

Heritability and Repeatability of Superovulatory Responses in Holstein Population in Hokkaido, Japan

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ABSTRACT : The aim of this study was to estimate heritability and repeatability for the number of embryos and transferable embryos collected per flush in Holstein population in Hokkaido, Japan. Data consisted of 306 MOET (Multiple Ovulation and Embryo Transfer) treatments on 224 Holstein cows from 1997 to 2000. Variance components for these traits were estimated using the REML procedure. The model included only non-genetic factors that were significant at the 0.05 level, through using generalized linear models, maximum likelihood methods, and stepwise regression procedure as fixed effects and sire and residual for heritabilities, donor and residual for repeatabilities as random effects. The factor identified as important in determining the results was the donor's estrous condition after superovulation. Heritabilities for the number of embryos and transferable embryos collected per flush were 0.14 and 0.09, respectively. The corresponding repeatabilities were 0.43 and 0.32, respectively. These results show that it was difficult to genetically improve these traits, thus, environmental and physical factors affecting the donor must be improved. These results also show that it is necessary to take the donor's estrous condition after superovulation and repeatabilities for the number of embryos and transferable embryos collected per flush into account when the genetic gains and inbreeding rates for MOET breeding schemes are predicted by a computer simulation. (*Asian-Aust. J. Anim. Sci.* 2002, Vol 15, No. 7: 944-948)

Key Words : Holstein, Superovulatory Responses, Heritability, Repeatability

INTRODUCTION

Earlier studies (Land and Hill, 1975; Nicholas and Smith, 1983; Ruane and Thompson, 1991) for MOET (Multiple Ovulation and Embryo Transfer) breeding scheme have suggested that by the use of MOET techniques it was possible to greatly increase the genetic gain per year due to increased selection intensities and reduced generation intervals. These studies assumed a constant number of embryos collected per donor per flush. However, in practice, the number of embryos collected per donor exhibited a high variability (Villanueva et al., 1995). Recent studies have presented the fear that the high variance in family size could lead to an increase in the inbreeding rates when MOET breeding schemes are carried out with a small MOET population.

Villanueva and Simm (1994) reported that the use of MOET technique can improve the genetic gain by greatly increasing the number of progeny to be produced by individuals, however, inbreeding rates accompany the increase, since fewer parents contribute to the next generation. Villanueva et al. (1995) suggested that repeatabilities concerning the embryo yields are important in determining the inbreeding rates, because increasing repeatabilities concerning the embryo yields can produce a high variance in family size, which leads to an increase in the inbreeding rates. Therefore, to estimate repeatabilities

for embryo yields need accurately to predict the genetic gains and inbreeding rates in MOET population. The number of embryos and transferable embryos collected per flush also gives considerably influences the genetic gains (Nicholas and Smith, 1983; Keller and Teepker, 1990; Villanueva and Simm, 1994; Terawaki and Asada, 2001). Therefore, it is very important to investigate the probability of genetic improvements for these traits using the estimated value of heritabilities.

However, prior to the estimation of genetic parameters for these traits, if these traits are affected by non-genetic factors, it is necessary to define these factors and include them in the models in order to estimate the exact genetic parameters. Several studies (Hasler et al., 1983; Donaldson, 1984; Isogai, 1992) indicated that the superovulatory responses were influenced by environmental and physical factors, as differences in the responses to superovulation between the various sources of hormones, the donor's condition, the season, the climate, and so on.

The objectives of this study were to define the non-genetic factors which influenced the number of embryos and transferable embryos collected per flush in Hokkaido, Japan, using generalized linear models, maximum likelihood methods, and the stepwise regression procedure, and to estimate heritabilities and repeatabilities for these traits using the REML procedure.

MATERIALS AND METHODS

Data

The data consisted of records of 306 superovulation and embryo recovery on 224 Holstein cows from 1997 to 2000

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at general dairy farms in Hokkaido, Japan. Observations contained the number of embryos and transferable embryos, and the classifying information on observations consisted of: the data on flush and artificial insemination, identification numbers of the donor cows, the donor's father, mother, and mate, the number of superovulation and flush, the technician, and the season of superovulation.

Factorial analysis

The initial analysis of data fitted a Poisson, a negative binomial, and a normal distribution to the observations, and compared the accuracy of the fit for the value.

In the present study, the non-genetic factors affecting the superovulatory responses of donors were examined using a generalized linear model and maximum likelihood methods (McCullagh and Nelder, 1983). The technicians, the age of donor at superovulation, the season at flush: spring (Mar. to May), summer (Jun. to Aug.), fall (Sep. to Nov.), and winter (Dec. to Feb.), the number of superovulations and flushes, the donor's estrous condition after superovulation, the genetic performance of milk production of the donor's father (based on the International evaluated value) as follows: $A \geq +1,500$ pound (p.), $+1,500$ p. $< B \geq +1,000$ p. $+1,000$ p. $< C \geq 0$, 0 p. $> D$, the genetic performance of milk production of the mate using artificial insemination on the donor: $A \geq +1,500$ pound (p.), $+1,500$ p. $< B \geq +1,000$ p. $+1,000$ p. $< C \geq 0$, and the year at flush were all included in a full model as fixed effects, and, through the stepwise regression procedure, only variables that were significant at the 0.05 level were defined as non-genetic factors affecting superovulatory responses.

