

## EFFECT OF BREEDING LENGTH ON GENETIC IMPROVEMENT IN JAPANESE HOLSTEIN POPULATION

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### Summary

The effect of breeding length of sire on genetic progress was examined in the Holstein dairy cattle population in Japan. Genetic progress was estimated by gene flow method. Breeding length of sires directly influences the replacement rates of sires and the selection intensity of sires because there are a fixed number of progeny tested young bulls per year. As breeding length of sires increased, rate of gene flow decreased and average proportions of genes deriving from selected animals had lower asymptotic values. When breeding length was short, average proportions of genes required a longer period to converge to asymptotic values. Changes of Rcow-sire's (sire to breed recorded cows) and Ncow-sire's (sire to breed non recorded cows) breeding length influenced not only transmission of their genes but also that of genes derived from all other selected animals. Irrespective of whether the discount rate was assumed to be 0 or 6%, longer term ( $\geq 20$  years) expected total genetic improvement was maximized by a sire breeding length of five years. For shorter term assessment (10 years), genetic improvement was maximized by a sire breeding length of three years. There was a linear increase in the contribution of the sire to bulls pathway to the total genetic improvement, with increase in the term of assessment.

(Key Words : Breeding Length, Genetic Improvement, Japanese Holstein)

### Introduction

Genetic improvement per year depends on phenotypic SD, the selection intensity, accuracy of selection and the generation interval. There have been many studies concerning estimation of genetic parameters (Suzuki and Mistumoto, 1981; Takebe, 1972) and evaluation of genetic performance (Suzuki and Mistumoto, 1982; Suzuki and Mistumoto, 1986; Suzuki and Mistumoto, 1987; Suzuki et al., 1989; Wada and Kashiwagi, 1990; Wada et al., 1991; Wada et al., 1993) for the Holstein population in Japan. However, there have been few reports on selection in and the structure of the Holstein population, and there has been only one study for the dairy population in Hokkaido

prefecture (Akabori et al., 1977). There are many factors relating to the structure of the Holstein population which influence genetic improvement. These include the breeding length of proven sires, the proportion of cows inseminated with young bulls, the number of progeny tested young bulls per year etc., and there is interaction between these factors in their effect on genetic improvement.

Assuming that the population has been kept in a constant size, the annual demand for semen straws is stable and the number of sires to be reared every year is necessarily determined. When the number of cows inseminated by young bulls to produce daughters for progeny testing is restricted by practical considerations, the number of progeny tested young bulls is automatically determined. Under these conditions, the increase in selection intensity results in fewer replacement sires, and consequently the breeding length of proven sires has to be prolonged in order to ensure the minimum number of proven sires to meet the annual demand for semen straws.

The objectives of the present study are to examine the effect of breeding length of proven sires on genetic improvement and to find the optimal breeding length for

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the Japanese Holstein population.

### Materials and Methods

The population structure used in this deterministic simulation is presented in figure 1. The population is divided into two sub populations, namely recorded cows, including cows to breed bulls, and unrecorded cows. Selection paths include those from sires to bulls, from sires to recorded cows, from dams to bulls, from dams to recorded cows and from sires to non recorded cows. Corresponding breeding animals are called Bull-sire, Rcow-sire, Bull-dam, Rcow-dam and Ncow-sire. Semen is collected from young bulls at 13 months of age and are mated to recorded cows in order to produce daughters for progeny testing. When young bulls are sixty months of age, some are selected as proven sires (Rcow-sire and Ncow-sires) based on the results of progeny testing. Rcow-sires and Ncow-sires are used to breed replacement heifers in recorded and non recorded groups, respectively. Moreover, a few proven sires are selected as Bull-sire to breed young bulls at 108 month of age for 1 year. Bull-dams are selected from recorded cows on the basis of two lactations at 48 months of age and are inseminated by semen from Bull-sire males for 3 years. Table 1 shows the

