

## Relationships between Distribution of Number of Transferable Embryos and Inbreeding Coefficient in a MOET Dairy Cattle Population

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**ABSTRACT :** Genetic gains and inbreeding coefficients in a Holstein MOET breeding population were predicted under different conditions relating to the distribution of the number of transferable embryos collected per flush using Monte Carlo simulation. The numbers of transferable embryos collected per flush were determined using five distributions (distributions 1, 3, 5, 7 and 9) with different aspects and similar means. Distributions 1, 3, 5, 7 and 9 were assumed to have gamma distribution's parameters ( $\alpha$  and  $\beta$ ) of (1 and 4.4), (3 and 1.47), (5 and 0.88), (7 and 0.63) and (9 and 0.49), respectively. Inbreeding rates were statistically significantly different among distributions but genetic gains were not. Relationships between inbreeding rates and variances of family size could be clearly distinguished. The highest inbreeding coefficients were predicted in distribution 1 with the largest variance of family size, while distributions 5, 7 and 9 with smaller variance of family size had lower inbreeding coefficients. (*Asian-Aust. J. Anim. Sci.* 2002, Vol 15, No. 12 : 1686-1689)

**Key Words :** Holstein, MOET, Transferable Embryos, Family Size, Inbreeding Coefficient, Genetic Gain

### INTRODUCTION

Many works have examined the effects of number of transferable embryos collected per flush on genetic gain and inbreeding coefficient in the MOET cattle population (Nicholas and Smith, 1983; Keller and Teeper, 1990; Leich et al., 1995). These studies indicate the significant effects of number of transferable embryos collected per flush on the genetic character of the population. In many studies, a fixed number of embryos collected per flush was assumed or a simple probability distribution (for example, the Poisson distribution) was used. Villanueva et al. (1995) investigated the effects of improved reproductive techniques on genetic progress and inbreeding in MOET schemes for beef cattle by simulation experiments. In this report, models were used to determine the number of transferable embryos collected per flush in the simulation experiments. There are few studies about the relationship between the models for determining the number of transferable embryos collected per flush and genetic gain in the MOET beef or dairy cattle population. Asada and Terawaki (2000) examined the adaptation of certain models and estimated the suitable parameters for each models based on the distribution of the number of transferable embryos collected per flush in a Japanese Holstein population. Additionally, Terawaki and Asada (2001a) estimated genetic gains in a Japanese Holstein MOET population using the models with suitable parameters established by Asada and Terawaki (2000). The

estimated genetic gains were significantly different between models. Terawaki and Asada (2001a) used three different models to determine the number of transferable embryos collected per flush. The mean numbers of transferable embryos collected per flush in simulation experiments were different for each models, and as a result, the data did not clearly indicate whether the mean or the distribution of the number of transferable embryos collected per flush is the more important factor in genetic gain and inbreeding rate in the MOET population.

The objective of the present study was to confirm the relationship between the distributions of the number of transferable embryos and genetic gain or inbreeding coefficient in a MOET population by changing the parameters of the distributions while maintaining a constant mean of the number of transferable embryos collected per flush.

### MATERIALS AND METHODS

A hypothetical Holstein MOET breeding population was simulated by infinitesimal genetic model. The basic population consisted of 200 cattle (male:female=1:1) assumed to be unrelated. Animals to be used for reproducing the next generation were selected based on estimated breeding values (EBVs) using the animal model BLUP at each generation. EBVs were estimated in two different ways. Coefficients of inbreeding were included in the BLUP evaluation in one estimation and ignored in the other. Ten males and 30 females were selected and randomly mated in each generation. The breeding program involved juvenile MOET, and the generation was discrete. Only one animal of each set of full-sib brothers was selected. Selected females were treated with MOET at 13

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month of age (Nicholas and Smith, 1983). The rate of conception was assumed to be 50%. The true breeding values of the offspring were generated by adding the mean of their parents' true breeding values and the Mendelian sampling term. A lactation trait with a heritability value of 0.3 was selected for examination. Multiple ovulation treatments on the same donor cow were performed at 2 month intervals. Eighty-five matings per generation were carried out in order to maintain the population size as close as possible to 200 animals.

