

L.S.

Dear Colleague, Dear Gene bank manager,

As you may remember, The IMAGE project is funded by EU H2020 to support innovative management of animal gene banks. Some time ago, you replied to the Europe wide IMAGE Genetic Collections survey, and you received the survey report. We are contacting you now for a different IMAGE activity. Your name was indicated as contact person for your germplasm or genomic collection.

In the final phase of the IMAGE project, we are developing a multi-species SNP array that can be used for genomic characterization of gene bank collections, globally. The array represent 6 species and contains per species 10K SNP markers. For detailed information on the choice of markers you can contact Richard Crooijmans (richard.crooijmans@wur.nl). This multi-species SNP array will be tested and validated in the last year of the IMAGE project, and will become publicly available for further use after the IMAGE project has ended.

In the validation and testing phase we will be able to genotype in total 1920 samples, funded by the IMAGE project, representing 6 species (approx. 320 samples per species) representing a variety of breeds and gene banks. Our offer and request to you is to indicate which samples (species and breeds) from your gene bank or genetic collection could be made available for this purpose.

Costs for genotyping in this validation and testing phase will be fully covered by the IMAGE project (WP4, partner Wageningen University). You will directly receive the data generated from your samples, and the data will be used by Wageningen University for validation of the multi-species SNP chip. As EU will fund the genotyping, the genotyping data will also be made publicly available through the EBI Biosamples database and in the EBI hosted European Nucleotide/Variation Archive (<https://www.ebi.ac.uk/ena>) following the analysis. If requested, an embargo period of half a year can be agreed upon, before making the data publicly available.

Your samples (isolated DNA with a total amount of at least 1 µg, with a concentration of 50 ng/µl and quality level OD260/OD280>1.8) will have to be sent to Wageningen University (att. Richard Crooijmans) before 1st of September. Wageningen University will send the DNA samples to a commercial genotyping service provider. Please note that we expect to receive good quality isolated DNA samples. Any commercial DNA isolation kit can be used for DNA extraction, but in case of sperm we recommend to use the EchoLUTION Semen DNA Kit (BioEcho). Please let us know in case you or your institute will not be able to do the DNA isolation.

Animal Sciences
Group

Animal Breeding and
Genomics

DATE
May 10, 2019

SUBJECT
Genotype samples request

OUR REFERENCE
19-028/RC/lb

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We will work in two steps. The first step as indicated in the commitment page below (next page), please indicate in the table how many and what type of samples per breed and per species you will be able to make available for this purpose. You can indicate a priority order as you wish. Then, please sign this page, and return by email to richard.crooijmans@wur.nl, before June 15, 2019.

In the second step, Wageningen University will make a selection of 1920 samples, representing a large variety of breeds, from the available samples as indicated in step one. We will contact you as soon as possible, before July 1, 2019, confirming the number of your samples, per breed/species, that can be genotyped and funded by the IMAGE project. Shipment details will be send to the providers of the DNA samples after selection. In case you need more information, please contact richard.crooijmans@wur.nl.

With kind regards,
On behalf of the IMAGE Consortium



Richard Crooijmans (Wageningen University, IMAGE WP4)
Michele Tixier-Boichard (IMAGE coordinator, INRA)
Sipke Joost Hiemstra (Centre for Genetic Resources, The Netherlands (CGN), IMAGE WP2)

Commitment page

I will be able to make available the following DNA samples for the purpose of testing and validation of the IMAGE multi-species SNP Array: IMAGE01A. Per species this array contains 10K SNPs (8K SNPs of existing arrays, 1K SNPs related to traits, mtDNA, X/Y or Z/W markers and 1 K SNPs ancestral markers.

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| Species | Breed | Number of DNA samples available for genotyping | Comments (motivation, priority) |
|---------|-------|--|---------------------------------|
| Cattle | A | | |
| | B | | |
| | C | | |
| Pig | | | |
| | | | |
| | | | |
| Chicken | | | |
| | | | |
| | | | |
| Goat | | | |
| | | | |
| | | | |
| Sheep | | | |
| | | | |
| | | | |
| Horse | | | |
| | | | |
| | | | |

I agree that the data generated with the multi-species SNP array will be made publicly available by Wageningen University after analysis and validation.

Wageningen University *will / will not* * respect an embargo period of half a year after receiving the genotypes, before making the data publicly available.

* Please indicate the preferred option

Provider signature:

Name:

Organisation:

Email contact person:

Date:

Signature: