

The value of conserved samples in gene banks for animal breeding in the MRIJ cattle breed

S.E. Eynard^{1,3}, M.P.L. Calus¹, B. Hulsege^{1,2}, S.J. Hiemstra² & J.J. Windig^{1,2}

¹Wageningen University & Research, Animal Breeding and Genomics, P.O. Box 338, 6700 AH Wageningen, The Netherlands

Jack.windig@wur.nl (Corresponding Author)

²Wageningen University & Research, Centre for Genetic Resources the Netherlands, P.O. Box 338, 6700 AH Wageningen, The Netherlands

³GABI, INRA, AgroParisTech, Université Paris-Saclay, 78350 Jouy en Josas, France

Summary

Population size of the Meuse-Rhine-Yssel cattle breed has decreased considerably between 1992 and 2014, while total genetic merit increased as a result of an effective breeding program. Genetic diversity decreased at the same time and inbreeding rate was 1.24% per generation. In addition to the genetic diversity in the live population, semen samples have been conserved in gene bank collections. We characterized genetic diversity in conserved samples and the current bull population by typing DNA with the 50K SNP chip, and investigated whether using conserved samples may help to restore genetic diversity in the breeding program, as measured by expected heterozygosity (H_{exp}), and what the effect is on total genetic merit. H_{exp} is 0.334 in the conserved bulls and 0.324 in the current breeding bulls. H_{exp} in the next generation can be maximised to 0.333 when using only current bulls, but to 0.344 when including conserved bulls. When the H_{exp} is constrained to 0.322 genetic merit can be maximised to 101 using current bulls only and to 105 when including conserved bulls. Under a more strict constraint of 0.331 genetic merit can increase to 56 for current and to 72 including conserved bulls. Conserved samples from gene bank collections may thus help to restore genetic diversity and even increase genetic merit when loss of diversity is constrained.

Keywords: genetic resources, conservation, animal breeding, cattle

Introduction

Livestock production is dominated by a few high producing international transboundary breeds while a large number of local breeds is “at risk”. Within breeds, both selection and genetic drift diminish genetic diversity. One way to prevent further loss of diversity is to store germplasm samples in gene banks. These samples may be later used to restore genetic diversity, or even to revive a breed after extinction.

The Maas-Rijn-IJssel cattle breed (MRIJ, or Meuse-Rhine-Yssel) is a local cattle breed in the Netherlands. Numbers have declined because farmers increasingly switch to the Holstein breed. However, an active breeding program is still in operation, and average genetic merit still increases. Semen samples have been stored in the national gene bank of the Centre for Genetic Resources, the Netherlands (CGN) and by breeding companies, for over 40 years. Apart from a backup in case of extinction stored samples may also serve as a pool to support breeding in the live population. Here we investigate what the effect is of using conserved

semen samples for breeding in the MRIJ cattle breed on genetic diversity and genetic merit.

Material and methods

Breed data and samples

The MRIJ breeding programme is managed by the breeding organisation CRV and supported by two regional breeders associations to maintain the breed that combines a good milk production with good health, fertility and meat value (The cattle site, 2017). Data, including year of birth and ancestry of all registered animals were extracted from the herd book. Average breeding values for total genetic merit of all cows per year of birth were extracted from yearly statistics published by the herd book (CRV, 2017). Semen samples of about 300 bulls have been stored in the national gene bank since the 1970s. 192 of these samples were available for genotyping. These samples were supplemented by 221 samples provided by CRV, which include all bulls currently used in the breeding program and bulls used in the past. The samples were split in two groups. Samples of 294 bulls born before 2000 were used to historic conserved population, which is still available for breeding, samples of 119 bulls born in or after 2000 were considered as the current population, as these contain the current cow ancestry.

DNA typing

Samples were typed with the BovineSNP50 BeadChip (Illumina Inc., San Diego, CA, USA), resulting in set of 49438 markers present in all the different genotyping batches. Data editing comprised i) individual call rate > 85% ii) marker call rate > 95%, iii) minor allele frequency > 0.0036 iv) at least one homozygous and one heterozygous genotype should be present, v) Mendelian inconsistencies < 5% per marker. After edits 39793 markers remained. Missing genotypes on the remaining markers were imputed using Fimpute (Sargolzaei et al. 2014).

Characterization of genetic merit and genetic diversity

Genetic merit was analysed using individual breeding values for the NVI, the Dutch Flemish total merit index combining production, health, fertility and conformation (GES 2016). Genetic diversity was analysed by calculating the inbreeding of animals using the available pedigree, and by the observed heterozygosity of the DNA markers.

