

Genomics in Small Populations: The MRY Breed

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Abstract

A feasibility study for a genomic evaluation for the Meuse-Rhine-Yssel (MRY) Red and White dual purpose breed was conducted. Aim was to improve genetic progress in this small population. For this, 550 MRY bulls were genotyped from the German and Dutch-Flemish populations. Added reliability of genomic evaluation was assessed in a validation study using approximately (trait dependent) 400 bulls as training population and another 100 as validation bulls. Mean gain in reliability over parent average was 8.4 percent (7.4 EDC). For production traits added reliability was on average 15.9 percent (1.2 EDC). For conformation added reliability averaged 9.6 percent (2.3 EDC). For functional traits, added reliability tended to be low. As a result of this study, a genomic evaluation for the MRY breed will be implemented in the breeding program. Another 2,000 cows are currently being genotyped to improve evaluation accuracies.

Introduction

The MRY breed is a local Dutch red and white breed, originating in the central region of the Netherlands (between the rivers Meuse, Rhine, and Yssel). It is a typical dual purpose breed, a strong, sober and robust cow, which makes it easy to manage, and very suitable for low input farming systems. Though numbers are low, with approximately 7,500 pure bred animals registered in 2016, interest in the breed is rising. Especially in the cross-breeding segment, as the MRY breed excels in good fertility, good longevity, and high milk protein. The breed may also benefit from gene exchange with the equivalent Doppelnutzung breed from Germany, which is in recent years promoted by a common MRY-Doppelnutzung ranking in both countries. The active breeders of the MRY breed have requested tools for better and more efficient selection in their breed, and an increase in the rate of genetic improvement to continue and enhance the competitive position of the MRY breed in the market. Therefore, in a joined effort, Germany and the Netherlands have conducted a pilot study to assess the added reliability of genomic information in a first set of genotyped MRY bulls.

Material & Method

A total of 480 MRY and 70 Doppelnutzung proven bulls were genotyped for this study. The MRY-DN breeding values (EBV) were used as phenotypes. These are MACE breeding values from the Interbull international evaluation, corrected in such a way that ranking of the bulls on both the Dutch and the German country scale is exactly the same. The EBV are then deregressed to DRP according to VanRaden to be used as input phenotypes. The SNP effect estimation is done using Bayes Stochastic Search Variable Selection (B-SSVS), where SNP effects are sampled from two distributions, with efficient right-hand-side updating for fast computing, according to Calus (2014). A classical validation was performed where DRP of the validation animals (~25% of available bulls) were discarded from the training population. Estimated breeding values for these bulls from a model without SNPs (BLUP model) and a model with SNPs (DGV model) were then correlated to their DRP to estimate the improvement in correlation. The squared difference in correlation - expressed as equivalent daughter contribution (EDC, which is a linear function, contrary to reliabilities),

corrected for average EBV reliability of the validation bulls, and extrapolated to the full training population size - is a measurement for added reliability due to genomics.

Results

Table 1 shows the results of the pilot study. Approximately 400 bulls were included in the training population. For most traits, approximately 40 bulls were available as validation set. Not all bulls had EBV for all traits. On average b-factor was 0.95, although there is a large variation between traits, which may be expected with such low number of bulls. Genomics adds some information to production traits, udder conformation traits, direct calving traits, fertility traits, and the beef index. Genomics adds no or very little information to leg conformation traits and udder health traits. Overall, genomics adds 7.4 EDC worth of information to the genomic breeding value, resulting in an overall increase in reliability of 4% on top of a conventional parent average. For production traits, the increase in reliability is 5-10%.

Discussion

Papers by Cooper *et al.* (2014, 2016) showed that, even in small population, there may be a benefit from genomic information. Indeed, even in this small pilot study, we have shown the added value of genomic information. In fact, results are quite comparable to the findings of Cooper *et al.* (2014) in Ayrshire. Still, practical implications of the current findings are limited.

The improvement in reliability due to genomic information, based on 400 bulls in the training population, is too limited to justify a population-wide introduction of genomics in the MRY-breed. Nonetheless, it can be shown that even with a small improvement in reliability, genomic selection for young bulls will be more effective than traditional selection methods, and moreover justifies a new set-up of the male selection program of the breeding company, not relying on progeny testing for information. As a second step, the first group of 17 active MRY farmers have now genotyped a set of 2,000, mostly lactating, cows. These cows will be a valuable addition to the small bull training population. This validation study will be repeated using a bull and cow training population of approximately 2,500 individuals autumn 2017.

References

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Table 1. Number of bulls in training population, regression of Direct Genomic Value on Deregressed Proof (b-factor), equivalent daughter contribution of genomic information (added EDC), and expected reliability of a genomically enhanced breeding value of a young bull (total R², assuming a conventional parent average with 30% reliability).

Trait	# bulls	b-factor	addEDC	total R ²
Kg milk	393	0.87	0.61	0.35
Kg fat	393	0.64	1.08	0.38
Kg protein	393	0.68	1.48	0.39
Kg lactose	393	1.04	1.72	0.41
Persistency	364	0.74	1.52	0.32
Rate of maturity	364	0.71	1.19	0.33
Stature	403	1.64	0.84	0.36
Chest width	403	0.81	0.00	0.30
Body depth	403	0.93	1.55	0.36
Angularity	403	1.05	8.71	0.40
Condition score	403	1.06	1.29	0.35
Rump angle	403	0.70	0.00	0.30
Rump width	403	1.15	0.00	0.30
Rear leg rear	403	0.67	0.00	0.30
Rear leg side	403	0.34	0.09	0.30
Foot angle	403	0.67	4.52	0.37
Locomotion	403	0.64	0.00	0.30
Front udder attach	403	0.98	1.02	0.33
Front teat	403	1.76	0.00	0.30
Teat length	403	0.51	0.93	0.34
Udder depth	403	1.38	1.34	0.36
Rear udder height	403	1.50	14.29	0.57
Udder support	403	1.29	6.44	0.45
Rear teat	403	1.70	0.47	0.32
SCS	401	1.26	0.00	0.30
Subclinical mastitis	401	1.25	0.00	0.30
Clinical mastitis	401	0.97	0.00	0.30
Direct longevity	400	1.29	0.00	0.30
Direct calving ease	357	1.11	4.42	0.34
Maternal calving ease	403	1.09	0.00	0.30
Direct livability	292	0.75	5.26	0.32
Maternal livability	370	0.91	0.00	0.30
Non-return 56	405	1.29	6.20	0.33
Interval-calving-1st ins	405	0.31	0.65	0.31
Calving interval	405	0.64	2.12	0.34
Interval-first-last-ins	405	1.28	6.21	0.36
Conception rate	404	1.65	0.00	0.30
Conception rate heifer	403	1.20	238.57	0.60
Age-first-insemination	373	0.35	0.82	0.30
Gestation length	325	0.12	0.00	0.30
Milking speed	350	0.52	0.00	0.30
Temperament	342	0.86	3.10	0.34
Beef index	383	0.60	1.89	0.36
Overall		0.95	7.40	0.34