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Genetic parameters for superovulatory response in Swedish Red Cattle and Swedish Holstein heifers

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Summary

The response to superovulatory treatment in terms of total number of collected embryos and number of transferable embryos per flush was studied for heifers in the Swedish nucleus herd Nötcenter Viken. The data was recorded during 2004 to 2006 and contained 761 treatments on 423 animals (212 Swedish Red, and 211 Swedish Holstein), sired by 90 bulls. Information on other fertility traits was available for 418 of these animals. The average result was 6.11 (SD 5.63) collected embryos and 3.55 (SD 4.03) transferable embryos per flush, non-responders included. Both number of embryos and quality of embryos increased in the herd during the studied period. The effect of breed was significant ($P<0.01$), with higher number of collected embryos in Swedish Red than in Swedish Holstein. The data was analysed using a linear animal model including fixed effects of breed, age, treatment number and year-season. Estimated repeatabilities were 0.40 and 0.44 for number of collected embryos and number of transferable embryos, respectively. Corresponding heritabilities were estimated at 0.11 and 0.12. Genetic and environmental correlations estimated between number of collected embryos and number of transferable embryos were strong, whereas weak correlations were estimated between number of transferable embryos and number of discarded embryos. No clear phenotypic relationships between superovulatory response and other fertility traits were detected in this data.

Introduction

An important feature of a nucleus herd for dairy cattle is the ability to test females of high genetic quality in a controlled environment. To fully benefit from a more accurate selection of dams, multiple ovulation and embryo transfer (MOET) is used to increase number of offspring per dam. The number of transferable embryos collected per animal is, however, variable and may be a limiting factor for a breeding program with MOET nucleus herd (Peixoto et al, 2004). There is a limited number of studies of genetic parameters for superovulatory response, and variable results have been presented. Heritabilities and repeatabilites in the range 0.00 – 0.65 and 0.13 – 0.51, respectively, have been reported by Peixoto et al. (2004), Michaux et al. (2002), Asada et al. (2002), Tonhati et al. (1999), and Liboriussen et al. (1995). In these previous studies, heifers as well as old cows have been included. The aim of this study was to analyse superovulatory response data from the Swedish nucleus herd Nötcenter Viken and to study phenotypic relationships with other fertility traits recorded in the herd.

Materials and Methods

Records of number of transferable embryos and number of discarded embryos were obtained from the Swedish nucleus herd Nötcenter Viken. Data from the start-up year 2003 were not included in the analyses as management routines were under development the first year. During January 2004 to September 2006, embryos were collected from 761 flushings of 423 heifers: 212 Swedish Red and 211 Swedish Holstein (Table 1). The heifers were sired by 90 bulls (32 Red and 58 Holstein), and were from 399 dams (203 Red and 196 Holstein). Most heifers were flushed twice, and a few three times. The age of the heifers at embryo collection was 18.1 month on average, ranging from 10-26 months. The distribution of number of embryos per flush in the data is shown in Figure 1.

Records were also available for a number of other fertility traits for most of the individuals: number of inseminations in first service period, interval first calving to first AI, and heat intensity score for heifers and cows (Table 2). Very few heifers had more than four inseminations and these were not included in the analyses as the practice of allowing more inseminations at the nucleus herd varied during the period studied. Records were also discarded if the heifer was more than 25 months at first insemination, younger than 26 months or older than 39 months at insemination after first calving.

The process of superovulatory treatment started with a natural oestrus, if a functional corpus luteum was found. Eight to twelve days after the onset of standing oestrus, treatment with follicle-stimulating hormone (FSH) begun. The FSH-treatments were given twice a day during four days. On the third day of FSH-treatment, the heifer was also given prostaglandin. Three days later an oestrus was induced, and the heifer was artificially inseminated (AI) twice. The non-surgical embryo flushing was done seven days after AI. The fluid was filtered into petri dishes. The embryos were classified and those of good enough quality were further prepared and then frozen. Embryos with a uniform cellular mass, without substantial defects and in development stages from compact morula to expanded, hatched blastocyst were classified as transferable (personal communication Geust, 2006).

