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Comparison of Genetic Responses Using Reproductive Techniques of MOET and *In Vitro* Fertilization in Cattle Populations

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다배란과 수정란이식 및 체외수정기술을 이용한 소의 유전적 개량량 비교

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요 약

다배란과 수정란이식(MOET)과 체외수정(IVF)기술을 이용한 육종체계에서 예상되는 유전적 개량량을 여러 집단의 크기에서 비교한 결과 체외수정기술이 MOET육종기술보다 특히 개량대상 유전력이 낮을때 훨씬 효율적으로 나타났다. 그러나 유전력이 높아지면 (h^2 = 0.3, 0.5), MOET와 IVF간의 상대적 차이는 미진하게 나타났다. 체외수정을 이용한 육종기술에서 암컷의 선발 강도는 대단히 높일 수 있는 반면 난자의 회수율이 많을수록 상대적으로 수컷에 대한 선발 강도는 낮아진다. 그 이유는 한 가계에서 근친을 피하기 위해 한 마리의 수컷만 선발해야 하므로 수소의 선발강도는 난자의 회수율이 높을수록 상대적으로 낮아진다. 여러 수준의 난자회수율(10, 20, 30, 50, 100)중에서 30일 때 가장 높은 유전적 개량을 나타내었다.

(Key words: MOET, IVF, selection responses)

INTRODUCTION

The advent of recent reproductive technologies including Multiple Ovulation and Embryo Transfer(MOET) and *in vitro* fertilization(IVF) has brought animal breeders a promising potential for acceleration of genetic improvement. Since the paper of Nicholas and Smith(1983) was the very first work published on practical application of MOET, many papers(Land and Hill, 1975; McDaniel and Cassel, 1981; Powell, 1981; Juga and Maki-Tanila, 1987; Jeon *et al.*, 1990) have been published on the implication of MOET and IVF techniques which has a great advantage over traditional artificial insemination(AI) breeding scheme. In traditional AI breeding schemes, most of genetic improvement comes from the bull to bull path and the dam to dam path contributes least to the genetic improvement. In the paper of Nicholas and Smith (1983), they examined the two MOET breeding schemes of Juvenile and Adult schemes. However, in practise, the mixture of the two MOET schemes was more appropriate(Jeon *et al.*, 1990). Various IVF breeding schemes were examined by Jeon and Smith(1995). The advantage of IVF over MOET was more intense selection in the dam to dam path and even diallele cross, as is in plant, is also possible. The objective of this study was to compare the relative efficiency of genetic responses between MOET and IVF breeding schemes in various population sizes and selection schemes in cattles.

MATERIALS AND METHODS

The selection response from a given breeding program is predicted by the well known Rendel and Robertson's equation(1950):

$$\triangle G = i.r_{TI}.\sigma G / L \quad [1]$$

where $\triangle G$ = estimated genetic gain, or selecytion response

i = standardized selection differential (selection intensity)

r_{TI} = selection accuracy

σG = genetic standard deviation

L = generation interval

To study a comparative efficiency of different breeding schemes, the following simple genetic model was used to approximate the selection accuracy. The selection accuracy, r_{TI}, can be thought as the coefficient of determination(R^2) in the genetic prediction model as:

$$G_{OWN} = G_{Sire} + G_{Dam} + G_{all\ relatives} \quad [2]$$

where G_{OWN} = own genetic merit

G_{Sire} = sire's genetic merit

G_{Dam} = dam's genetic merit

$G_{all\ relatives}$ = relative's genetic merit

From equation [2], the accuracy of predictability(or, equivalently selecion accuracy) depends upon the amount of information from related animals(relatives) and was expressed as the coefficient of determination, R^2. The theoretical maximum of R^2 from the model including only sire and dam information is 50%, which is derived as:

$$G_{OWN} = 0.5(G_{Sire} + G_{Dam}) + m \quad [3]$$

for m being the mendelian segregation effect.

