

Breeding Scheme for Beef Cattle by Use of Embryo Transfer

By HIROTAKA TANAKA, TSUTOMU FURUKAWA
and YUKIO YAMADA*

Animal Breeding and Genetics Division, National Institute of Animal Industry
(Yatabe, Ibaraki, 305 Japan)

* College of Agriculture, Kyoto University
(Kyoto, 606 Japan)

In spite of a very high demand for beef, the rate of increase of beef production is much slower than that of pork or broiler production, and consequently its price is also higher. Major reasons ascribed to the slower increase of beef production are a long generation interval, a lower reproduction rate of cattle, and almost negligible selection pressure on cows per generation. Under such situations, a breeding scheme for beef cattle by using new technologies is desired. Technology of embryo transfer, which has developed to a commercially applicable level in Japan, is one of the new technologies that has stimulated further research on super-ovulation, embryo recovery, oestrus synchronization, deep freezing of embryos and embryo transfer.

In cattle breeding, 4 expected sources of genetic gains are i) production of young bulls by bulls, ii) heifers by bulls, iii) young bulls by cows and iv) heifers by cows. Ranking of relative genetic gains from these 4 sources will be partly changed by the adoption of embryo transfer. It is unlikely that very high genetic gain could be expected from selection of cows to produce heifers. Hence, selection of cows to produce young bulls will be most important in the application of embryo transfer in cattle breeding. Therefore a new breeding scheme with the objective of increasing intensity of selection on female side and shortening the generation interval by carrying out a sib test instead of a progeny test, is desired.

The aim of this research is to present a breeding scheme by using embryo transfer, and to predict genetic improvement in comparison with the conventional breeding scheme in a nucleus herd and a

commercial herd.

Standard plan in the breeding herd and prediction of genetic gain

In this section, a breeding scheme by using embryo transfer in the nucleus breeding herd is presented and predicted genetic gain is compared with that of the conventional breeding scheme in a nucleus herd.

1) Assumptions and calculation

(1) Suppose a closed herd of 300 cows in the conventional scheme (CS). As for the embryo transfer scheme (ETS), number of donors and live calves per donor are determined equally by the number of live calves expected in CS.

(2) In CS, selection of young bulls for the growth trait is done firstly by their own records and secondly for the carcass trait by their son's records. In ETS, on the contrary, selection of young bulls and heifers for the growth trait is carried out first by assessing their own records, and then by selection of bulls based on the records of their male sibs (Figs. 1, 2).

(3) Heritabilities are assumed 0.5 for the growth trait, and 0.4 or 0.6 for the carcass trait. The genetic correlation between the two traits is assumed to be 0.0 ± 0.2 .

(4) Accuracy of selection (r_{GP}) is calculated by the following equations.