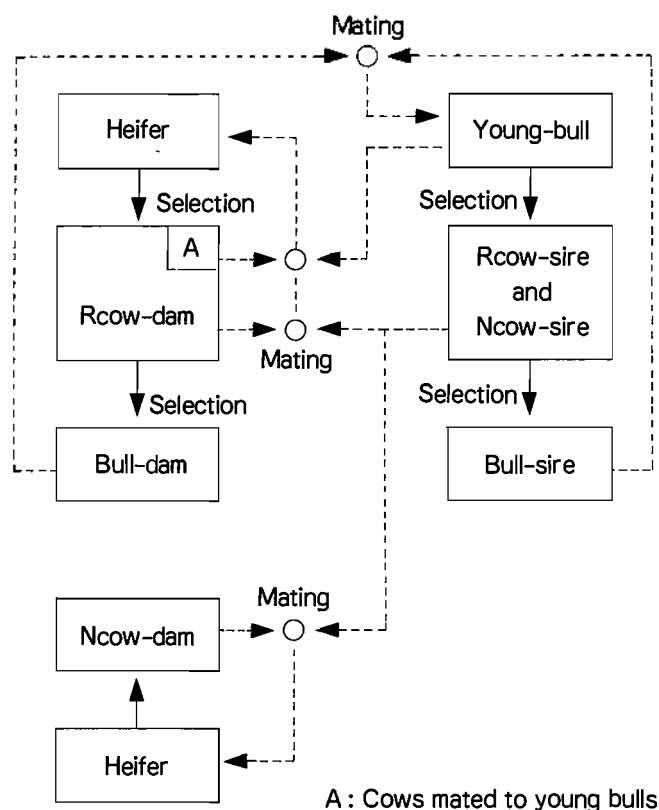


Figure 1. Structure of dairy cattle population.

TABLE 1. CONDITIONS OF THE SIMULATION

Total number of cows	2,000,000
Proportion of recorded cows	40%
Proportion of recorded cows inseminated with young bulls	10%
Number of daughter's record used for progeny testing per young bull	40
Number of progeny tested young bulls per year	166
Demand for semen straw per year	3,000,000
Number of straws produced per sire per year	30,000
Breeding length of Rcow- and Ncow-sire	1,3,5,7 or 10 year

data on which the simulation was based. The number of cows inseminated with young bulls for progeny testing is 60,000 which is calculated from total number of cows, the proportion of recorded cows, proportion of recorded cows inseminated with young bulls and proportion of cows which may be inseminated (75%). The annual number of progeny tested young bulls is derived by dividing the number of cows inseminated with young bulls (60,000) by number of cows inseminated with a young bull (360 cows). There were five breeding lengths of sires 1, 3, 5, 7 or 10 years. The age structures of the recorded and non-recorded cows in the present study were the same as those described by Shimizu et al. (1985). The number of selected Bull-sires, Rcow-sires and Ncow-sires, and the selection intensity are presented in table 2.

TABLE 2. THE SELECTION INTENSITIES OF SELECTED MALE ANIMALS

Selection animal	Breeding length	Number of selected animal	Selection intensity
Bull-sire	1	20	1.650 (1.0) <sup>a</sup>
	3	7	2.100 (1.273)
	5	4	2.301 (1.394)
	7	3	2.393 (1.451)
	10	2	2.513 (1.523)
Rcow-sire and Ncow-sire	1	96	0.669 (0.406)
	3	33	1.393 (0.844)
	5	20	1.650 (1.0)
	7	15	1.784 (1.08)
	10	10	1.959 (1.187)

<sup>a</sup> Numbers in the parentheses indicate relative values on Rcow- and Ncow-sire with 5-year breeding length.

The proportions of genes transmitted from selected animals into the groups of recorded and non-recorded cows are examined using the gene flow method (Brascamp, 1978; Hill, 1974; McClintock and Cunningham, 1974). The proportions of genes in each group-sex-age class are estimated by

$$m_t = P \cdot m_{t-1} + R \cdot n_{t-1} \dots\dots\dots (1)$$

$$n_t = Q \cdot n_{t-1} \dots\dots\dots (2)$$

where,

$m_t$ : vector indicates proportions of genes deriving from selected animals into group-sex-age classes in year  $t$ ,

$P$ : matrix describes transmission of genes to the next year,

$n_t$ : vector indicates age structure of selected animals in year  $t$ ,

$R$ : matrix specifies the passage of genes by reproduction,

$Q$ : matrix describes aging of selected animals.

Expected genetic improvement is estimated by following formulas.

$$C_{jt} = \sum_{i=0}^t m_{ji} \dots\dots\dots (3)$$

where,

$C_{jt}$ : vector indicates cumulative expression in group-sex-age classes until  $t$  year by  $j$  th selected animals,

$m_{ji}$ :  $m$  vector in  $i$  year by  $j$  th selected animals.

$$G_{j(tz)} = h' \cdot C_{jt} \cdot S_j \dots\dots\dots (4)$$

where,

$G_{j(tz)}$ : scalar indicates the genetic improvement expected to be obtained in the groups of recorded or non-

recorded cows (cows over 36 month of age) until  $t$  year by  $j$  th selected animals,

$h'$ : vector describes the proportion of expressed animals in recorded cows or non-recorded cows,

$S_j$ : genetic superiority of  $j$ th selected animal.

When the rate of discount is considered, formula (3) is modified as follows.

$$C_{jt} = \sum_{i=0}^t [1/(1+d)^i] \cdot m_{ji} \dots\dots\dots (5)$$

where,  $d$  is rate of discount and 0.00 or 0.06 in present study.

Expected genetic improvement is estimated when only male animals are selected, namely Bull-sire, Rcow-sire and Ncow-sire because of the unreliable low intensity of selected female animals in practice.