Taking variances of above equation,

$$V(G_{OWN}) = V[0.5(G_{Sire} + G_{Dam})] + V(m)$$
$$= 0.25V(G_{Sire}) + 0.25V(G_{Dam}) + V(m)$$

Assuming that they are from the same population, then the equality holds such that

$$V(G_{OWN}) = V(G_{Sire}) = V(G_{Dam}) = V(G)$$

then,

$$V(G_{OWN}) = 0.25V(G_{Sire}) + 0.25V(G_{Dam}) + V(m)$$
$$V(G) = 0.25V(G) + 0.25V(G) + V(m)$$
$$= 0.5V(G) + V(m)$$

Thus, $V(m) = 0.5V(G)$, which determines that the unknown genetic variation due to the model including only Sire and Dam infomation can theoretically predict only 50% of the own genetic merit, which is equivalently said that R^2 of the model is 50%. Then, the rest of unknown genetic vatriation is accounted for by other information, the term of "$G_{All\ relatives}$", in the right hand of equation [2]. The relatives other than the parents are possibly halfsibs(HS) and fullsibs(FS). Since the other distant relatives other than HS and FS are contributing so little to account for the variation of the model wherein sire and dam were already included. The additional genetic variation accounted for by the addition of HS and FS in the model with sire and dam is:

1. Halfsib(HS) added(Assumed Paternal Halfsib, PHS)

$$E(G_{OWN}) = E(0.5G_{Sire} + 0.5G_{Dam} + 0.25G_{PHS})$$
$$V(G_{OWN}) = V(0.5G_{Sire} + 0.5G_{Dam} + 0.25G_{PHS})$$
$$= 0.5^2V(G_{Sire}) + 0.5^2V(G_{Dam}) + 0.25^2V(GPHS) + 2[COV(G_{Sire}, G_{Dam}) +$$

$COV(G_{Sire}, G_{PHS})+COV(G_{Dam}, G_{DPHS})]$

where E(.) is the expected value and all COVs (G_i, G_j) were assumed so small to be ignored. Then, the proportion of genetic variability for each component is simply the square of the additive relation with G_{OWN}. An additional variability due to P_{HS} information is 0.252, which is 0625.

2. Fullsib(FS) added

$$E(G_{OWN})=E(0.5G_{Sire}+0.5G_{Dam}+0.5G_{FS})$$
$$V(G_{OWN}) =V(0.5G_{Sire}+0.5G_{Dam}+0.5G_{FS})$$
$$=0.5^2V(G_{Sire})+0.5^2V(G_{Dam})+0.5^2V(G_{FS})+2[COV(G_{Sire}, G_{Dam})+COV(G_{Sire}, G_{FS})+COV(G_{Dam}, G_{FS})]$$

where E(.) is the expected value and all COVs (G_i, G_j) were assumed minimal to be ignored. An additional variability due to FS information is 0.5^2, which is 0.25.

3. Both PHS and FS added

$$E(G_{OWN})=E(0.5G_{Sire}+0.5G_{Dam}+0.5G_{FS}+0.25G_{PHS})$$
$$V(G_{OWN})=V(0.5G_{Sire}+0.5G_{Dam}+0.5G_{FS}+0.25G_{PHS})$$
$$=0.5^2V(G_{Sire})+0.5^2V(G_{Dam})+0.5^2V(G_{FS})+0.25^2V(G_{PHS})+\text{all COV's}(G_i, G_j)$$

Table 1. Additional variability accounted for by the various relatives' information added in genetic models

Model	Genetic variability explained(R^2)
(1) Sire+Dam	0.5000
(2) Sire+Dam+PHS	0.5625
(3) Sire+Dam+FS	0.7250
(4) Sire+Dam+FS+PHS	0.8125

Table 2. Parameters used in this study

Traits : Economic traits
Population size : 10^3, 10^4, 10^5 (dairy or beef cattles)
Heritability(h^2) : 0.05, 0.3, 0.5
Phenotypic standard deviation(σP) = 1.0 (unit)
Selection method : Truncation selection
Selection criteria : Selection Index with various information
1) MOET : Own+Sire+Dam+FS+PHS
2) ivf : Own+Sire+Dam+FS