Table 1a. Superovulatory response traits in heifers included in the study

Trait	No. of obs.	No. of animals	Mean	S.D.	Min	Max
Number of collected embryos	761	423	6.11	5.63	0	34
Number of transferable embryos	761	423	3.55	4.03	0	21
Number of discarded embryos	761	423	2.57	3.53	0	29

Table 1b.Other fertility traits included in the study

Trait	No. of obs.	Mean	S.D.	Min	Max
Number of inseminations 1st service period	395	1.54	0.86	1	4
Interval first calving – first AI (days)	151	69.40	17.22	42	128
Heat intensity score heifers	416	2.16	0.84	1	3
Heat intensity score cows	155	2.39	0.69	1	3

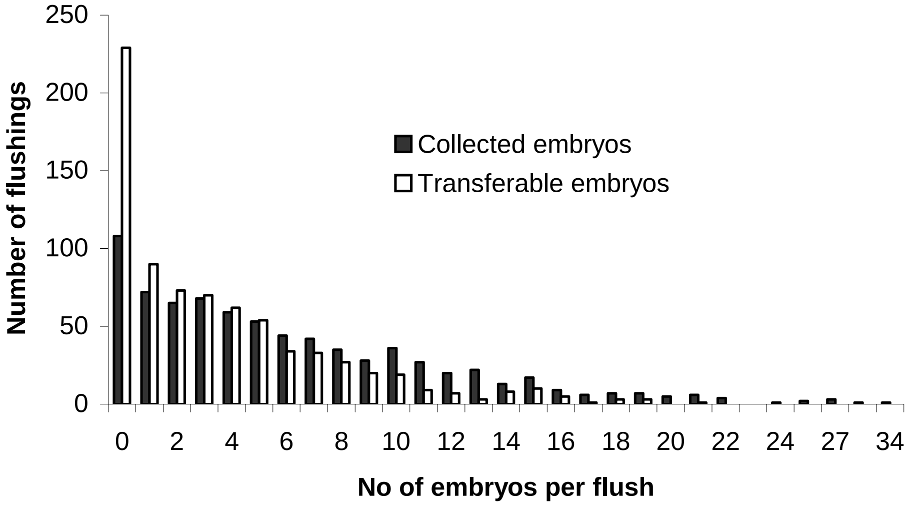

Fig.1. Distribution of superovulatory response variables in the data.

Estimation of genetic parameters

Statistical models were evaluated by using the MIXED procedure in SAS package (SAS Institute Inc., 2007).

The superovulatory traits were analyzed using the following animal model.

$$y_{ijklm} = \text{breed}_i + \text{age}_j + \text{flush number}_k + \text{year-season}_l + \text{pe}_m + a_m + e_{ijklm}$$

where:

y_{ijklm} is observed number of collected embryos, number of transferable embryos or number of discarded embryos, breed_i is the fixed effect of breed (Swedish Red or Holstein), age_j is fixed effect of the j^{th} age class, flush number_k is fixed effect of the flush number (first or later), year-season_l is the fixed effect of combination of year and season of embryo collection, pe_m is the random permanent environmental effect of animal m, a_m is the random additive genetic effect of animal m, and e_{ijklm} is the random residual effect. The random effects are assumed to be normally distributed, have zero means and the variances $I\sigma^2_{pe}$, $A\sigma^2_a$, and $I\sigma^2_e$, respectively, where A is a numerator relationship matrix and I is an identity matrix.

Five age classes were used: 10-13, 14-15, 16-17, 18-19, and 20-24 months of age at embryo collection. The seasons were defined as: March-May, June-August, September-November, and December-February.

Bivariate analyses were used for estimation of correlations between traits. (Co)variances were estimated using the average information algorithm (Jensen et al., 1997) for restricted maximum likelihood included in the DMU package (Jensen and Madsen, 2000). Asymptotic standard errors of variance components were computed from the inverse average information matrix. Heritabilities were calculated as $\sigma^2_a/(\sigma^2_{pe}+\sigma^2_a+\sigma^2_e)$.

Correlations between residuals for superovulatory traits and the other fertility traits were estimated in the SAS-package (SAS Institute Inc., 2007). The models for all traits included the fixed effects of breed, year, season and age class. The effect of number of flushings was included for all other fertility traits but heat intensity score for heifers. We also tried including the effect of number of embryos as an explanatory variable in the model for other fertility traits, to find out if this was significant.

