Removing Undesired Introgression Using Markers

C. Amador[*], M.A. Toro[†], J. Fernández[*]

Introduction

Loss of genetic diversity reduces species ability to adapt to new environments and causes decreases in fitness. The benefits of the interchange of genetic resources are known and widely used among livestock. Nevertheless, sometimes a new input of genetic material could be considered undesired when the species or breed we are working with has to be kept pure.

Maintaining the original genetic background could be required because of an economical interest due to several reasons, like quality products provided by the specific breed (Tajima or Kobe ox in Japan, Iberian pigs), association with particular activities (Spanish pure breed horses, bullfight cattle), aesthetics (dog breeds), or just for conservational purposes. In the last case, foreign species and breeds can become extinct by introgresed individuals removing their native equivalent (see examples of this phenomenon in Rhymer and Simberloff 1996; Allendorf *et al*. 2001).

Cryopreservation of livestock breed biodiversity is also an interesting and cheap option which is usually accomplished by keeping only male information. Recovering a population exclusively from a semen bank would involve females from another population whose background should be eliminated to succeed (Hall and Bradley 1995).

Results from a previous study about removing undesired introgression using the genealogical information (unpublished data) showed that the most powerful method to maintain the original information when genealogy is available was to minimize the coancestry of the population with the foreign founders. Despite the efficiency of the strategy in cases with low percentage of introgression and a few generations of admixture, it became difficult to recover the original information when the introgression was high. Moreover, for using this method the whole genealogy had to be recorded, which is not the most usual situation.

In this study, we used the information of a varying number of biallelic markers as a tool to identify and remove the exogenous pieces of genome. The alleles for all markers were unique for each population and they were always correctly identified (*i.e.* no genotyping errors assumed). The objective was mantaining the population as pure as possible removing the exogenous information from it.

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[*] INIA, Ctra. Coruña Km. 7.5, 28040 Madrid, Spain

[†] ETSIA, UPM, Ciudad Universitaria, 28040 Madrid, Spain

Methods

Simulation of the population: We simulated a population of 10 individuals with constant census size over discrete generations. Their genome was 20 cM in length, with a total of 2000 multiallelic loci and different number of biallelic markers. In the base population, all individuals carried two different alleles for all multiallelic loci. All markers were defined as private of the native or the introgressed individuals (*i.e.* two different alleles for every marker, each fixed for foreigners or natives).

Simulation of the introgression: Different scenarios were simulated by varying the following factors:

- Number of exogenous individuals: 1 to 5 exogenous individuals (10 to 50% of introgression), sex randomly set, were included as part of the base population.
- Number of generations without management**:** The population started running for 1 to 5 unmanaged generations to carry out the admixture of the foreign information and get some relatedness among individuals.
- Number of markers**:** 1 to 20 biallelic codominant markers were set. They were always evenly spaced along the chromosome.

Desintrogression: Contributions to next generation were decided based on the information the markers provided. Those individuals with less exogenous alleles were chosen to be parents of the next generation. The management method was applied during ten generations. Solutions with more individuals effectively contributing offspring were chosen among those achieving the same desintrogression level, in order to increase the effective population size.

Parameters: To evaluate the efficiency of the strategies, we calculated the Native-founder Genomic Representation (NGR) that is the percentage of population information (calculated from the multiallelic loci in the genome) coming from non-exogenous founders, and the inbreeding coefficient (F) on every generation for each simulated scenario.

Results and Discussion

Elimination of the undesired information.

Results of the simulations for NGR are shown in Figure 1. Different lines represent simulations with different number of markers and results obtained in the previous work, where desintrogression was driven by pedigree information (solid line), are also included. As expected, the larger the number of markers used for purifying purposes, the better the results. Benefits of the strategy based on markers became larger when the level of introgression was high (*i.e.* in cases with a large number of exogenous individuals, or when the time of admixture was long). The use of markers is better justified in these cases. It has to be taken into account that we are using exclusive markers, which could be difficult to find between not too distant populations, so the ideal 20 markers simulation could be a little unreal in most cases.

Contrarily to what happened when using the pedigree, where all the elimination of undesired information took place in the first generation of management, in some cases (many individuals, great admixture) the markers allowed to eliminate information for a couple of generations more, although most of the recovery still took place in the first generation of management.

Evolution of inbreeding.