Selection intensity :
1) MOET : Top 5 sires and no of donors depending upon number of transferable embryos(N_{ET})
N_C = no. of breeding females
N_D = no. of donors selected
N_{ET} = no. of transferable embryos (2, 4, 8, 16, 32 were assumed)
2) ivf : Top 5 sires and no of donors depending upon number of oocytes collected(N_{ET}) (10, 20, 30, 50, 100)

Again, assumed all COV's(G_i, G_j) were zero's. An additional variability due to FS plus PHS information is 0.52+0.252, which is 0.3125. The additional variability for the cases of 1), 2), and 3) were summarized in Table 1.

To compare the general efficiency of breeding schemes using different reproductive techniques of MOET and IVF, the parameters used in this study were in Table 2.

The selection intensity(i) for MOET and IVF breeding schemes is defined as:

4. MOET

Let NC be the number of breeding females, ND the number of donor selected, and NET the number of transferable embryos. Then the selection percentage(%) is ND/NC. The ND is depending upon NET. ND is determined as NC/NET.

5. IVF

For IVF, almost infinite number of oocytes can be collected. However, in this study, 6 levels of oocyte collection were assumed(10, 20, 30, 40, 50, 100). If possible, ND is recommended to be kept nearly to minimum for high selection intensity. The main advantage of IVF is that diallele cross, as is in plant, is also possible.

RESULTS AND DISCUSSION

As heritability(h^2) decreased, selection responses were greater for *in vitro* fertilization (IVF) than for MOET breeding schemes. For population size of 10^3 with the number of transferable embryos(N_{ET}) of 2, the selection response($\triangle G$) was 0.015 and increased double when N_{ET} increased to 4(Table 3). However, the selection responses were not much changed as N_{ET} increased more than 4. The similar trend was observed for the population sizes of 10^4 and 10^5. For IVF breeding schemes in all population sizes(10^3, 10^4, 10^5), the selection responses were not continuously increased as the yield of oocytes increased. If more oocytes from a donor were collected, the selection percentage of males became less, resulting in lower selection intensity and cosequently, low selection response. The optimum number of oocytes collected from donors for IVF breeding schemes were found around 30 per donor. When h^2 became larger,

Table 3. Expected genetic gain from breeding schemes using different reproductive techniques

h^2	Scheme	NC	N_{ET}	$\triangle G$
0.05	MOET	1,000	2	0.0150
		1,000	4	0.0256
		1,000	8	0.0273
		1,000	16	0.0281
		1,000	32	0.0284
	IVF	1,000	10	0.0584
		1,000	20	0.0604
		1,000	30	0.0608
		1,000	50	0.0606
		1,000	70	0.0599
		1,000	100	0.0590

Table 4. Expected genetic gain from breeding schemes using different reproductive techniques

h^2	Scheme	NC	N_{ET}	$\triangle G$
0.30	MOET	1,000	2	0.1045
		1,000	4	0.1249
		1,000	8	0.1334
		1,000	16	0.1374
		1,000	32	0.1383
	IVF	1,000	10	0.1566
		1,000	20	0.1603
		1,000	30	0.1606
		1,000	50	0.1596
		1,000	70	0.1575
		1,000	100	0.1550

Table 5. Expected genetic gain from breeding schemes using different reproductive techniques

h^2	Scheme	NC	N_{ET}	$\triangle G$
0.50	MOET	1,000	2	0.1136
		1,000	4	0.1407
		1,000	8	0.2035
		1,000	16	0.2096
		1,000	32	0.2112
	IVF	1,000	10	0.2155
		1,000	20	0.2204
		1,000	30	0.2208
		1,000	50	0.2194
		1,000	70	0.2165
		1,000	100	0.2131