① Individual selection $r_{GP} = h$

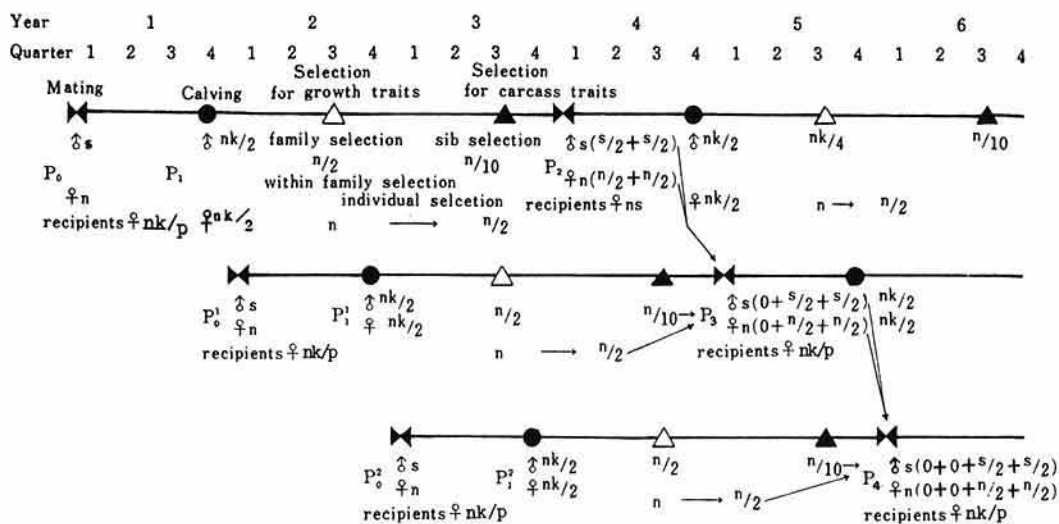


Fig. 1. An example of selection program by embryo transfer method

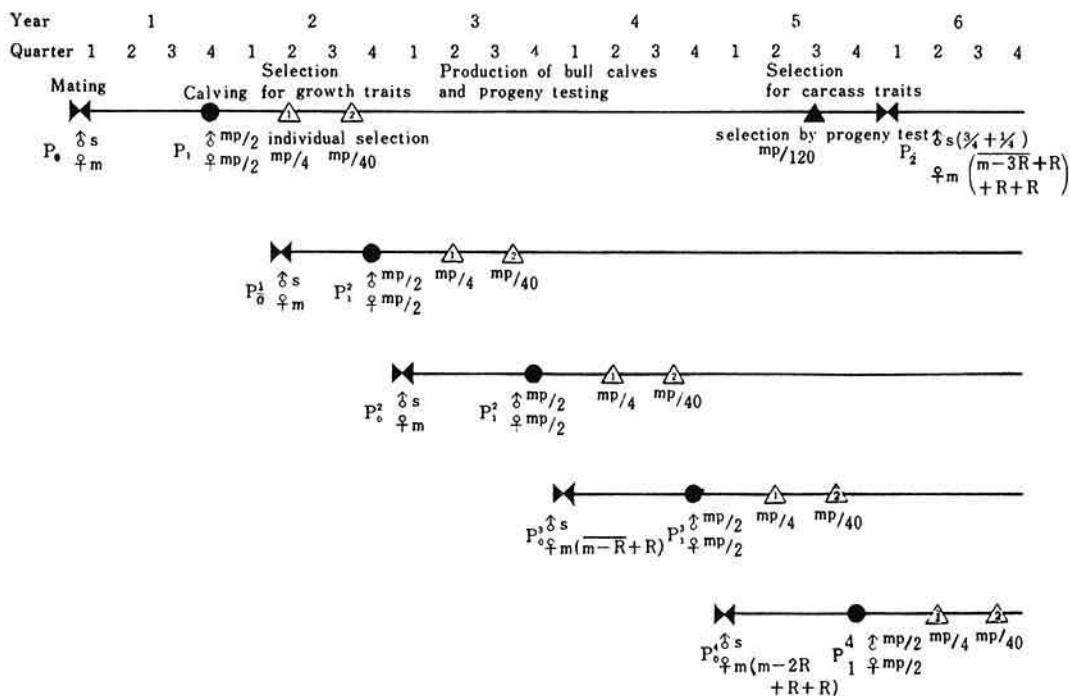


Fig. 2. An example of selection program by conventional method

- ② Within family selection $r_{GP} = h \sqrt{\frac{1 - \frac{1}{2}}{1 - t}}$
- ③ Full sib test $r_{GP} = \frac{1}{2} h \sqrt{\frac{n}{1 + (n-1)t}}$
- ④ Progeny test $r_{GP} = \frac{1}{2} h \sqrt{\frac{q}{1 + (q-1)t}}$
- ⑤ Combined selection with individual records and full sib records

$$r_{GP} = h \sqrt{1 + \frac{\left(\frac{1}{2} - t\right)^2}{1 - t} \cdot \frac{n}{1 + nt}}$$

where h : Square root of heritability
 n : Number of full sibs tested
 q : Number of progenies per sire
 t : Intraclass correlation

(5) Genetic gain is calculated as follows, assuming additive genetic effects, no sex-linkage and no maternal effects.

