"post-print version"
DOI: http://dx.doi.org/10.3168/jds.2014-8267

INTERPRETIVE SUMMARY

Short Communication: Genetic parameters for fertility related disorders. *Haugaard et al pages 000*. Genetic parameters were estimated for the 4 fertility related disorders cystic ovaries, metritis, retained placenta and silent heat in lactations 1 to 5. Data on 1,747,500 lactations from 780,114 Norwegian Red cows were used to estimate genetic correlations between the lactations within each disorder. Heritabilities ranged from 0.02 (silent heat) to 0.12 (cystic ovaries). Genetic correlations between the lactations within disorder were positive and moderate to high, 0.79-0.95 for cystic ovaries, 0.40-0.75 for metritis, 0.53-0.94 for retained placenta and 0.39-0.83 for silent heat.

SHORT COMMUNICATION

SHORT COMMUNICATION: Genetic parameters for fertility related disorders in Norwegian Red

Katrine Haugaard* 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

Corresponding author:

Katrine Haugaard

PO BOX 5003, 1432 Ås, Norway

Phone: (0047) 67 23 26 96

Fax: (0047) 64 96 51 01

e-mail: katrine.haugaard@nmbu.no

ABSTRACT

Heritabilities and genetic correlations were estimated for the 4 most common fertility related disorders in Norwegian Red: retained placenta, cystic ovaries, silent heat and metritis. Data on 1,747,500 lactations from 780,114 cows calving from January 2001 through December 2011 were analyzed using multivariate threshold sire models to estimate variance components for the 4 disorders in the first 5 lactations. The traits were defined as binary within lactation (0=unaffected, 1=affected), and each fertility related disorder was analyzed separately with the 5 lactations as correlated traits. The mean frequency of affected cows ranged from 0.5% to 1.7% for cystic ovaries, 0.7% to 1.1% for metritis, 1.3% to 3.4% for retained placenta and from 1.7% to 2.7% for silent heat. Posterior means (SD) of heritability of liability ranged from 0.02 (0.01) to 0.12 (0.01), and were lowest for silent heat and highest for cystic ovaries. Genetic correlations across lactation within disorder were positive and moderate to high, ranging from 0.79 to 0.95 for cystic ovaries, 0.40 to 0.75 for metritis, 0.53 to 0.94 for retained placenta and 0.39 to 0.83 for silent heat.

Key words: Retained placenta, cystic ovaries, silent heat, metritis, genetic correlations

Fertility related disorders can decrease cow fertility, increase the calving interval, and are of economical importance due to increased labor, veterinary cost and reduced production. Cystic ovaries (**CO**), metritis (**MET**), retained placenta (**RP**) and silent heat (**SH**) are the most common fertility related disorders in Norway, and this category of diseases was the only category that increased in frequency in Norway in 2013 (Norwegian Cattle Health Services, 2014). Like many other disease traits, heritability of fertility related disorders are in general low. Heritability estimates from threshold models range from 0.05 to 0.08 for CO and 0.03 – 0.08 for MET (Zwald et al., 2004; Heringstad, 2010; Koeck et al., 2010), 0.06 – 0.08 for RP (Heringstad et al., 2005; Heringstad, 2010; Koeck et al., 2010) and 0.01 – 0.06 for SH

(Heringstad, 2010; Koeck et al., 2010). Studies have shown that heritability varies between lactations, e.g. Zwald et al. (2004) reported larger heritability estimates for CO and MET from the first lactation relative to estimates from all available lactations. Heringstad et al. (2005) reported a heritability of 0.08 for RP in lactations 1 to 3 in Norwegian Red, but the genetic correlations between the lactations ranged from 0.55 to 0.65, indicating that the disorder genetically is not the same trait across lactations.

As some of the fertility related disorders increase in frequency in the later lactations, it may be advantageous to use multiple lactations in genetic evaluations. The aims were to estimate heritabilities for CO, MET, RP and SH in the first 5 lactations, and to evaluate whether these disorders genetically can be considered to be the same trait across lactations based on genetic correlations between the lactations within each disorder.

