

Differences in genetic diversity in Holstein cattle with high and low genetic merit

K.A. Engelsma^{*†}, R.F. Veerkamp[†], M.P.L. Calus[†], and J.J. Windig^{*†}

Introduction

Loss of genetic diversity in Holstein cattle has been the result of the intensive selection for milk production. Genetic diversity is necessary for the future of the Holstein breed, and therefore evaluation of the loss of genetic diversity in this breed is of importance.

Evaluations of genetic diversity in Holstein cattle based on pedigree data, indicate a decrease in genetic diversity in Holstein cattle, because of a lower effective population size and a higher relatedness compared to other cattle breeds (Adamec *et al.* (2006), Kearney *et al.* (2004), Koenig and Simianer (2006), Sorensen *et al.* (2005)). However, pedigree based diversity reflects only the overall genetic diversity, while for specific regions on the genome the genetic diversity might be completely different. Additionally, genome regions with high or low genetic diversity might be missed completely.

With the availability of dense marker maps, information from large numbers of SNPs can be used to estimate the genetic diversity for specific genome regions. In simulation studies the loss of genetic diversity is largest in genome regions where selection has acted (Pedersen *et al.* (2009)). Less is known about the effect of selection on the genetic diversity in a population that has been under selection such as the Holstein cattle population.

The objective in this study was to compare genetic diversity across the genome between Holstein cattle with high and low genetic merit for milk production, using pedigree information and SNP data.

Material and methods

Animals. 90 Holstein heifers with either a high or a low EBV for milk, fat and protein production were selected on the basis the Dutch production index for milk, fat, and protein (Inet, calculated as: $0.06 \times \text{EBV kg of milk} + 0.7 \times \text{EBV kg of fat} + 4.2 \times \text{EBV kg of protein}$). Of the 90 heifers, 51 had a relatively high genetic merit and 39 had a relatively low genetic merit. The group with high EBV (EBV_{high}) had an average Inet value of 171, ranging from 112 to 241, and the group with low EBV (EBV_{low}) had an average Inet value of -24, ranging from -117 to 34. The average difference in Inet between the two groups was 195 Euros, corresponding to about 10 years of ongoing selection (Beerda *et al.* (2007)).

* Centre for Genetic Resources The Netherlands (CGN), P.O. Box 65, 8200 AB Lelystad, The Netherlands

† Wageningen UR Livestock Research, Animal Breeding and Genomics Centre, P.O. Box 65, 8200 AB Lelystad, The Netherlands

Genotyping. For the genetic diversity evaluation, DNA was extracted from the 90 heifers and used to determine genotypes at 54,001 SNP loci with the Illumina BovineSNP50[™] array. A SNP quality check was done before analysis, removing monomorphic SNPs, SNPs without known genome position, SNPs with >5% missing genotype, and SNPs not in Hardy Weinberg equilibrium. After cleaning 47,213 SNPs were left and used for analysis.

Genetic diversity evaluation. The overall genetic diversity based on pedigree information was estimated for the two groups, using the coefficient of kinship and the inbreeding coefficient (Falconer and Mackay (1996)).

The genetic diversity across the genome based on SNP data was evaluated for the two groups using expected heterozygosity based on allele frequencies (H_{exp}) (Falconer and Mackay (1996)) for each SNP. For each SNP a Chi-square test was performed to determine whether the frequencies of the alleles deviate from a random distribution over the two groups.

Results and discussion

Based on pedigree information, the average mean kinship was higher within group EBV_{high} ($f=0.12$) compared to group EBV_{low} ($f=0.07$), indicating a higher overall genetic diversity in this group due to the selection for milk production. Comparable results were found by Mrode *et al.* ((2009)), suggesting that there is indeed a measurable effect of selection for production traits on the genetic diversity in the Holstein cattle.

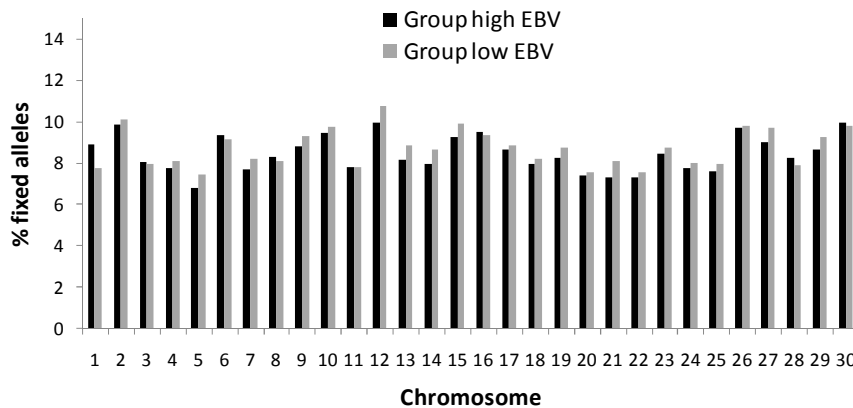


Figure 1: Percentage fixed alleles for two Holstein groups, with high and low EBV for milk production, for 30 chromosomes.