Table 6. Expected genetic gain from breeding schemes using different reproductive techniques

h^2	Scheme	NC	N_{ET}	$\triangle G$
0.05	MOET	10,000	2	0.0152
		10,000	4	0.0310
		10,000	8	0.0331
		10,000	16	0.0343
		10,000	32	0.0349
	IVF	10,000	10	0.0706
		10,000	20	0.0737
		10,000	30	0.0748
		10,000	50	0.0755
		10,000	70	0.0759
		10,000	100	0.0760

Table 7. Expected genetic gain from breeding schemes using different reproductive techniques

h^2	Scheme	NC	N_{ET}	$\triangle G$
0.30	MOET	10,000	2	0.0613
		10,000	4	0.1517
		10,000	8	0.1616
		10,000	16	0.1672
		10,000	32	0.1702
	IVF	10,000	10	0.1893
		10,000	20	0.1752
		10,000	30	0.1976
		10,000	50	0.1989
		10,000	70	0.1998
		10,000	100	0.1998

Table 8. Expected genetic gain from breeding schemes using different reproductive techniques

h^2	Scheme	NC	N_{ET}	$\triangle G$
0.50	MOET	10,000	2	0.0935
		10,000	4	0.2314
		10,000	8	0.2466
		10,000	16	0.2550
		10,000	32	0.2596
	IVF	10,000	10	0.2606
		10,000	20	0.2687
		10,000	30	0.2716
		10,000	50	0.2735
		10,000	70	0.2746
		10,000	100	0.2746

the relative efficiency of selection responses between MOET and IVF breeding schemes was lessened. Therefore, more advantage was achieved for lower heritable traits. This implies that IVF breeding scheme could be more effective in selection for reproductive traits, which have in general low heritabilities(h^2 = 0.0 to 0.1).

SUMMARY

Relative efficiency of selction responses between MOET and IVF breeding schemes for closed cattle populations with sizes of 10^3, 10^4, and 10^5 were studied for various population sizes and selection schemes in cattles. The breeding schemes employing IVF technique were more effective than those with MOET technique when heritabilities(h^2) of traits of interest were very low(h^2=0.05). However, when h^2 were 0.3 or greater, the efficiency of IVF over MOET was less significant, which was due to the fact that for a given breeding population size in IVF

Table 9. Expected genetic gain from breeding schemes using different reproductive techniques

h^2	Scheme	NC	N_{ET}	$\triangle G$
0.05	MOET	100,000	2	0.0250
		100,000	4	0.0310
		100,000	8	0.0346
		100,000	16	0.0374
		100,000	32	0.0398
	IVF	100,000	10	0.0750
		100,000	20	0.0816
		100,000	30	0.0848
		100,000	50	0.0885
		100,000	70	0.0875
		100,000	100	0.0884

Table 10. Expected genetic gain from breeding schemes using different reproductive techniques

h^2	Scheme	NC	N_{ET}	$\triangle G$
0.30	MOET	100,000	2	0.1226
		100,000	4	0.1517
		100,000	8	0.1689
		100,000	16	0.1825
		100,000	32	0.1941
	IVF	100,000	10	0.2012
		100,000	20	0.2163
		100,000	30	0.2243
		100,000	50	0.2332
		100,000	70	0.2303
		100,000	100	0.2325

breeding schemes, as the more intense selection was practised on dams, the less selection intensity was possible in sires. The optimum number of oocytes to be collected in IVF breeding schemes was found to be 30 per donor.

Table 11. Expected genetic gain from breeding schemes using different reproductive techniques

h^2	Scheme	NC	N_{ET}	$\triangle G$
0.50	MOET	100,000	2	0.1871
		100,000	4	0.2314
		100,000	8	0.2576
		100,000	16	0.2784
		100,000	32	0.2961
	IVF	100,000	10	0.2769
		100,000	20	0.2975
		100,000	30	0.3085
		100,000	50	0.3206
		100,000	70	0.3165
		100,000	100	0.3148

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