The Value of Increased Heterozygosity in Dairy Cattle

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Abstract

Today mating decisions are mostly based on pedigree information. However, genomic information could be used to minimize inbreeding or increase heterozygosity in mating decisions, because it contributes with more information on the expected heterozygosity (He) than pedigree information. The underlying hypothesis is that the more heterozygous the offspring of a mating is, the larger the dominance effect and less inbreeding depression in purebred offspring. The purpose of this study was to estimate the size of He using single nucleotide polymorphism (SNP) marker information and further the effect of increased heterozygosity on milk, fat and protein yield in Holstein (HOL), Red Dairy Cattle (RDC) and Jersey (JER) cows. He was calculated SNP by SNP for all couples of genotyped parents. Genome-wide He was calculated as the mean heterozygosity over all the SNPs. Data from 5,423 HOL, 2,245 RDC and 5,975 JER genotyped cows born between 2015 and 2017, which all had parents with GEBV were analyzed. The mean He levels were 0.328 for HOL, 0.336 for RDC and 0.308 for JER with standard deviations between 0.007 and 0.008. Results showed a significant effect of He on milk, fat and protein for all breeds. For HOL, a 1%-point increase in He corresponds to an increase in 305 days yield of 122 kg milk, 3.7 kg fat and 3.7 kg protein. For RDC the effect was 99 kg milk, 2.9 kg fat and 2.9 kg protein per heterozygosity percentage point. For JER the effect was 42 kg milk, 3.2 kg fat and 1.8 kg protein per heterozygosity percentage point. This indicates that it could be beneficial to include He in the mating plan decisions.

Key words: Dairy Cattle, mating decisions, inbreeding, heterozygosity, production traits

Introduction

Today mating decisions are primarily based on pedigree information. However, genomic information could be used to minimize inbreeding or increase heterozygosity in mating decision, because it contributes with more information on the expected heterozygosity (He) than pedigree information. Inbreeding depression has been shown to affect many traits affecting the profitability of dairy cows such as milk, fat and protein yield (Rokouei et al. 2010, Cassell 2009), but also mastitis (Sørensen et al. 2006) and some fertility traits (Rokouei et al., 2010). Accounting for genomic information increases the estimation accuracy of inbreeding coefficients because it captures realized autozygosity. As a result, it also allows for more accurate estimation of inbreeding depression effects than pedigree information. For example, Pryce et al. (2014) found that a 1% increase in pedigree inbreeding results in a decrease in milk yield of 21 L for Holstein dairy cows whereas the same 1% increase in genomic inbreeding leads to a decrease in milk yield of 27.8L and the effect of increased homozygosity was -63 L. Bjelland et al. (2013) also found a decrease in yield traits with an increase of genomic inbreeding.

The expected genome-wide heterozygosity for a progeny from a prospective mating can be computed from the parents' genotypes. The expected heterozygosity is assumed to reflect part of inbreeding depression effect that would be expected for an "average" progeny of a specific mating. When the effect of increased expected heterozygosity on traits is known, it is possible to implement it in the mating plan. This will make it possible for the farmer to select the sire for the specific cows, that will give the highest profit considering both breeding values and heterozygosity.

In this study we calculated the expected heterozygosity of purebred animals, using SNP information and further the effect of increased heterozygosity on milk, fat and protein yield in Holstein (HOL), Red Dairy Cattle (RDC) and Jersey (JER) cows. The underlying hypothesis is that the more heterozygous the offspring of a mating is, the larger the dominance effect and less inbreeding depression in purebred offspring.

Material and Methods

Data

Data from 5423 Holstein (4833 dams and 517 sires), 2245 RDC (1978 dams and 212 sires) and 5975 Jersey cows (5148 dams and 214 sires) born in Denmark in 2015, 2016 and 2017 were included in the analyse. All cows were genotyped and had deregressed proofs. The parents of the cows were also genotyped and had GEBVs. For HOL 46,342 SNPs were used to calculate He, 41,897 SNPs were used to calculate He for RDC and 46,914 SNPs were used to calculate He for JER.

Methods

Expected heterozygosity was calculated SNP by SNP for the genotyped parents. If both parents were opposite homozygotes for the SNP, the He was set to 1. If both parents were homozygous for the same SNP, the expected heterozygosity was set to 0. If one or both parents were heterozygous for the SNP, He was set to 0.5. The genome-wide He was then calculated as the sum of all He over all the SNPs divided by the total number of SNPs.

Effect of He on each trait was estimated using a linear regression model with software SAS (version 9.4; SAS Institute Inc.).

$$\mathrm{DRP} = \mu 1 + \alpha \mathrm{He} + \beta \frac{\mathrm{GEBV_s} + \mathrm{GEBV_d}}{2} + e$$

where:

$\mu 1$ is the intercept, He is the expected heterozygosity fitted as covariate, and $\frac{\mathrm{GEBV_s} + \mathrm{GEBV_d}}{2}$ is the mean parental GEBV for the traits milk yield, fat yield and protein yield. DRP is the deregressed proof (Stránden and Mäntysaari, 2010) expressed in index units.

The phenotypic effect of He for each trait in trait units was calculated by scaling He according to the value of 1 index unit (see Table 1).