Based on SNP data, over all 30 chromosomes only a slight difference between the two groups was found for the percentage fixed alleles (8.5% for EBV_{high}, 8.7% for EBV_{low}) and no difference for the expected heterozygosity ($H_{exp}=0.31$ for both groups). Within chromosomes there were differences between the groups. For the percentage fixed alleles, the highest difference between the two groups was found on chromosome 1, where the

percentage fixed alleles was higher for group EBV_{high} (8.9% for EBV_{high} versus 7.7% for EBV_{low}; Figure 1). The difference in H_{exp} between the two groups showed a large variation over individual SNPs within chromosomes, illustrated in Figure 2 for chromosome 1.

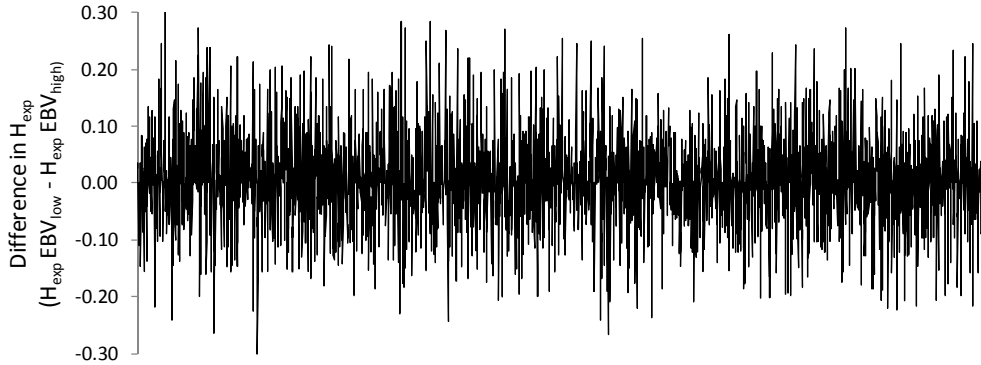


Figure 2: Differences in expected heterozygosity (H_{exp}) between two Holstein groups, with high and low EBV for milk production, for the individual SNPs on chromosome 1.

For 2.0% of the SNPs over the whole genome allele distribution over the two groups differed significantly ($p < 5\%$) from random, indicating less than expected differences between the two groups. However, on chromosome level 13.4% of the SNPs on chromosome 1 showed a non-random distribution (Table 1).

Table 1: Percentage of SNPs with a significant difference in allele frequency per chromosome for (a) the chromosome with the highest percentage; (b) the chromosome with the lowest percentage; (c) the average percentage over all 30 chromosomes. Significance is based on a Chi-square test with significance level of 5%.

Chromosome	% significant SNPs
1 (a)	13.4
27 (b)	0.8
All (c)	2.0

Although the average expected heterozygosity for each chromosome did not show differences between the two groups, a large variation in the difference in expected heterozygosity between the groups was found for individual SNPs. A lower heterozygosity would be expected on those genome regions where selection has taken place, expected to be found in group EBV_{high}. In a study of Hayes *et al.* ((2008)) higher values of homozygosity (similar to lower heterozygosity values) were found in genome regions linked to QTL related to production traits, and where selection had taken place. In further research, we will investigate the link with important QTL connected to milk production situated in the regions

where we found large differences in heterozygosity between the two groups, and if the LD around the QTL and in the regions found in our study is comparable.

Conclusion

Pedigree information showed a higher genetic diversity in the group with high EBV for milk production. Based on SNP data, over the whole genome there were no large differences in fixed alleles and expected heterozygosity between the two groups. However, within chromosomes there was a large variation in the difference between the two groups, where the largest differences were found on chromosome 1.

References

- Adamec, V., Cassell, B. G., Smith, E. P., et al. (2006). *J. Dairy Sci.* 89(1):307-314.
- Beerda, B., Ouweltjes, W., Sebek, L. B. J., et al. (2007). *J. Dairy Sci.* 90(1):219-228.
- Falconer, D. S. and Mackay, T. F. C. 1996. Longman Group, Essex, UK.
- Hayes, B. J., Lien, S., Nilsen, H., et al. (2008). *Anim. Genet.* 39(2):105-111.
- Kearney, J. F., Wall, E., Villanueva, B., et al. (2004). *J. Dairy Sci.* 87(10):3503-3509.
- Koenig, S. and Simianer, H. (2006). 103(1-2):40-53.
- Mrode, R., Kearney, J. F., Biffani, S., et al. (2009). *J. Dairy Sci.* 92(11):5760-5764.
- Pedersen, L. D., Sorensen, A. C., and Berg, P. (2009). *Proc 60th EAAP*: Page 319.
- Sorensen, A. C., Sorensen, M. K., and Berg, P. (2005). *J. Dairy Sci.* 88(5):1865-1872.