Information on calving and fertility related health records were extracted from the Norwegian Dairy Herd Recording System. Information included up to 5 lactations from 780,114 cows sired by Norwegian Red AI bulls, calving from January 2001 to December 2011. Cows without first lactation data were omitted from the dataset. Age at calving had to be within defined intervals for the lactation record to be included (20-36 months, 32-48 months, 44-60 months, 56-72 months and 68-84 months for lactation 1-5, respectively). The definition of lactation were from the day of calving until 15 days before next calving, culling or 400 days after calving, whichever occurred first. The dataset contained 20 traits, 5 lactations for each of the 4 disorders, where each trait was defined as a binary (0 = unaffected, 1 = affected). 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 defined lactation were used. Number of records and mean frequency for the traits are given in Table 1. A total of 27,185 animals were in the pedigree file, which consisted of the 1,247 bulls with daughters in the dataset and their dams and sires traced back as far as possible.

Each of the 4 fertility related disorders was analyzed separately, with the 5 lactations as correlated traits in a multivariate threshold sire model. In matrix notation the model can be written as $\boldsymbol{\lambda} = \mathbf{X\beta} + \mathbf{Z_h h} + \mathbf{Z_s s} + \mathbf{e}$, where $\boldsymbol{\lambda}$ is a vector of unobserved liabilities, $\boldsymbol{\beta}$ is a vector of systematic effects (described below), **h** is a vector of random herd-5-year effects (30,583 levels), **s** is the random effect of sire (1,247 levels), **e** is the vector of residual, and **X**, $\mathbf{Z_h}$ and $\mathbf{Z_s}$ are the corresponding incidence matrices. The systematic effects were year-season of calving (seasons defined as January-March, April-June, July-September and October-December)(44, 41, 37, 33 and 29 levels for lactation 1-5 respectively) and age at calving in months (17 levels). Herd-5-year classes were defined by using 2 time periods of approximately 5 years (2001-2006 and 2007-2011). Heritability was calculated as $h^2 = 4*\sigma^2_{sire} / \sigma^2_{sire} + \sigma^2_{herd} + \sigma^2_{residual}$. A Bayesian approach using Gibbs sampler in the RJMC-routine of the DMU package (Madsen and Jensen, 2007) was used for analyses. Based on Raftery and Lewis convergence statistics in BOA (Smith, 2003) it was decided to use a total chain length of 300,000 iterations after 10,000 iterations burn in for all traits.

The mean frequency were low in all lactations for all disorders, less than 4% (Table 1). For 2 of the disorders (CO and RP) the frequency increased in later lactations, and for CO the frequency was 3 times as high in the fifth lactation (1.7%) as in the first lactation (0.5%). For RP the frequency more than doubled from the first lactation (1.3%) to the fifth lactation (3.4%). For MET the frequency was stable (0.6-0.8%) in the first four lactations, but with an increase in the fifth lactation (1.1%). The frequency of SH decreased with increasing lactations, from 2.7% to 1.7%. In general these frequencies were lower than disease frequencies reported in other studies; for CO frequencies range from 3.1% (Canadian Holstein, van Dorp et al., 1998) to 13% (Finnish Ayrshire, Mäntysaari et al., 1993), while for MET they range from 2.5%

(Finnish Ayrshire, Pösö and Mäntysaari, 1996) to 21% (US Holstein, Zwald et al., 2004). Koeck et al. (2010) reported a frequency for SH of 6.3% in Austrian Fleckvieh. For RP, the frequencies were more similar to those presented in the present study, where most range between 1.3% (Canadian Holstein, van Dorp et al., 1998) and 5.8% (Austrian Simmental, Schnitzenlehner et al., 1998), although Lin et al. (1989) presented frequencies for RP in US Holstein of 8.3% and 12.7% for second lactation cows and older cows, respectively