① ETS

Genetic improvement does not proceed until individuals selected produce their progenies. In ETS, it takes 3 years to complete a sib test before selection is done. Then, half of the breeding herd is replaced by young bulls and heifers selected.

$$\begin{aligned} A_2 &= A_1 \\ A_3 &= A_1 + (1/4)(\Delta G_m + \Delta G_f) \\ A_4 &= A_1 + (1/2)(\Delta G_m + \Delta G_f) \\ A_5 &= A_1 + (1/2)(\Delta G_m + \Delta G_f) \\ &\vdots \\ A_Y &= (1/2)\{A_{(Y-3)} + A_{(Y-4)} + (\Delta G_m + \Delta G_f)\} \end{aligned}$$

where A_Y : Genetic gain in yth year
 ΔG_m : Genetic gain per generation on male
 ΔG_f : Genetic gain per generation on female

② CS

In CS, it takes 5 years to complete a progeny test. A quarter of the bulls in the breeding herd are replaced by young bulls selected. After 3 years since the start of the breeding scheme, cows in the breeding herd are replaced by heifers selected, each year at the rate of R .

$$\begin{aligned} B_{m5} &= B_{m4} = B_{m3} = B_{m2} = B_{m1} \\ B_{m6} &= B_{m5} + (1/4)\Delta G_m' \end{aligned}$$

$$\begin{aligned} B_{m7} &= B_{m6} + (1/4)\Delta G_m' \\ B_{m8} &= B_{m7} + (1/4)\Delta G_m' \\ B_{mY} &= (1/4)\{B_{(Y-5)} + B_{(Y-6)} + B_{(Y-7)} + B_{(Y-8)}\} + \Delta G_m' \\ B_{f3} &= B_{f2} = B_{f1} \\ B_{f4} &= B_{f3} + \Delta G_f \cdot R \\ B_{f5} &= B_{f(Y-1)} \cdot (1-R) + (B_{(Y-3)} + \Delta G_f)R \\ B_{f1} &= B_{m1} = B_1 \\ B_Y &= (1/2)(B_{mY} + B_{fY}) \end{aligned}$$

where B_Y : Genetic gain in yth year
 B_{mY} : Genetic gain on male in yth year
 B_{fY} : Genetic gain on female in yth year
 $\Delta G_m'$: Genetic gain per generation on male
 $\Delta G_f'$: Genetic gain per generation on female
 R : Rate of female replacement per year

2) Result and discussion

For the growth trait, Fig. 3 shows prediction of genetic gain by different breeding schemes when the female selection rate is 67% in CS. Genetic gain in 15th year is 2.1 standard deviation unit (σ) in ETS and 1.1 σ in CS when genetic correlation between the growth trait and the carcass trait is

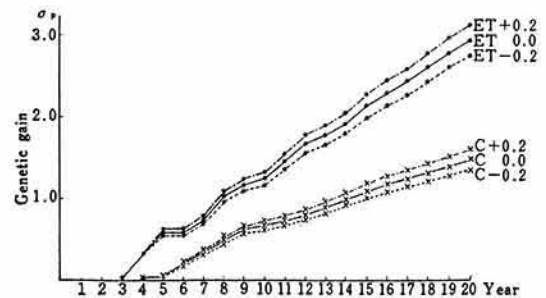


Fig. 3. Prediction of genetic gain on growth trait by different breeding methods when female selection rate is 67% in the conventional method
 ●---● ET+0.2 (Embryo transfer method, genetic corr. +0.2)
 ●—● ET 0.0 (Embryo transfer method, genetic corr. 0.0)
 ●---● ET-0.2 (Embryo transfer method, genetic corr. -0.2)
 ×---× C +0.2 (Conventional method, genetic corr. +0.2)
 ×—× C 0.0 (Conventional method, genetic corr. 0.0)
 ×---× C -0.2 (Conventional method, genetic corr. -0.2)

