Genomic predictions of fertility related disorders in Norwegian Red using 30 years of data

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ABSTRACT: The aim was to investigate whether including information from later lactations improve accuracy of genomic breeding values for the 4 fertility related disorders cystic ovaries, retained placenta, metritis and silent heat. Data consisted of health records from 6,015,245 lactations from 2,480,976 Norwegian Red cows, recorded from 1979 to 2012. These were daughters of 3,675 AI-bulls. Genomic information was available for all sires. The 312 youngest bulls were used for validation. Genomic breeding values were predicted using G-BLUP for first lactation only (GEBV1) and for the first 5 lactations (GEBV5). Correlations between EBV for the 4 traits in 5 lactations with GEBV1 and GEBV5, respectively, were compared. Accuracy ranged from 0.17 to 0.65. Including later lactations improved accuracy of GEBV for cystic ovaries and retained placenta, while for metritis and silent heat no obvious advantage was found.
Keywords: fertility related disorder; genomic prediction; dairy cattle

Introduction

In a progeny testing scheme, only first lactation information is available from the daughters when the bulls get their first official proofs. The frequency of fertility related disorders such as cystic ovaries (CO), retained placenta (RP) and metritis (MET) however, often increase as the cow gets older. This implies that potentially valuable information is not available at the time when the elite-bulls are selected. With the introduction of genomic selection, information from later lactations may more easily be utilized as the reference population includes older bulls with information from daughters in the later lactations. Fertility related disorders have so far not been included in routine genetic evaluations in Norway, except RP which is included in "other diseases", a trait with 2% relative weight in the current total merit index-

The main aim was to compare accuracy of genomic predictions for fertility related disorders in Norwegian Red based on data from first lactation only vs. using lactation 1 to 5. More than 30 years of health recordings of the 4 most common fertility related disorders; CO, RP, MET and silent heat (SH) were used.

Material and methods

Data: Records on calving and health (veterinary treatments of disease) from 2,480,976 cows calving from January 1979 through December 2012, and sired by Norwegian Red AI bulls, was extracted from the Norwegian Dairy Herd Recording System. Information from the first 5 lactations on CO, RP, MET and SH was used. The four disorders were chosen as these are the most frequent fertility related disorders in Norway. Cows without first lactation records in the dataset were omitted, and the cows had to be 20 to 36 months old at first calving and have reasonable calving intervals (280-500 d). The traits were defined as binary (0=healthy, 1=affected) for each disorder in each lactation. For RP the veterinary treatment had to occur within the first 5 days after calving, while for the other disorders all health records within the lactation was used. The overall mean frequency of each disorder in each lactation is presented in Table 1. Only daughters of bulls with at least 150 first lactation daughters were included in the dataset. There were a total of 11,253 animals in the pedigree file which consisted of the 3,675 bulls with daughters in the dataset and their dams and sires traced back as far as possible.

Table 1. Number of records and mean frequency of cystic ovaries (CO), retained placenta (RP), metritis (MET) and silent heat (SH) in the full dataset.

		Frequency			
Lactation number	No of lactations	CO %	RP %	MET %	SH %
1	2,480,976	0.6	1.9	1.5	3.8
2	1,645,094	1.4	2.5	1.0	2.9
3	1,021,604	2.0	3.1	1.1	2.8
4	576,709	2.3	3.6	1.2	2.6
5	290,862	2.4	4.1	1.2	2.4
	6,015,245	1.3	2.6	1.2	3.2

Genomic information was available for all sires. An imputed 25k/54k SNP dataset (imputed both ways) that after standard editing had 48,249 SNP loci was used for genomic predictions.

For estimation of breeding values of the reference population a subset containing only records from lactations starting before January 1st 2008 was used. The 3,363 bulls with at least 150 first lactation daughters in this sub-dataset was used as reference population, while the youngest 312 bulls that not yet had 150 first lactation daughters was defined as the validation set.

Model: Each fertility related disorder was analyzed separately using linear sire models. For MET and SH the 5 lactations were analyzed as genetically correlated traits in multivariate models, while for CO the 5 lactations was analyzed as repeated records in a univariate repeatability model. A repeatability model was also used for RP in lactation 2 to

5, while RP in the first lactation was analyzed as a correlated trait in a bivariate model. The choice of models was based on Haugaard and Heringstad (2013). Single-trait analyses for the first lactation of each disorder were also performed. All analyses was done in DMU (Madsen and Jensen (2006))

Genomic predictions: Solutions from the linear models were used to calculate daughter-yield-deviations (DYD) to use as response variable in the genomic predictions. A genomic relationship matrix was calculated with the G-matrix program (Su and Madsen (2012)). Genomic breeding values (GEBV) were predicted by single trait G-BLUP, using DMU (Madsen and Jensen (2006)) for first lactation only (GEBV1) and for the first 5 lactations (GEBV5). Accuracy of genomic predictions was calculated as the correlation between EBV for the 4 disorders and 5 lactations estimated from the full dataset, and the GEBV1 and GEBV5, respectively, for the 312 sires in the validation set. When using 5 lactations EBV was correlated with GEBV of the same lactation, while in the first lactation only approach, EBV for all five lactations was correlated to GEBV1.

