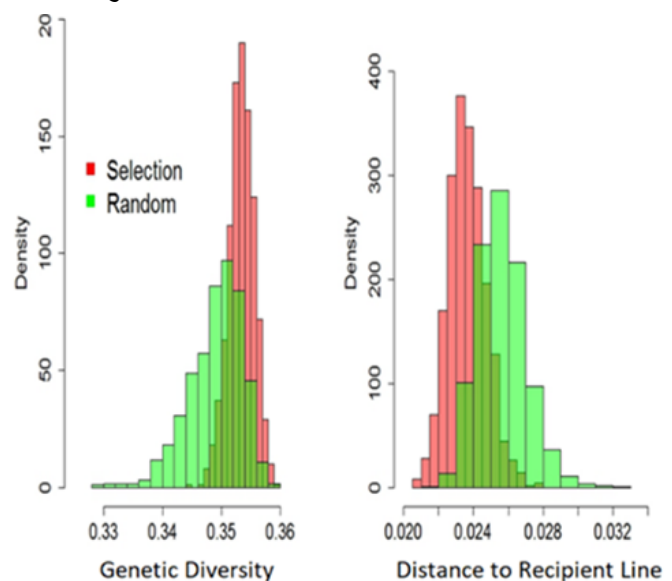
WP4 is all about 'Characterization of genetic resources by means of DNA sequence data'. We are entering the second phase of that characterization step –

interpreting what it all means. Stay tuned for some really cool stories on some of the case studies in the next newsletters!

A new flexible and powerful software for the optimization of breeding and conservation schemes

A first version of an R-package "RekomBre" has been developed, a stochastic simulation program for the optimization of complex breeding and conservation schemes. At the current stage, the software can simulate up to millions of markers across the whole genome for many generations in a flexible and realistic way. It is able to incorporate real genetic information, such as genotype data of the starting population, mutation rates and separate male and female recombination maps, with options for selfing, cloning and gene editing while allowing for the simulation of different genetic models of phenotypic traits. A broad range of approaches for breeding value estimation is available, e.g. conventional BLUP, Genomic BLUP and Bayesian methods.

Comparing different selection strategies to select the best F1 animals



Using the R-package "RekomBre", we simulated the whole introgression scheme (Task 6.3, WP6) using different selection strategies (1,000 repetitions). The histograms show the outcome of the 1,000 simulations, i.e. the genetic diversity (left panel) and distance to the recipient line (right panel) for two different strategies in the final IC population.

The R-package has already been applied to several simulation studies, including the optimization of the first step of introgression scheme of the WP6 case study “from gene banks to breeding lines”. Using this new software, several selection strategies were compared to select the best F1 animals ensuring the highest genetic diversity and the best preservation of the genetic make-up of the recipient line.

Nevertheless, the software is under continuous optimization and refinement for a computationally

efficient simulation and a widespread application. Among others, a visual program interface is under development, which should enable also non-programming specialists to perform simulations for their own customized breeding schemes. After all the developments, RekomBre will be made publicly available.

profiles



Sipke Joost Hiemstra (MSc), CGN

WP2 Leader—Enhancing gene bank functioning to improve quality and access transparency

sipkejoost.hiemstra@wur.nl

Sipke Joost Hiemstra is the director of the Centre of Genetic Resources, the Netherlands (CGN) at Wageningen University and Research. He is also the head of the Animal Genetic Resources Group. Sipke Joost worked at the interface between science, policies and practice during the past 20 years, in particular in the area of conservation and use of genetic resources, animal breeding, sustainable livestock sector development and agrobiodiversity. As the National Coordinator of Animal Genetic Resources, he is strongly involved in the development and implementation of the FAO Global Plan of Action for Animal Genetic Resources at national and international level. For the European region he is currently chair of the Steering Committee of the European Regional Focal Point for Animal Genetic Resources (ERFP) and he initiated the development of the European Gene Bank Network for Animal Genetic Resources (EUGENA) within the ERFP framework.



Dr. Elisabeth Blesbois, INRA

WP3 Leader—Improving reproductive technologies for gene banking

elisabeth.blesbois@inra.fr

Elisabeth Blesbois is the head of the department “Gonad and Fertility” at the department of Animal Breeding, UMR Physiology of Reproduction and Behaviours at the French National Institute of Agronomic Research (INRA). Elisabeth has been working at INRA for 30 years. Recruited in the Poultry Research Unit of INRA, she joined the Reproductive Physiology and Behaviour Research Unit in 2007. As a scientist working in the field of reproductive biology and then as the head of different groups involved in Gonadic Development and Gamete Quality, she initially worked on bird semen biology. She thereafter focused her activity on the biological activity of gametes and on sperm ability to *in vivo* and *in vitro* storage. Since 2000, she enlarged her field to the cryobanking and initiated the French Avian National Cryobank Program. She coordinates a number of national and international programs involved in the development of reproductive biotechnologies to maintain and protect genetic diversity and is member of the High French Council of Biotechnologies.

publications

An overview of all IMAGE publications can be found on the website: www.imageh2020.eu



contact



WP7 Outreach

Prof. Luís Telo Gama

ltgama@fmv.ulisboa.pt



IMAGE Newsletter

Dr. Çağla Yüksel Kaya Kuyululu

cagla.kaya@effab.info



@imageh2020

@imageh2020



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