



Information from later lactations improves accuracy of genomic predictions of fertility-related disorders in Norwegian Red

Katrine Haugaard,*¹ Morten Svendsen,† and Bjørg Heringstad*†

*Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, PO Box 5003, 1432 Ås, Norway

†Geno Breeding and A.I. Association, PO Box 5003, 1432 Ås, Norway

ABSTRACT

Our aim was to investigate whether including information from later lactations improves accuracy of genomic breeding values for 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 artificial insemination bulls. The mean frequency of these disorders for cows in lactation 1 to 5 ranged from 0.6 to 2.4% for cystic ovaries, 1.0 to 1.5% for metritis, 1.9 to 4.1% for retained placenta, and 2.4 to 3.8% for silent heat. Genomic information was available for all sires, and the 312 youngest bulls were used for validation. After standard editing of a 25K/54K single nucleotide polymorphism data set that was imputed both ways, a total of 48,249 single nucleotide polymorphism loci were available for genomic predictions. Genomic breeding values were predicted using univariate genomic BLUP for the first lactation only and for the first 5 lactations and multivariate genomic BLUP with 5 lactations for each disorder was also used for genomic predictions. Correlations between estimated breeding values for the 4 traits in 5 lactations with predicted genomic breeding values were compared. Accuracy ranged from 0.47 and 0.51 for cystic ovaries, 0.50 to 0.74 for retained placenta, 0.21 to 0.47 for metritis, and 0.22 to 0.60 for silent heat. Including later lactations in a multitrait genomic BLUP improved accuracy of genomic estimated breeding values for cystic ovaries, retained placenta, and silent heat, whereas for metritis no obvious advantage in accuracy was found.

Key words: fertility-related disorders, genomic prediction, dairy cattle

INTRODUCTION

In a progeny testing scheme, only first lactation information from the daughters is available 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 increases as the cow gets older (Haugaard and Heringstad, 2013). This implies that potentially valuable information is not yet available at the time when the elite sires are selected. With the introduction of genomic selection, information from later lactations may more easily be used, as the reference population includes older bulls with information from daughters of all ages.

Some of the factors affecting the accuracy of genomic predictions are the size of the reference population, heritability of the trait, quality and number of available phenotypes, population structure and effective population size, as well as the density of the genomic markers (Hayes et al., 2009). Functional traits, such as fertility and health, have low heritability and show lower accuracy in genomic predictions compared with production traits (Luan et al., 2009; Zhou et al., 2014). Few populations record direct health traits, though several countries have recently started recording health traits as well as production traits in contract herds (Gernand et al., 2012) or in the main population (e.g., Koeck et al., 2012; Egger-Danner et al., 2012). In the Scandinavian countries, disease records have been collected for more than 30 yr, and direct health traits (e.g., mastitis) are included in routine genetic evaluations. Fertility-related disorders have so far not been included in the 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 for Norwegian Red. Fertility-related disorders is a disease category that has increased somewhat in frequency in recent years. The number of cows treated for any fertility-related disorder per cow-year (incidence rate) increased from 6.6% in 2008 to 8.5% in 2013 (Norwegian Cattle Health Services, 2014), and inclusion in the breeding scheme may therefore become desired.

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¹Corresponding author: katrine.haugaard@nmbu.no

The main aim of the current study was to examine whether including information from later lactations would increase accuracy of genomic predictions for fertility related disorders in Norwegian Red. Accuracy of genomic predictions based on data from first lactation only versus using lactations 1 to 5 was compared. More than 30 yr of health recordings of the 4 most common fertility-related disorders, CO, RP, MET, and silent heat (SH), were used.

MATERIALS 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 were extracted from the Norwegian Dairy Herd Recording System. Information on CO, RP, MET, and SH from the first 5 lactations were used. The 4 disorders were chosen as these are the most frequent fertility-related disorders in Norway. Cows without first lactation records in the data set were omitted, and the cows had to be 20 to 36 mo old at first calving and have reasonable calving intervals (280–500 d) thereafter. 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 d after calving, whereas for the other disorders all health records within a lactation were used. The overall mean frequency of each disorder in each lactation is presented in Table 1. The mean frequency varied from 0.6 (CO in first lactation) to 4.1% (RP in fifth lactation). Only daughters of bulls with at least 150 first-lactation daughters were included in the data set. There were a total of 26,858 animals in the pedigree file, which consisted of the 3,675 bulls with daughters in the data set and their dams and sires traced back as far as possible, back to the 1950s.

Genomic information was available for all 3,675 sires, where 2,165 were genotyped with the 25K SNP chip

from Affymetrix (Affymetrix Inc., Santa Clara, CA) and 1,967 were genotyped with the 55K SNP chip from Illumina (Illumina Inc., San Diego, CA). A total of 457 of the sires were genotyped with both. An imputed 25K/54K SNP data set (imputed both ways, imputation procedure described in Solberg et al., 2011) after standard editing had 48,249 SNP loci used for genomic predictions.

Daughter Yield Deviations

Daughter yield deviations (DYD) of the reference population were used as the response variable for the genomic predictions. These were estimated using a subset containing only records from lactations starting before January 1, 2008. The 3,363 bulls with at least 150 first-lactation daughters in this subset of data were included in the reference population, whereas the youngest 312 bulls that by January 1, 2008, did not have 150 first-lactation daughters was defined as the validation set. The mean number of first lactation daughters per sire in the reference population and validation set was 675 (minimum = 150; maximum = 10,197) and 227 daughters (minimum = 150; maximum = 2,742), respectively.

Each of the 4 fertility-related disorders was analyzed separately using linear sire models to predict parameters for calculation of DYD using the subset and to predict EBV using the full data set for comparison with genomic EBV (GEBV) from the genomic predictions. For MET and SH, the 5 lactations were analyzed as genetically correlated traits in multivariate models. Cystic ovaries were analyzed treating the 5 lactations as repeated records in a univariate repeatability model. A repeatability model was also used for RP in lactation 2 to 5, whereas 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). For CO, the systematic effects were year-season of calving (132 levels, seasons defined as January–March, April–June, July–September, and October–December) and age at calving in months (76 single-month classes).

Table 1. Number of records and mean frequency of cystic ovaries (CO), retained placenta (RP), metritis (MET), and silent heat (SH) in lactation 1 to 5 in the full data set

Lactation number	No. of records	Frequency, ¹ %			
		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
Overall	6,015,245				

¹Frequency of at least 1 veterinary treatment.

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