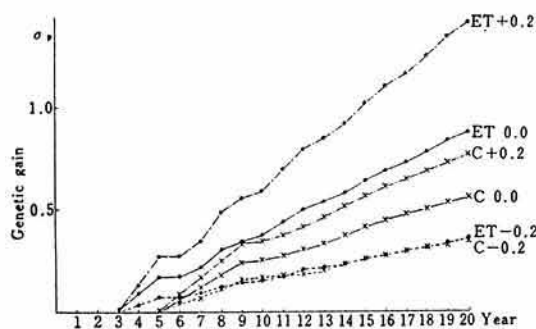


Fig. 4. Prediction of genetic gain on carcass trait by different breeding methods when no female selection is practiced in the conventional method

- ET+0.2(Embryo transfer method, genetic corr. +0.2)
- ET 0.0(Embryo transfer method, genetic corr. 0.0)
- - -● ET-0.2(Embryo transfer method, genetic corr. -0.2)
- ×- - -× C +0.2(Conventional method, genetic corr. +0.2)
- ×—× C 0.0(Conventional method, genetic corr. 0.0)
- ×- - -× C -0.2(Conventional method, genetic corr. -0.2)

zero. For the carcass trait, no female selection is practised. Genetic gain in 15th year is 0.6σ in ETS and 0.4σ in CS when genetic correlation between the two traits is zero (Fig. 4). Genetic response of the carcass trait is greatly influenced by the correlated traits.

Hence it is concluded that genetic gain in ETS exceeds that of CS by shortening the generation interval and increasing the female selection intensity in the growth trait. Introduction of a sib test instead of a progeny test can reduce the time required for testing from 5 to 3 years. Genetic gain on the carcass trait remains rather low, particularly when the genetic correlation with growth trait is negative, because accuracy of selection is lower in the sib test than in the progeny test.

Standard plan in the commercial herd and prediction of genetic progress

In this section, genetic progress in the commercial herd is predicted. In the nucleus breeding herd

system, all efforts for breeding are concentrated on the breeding herd and the commercial herd receives its gain but shares the whole cost. In this system, nucleus breeding stations are established on each district, assuming a whole breeding scheme of the country consists of several geographically divided subsystems according to districts. Semen of the bulls produced is used within the district and some doses of semen, brought from outside of this program are also used.

1) Assumptions

(1) Suppose a certain district with cow population of 150,000.

(2) The commercial herd receives the semen supply from the nucleus herd every year. It is not closed completely and some doses of semen brought from outside of the program are served randomly.

(3) The initial genetic superiority of the nucleus herd over the commercial herd is 0.25σ or 0.5σ and that of the sire's breeding values from outside of the program is zero or 0.25σ .

(4) For the comparison of breeding efficiencies, selection in the nucleus herd is terminated at 15th year and thereafter the genetic gain attained in the

Table 1. Definition of symbols

Symbol	Definition
G_{MY}	Mean breeding value of the male in the nucleus herd
ΔG_M	Genetic gain of the male per generation in the nucleus herd
ΔG_F	Genetic gain of the female per generation in the nucleus herd
M_{SY}	Mean breeding value of the male selected in yth year in the nucleus herd
B_Y	Mean breeding value of the sire outside the program in yth year
B_0	Mean genetic difference between nucleus herd in the conventional scheme and the sire outside the program at the start of selection program
C_{FY}^*	Mean breeding value of the female in yth year in the conventional scheme
C_{MY}	Mean breeding value of the sire mated to the commercial herd
C_{FY}	Mean breeding value of the female commercial herd in yth year
D_0	Mean genetic difference between nucleus and commercial herds at the start of selection program
R_M	Percentage of semen supply of the male in the nucleus to the commercial herd

**Table 2. Yearly genetic gain in the commercial herd
(Embryo transfer scheme; cows were culled in the order of their ages)**