Results and discussion

Accuracy of genomic predictions ranged from 0.17 to 0.65 (Table 2). The highest accuracy was found for RP in the second to fifth lactation (0.65). For SH the accuracy was highest for the first lactation (0.45) and lowest for the fifth lactation (0.20), while for MET the highest and lowest accuracy was for the second (0.41) and fourth (0.17) lactation, respectively. The two disorders modeled with a repeatability model (CO and RP) had the highest accuracy, and these were higher than those previously reported for health and fertility traits in Norwegian Red (Svendsen et al. (2013)). The accuracy of MET and SH was in the same range as those previously reported. Luan et al. (2009) and Svendsen et al. (2013) found accuracies for various production and health traits in Norwegian Red ranging from 0.15 to 0.41 and 0.16 to 0.77, respectively. In both studies health and fertility traits showed lower accuracies than production traits. Ødegård et al. (2014) presented accuracies of GEBV for claw health in Norwegian Red ranging from 0.29 to 0.32, which is in general lower than the accuracies presented in here.

Table 2. Correlation between EBV for cystic ovaries (CO), retained placenta (RP), metritis (MET) and silent heat (SH) in lactations 1-5, with genomic predictions based on 5 lactations (GEBV5) or first lactation only (GEBV1).

	Genomic predictons	
Trait[1]	**GEBV5 [2]**	**GEBV1[3]**
CO1-5	0.44	0.42
RP1	047	0.39
RP2-5	0.65	0.42
MET1	0.39	0.42
MET2	0.41	0.38
MET3	0.21	0.39
MET4	0.17	0.36
MET5	0.24	0.41
SH1	0.45	0.46
SH2	0.24	0.36
SH3	0.39	0.31
SH4	0.40	0.21
SH5	0.20	0.35

[1]CO was analyzed with 5 lactations as repeated records in a univariate repeatability model. RP in lactation 2 to 5 where analyzed as repeated records in a repeatability model, while RP in the first lactation was analyzed as a correlated trait in a bivariate model. MET and SH were analyzed with 5 lactations as genetically correlated traits in multivariate models.
[2]EBV correlated with GEBV of the same lactation for the same disorder
[3]EBV for the five lactations of a disorder correlated to the GEBV of the first lactation of the same disorder.

Table 2 shows accuracies for genomic predictions based on 5 lactations vs. first lactation only. For CO and RP using 5 lactations yielded higher accuracies of GEBV, while using first lactation only gave better accuracy for MET except for prediction of second lactation MET. For SH the 5 lactation model gave better predictions in lactation 3 and 4, but lower in lactation 1, 2 and 5. Including later lactations provide valuable information and thus increased accuracy of genomic prediction for CO and RP. For MET and SH, the results were more inconclusive. Among the 4 fertility related disorders, MET had the lowest mean frequency and the same level across lactations. Estimates of variance components and EBV for MET were therefore less accurate, especially in the later lactations where information was sparse (Haugaard and Heringstad (2013)). SH had the highest mean frequency among the 4 disorders, but decreasing with increasing lactation number. This is a difficult disorder to record. Here we used information on veterinary treatments, however, many cases of SH may go unnoticed and therefore untreated, or the cow may be culled instead of treated

In the present study, the validation set consisted of the 312 youngest bulls from the full dataset. Some of these have few records of daughters in the later lactations which will make their EBV less accurate. Including more bulls in the validation set could be an alternative, although this would reduce the size of the reference population. An important question is which EBV the GEBV are to be compared with. In the present study, EBV for each lactation and disorder was correlated with the GEBV of the same lactation or with GEBV for the first lactation. The latter is a measure of how well first lactations GEBV predict the later lactations. Another approach could be to use GEBVs from the 5 first lactations (together or separately) to predict the first and perhaps the second lactation of the disorder.

Conclusions

Using information from later lactations for genomic predictions yielded higher accuracy of GEBV for CO and RP than when using information from the first lactation only, while for MET and SH the results were inconclusive. The accuracy of GEBV for fertility related disorders were similar or better than the accuracy of GEBV for other health traits and fertility traits in Norwegian Red. This is promising results if these traits are considered to be included in the total merit index in the future.

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