

## **The use of genomic variation in European livestock genebank collections**

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The majority of the SNP arrays developed so far from whole genome sequencing data are biased towards genomic variation found in a few commercial populations. Moreover, the set of markers contained in the SNP arrays is changing often in time and overlap between the different versions and platforms is not always guaranteed. Furthermore, in several cases arrays are not freely available without permission of the consortia involved in their development. In the framework of the Horizon2020 IMAGE project, we have identified a large pool of SNP variants by whole genome sequencing of over 500 individuals from a large variety of local breeds and species and combined this with publicly available SNPs to develop panels to be used for different applications and analyses. One of these applications is the development of a multi- species SNP array (that might include cattle, sheep, goat, pig chicken, turkey, buffalo, horse, duck, rabbit, camel, camelids, honey bee) containing 10k SNPs per species selected from the total SNP pool. This low cost SNP array will make it possible to genotype a large number of samples of the different species collected in gene banks worldwide. Opening the molecular reservoir of variation in these gene bank collections will add value to the material stored, detect the uniqueness of the collections and monitor variation changes over time. The generated whole genome sequences will also be used in genome wide association studies (GWAS) for specific traits present in traditional breeds, like e.g. ptilopody and bantam traits in chicken. The variants related to these and other traits of interest, detected in the course of IMAGE project, or variants presented in literature for specific traits, will also be selected and added on the multi-species SNP array.

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