Estimation of variance components

Variance components for the number of embryos and transferable embryos collected per flush were estimated using the REML procedure. The model included the significant non-genetic factors defined by factorial analysis as fixed effects, the sire and residual for heritabilities, and the donor and residual for repeatabilities as random effects. The heritabilities and repeatabilities for these traits were calculated using the variance components by the following formula:

$$R = \sigma_{donor}^2 / \sigma_P^2$$

R = repeatability.

σ_{donor}^2 = among donor variance component.

σ_P^2 = phenotypic variance component.

$$h^2 = 4 * \sigma_{sire}^2 / \sigma_P^2$$

h^2 = heritability.

σ_{sire}^2 = among sire variance component.

σ_P^2 = phenotypic variance component.

All analyses were conducted using GENSTAT5-Release 4.2 (2000).

RESULTS AND DISCUSSION

Table 1 shows the results of flushes with the donor cows. The total number of flushes, embryos, and transferable embryos were 306, 2,042 and 1,352, respectively. The value of mean, standard deviation, and coefficient of variation for the number of embryos collected per flush were 6.67, 5.78, and 0.87, respectively. The corresponding value for the number of transferable embryos collected per flush were 4.42, 4.11, and 0.93, respectively. The value of the mean number of embryos was lower than the estimates in some studies (8.96: Woolliams et al., 1995; 10.3: Hasler et al., 1983), and for the mean number of transferable embryos was equal to or lower than the estimate in some studies (6.4: Hasler et al., 1983; 6.85: Lohuis et al., 1993; 4.42: Woolliams et al., 1995; 5.90: Tonhati et al., 1999). The coefficient of variation was higher than most reproductive traits, which are normally between 0.1 and 0.3 (Smith, 1984).

Figure 1 shows the frequency distribution of the number of embryos and transferable embryos collected per flush. The frequency of treatments that collected no embryos or transferable embryos was highest.

Table 2 shows the goodness of fit of a normal, a Poisson, and a negative binomial distribution with the observation.

Table 1. Treatment situation of donors

	No. of flush	No. of embryos	No. of transferable embryos	Ave. no. of embryos per flush	Ave. no. of transferable embryos per flush
Total	306	2,042	1,352	6.67	4.42
Year					
1997	113	667	410	5.90	3.63
1998	117	789	542	6.74	4.63
1999 [#]	76	586	400	7.71	5.26

* No.: Number. * Ave.: Average. [#] Included result of flushes in 2000.

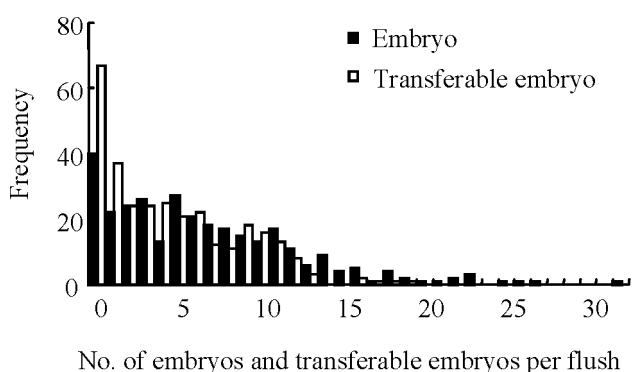


Figure 1. Frequency distribution of number of embryos and transferable embryos collected per flush

Table 2. Goodness of fit for a Poisson, a normal and a negative binomial models on the field data of the number of embryos and transferable embryos obtained

Data	Distribution	Goodness of fit	
		D.F.	χ^2
Embryos	Poisson	14	4,915.8
	Normal	13	2,369.8
	Negative binomial	12	23.39
Transferable embryos	Poisson	12	1,809.7
	Normal	11	4,538.5
	Negative binomial	8	49.25

These results indicate that a negative binomial distribution had the best fit with the observation among the three distributions.

The χ^2 -values and degree of freedom associated with the factors including generalized linear models for the number of embryos and transferable embryos collected per flush are shown in table 3. There was a significant effect ($p > 0.05$) on these traits of the donor's estrous condition after superovulation. There was no evidence for the season and genetic performance of milk production of the donor's father, which is consistent with the results of Asada and Terawaki (2000).