Heritabilities of liability were low for all traits (Tables 2-5). The posterior mean ranged from 0.02 (SH2 and SH3) to 0.12 (CO2) with small SD (0.01-0.02) for all traits, indicating fairly accurate heritability estimates. All first lactation estimates were in accordance with those reported by Heringstad (2010), which analyses were based on partly the same dataset as in the present study. The highest heritabilities were found for CO, ranging from 0.08 to 0.12 (Table 2), which is in agreement with previously reported heritability estimates for CO (e.g. Zwald et al., 2004; Koeck et al., 2010). The lowest heritabilities of liability were estimated for SH (0.02-0.04; Table 5) and MET (0.03-0.06; Table 3). Very few studies have published heritability of SH, so comparisons are sparse. Koeck et al. (2010) reported a heritability from a threshold model of 0.012 for SH and anestrus in the first 5 lactations, which is slightly lower than the estimates reported here. Threshold model heritability estimates for MET range from 0.06 (Koeck et al., 2010) to 0.08 (Zwald et al., 2004), which is in accordance with our estimates. The heritabilities of liability to RP ranged from 0.06 to 0.09 (Table 4). This is in agreement with previous estimates of 0.06 (Koeck et al., 2010) and 0.08 (Heringstad et al., 2005).

Generally, the genetic correlations (Table 2-5) among the lactations within each disorder were positive and moderate to high. The highest genetic correlations were found between the CO-traits (Table 2), with posterior mean ranging from 0.79 (CO1-CO5) to 0.95 (CO2-CO3), and

the upper bound of the 95% highest posterior density (**HPD**) intervals were all above 0.94. This was higher than genetic correlations of ovulatory disorders between lactations reported earlier, ranging from 0.60 to 0.94 (Mäntysaari et al., 1993; Pösö and Mäntysaari, 1996). However, those studies included anestrus, subestrus and other infertilities in addition to CO, and comparison is therefore difficult.

The posterior means of genetic correlations for SH ranged from 0.39 (SH1-SH4) to 0.83 (SH3-SH4), while for MET the posterior means of genetic correlations ranged from 0.40 (MET4-MET5) to 0.75 (MET2-MET4). The 95% HPD intervals for the genetic correlations among these traits were relatively wide indicating uncertain estimates, especially for the later lactations. For MET5, the 95% HPD interval of the genetic correlations to MET3 and MET4 even included 0. Previous genetic correlation estimates for MET between lactations range from -0.58 to 0.62 (Mäntysaari et al., 1993; Pösö and Mäntysaari, 1996). Also in these studies, the standard errors were large.

The posterior means of genetic correlations for RP showed a difference between the correlations involving the first lactation (0.53-0.69) and the correlations among the second to fifth lactation (0.84-0.94) (Table 4). These genetic correlations were slightly higher than those reported by Heringstad et al. (2005), with estimates from 0.55 to 0.65 for RP in the three first lactations. Schnitzenlehner et al. (1998) reported genetic correlation for RP in the first and second lactation of 0.79, which is higher than the corresponding estimate of the present study.

The posterior means of herd correlations between lactations were positive and high (0.71-0.98) for all the fertility related disorders (Tables 2-5). The posterior means of residual correlations (results not shown) between lactations were low for all disorders, 0.06-0.31, -0.04-0.14, 0.11-0.19 and -0.05-0.19 for CO, MET, RP and SH, respectively.

The main challenge with the fertility related disorders is the low frequency and the definition of the traits. In Norway only the veterinary treatments of disease are recorded, and in the analyses a cow was considered "affected" if she had one or more veterinary treatments of the given disorder during the lactation. For some disorders, like RP, this covers most of the actual cases of the disorder as it is easy to discover. Other disorders are more challenging and likely with more false negatives, like for example SH. Some cases of SH may not be discovered by the farmer and therefore not treated (and in consequence, not recorded), or the disorder is discovered but the cow is culled instead of treated. The actual incidence of disease is therefore probably larger than what the records show, valuable information is lost and genetic analyses may be less accurate. From Tables 2 to 5 it is shown that the SD and 95% HPD intervals for the genetic correlations between lactations is large for MET and SH. This may possibly reflect the low frequency and the complexity of these traits, relative to CO and RP which have low SD and smaller 95% HPD intervals.