To estimate the effect of using samples of the conserved population for current breeding one generation of breeding using genetic contributions was simulated. With this method contributions of animals to the next generation are based on their relatedness and on constraints set by the user (Meuwissen 1997). We compared three scenarios. In the first scenario genetic diversity was maximised (conservation scenario). In the second scenario breeding values were maximised given a restriction on the inbreeding to a level of 1% above the current bulls, while in the third scenario the restriction was to 1% above all bulls. Comparisons were made for when using only current animals to using both all animals.

Results

Number of calves born in the early 1980s was around 160 000 per year. Since then numbers dropped sharply (Figure 1). Since 2005 less than 4000 purebred calves are born per year. The breed is nowadays more frequently used in cross breeding and in 2014 more than 20000 calves were born with at least 25% MRIJ ancestry. In 2014, 3452 purebred calves (>87%

MRIJ ancestry) were born.

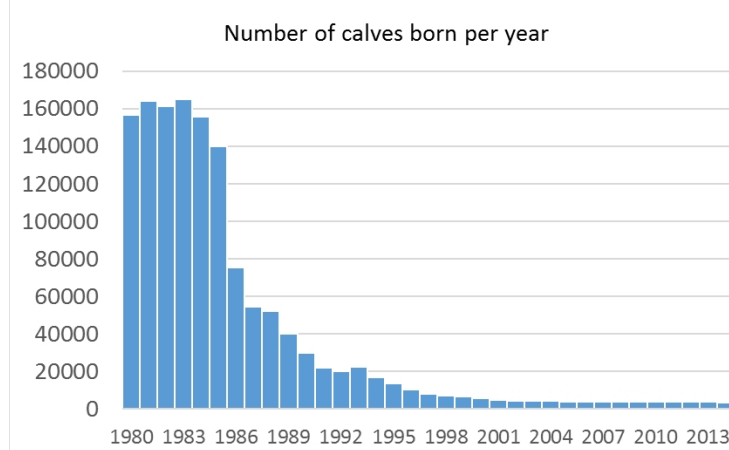


Figure 1. Population size of the MRIJ breed.

Evolution of genetic merit and diversity over time

Average genetic merit of the total cow population increased from around -250 for animals born in 1980 to +5 for animals born in 2014 (figure 2). The genetic merit of bulls followed the same pattern, but preceded the cow population by about 5 to 10 years, roughly the generation interval. The average genetic merit of bulls born in 2014 was +65. The average of the conserved bull population, animals born before 2000, was -183, while the average of the current population was +5. The yearly increase in genetic merit since 1990 was about 7.5 points per year.

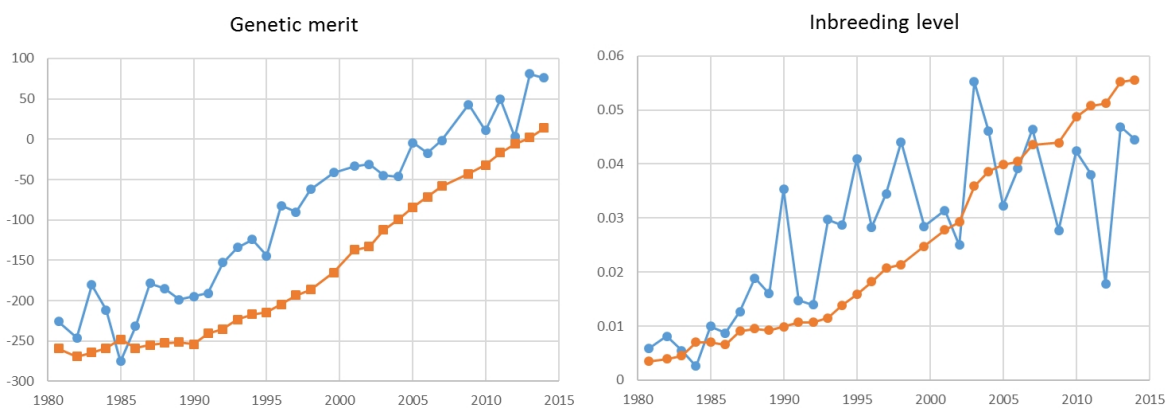


Figure 2 Average genetic merit (left panel) and average inbreeding coefficient (right panel) for bulls with conserved semen samples (blue lines) and for the live population = female calves in farms (orange lines)

The average inbreeding level also increased from just above 0.0 to 0.055 for the cow population. Although roughly following the same pattern, the average inbreeding level of bulls was more irregular, and before 2000 somewhat higher than in the cow population and after 2000 somewhat below (Figure 2). The average inbreeding level was 0.02 in the conserved bull population and 0.04 in the current bull population, while average observed heterozygosity was 0.32 and 0.33, respectively. Before 1992, the inbreeding rate (ΔF) in the cow population was 0.06% per year, and 0.34% per generation. After 1992 it increased to 0.22% per year and 1.24% per generation.