The numbers of transferable embryos collected per flush were generated following Model 2 as described by Villanueva et al. (1995). Although Villanueva et al. (1995) indicate the superiority of Model 1, Model 2 was chosen for this study because a study by Asada and Terawaki (2000) examined the adaptation of different models for generating the number of transferable embryos, and found Model 2 to be the most appropriate for the Japanese Holstein MOET breeding population. Parameters ( $\alpha$  and  $\beta$ ) of gamma distribution for generating the number of the transferable embryos were set at (1 and 4.4), (3 and 1.47), (5 and 0.88), (7 and 0.63) and (9 and 0.49) for distribution 1, distribution 3, distribution 5, distribution 7 and distribution 9 respectively. Distribution 1 reflects the present condition of MOET techniques in the field in Hokkaido, Japan. The parameters of distributions 3, 5, 7 and 9 were determined so that the expectations of the number of transferable embryos collected per flush were the same as for distribution 1. Simulations for each distribution were repeated 50 times.

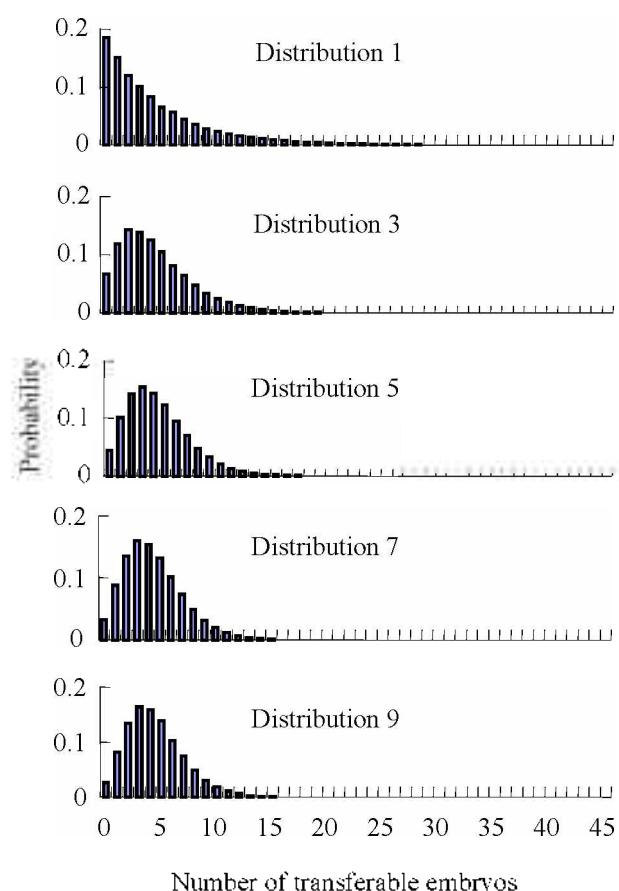
## RESULTS

The distributions of the number of transferable embryos collected per flush are shown in Figure 1. Aspects of five different distributions were classified into two groups. One group included only distribution 1 and the other included distributions 3, 5, 7 and 9. For distribution 1, the highest frequency occurred at no transferable embryos, and its probability decreased remarkably with the increase of the number of transferable embryos. For distribution 3, the highest frequency was recognized at 2 transferable embryos collected per flush, and for distributions 5, 7 and 9, 3 transferable embryos were most frequently collected in a flush. Distribution 1, furthermore, had the longest slope toward more transferable embryos. In contrast, both the highest peak and the shortest slope characterized distribution 9.

The statistics for the number of transferable embryos collected per flush in each distribution are shown in Table 1. The means of the number of transferable embryos collected per flush in the five distributions were similar, while the standard deviations were remarkably different across distributions. Standard deviations increased as parameter  $\alpha$

increased. The standard deviation of distribution 9 decreased by 47% compared with one of distribution 1. Skewnesses estimated for the five distributions were positive and indicated that the five distributions were skewed to the right. Distribution 1 in particular had remarkable skewness as can be seen in Figure 1. Kurtoses of the five distributions were positive, indicating that the densities of the five distributions were more peaked around the center than the density of a normal curve.