The inbreeding coefficient is considered an interesting parameter because it is connected to inbreeding depression and, with random mating, also reflects the level of diversity, which is especially important for conservational purposes. Inbreeding values obtained after the tenth generation of management are showed in Figure 2. As in the previous graphic, lines represent simulations with different number of markers and F reached in the pedigree simulations is included (solid line).

The increase of F during the management was very high, with values ranging from 30 to 80% in generation 10. These high values were reached because, as stated previously, desintrogression took place in the first two or three generations. During the rest of the simulation no changes in the level of foreign information are attained but inbreeding is not controlled at all. Consequently, the recommendation could be to implement an strategy of optimization of contributions (via the minimization of coancestry, Caballero and Toro 2000) after these initial generations.

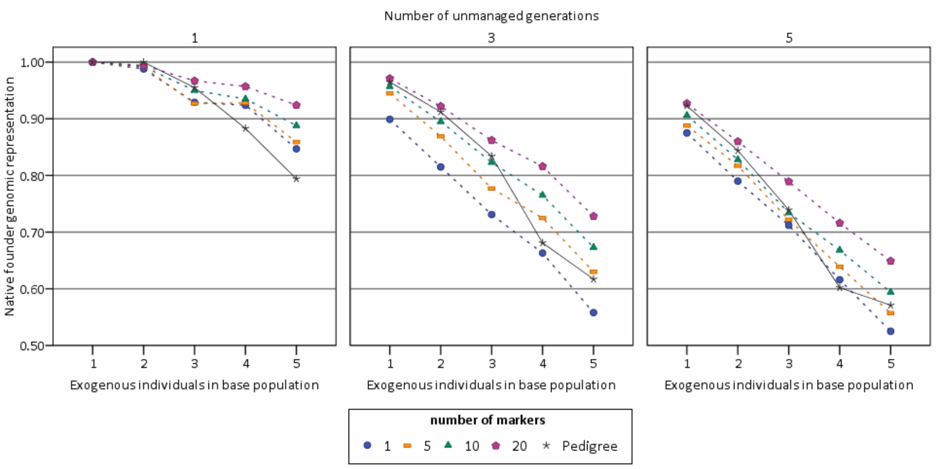

Figure 1: Genomic representation of the non-exogenous founders in the 10th generation of management of the simulations over the number of exogenous individuals, for 1, 3 or 5 previous generations without management.

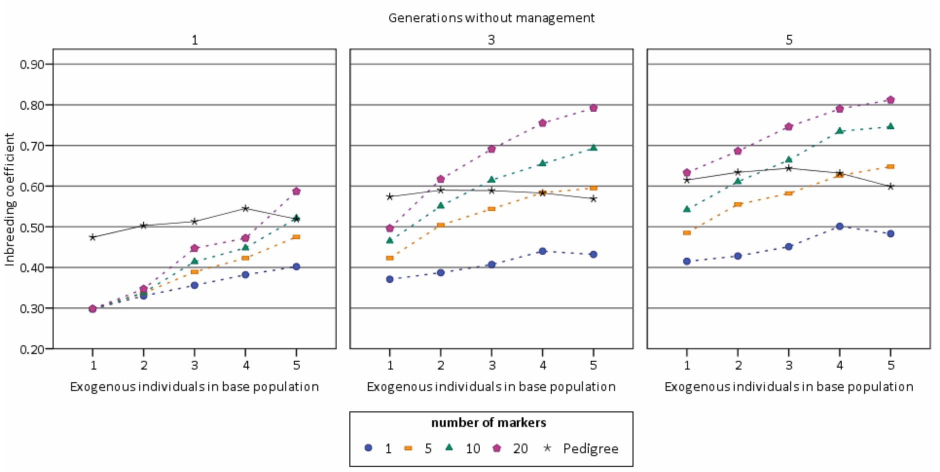

Figure 2: Inbreeding coefficient in the 10th generation of management of the simulations over the number of exogenous individuals, for 1, 3 or 5 previous generations without management.

Conclusion

The results showed that is possible to get a substantial improvement in the recovery of a genetic background contaminated by another a few generations earlier using private biallelic markers. Although the potential is limited (a big introgression is very difficult to be completely eliminated) the information given by the markers helps to reach a great level of depuration, which is larger the sooner we act and the more information we can use. The big increase of the inbreeding coefficient request to employ the method the fewest possible generations and keep on managing by controlling the relationship between individuals.

References

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