Table 4 shows the values for the components of phenotypic variance among the sire (donor's father), among the donor, heritabilities, and repeatabilities for the number of embryos and transferable embryos collected per flush. Repeatabilities for these traits were estimated as 0.43 and 0.32, respectively (table 4). Repeatability for the number of transferable embryos has been reported previously, and ranges from 0.11 to 0.35 (Bastidas, 1987; Lamberson, 1986; Lohuis et al., 1993; Woolliams et al., 1995; Tonhati et al., 1999). The repeatability estimate for the number of transferable embryos in our study (table 4) is similar to the estimate 0.31 obtained by Lohuis et al. (1993) using the REML procedure. Villanueva et al. (1995) reported that the

Table 3. Analysis of deviance for number of embryos and transferable embryos collected per flush (Number of embryos and transferable embryos was analysed assuming negative binomial model)

Source	Embryos		Transferable embryos	
	D.F.	χ^2	D.F.	χ^2
Season	3	0.94	3	0.75
Sire ¹⁾	3	0.95	3	1.66
Age	5	3.14	5	4.44
Flush	3	0.56	3	0.43
Mate ²⁾	2	0.99	2	0.45
Year	2	2.91	2	4.95
Superovulation	2	4.02	2	2.11
Technician	8	15.50	8	13.09
Estrous condition ³⁾	2	28.16*	2	33.06*

^{1),2)} Based on International evaluated value (pound) for genetic performance of milk production of donor's father or mate used artificial insemination on donor.

³⁾ Donor's estrous condition after treatment.

* $p < 0.05$.

Table 4. Value of variance components, heritability and repeatability for number of embryos and transferable embryos

Source	σ^2_{donor}	σ^2_{sire}	σ^2_P	h^2 * ¹	R^2 * ²
Embryos	14.3	1.13	33.46	0.14	0.43
Transferable embryos	5.47	0.38	16.29	0.09	0.34

σ^2_{donor} =Between donor variance component, σ^2_{sire} =Among sire

variance component, σ^2_P =Phenotypic variance component, h^2 =Heritability, R =Repeatability.

*¹ Fixed effects: Donor's estrous condition after superovulation, Random effects: Sire, residual.

*² Fixed effects: Donor's estrous condition after superovulation, Random effects: Donor, residual.

inbreeding rates obtained when repeatability (0.22) was included in a generating method of the number of embryos and transferable embryos collected per flush was higher than that when repeatability was ignored. It would be possible to make a more realistic prediction of simulation which includes repeatability in the method of generating the number of transferable embryos, because estimated repeatabilities in our study isn't so low that its values can be ignored.

The heritability estimate for the number of embryos and transferable embryos were estimated as 0.14 and 0.09, respectively. Tonhati et al. (1999) obtained considerably lower estimates for heritability (about the number of transferable embryos: 0.03) using MTDFREML. The results of heritability estimates in our study show that it isn't

advisable to try for a genetically improvement of these traits.

Keller and Teepker (1990) reported that the phenotypic correlation for the donor cow embryo yield with the milk yield was a negative (-0.3). Damatawewa and Berger (1998) reported genetic correlation between the yield and fertility traits, although there wasn't a direct relationship between the embryo yield and the milk yield. In their study, the genetic correlations were positive and undesirable between the yield traits and fertility traits, indicating that the genetic correlation between days open and 305-day adjusted yields for milk, fat, and protein in first-parity cows were 0.55, 0.53, and 0.55, and the genetic correlation between number of services and the corresponding yield traits in first-parity cows were 0.53, 0.63 and 0.62, respectively. They also showed that heritabilities for the fertility traits were low, estimating that heritabilities for days open and number of services were 0.12 and 0.03, respectively. Hansen et al. (1983) estimated that the genetic correlation for 305-days adjusted milk yield with days open was 0.34, and the number of services was 0.20 in first parity cows. Veerkamp et al. (2001) reported that genetic correlations for fertility traits with yields were unfavorable, ranging from 0.37 to 0.74. In the case of defined superovulatory responses as fertility traits, superovulatory responses seemed to have an undesirable relationship with yield traits. Therefore, the more yield traits improve genetically, the more difficult it is to make the number of embryos and transferable embryos collected per flush increase over the present number.

The results of our study suggested that improvements of physical factors (found in the present study), such as the donor's estrous condition after superovulation and the source of the superovulatory drug used, and environmental factors, such as the conditions of breeding, climate, and nutrition peculiar to the district (the donor cows included in MOET breeding schemes in Hokkaido, Japan, were dispersed at dairy farms across Hokkaido) are necessary, because the results of our study indicate that genetic improvement for these traits is difficult.

CONCLUSION

These results show that when the genetic gains and inbreeding rates for MOET population in Hokkaido, Japan, were predicted by a computer simulation, it was necessary to take the donor's estrous condition after superovulation and repeatabilities for the number of embryos and transferable embryos collected per flush into account. In the future, the more MOET techniques are actively used in Hokkaido, Japan, the more information for donors may be collected. It should be possible to investigate other non-genetic factors, aside from the factors investigated in the present study. If more information is obtained, it may be

possible to more accurately and realistically predict the genetic gains and inbreeding rates. These results also show that it is difficult to genetically improve these traits by selection, since heritabilities for the traits estimated in the present study were low, and improvements for these traits depend on improvements of the environmental and physical factors.

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