Effect of using conserved semen samples in breeding

Average heterozygosity will increase from 0.324 to 0.333 when only bulls of the current population are used in breeding and genetic diversity is maximised. Under this conservation scenario the genetic merit decreases from 5 to 0.2 (Figure 3). When both conserved and current bulls are used under the conservation scenario the heterozygosity increases from 0.333 to 0.344, and the average genetic merit decreases from -129 to -143.

Under the improvement plus conservation scenario, the heterozygosity is constrained to either 0.322 or 0.331. In the first case genetic merit increases to 101 when using only current bulls and slightly higher (105) when using all bulls. In the second case genetic merit increases less, to 56 when using current bulls, but to 72 when using all bulls. Thus using conserved bulls in the breeding program allows to increase genetic merit more when inbreeding is restricted more severely.

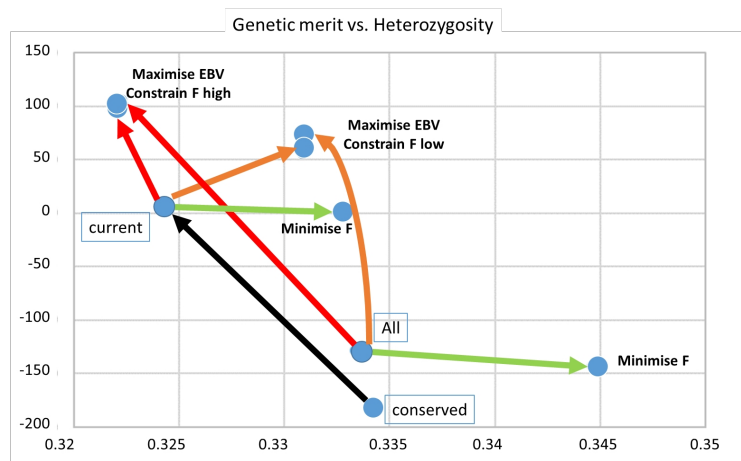


Figure 3. Genetic merit (average EBV) and diversity (expected heterozygosity) for current bull population (born in 2000 or later) and conserved bull population (= born before 2000), and resulting next generation when bred using optimal contributions, either from current or combined bull population, and either maximising diversity by minimising inbreeding level (F) only, or when maximising EBV and constraining inbreeding level to +1% either from combined population (F low) or from current population (F high)

Discussion

The MRIJ breed was one of the dominant breeds before the introduction of Holstein Friesian in the Netherlands. Population size has decreased sharply but the MRIJ breed is still considered as a viable breed with an active breeding population providing livelihood for a large group of farmers, in contrast to other endangered breeds for which number of breeding animals became very small. Currently, efforts are underway to implement genomic selection in MRIJ. Although the MRIJ breed is not endangered based on number of breeding animals, the genetic diversity in the breed has been clearly reduced since the 1970s. This is probably due to both the reduced population size and selection for improved genetic merit at the same time.

The lost genetic diversity, however, has been at least partly conserved in stored semen

samples. Use of stored samples from gene bank collections in the current breeding program may increase the effective population size and prevent problems associated with excessive inbreeding rates (Berg and Windig 2017). Here we show for an actual population that genetic diversity indeed can be increased by using stored samples. The loss in genetic merit, can be limited when using the optimal contribution method.

Acknowledgements

We thank CRV for providing data sets. This work was funded by the EU Horizon 2020 consortium "Innovative Management of Animal Genetic Resources" (acronym IMAGE). The Dutch Ministry of Economic Affairs also contributed financially to this study through the programs 'Kennisbasis Dier' (code KB-12-005.03.001) and 'WOT' (code WOT-03-003-056).

List of References

- Berg, P. & J.J. Windig, 2017. Management of cryo-collections with genomic tools. In: Genomic management of animal genetic diversity, K. Oldenbroek (editor), Wageningen Academic Publishers, Wageningen, The Netherlands, p 155-178.
- CRV, 2017. Genetic trends of cows in the Netherlands (in Dutch). https://crvnl-be6.kxcdn.com/wp-content/uploads/2017/08/gen_trend_koe_nl_20170811.pdf, accessed 15/09/2017.
- Meuwissen, T.H.E., 1997. Maximising the response of a selection with a predefined rate of inbreeding. *J. Anim. Sci.* 75: 934-940.
- Sargolzaei, M., J. P. Chesnais and F. S. Schenkel. 2014. A new approach for efficient genotype imputation using information from relatives. *BMC Genomics*, 15:478
- The cattle site, 2017. The Meuse Rhine Issel. <http://www.thecattlesite.com/breeds/dairy/111/meuse-rhine-issel/> accessed 12/09/2017.