Year	Mean breeding value of the male in the nucleus herd	Sire from outside the program	Sire mean	Cow mean	Mean breeding value of the progeny
Y	G_{MY}	B_Y	C_{MY}	C_{FY}	C_Y
0	D_0	B_0	$R_M D_0 + (1-R_M)B_0$	0	
1	D_0	B_0	$R_M D_0 + (1-R_M)B_0$	0	$1/2\{R_M D_0 + (1-R_M)B_0\}$
2	D_0	B_0	$R_M D_0 + (1-R_M)B_0$	0	$1/2\{R_M D_0 + (1-R_M)B_0\}$
3	$D_0 + 1/8 \Delta G_M$	$G_{F_3}^* + B_0$	$R_M G_{M_3} + (1-R_M)B_3$	$1/4 C_1$	$1/2\{R_M G_{M_3} + (1-R_M)B_3 + C_{F_3}\} = 1/2(C_{M_3} + C_{F_3})$
4	$D_0 + 1/4 \Delta G_M$	$C_{F_4}^* + B_0$	$R_M G_{M_4} + (1-R_M)B_4$	$1/4(C_1 + C_2)$	$1/2(C_{M_4} + C_{F_4})$
5	$D_0 + 3/8 \Delta G_M$	$C_{F_5}^* + B_0$	$R_M G_{M_5} + (1-R_M)B_5$	$1/4(C_1 + C_2 + C_3)$	$1/2(C_{M_5} + C_{F_5})$
6	$1/8(G_3 + 7D_0 + 4 \Delta G_M)$	$C_{F_6}^* + B_0$	$R_M G_{M_6} + (1-R_M)B_6$	$1/4(C_1 + C_2 + C_3 + C_4)$	$1/2(C_{M_6} + C_{F_6})$
7	$1/8(G_3 + G_4 + 6D_0 + 5 \Delta G_M)$	$C_{F_7}^* + B_0$	$R_M G_{M_7} + (1-R_M)B_7$	$1/4(C_2 + C_3 + C_4 + C_5)$	$1/2(C_{M_7} + C_{F_7})$
8	$1/8(G_3 + G_4 + G_5 + 5D_0 + 6 \Delta G_M)$	$C_{F_8}^* + B_0$	$R_M G_{M_8} + (1-R_M)B_8$	$1/4(C_3 + C_4 + C_5 + C_6)$	$1/2(C_{M_8} + C_{F_8})$
9	$1/8(G_3 + G_4 + G_5 + G_6 + 4D_0 + 7 \Delta G_M)$	$C_{F_9}^* + B_0$	$R_M G_{M_9} + (1-R_M)B_9$	$1/4(C_4 + C_5 + C_6 + C_7)$	$1/2(C_{M_9} + C_{F_9})$
10	$1/8(G_3 + G_4 + G_5 + G_6 + G_7 + 3D_0 + 8 \Delta G_M)$	$C_{F_{10}}^* + B_0$	$R_M G_{M_{10}} + (1-R_M)B_{10}$	$1/4(C_5 + C_6 + C_7 + C_8)$	$1/2(C_{M_{10}} + C_{F_{10}})$
	$G_{MY} = 1/8 \sum_{i=1}^8 M_{S(Y-i+1)}$	$B_Y = C_{FY}^* + B_0$	$C_{MY} = R_M G_{MY} + (1-R_M)B_Y$	$C_{FY} = 1/4 \sum_{i=1}^4 C_{(Y-i-1)}$	$C_Y = 1/2(C_{MY} + C_{FY})$

**Table 3. Yearly genetic gain in the commercial herd
(Conventional scheme; cows were culled in the order of their ages)**