Genetic correlations between lactations within disorder were positive and moderate to high and suggest that it is reasonable to assume that CO in lactations 1-5 genetically is the same trait, whereas MET and SH can not be considered to be the same trait across lactations.

Acknowledgement

The authors would like to thank the Norwegian Dairy Herd Recording System and the Norwegian Cattle Health Service (Ås, Norway) for access to data. This work is part of project no 217553/97225 financed by Regionale Forskningsfond, Norway.

REFERENCES

175 Heringstad, B., Y.M. Chang, D. Gianola and G. Klemetsdal. 2005. Genetic analysis of clinical
176 mastitis, milk fever, ketosis, and retained placenta in three lactations of Norwegian Red cows.
177 J. Dairy Sci. 88:3273-3281.
178 Heringstad, B. 2010. Genetic analysis of fertility-related diseases and disorders in Norwegian
179 Red cows. J. Dairy Sci. 93:2751-2756.
180 Koeck, A., C. Egger-Danner, C. Fuerst, W. Obritzhauser and B. Fuerst-Waltl. 2010. Genetic
181 analysis of reproductive disorders and their relationship to fertility and milk yield in Austrian
182 Fleckvieh dual-purpose cows. J. Dairy Sci. 93:2185-2194
183 Lin, H. K., P. A. Oltenacu, L. D. van Vleck, H. N. Erb and R. D. Smith. 1989. Heritabilities of
184 and genetic correlations among six health problems in Holstein cows. J. Dairy Sci. 72:180-186.
185 Madsen, P. and J. Jensen. 2007. An User's Guide to DMU. A package for analyzing
186 multivariate mixed models. Version 6. Release 4.7. University of Aarhus, faculty of
187 Agricultural Sciences (DFJ), Dept. Genetics and Biotechnology, Research Centre Foulum,
188 Tjele, Denmark.
189 Mäntysaari, E.A., Y.T. Gröhn and R.L. Quaas. 1993. Repeatability and heritability of
190 lactational occurrence of reproductive disorders in dairy cows. Prev. Vet. Med. 17:111-125.
191 Norwegian Cattle Health Services. 2014. Årsmelding fra helsetjenesten for storfe 2013 (In
192 Norwegian with English tables). Available at http://storfehelse.tine.no/om-
193 oss/%C3%A5rsmeldinger-og-rapporter/%C3%A5rsmeldinger-helsetjenesten (accessed
194 September 2014)
195 Pösö, J. and E.A. Mäntysaari. 1996. Genetic relationship between reproductive disorders,
196 operational days and milk yield. Livest. Prod. Sci. 46(1):41-48.
197 Schnitzenlehner, S., A. Essl and J. Sölkner. 1998. Retained placenta: estimation of nongenetic
198 effects, heritability and correlations to important traits in cattle. J. Anim. Breed. Genet.
199 115:467-478.

Smith, B. J. 2003. Bayesian Output Analysis Program (BOA) Version 1.0 User's Manual.

Van Dorp, T.E., J.C.M. Dekkers, S.W. Martin, and J.P.T.M. Noordhuizen. 1998. Genetic parameters of health disorders, and relationships with 305-day milk yield and conformation traits of registered Holstein cows. J. Dairy Sci. 81:2264-2270.