Results

The average superovulatory response increased markedly during the period 2004-2006 (Figure 2), and the effect of year was highly significant for all superovulatory traits studied. The number of collected embryos and number of discarded embryos were significantly (<0.01) higher for Swedish Red, but there was no significant breed difference in number of transferable embryos. The effects of age group and flush number were not significant. There was a tendency for lower number of transferable embryos collected during the grazing season in the summer (June-Aug). There was no clear time trend for the other fertility traits during the period studied.

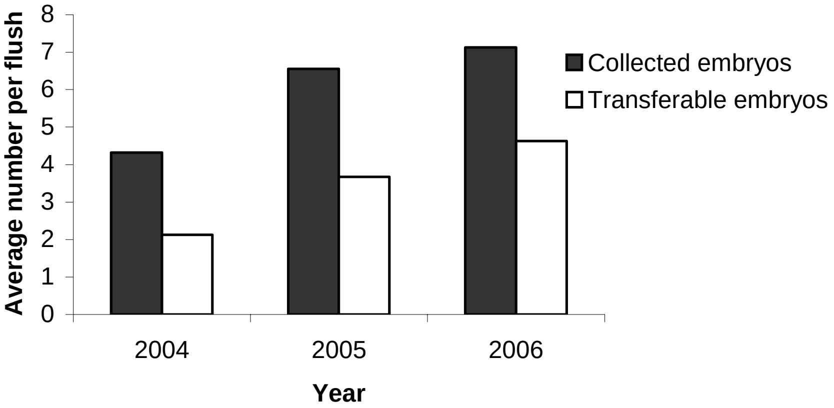

Fig.2. Average superovulatory response per year.

Estimated heritabilities were about 0.1 and repeatabilities about 0.4 for all superovulatory traits studied (Table 2). Genetic correlations were as expected high between total number of collected embryos and both other traits (Table 3). Weak genetic correlations were estimated between number of transferable embryos and number of discarded embryos.

We estimated weak residual correlations between superovulatory traits and other fertility traits in this study (Table 4). The strongest correlations were also favourable: with heat intensity in cows (0.10-0.14) and with number of inseminations (-0.07). The effect of number of embryos as an explanatory variable in the model for other fertility traits was not found to be significant.

Table 2. Estimated variance component[1] for permanent environmental (σ^2_{pe}), genetic (σ^2_a) and residual (σ^2_e) effects, and heritabilites (h^2) and repeatabilities (r) for the different superovulatory traits with SE as subscripts

Trait	σ^2_{pe}	σ^2_a	σ^2_e	h^2	R
Number of collected embryos	$10.0_{3.08}$	$3.21_{2.96}$	$16.7_{1.31}$	0.11	0.44
Number of transferable embryos	$4.31_{1.47}$	$1.85_{1.43}$	$9.09_{0.71}$	0.12	0.40
Number of discarded embryos	$3.50_{1.34}$	$1.70_{1.32}$	$7.04_{0.56}$	0.13	0.42

[1] From single-trait analyses.

Table 3. Estimated permanent environmental (r_{pe}), genetic (r_g), and residual (r_e) correlations with SE as subscripts

Correlated traits	r_{pe}	r_g	r_e
No of collected embryos – No of transferable	$0.82_{0.09}$	$0.70_{0.28}$	$0.76_{0.02}$
No of embryos – No of discarded	$0.78_{0.10}$	$0.67_{0.31}$	$0.67_{0.03}$
No of transferable – No of discarded	$0.28_{0.25}$	$-0.07_{0.57}$	$0.03_{0.06}$

Table 4. Estimated residual correlations between superovulatory traits and other fertility traits

Trait	Average no. of collected embryos	Average no. of transferable embryos
No of inseminations	-0.07	-0.07
Interval calving-AI	0.03	-0.04
Heat Intensity heifer	0.02	0.02
Heat Intensity cow	0.14	0.10

Discussion

This study differs from most earlier studies in that only superovulatory response data from heifers were included. The level of heritabilities and repeatabilities agree closely with previous studies by Asada and Terawaki (2002) and Bényei et al. (2004), even though the genetic variance was not significant due to a limited amount of data. Similar heritabilities were reported by Liboriussen et.al. (1995) and Michaux el.al. (2002), but they found lower repeatabilities. Higher heritabilities (0.20-0.65) for number of viable embryos was reported by Peixoto (2004), whereas a very low heritability of 0.03 was estimated in a study of field data by Tonhati et.al. (1999).