Year	Mean breeding value of the male in the nucleus herd	Sire from outside the program	Sire mean	Cow mean	Mean breeding value of the progeny
Y	G_{MY}	B_Y	C_{MY}	C_{FY}	C_Y
0	D_0	B_0	$R_M D_0 + (1-R_M)B_0$	0	
1	D_0	B_0	$R_M D_0 + (1-R_M)B_0$	0	$1/2(C_{M_0} + 0)$
2	D_0	B_0	$R_M D_0 + (1-R_M)B_0$	0	$1/2(C_{M_1} + 0)$
3	D_0	$C_{F_3}^* + B_0$	$R_M D_0 + (1-R_M)B_3$	$1/4 C_1$	$1/2(C_{M_2} + 0)$
4	D_0	$C_{F_4}^* + B_0$	$R_M D_0 + (1-R_M)B_4$	$1/4(C_1 + C_2)$	$1/2(C_{M_3} + C_{F_3}^*)$
5	$D_0 + 1/6 \Delta G_M$	$C_{F_5}^* + B_0$	$R_M G_{M_5} + (1-R_M)B_5$	$1/4(C_1 + C_2 + C_3)$	$1/2(C_{M_4} + C_{F_4}^*)$
6	$D_0 + 1/3 \Delta G_M$	$C_{F_6}^* + B_0$	$R_M G_{M_6} + (1-R_M)B_6$	$1/4(C_1 + C_2 + C_3 + C_4)$	$1/2(C_{M_5} + C_{F_5}^*)$
7	$D_0 + 1/2 \Delta G_M$	$C_{F_7}^* + B_0$	$R_M G_{M_7} + (1-R_M)B_7$	$1/4(C_2 + C_3 + C_4 + C_5)$	$1/2(C_{M_6} + C_{F_6}^*)$
8	$1/6(G_3 + 5D_0 + 4 \Delta G_M)$	$C_{F_8}^* + B_0$	$R_M G_{M_8} + (1-R_M)B_8$	$1/4(C_3 + C_4 + C_5 + C_6)$	$1/2(C_{M_7} + C_{F_7}^*)$
9	$1/6(G_3 + G_4 + 4D_0 + 5 \Delta G_M)$	$C_{F_9}^* + B_0$	$R_M G_{M_9} + (1-R_M)B_9$	$1/4(C_4 + C_5 + C_6 + C_7)$	$1/2(C_{M_8} + C_{F_8}^*)$
10	$1/6(G_3 + G_4 + G_5 + 3D_0 + 6 \Delta G_M)$	$C_{F_{10}}^* + B_0$	$R_M G_{M_{10}} + (1-R_M)B_{10}$	$1/4(C_5 + C_6 + C_7 + C_8)$	$1/2(C_{M_9} + C_{F_9}^*)$
	$G_{MY} = 1/6 \sum_{i=1}^6 M_{S(Y-i+1)}$	$B_Y = C_{FY}^* + B_0$	$C_{MY} = R_M G_{MY} + (1-R_M)B_Y$	$C_{FY} = 1/4 \sum_{i=1}^4 C_{(Y-i-1)}$	$C_Y = 1/2(C_{MY-1} + C_{FY-1})$

nucleus herd was disseminated to the commercial herd.

(5) The bulls serve until the age of 10 and cows in the commercial herd are replaced either randomly or in the order of their ages after their 4th parturition.

(6) The number of bulls selected every year in the nucleus herd is 4 in ETS and 2 in CS, thus making the total number of bulls serving to the commercial herd as 32 in ETS and 12 in CS. Consequently, the number of cows served in a year is 96,000 and 36,000 in ETS and in CS, respectively.

2) Calculation

Symbols used are shown in Table 1.

Genetic improvement is calculated as shown in Tables 2 and 3.