Zwald, N.R., K.A. Weigel, Y.M. Chang, R.D. Welper and J.S. Clay. 2004**.** Genetic selection for health traits using producer-recorded data. I. Incidence rates, heritability estimated and sire breeding values. J. Dairy Sci. 87:4287-4294

Table 1: Number of records and mean frequency of cystic ovaries (CO), metritis (MET), retained placenta (RP) and silent heat (SH) in lactations 1 to 5 for Norwegian Red

Lactation no	**No of records**	**Frequency (%)**			
		CO	**MET**	**RP**	**SH**
1	780,114	0.5	0.7	1.3	2.7
2	489,903	1.0	0.6	2.1	2.1
3	280,085	1.5	0.7	2.6	2.0
4	138,938	1.6	0.8	3.1	1.8
5	58,461	1.7	1.1	3.4	1.7

Table 2: Posterior mean (SD) of heritability of liability (diagonal), genetic correlations (below diagonal) and herd correlations (above diagonal) for cystic ovaries (CO_i), in five lactations (i=1-5), with 95% highest posterior density interval given in brackets

	CO1	**CO2**	**CO3**	**CO4**	**CO5**
CO1	*0.08 (0.01)*	0.92 (0.02)	0.88 (0.03)	0.79 (0.03)	0.76 (0.05)
	[0.06 – 0.11]	[0.89 – 0.96]	[0.83 – 0.93]	[0.73 – 0.86]	[0.66 – 0.85]
CO2	0.91 (0.04)	*0.12 (0.01)*	0.97 (0.01)	0.93 (0.02)	0.90 (0.02)
	[0.83 – 0.97]	*[0.09 – 0.14]*	[0.94 – 1.00]	[0.88 – 0.98]	[0.83 – 0.97]
CO3	0.83 (0.06)	0.95 (0.02)	*0.11 (0.01)*	0.94 (0.03)	0.86 (0.04)
	[0.70 – 0.94]	[0.90 – 0.99]	*[0.08 – 0.14]*	[0.89 – 0.99]	[0.78 – 0.94]
CO4	0.88 (0.06)	0.94 (0.03)	0.93 (0.04)	*0.09 (0.02)*	0.88 (0.05)
	[0.77 – 0.97]	[0.89 – 0.99]	[0.85 – 0.99]	*[0.06 – 0.12]*	[0.80 – 0.97]
CO5	0.79 (0.09)	0.90 (0.07)	0.92 (0.06)	0.91 (0.06)	*0.09 (0.02)*
	[0.61 – 0.94]	[0.77 – 0.98]	[0.79 – 0.99]	[0.79 – 0.99]	*[0.06 – 0.13]*

Table 3: Posterior mean (SD) of heritability of liability (diagonal), genetic correlations (below diagonal) and herd correlations (above diagonal) for metritis (MET_i), in five lactations (i=1-5) , with 95% highest posterior density interval given in brackets

	MET1	**MET2**	**MET3**	**MET4**	**MET5**
MET1	*0.04 (0.01)*	0.87 (0.03)	0.77 (0.05)	0.76 (0.08)	0.71 (0.08)
	[0.02 – 0.05]	[0.81 – 0.93]	[0.67 – 0.86]	[0.61 – 0.91]	[0.54 – 0.86]
MET2	0.57 (0.13)	*0.03 (0.01)*	0.85 (0.06)	0.82 (0.06)	0.86 (0.06)
	[0.31 – 0.81]	*[0.01 – 0.04]*	[0.75 – 0.96]	[0.71 – 0.94]	[0.73 – 0.96]
MET3	0.59 (0.15)	0.74 (0.13)	*0.03 (0.01)*	0.74 (0.08)	0.81 (0.07)
	[0.28 – 0.84]	[0.50 – 0.96]	*[0.02 – 0.05]*	[0.58 – 0.89]	[0.66 – 0.94]
MET4	0.48 (0.23)	0.75 (0.14)	0.55 (0.20)	*0.03 (0.01)*	0.68 (0.13)
	[0.07 – 0.89]	[0.48 – 0.95]	[0.16 – 0.91]	*[0.01 – 0.05]*	[0.45 – 0.92]
MET5	0.72 (0.13)	0.47 (0.21)	0.42 (0.27)	0.40 (0.23)	*0.06 (0.02)*
	[0.47 – 0.93]	[0.05 – 0.82]	[-0.05 –0.86]	[-0.03 -0.82]	*[0.02 – 0.10]*