The influences of the shape of the distribution and the inclusion of coefficients of inbreeding in MME on genetic gains and the inbreeding coefficients of simulated



**Figure 1.** Probability distributions of the number of transferable embryos collected per flush generated with different parameters

**Table 1.** Means, standard deviations, maximum, skewness and kurtosis for the five distributions

Distribution	Mean	S.D.	Maximum	Skewness	Kurtosis
Distribution 1	4.39	4.84	43	1.93	5.06
Distribution 3	4.39	3.29	28	1.19	2.05
Distribution 5	4.38	2.87	25	0.95	1.26
Distribution 7	4.41	2.66	22	0.82	0.95
Distribution 9	4.43	2.57	20	0.78	0.77

population were examined by analysis of variance. Analysis

by GLM procedure (SAS, 1988) indicated that the distribution significantly influenced the inbreeding coefficients of the population, but had no effect on genetic gains. The inclusion of coefficients of inbreeding in MME had no influence on genetic gain nor on the inbreeding coefficient of a simulated population. Tables 2 and 3 show the least square means of genetic gains and inbreeding coefficients for the distributions. The genetic gains of distribution 5 tended to be larger than those of other distributions, but these trends were not clear. On the other hand, the differences in the inbreeding coefficients of the distributions were obvious and significant. No differences in inbreeding coefficients among the distributions were recognized until the third generation. For the most part, the inbreeding coefficients of distributions 1 and 3 changed comparably with generation, while the changes of inbreeding coefficients with generation were likewise comparable for distributions 5, 7 and 9. The inbreeding coefficients of distribution 5 were the lowest from the 4th generation to the 10th, in contrast with those of distribution 1, which were estimated to be the highest at the 4th.

**Table 2.** Least square means of genetic gain for distributions of the number of transferable embryos collected per flush

Generation	Distribution				
	1	3	5	7	9
1	0.01	0.02	0.04	0.03	0.03
2	0.34	0.30	0.38	0.29	0.36
3	0.70	0.69	0.73	0.71	0.76
4	1.03	1.04	1.14	1.05	1.13
5	1.39	1.43	1.48	1.42	1.46
6	1.66	1.83	1.80	1.72	1.72
7	1.97	2.11	2.12	2.00	2.03
8	2.25	2.43	2.46	2.32	2.30
9	2.55	2.72	2.76	2.61	2.62
10	2.83	2.98	3.04	2.92	2.91

The different family sizes for the five distributions are

**Table 3.** Least square means of inbreeding coefficient for distributions of the number of transferable embryos collected per flush

Generation	Distribution				
	1	3	5	7	9
1	0.01 <sup>aA</sup>	0.0 <sup>aA</sup>	0.0 <sup>aA</sup>	0.0 <sup>aA</sup>	0.0 <sup>aA</sup>
2	0.037 <sup>aA</sup>	0.040 <sup>aA</sup>	0.034 <sup>aA</sup>	0.034 <sup>aA</sup>	0.034 <sup>aA</sup>
3	0.082 <sup>aA</sup>	0.079 <sup>aA</sup>	0.082 <sup>aA</sup>	0.082 <sup>aA</sup>	0.080 <sup>aA</sup>
4	0.134 <sup>aA</sup>	0.128 <sup>abAB</sup>	0.120 <sup>bB</sup>	0.126 <sup>abB</sup>	0.122 <sup>bAB</sup>
5	0.180 <sup>aA</sup>	0.170 <sup>abAB</sup>	0.163 <sup>bB</sup>	0.173 <sup>abAB</sup>	0.166 <sup>bAB</sup>
6	0.223 <sup>aA</sup>	0.215 <sup>abAB</sup>	0.201 <sup>cB</sup>	0.210 <sup>bcAB</sup>	0.207 <sup>bcAB</sup>
7	0.266 <sup>aA</sup>	0.260 <sup>abAB</sup>	0.235 <sup>cC</sup>	0.248 <sup>bcABC</sup>	0.243 <sup>cBC</sup>
8	0.303 <sup>aA</sup>	0.293 <sup>abAB</sup>	0.272 <sup>cC</sup>	0.282 <sup>bcBC</sup>	0.279 <sup>bcBC</sup>
9	0.339 <sup>aA</sup>	0.330 <sup>aAB</sup>	0.307 <sup>bBC</sup>	0.314 <sup>bBC</sup>	0.312 <sup>bBC</sup>
10	0.374 <sup>aA</sup>	0.363 <sup>aAB</sup>	0.340 <sup>bc</sup>	0.347 <sup>bBC</sup>	0.347 <sup>bBC</sup>

