

Rationalization and characterization of gene bank collections: a case study

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The French national cryobank is holding cryoconserved semen from six rare goat breeds. Most males were sampled when the breeds' conservation programs started and very limited information was available at the time. Pedigree data were scarce or even unknown, and bucks were often chosen from information based on their phenotypes and region of origins. The IMAGE project presented an opportunity to better characterize these animals thanks to genotype analysis. DNA was extracted from the frozen semen of the oldest bucks and genotyped with a 54k SNP chip. Their data were compared with animals from the live populations. An analysis was performed by using the PLINK, Admixture and TreeMix software. Our study revealed what was the real kinship between animals, including the ones without pedigrees, pinpointed the animals that were crossbred, and helped us target the strains present in the live population without representatives in the French cryobank. On a different perspective, since some of the goat breeds were genotyped for the first time with SNP data, it allowed us to have more insights on how the French goat breeds were related between each other. Finally, our study showed that the various diversity indicators calculated, based on SNP data, still need a better consensus from the research community. Indeed, most indicators and parameters were defined with population genetics hypothesis fit for Human and/or wild species and do not correspond well to rare livestock breeds. The small number of animals, recent bottlenecks and short generation intervals do not comply with some of the hypothesis used in various SNP analysis programs. Depending on the parameters used, results could vary in a quite wide range, which could lead to erroneous answers. Some tips learnt from our experience are described during the process analysis but further researches are still needed in this area.