Other, more traditional traits related to female fertility in cattle, such as heat intensity, number of inseminations or interval between calving and insemination, are generally lowly heritable (heritabilities of less than 4%) (Roxtröm, 2001a,b). Compared with these, the heritability of number of collected embryos or number of transferable embryos is considerably higher. The ability to respond to superovulatory treatment is a less complex trait, as it involves only some of the important factors related to fertility.

The environmental influence is of great importance, both for number of embryos produced and the quality of embryos. In our study the time-trend was strikingly positive. Increasing knowledge and experience among the staff and responsible veterinary could explain a large part of the difference between years.

In our study, the average number of collected embryos was higher for Swedish Red than for Holstein. The difference between number of transferable embryos was however not significant. Liboriussen et.al. (1995) reported that red cattle breeds in Denmark responded better to superovulatory treatment than did Danish Friesian.

The estimated genetic correlation between total number of collected embryos and number of transferable embryos was high. This is to be expected as the measures are auto-correlated, and a high genetic correlation between these traits was also reported by Michaux et al. (2002).

It would be possible to select for response to superovulatory treatment in terms of number of transferable embryos, and an indirect selection may take place as the MOET nucleus scheme increases in importance in the breeding program. It has been suggested that this may also result in an unwanted increased natural twinning rate unless family size is standardised in MOET programs (Liboriussen et al. 1995).

In our study, we found weak phenotypic relationship between number of collected or transferable embryos and other fertility traits. The higher correlations with heat intensity in cows than in heifers was likely an effect of housing system, as the heifers are in tied stalls and the cows in loose-housing system.

Acknowledgements

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References

Asada, Y., and Terawaki, Y., 2002. Heritability and repeatability of superovulatory responses in Holstein population in Hokkaido, Japan. Asian-Aust. J. Anim. Sci. 15, 944-948.

Bényei, B., Gáspárdy, A., Komlósi, I. and Pécsi, A. 2004. Repeatability and heritability of ovulation number and embryos in dam-daughters pairs in superovulated Holstein-Friesian cows. Reprod. Dom. Anim. 39, 99-102.

Jensen, J., Mäntysaari, E. A., Madsen, P., and Thompson, R. (1997) *J. Ind. Soc. Ag. Stat.* 49 : 215-236.

Liboriussen, T., Makulska, J., Callesen, H. 1995. Genetic responsiveness of dairy cattle to superovulatory treatment. Acta Agric. Scand. Sect. A. Animal Sci. 45, 99-105.

Madsen, P. and Jensen, J. (2000) A user's guide to DMU. Version 6, release 4. Danish Institute of Agricultural Sciences, Research Centre Foulum, Denmark, 18 pp.

Michaux, C., Bagore, B., Chapaux, P., Hanzen, C., Leroy, P. and Massip, A. 2002. Genetic parameters for responsiveness of Belgian Blue Cattle to superovulatory treatment. Proc. 7th World Congr. Genetics Appl. Livest. Prod. Aug. 19-23 Montpellier, France. No 08-41.

Peixoto, M.G.C.D., Pereira, C.S., Bergmann, J.A.G., Penna, V.M. and Fonseca, C.G. 2004. Genetic parameters of multiple ovulation traits in Nellore females. Theriogenology 62, 1459-1464.

Roxström, A., Strandberg, E., Berglund, B., Emanuelson, U. and Philipsson, J. 2001a. Genetic and environmental correlations among fertility traits and milk production in different parities of Swedish red and white dairy cattle. Acta Agric. Scand. Sect. A. Animal Sci. 51, 7-14.

Roxström, A., Strandberg E., Berglund B., Emanuelson, U. and Philipsson, J. et al. 2001b.
Genetic and environmental correlations among female fertility traits, and between the ability to show oestrus and milk production in dairy cattle. Acta Agric. Scand.. Sect. A, Animal Sci. 51, 192-199.

SAS Institute Inc. 2007. SAS OnlineDoc® 9.1.3. Cary, NC: SAS Institute Inc.

Tonhati, H., Lôbo, R.B. and Oliviera, H.N. 1999. Repeatability and heritability of response to superovulation in Holstein cows. Theriogenology 51, 1151-1156.