Cumulative genetic progress in the commercial herd (A_{CY}) is calculated by the following equation.

$$A_{CY} = \frac{1}{2} \sum_{Y=1}^y (C_{MY} + C_{FY})$$

3) Result and discussion

Assuming that heritabilities of the growth and

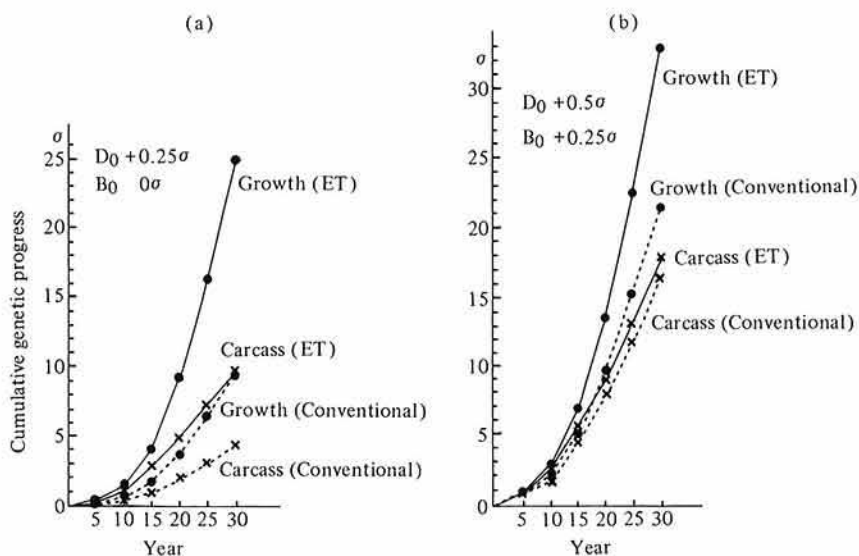


Fig. 5. Prediction of cumulative genetic progress in the commercial herd

It is assumed that heritabilities of the growth trait (●) and carcass trait (×) are 0.5 and 0.4, respectively and that the genetic correlation between the two traits is -0.2 . The percentage of semen supply to the commercial herd is 60% for ET (—) and 20% for conventional (----).

D_0 : Mean genetic difference between nucleus and commercial herds at the start of selection program

B_0 : Mean genetic difference between nucleus herd in the conventional scheme and the sires outside the program at the start of selection program

carcass traits are 0.5 and 0.4, respectively, genetic correlation between two traits is -0.2 , the initial genetic superiority of the nucleus herd over the commercial is 0.25σ , the average superiority of the sires introduced from outside of the program is zero and cows are replaced in the order of their seniority, the following results are obtained.

For the growth trait, the cumulative genetic progress in the commercial herd during 25 years is estimated at 16.3σ in ETS and 6.4σ in CS. For the carcass trait, the progress is estimated at 7.2σ in ETS and 3.0σ in CS.

Fig. 5 shows predicted cumulative genetic progress in the growth and the carcass traits according to years. It appears that genetic progress cumulates noticeably after 15 years and that relative advantage of ETS over CS is greater in case when initial genetic superiority of the nucleus herd is not large. The application of ETS to the commercial herd will promise a great deal of monetary returns.

References

- 1) Church, R. B. & Shea, B. F.: The role of embryo transfer in cattle improvement programs, *Can. J. Anim. Sci.* **57**, 33-45 (1977).
- 2) Hill, W. G. & Land, R. B.: Super ovulation and ovum transplantation in genetic improvement programs, in *Egg transfer in cattle* ed. Rowson, L.E.A., 355-367, Luxembourg, Commission of European Communities (1976).
- 3) Land, R. B. & Hill, W. G.: The possible use of super-ovulation and embryo transfer in cattle to increase response to selection, *Anim. Prod.* **21**, 1-12 (1975).
- 4) Nicholas, F. W.: The genetic implications of multiple ovulation and embryo transfer in small dairy herds, 30th Annual Meeting of EAAP, CG1, **11**, 1-4 (1979).
- 5) Tanaka, H., Furukawa, T. & Yamada, Y.: Breeding plan for beef cattle by embryo transfer. I. Prediction of genetic gain in breeding stock, *Jpn. J. Zootech. Sci.*, **53**(4), 283-288 (1982) [In Japanese with English summary].

(Received for publication, October 16, 1985)