Introducing genetic diversity in animal populations from germplasm collections

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Genetic diversity is essential for the conservation and adaptation of animal populations. However, in a closed population, genetic variability inevitably decreases under the effect of genetic drift, inbreeding or selection. This is the case for domestic animals, where strong selection takes place in a few breeds, drastically reducing their effective population size whereas other breeds become endangered. *Ex situ* genetic resources, particularly cryopreserved ones such as semen or embryos, offer a unique opportunity to reintroduce or manage genetic diversity in domestic animal *in situ* populations. However, these resources are rarely used for this purpose. Indeed, there are no recommendations to help population managers use them in a way that addresses their objectives (e.g. conservation, selection...) and to the species involved. In fact, reintroducing diversity from "old" material might increase inbreeding and decrease performances if not carefully planned.

By combining the analysis of real data with simulations, this thesis aims at i) proposing a framework for evaluating *ex situ* genetic resources in the perspective of using them to manage the diversity of *in situ* populations, ii) understanding the determinants of their effective use and iii) proposing general recommendations for their future use and the setting of new collections.

Analysis of data from the French National Cryobank has enabled us to propose several standardized indices for measuring the diversity present in collections at different scales, from the breed to the individual. It has also been shown that the collection effort depends heavily on the species in question, as well as on whether it is accustomed to using artificial insemination. Analysis of a specific case in the Abondance breed, where semen from a bull born in 1977 was re-used between 2004 and 2009, demonstrated the positive impact of using cryopreserved resources on the genetic diversity of *in situ* populations, even when under selection (Jacques et al., 2023). This made it possible to reintroduce genetic variability, as well as to improve certain traits that had deteriorated over time, while limiting the negative impact on production performance, for which a certain lag was expected. This potential of "old" *ex situ* genetic resources has been confirmed in other contexts, by simulating various selection schemes ranging from conservation to selection with changing or unchanging objectives. Whatever the situation, few individuals were used, but this was enough to significantly reintroduce genetic diversity while maintaining the objectives set in each situation. Prolificity, on the other hand, seemed to have little effect on results. Finally, still using simulations, recommendations were made for building up a collection to optimize its use in managing the diversity of *in situ* populations. This was done with a gene bank collection of fixed size to mimic the financial and human limitations inherent in such programs.

This work has therefore provided validation of the long-term usefulness of *ex situ* collections for managing the genetic diversity of *in situ* populations, while also providing recommendations for end-users and managers. These results could be transposed to wild populations in zoos or parks.

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