<sup>a,b,c</sup> Values on the same line without a common superscript differ ( $p < 0.05$ ).

<sup>a,b,c</sup> Values on the same line without a common superscript differ ( $p < 0.01$ ).

shown in Table 4. Paternal half-sib family sizes were similar in all distributions, while maternal half-sib and full-sib family sizes in distribution 1 were larger than in the other distributions. Three kinds of family size variances were remarkably larger in distribution 1 than in the other distributions. On the other hand, variances of family size in distributions 5, 7 and 9 were similar and smaller than those in distributions 1 and 3.

## DISCUSSION

The means of the five distributions of the number of transferable embryos collected per flush were similar (4.38 to 4.43). This indicates that the shapes of distributions caused differences of results in the five simulation experiments using the different distributions.

No statistical differences of the genetic gains predicted using different distributions were found. On the other hand, the means of inbreeding coefficient were statistically different across the distributions. These results indicate that the aspect of distributions of the number of transferable embryos collected per flush, rather than genetic gains, influenced inbreeding coefficients in the MOET population.

Variance of family size has an effect on ideal population size, and the rate of inbreeding in a given population is influenced by the ideal population size. Specifically, an increase of variance of family size results in an acceleration of inbreeding rate in a population (Falconer and Mackay, 1989). A comparison of tables 3 and 4 clearly shows the relationship between inbreeding rate and variance of family size. The distributions with smaller variance of family size (5, 7 and 9) had smaller means of inbreeding coefficient.

The shape of the distribution of the number of transferable embryos collected per flush influenced variance of family size in the MOET population. Consequently, smaller inbreeding coefficients were predicted for distributions 5, 7 and 9 in which variance of family size was smaller than in distributions 1 and 3. The aspect of the distributions of the number of transferable embryos collected per flush had no effect on genetic gains in the MOET population.

## CONCLUSION

This study demonstrates that inbreeding rates of Holstein MOET breeding population are influenced by the aspects of the distribution of the number of transferable embryos collected per flush. Moreover, variances of family size are clearly dependent on the aspects of the distribution. Both Woolliams et al. (1995) and Asada and Terawaki (2001, 2002) identified factors affecting superovulatory responses in cattle, and Asada and Terawaki reported that the aspects of the distribution of the number of transferable embryos collected

**Table 4.** Family size for distributions of the number of transferable embryos collected per flush

Distribution	Paternal-half-sib		Maternal-half-sib		Full-sib	
	Mean	Variance	Mean	Variance	Mean	Variance
1	18.7	96.10	7.2	30.45	3.5	8.48
3	18.6	67.26	6.9	21.89	3.0	4.55
5	18.5	61.62	6.8	19.95	2.9	3.78
7	18.7	61.52	6.8	18.88	2.9	3.56
9	18.8	60.77	6.8	19.47	2.9	3.45

per flush were dependent on the degree of estrus of the donor cow. Terawaki and Asada (2001b) suggested the possibility that the ratio of the degree of estrus influenced genetic gain and inbreeding rate in the Holstein MOET breeding population. It will therefore be necessary to conduct further and detailed research on the relationships among the degree of the donor cow's estrus, the aspect of the distribution and mean of the number of transferable embryos collected per flush, and genetic gain and inbreeding rate in the Holstein MOET breeding population. It is also important to investigate relationships between variances of family size and the aspects of the distribution of the number of transferable embryos collected per flush.

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