Table 1. Value of + 1 index unit (NAV 2023)

	HOL	RDC	JER
Milk (305-d, kg)	66.0	72.5	57.3
Fat (305-d, kg)	2.4	2.5	2.1
Protein (305-d, kg)	2.0	2.0	1.7

Results & Discussion

The mean He at SNP markers for HOL was 0.328 with a standard deviation of 0.007. RDC had, as expected the highest He of 0.336 with a standard deviation of 0.008, and JER the lowest He with a mean on 0.308 with a standard deviation of 0.008.

The effect of expected heterozygosity on milk, fat and protein yield is shown in Table 2 for HOL, in Table 3 for RDC and in Table 4 for JER. The estimates for regression coefficients represent the increased value, expressed in index units, when going from an He of 0 to 1 or 100%. All regression coefficients were significant, irrespective of the breeds and traits. They were consistently higher for HOL. The effect of an 1%-point increase in He was 1.85 index units for milk, equivalent to 122 kg milk. For fat yield the effect of 1%-point increase in He increases fat yield by 3.7 kg corresponding to 1.54 index units of fat. The effect of increased He is the same for protein yield as for fat yield, where 1%-point increase of He resulted in 3.7 kg (1.87 index units).

Table 2. Regression coefficient estimated for deregressed proofs on expected heterozyosity for Holstein

	Estimate	Standard error
He milk	185	52
He fat	154	54
He protein	187	47

He = estimated heterozygosity

For milk regression coefficients were lower for RDC and JER than for HOL: the effect of 1%-point increase in He was 1.37 index units in RDC (equivalent to 99 kg of milk) and 0.74 index units for JER (equivalent to 42 kg of milk). The effect of heterozygosity on fat yield of JER (1.51 index units per 1%-increase in He, i.e. 2.9 kg fat yield) was as high as the HOL estimate and higher than the RDC estimate.

Table 3. Regression coefficient estimates for deregressed proofs on expected heterozygosity for RDC

	Estimate	Standard error
He milk	137	50
He fat	115	49
He protein	187	47

He = estimated heterozygosity

In contrast, the regression coefficient of protein yield DRP on He was lower in JER (1.03 index units per 1% increase in He, i.e. 1.8kg protein yield) than in HOL and RDC.

Table 4. Regression coefficient estimated for deregressed proofs on expected heterozygosity for Jersey

	Estimate	Standard error
He milk	74	33
He fat	151	33
He protein	103	30

He = estimated heterozygosity

Pryce et al. (2014) and Bjelland et al. (2013) focused on increase in homozygosity instead of heterozygosity but because 1% increase in heterozygosity is the same as 1% decrease in heterozygosity these results are comparable, even though there are difference in the models used, where Pryce et al. (2014) used phenotypic data instead of deregressed proof. Pryce et al. (2014) found a decrease in milk yield of 63 L for Holstein and 71 L for Jersey, with a mean of 7286 L milk for Holstein and 5197 L milk for Jersey in the population, corresponding to a decrease of 0.9% and 1.4% in milk. Bjelland et al. (2013) found a decrease in milk yield of 53 kg with one percentage increase in homozygosity, this is for 205 days yield with a mean of 8453 kg which corresponds to a decrease on 0.6%. The mean milk, protein and fat yield (305 days) for Danish Holstein, RDC and Jersey cows are shown in Table 5. Converted to percentage of total milk yield the effect of 1%-point increase in estimated heterozygosity are between 0.6% increase in milk yield (Jersey) and 1.1% increase in milk yield (Holstein), which are similar to the results found by Pryce et al. (2014) and Bjelland et al. (2013). Bjelland et al. (2013) did not find a significant effect of increased homozygosity on fat- and protein percentages. Pryce et al. (2014) found a decrease in fat yield of 3 kg for Holstein and 3.9 kg for Jersey corresponding to 1.1% and 1.5% which is higher than our estimates, that, converted to increase in percentage of fat yield is between 0.7% (RDC and Jersey) and 0.8% (Holstein). The increase in fat yield with increased heterozygosity was between 0.6% (Jersey) and 0.9% (Holstein) which for Holstein is comparable to results by Pryce et al. (2013) with a decrease in protein yield of 0.8% for Holstein with increase in homozygosity, but lower for Jersey where Pryce et al. (2014) found a decrease in protein yield of 1.4%.

Table 5. Mean 305 days yield in Denmark 2021/2022 (Viking Danmark 2022)

	Milk	Fat	Protein
Holstein	11,271	462	396
RDC	9,735	428	360
Jersey	7,598	453	326

Conclusions

There is a significant effect of He on milk, protein and fat yield across all three breeds and traits. Including this information in the mating plan is straightforward. It is expected to increase the average genome-wide heterozygosity of offspring compared to random mating and thereby their phenotypic performance. Before being implemented in the mating plan with full added value, there is a need to estimate the effect of He for all other traits in the breeding goal and for the total merit.

Acknowledgments

This work was funded by the DairyCross project supported by the green development and demonstration programme (GUDP) from the Danish ministry of food, agriculture and fisheries (J. nr. 34009-18-1365).

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