Table 4: Posterior mean (SD) of heritability of liability (diagonal), genetic correlations (below diagonal) and herd correlations (above diagonal) for retained placenta (RP_i), in five lactations (i=1-5) , with 95% highest posterior density interval given in brackets

	RP1	**RP2**	**RP3**	**RP4**	**RP5**
RP1	*0.06(0.01)*	0.89 (0.03)	0.93 (0.03)	0.84 (0.04)	0.84 (0.05)
	[0.04 – 0.07]	[0.84 – 0.95]	[0.88 – 0.98]	[0.76 – 0.93]	[0.74 – 0.93]
RP2	0.69 (0.06)	*0.07 (0.01)*	0.96 (0.02)	0.92 (0.03)	0.87 (0.05)
	[0.56 – 0.80]	*[0.05 – 0.08]*	[0.93 – 0.98]	[0.86 – 0.99]	[0.77 – 0.96]
RP3	0.60 (0.07)	0.92 (0.03)	*0.08 (0.01)*	0.92 (0.03)	0.88 (0.05)
	[0.47 – 0.74]	[0.86 – 0.98]	*[0.06 – 0.10]*	[0.86 – 0.98]	[0.80 – 0.98]
RP4	0.60 (0.08)	0.84 (0.05)	0.94 (0.03)	*0.09 (0.01)*	0.83 (0.06)
	[0.45 – 0.74]	[0.74 – 0.94]	[0.89 – 0.99]	*[0.06 – 0.11]*	[0.70 – 0.93]
RP5	0.53 (0.10)	0.84 (0.06)	0.87 (0.06)	0.86 (0.07)	*0.09 (0.02)*
	[0.32 – 0.73]	[0.72 – 0.95]	[0.76 – 0.98]	[0.73 – 0.97]	*[0.05 – 0.12]*

Table 5: Posterior mean (SD) of heritability of liability (diagonal), genetic correlations (below diagonal) and herd correlations (above diagonal) for silent heat (SH_i), in five lactations (i=1-5), with 95% highest posterior density interval given in brackets

	SH1	**SH2**	**SH3**	**SH4**	**SH5**
SH1	*0.04 (0.01)*	0.96 (0.01)	0.93 (0.01)	0.90 (0.01)	0.88 (0.02)
	[0.03 – 0.05]	[0.95 – 0.97]	[0.92 – 0.94]	[0.88 – 0.93]	[0.85 – 0.92]
SH2	0.78 (0.06)	*0.02 (0.01)*	0.98 (0.01)	0.96 (0.01)	0.94(0.02)
	[0.65 – 0.89]	*[0.02 – 0.03]*	[0.96 – 0.99]	[0.95 – 0.98]	[0.91 – 0.98]
SH3	0.58 (0.11)	0.78 (0.10)	*0.02 (0.01)*	0.98 (0.01)	0.97 (0.02)
	[0.37 – 0.78]	[0.59 – 0.97]	*[0.01 – 0.03]*	[0.96 – 1.00]	[0.93 – 1.00]
SH4	0.39 (0.14)	0.64 (0.11)	0.83 (0.09)	*0.03 (0.01)*	0.96 (0.02)
	[0.13 – 0.64]	[0.42 – 0.87]	[0.95 – 0.98]	*[0.01 – 0.04]*	[0.93 – 0.99]
SH5	0.45 (0.18)	0.54 (0.20)	0.51 (0.22)	0.47 (0.18)	*0.04 (0.02)*
	[0.14 – 0.82]	[0.16 – 0.92]	[0.10 – 0.88]	[0.11 – 0.81]	*[0.01 – 0.08]*