**Results**

The proportions of genes transmitted from selected animals to recorded or non-recorded cows are presented in figure 2, 3 and 4 by each path of selection. In general, the proportions decreased with increase in breeding lengths of Rcow-sire and Ncow-sire. Moreover, their asymptotic values became higher with shorter breeding lengths. As breeding length of sires decreased, the proportion of genes transmitted to cows rose more sharply in earlier years and converged to higher asymptotic values, fluctuates more in late years. These trends were similar to those obtained by Shimizu et al. (1988) on beef cattle. Bull-sire's genes (figure 2) were transmitted earlier to recorded cows than

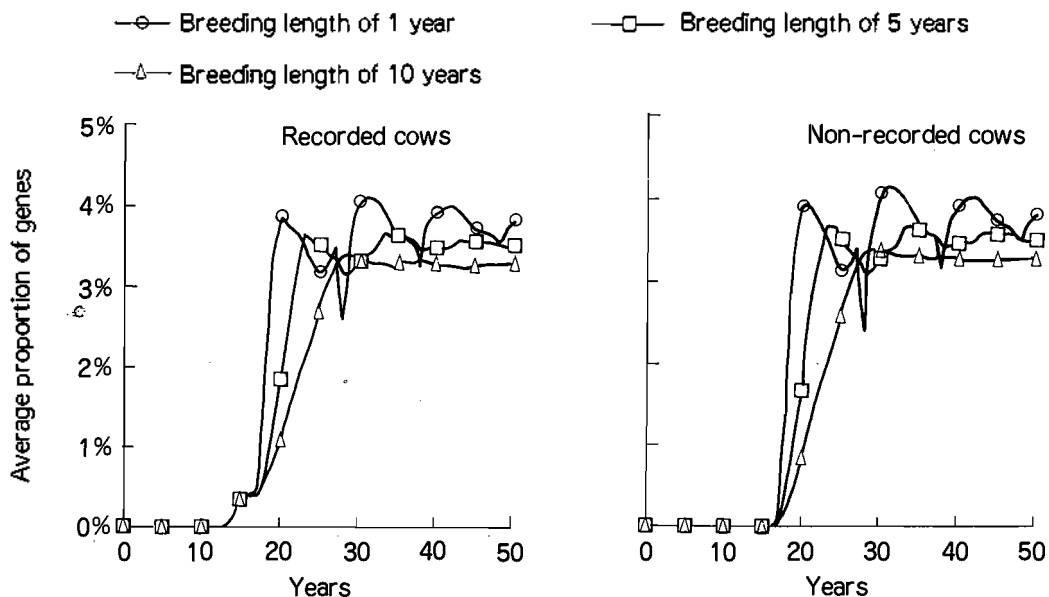


Figure 2. Proportions of genes transmitted from Bull-sire into recorded and non-recorded cows.

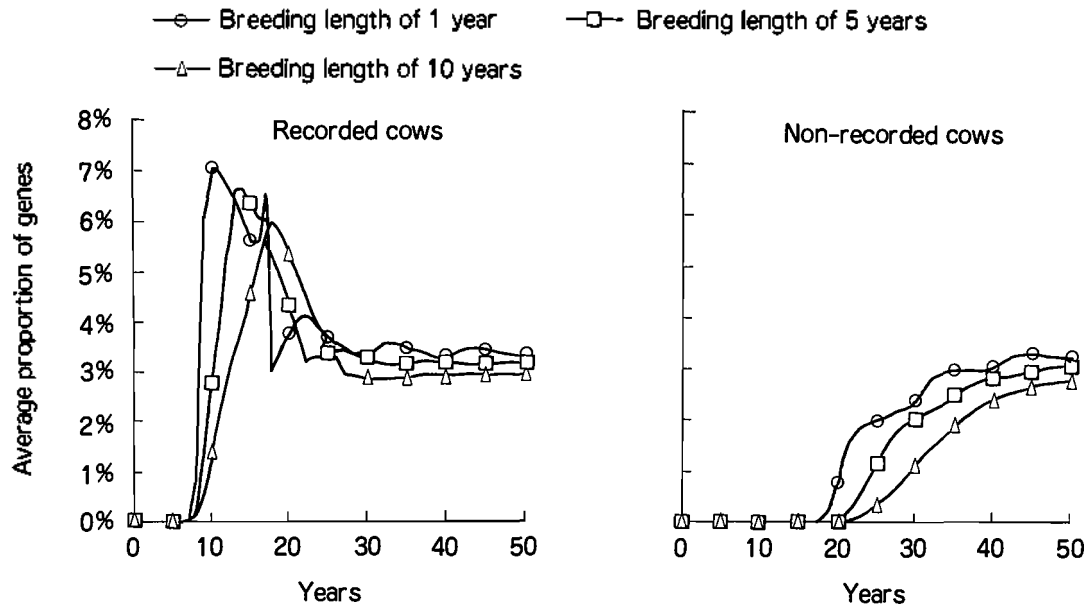


Figure 3. Proportions of genes transmitted from Rcow-sire into recorded and non-recorded cows.

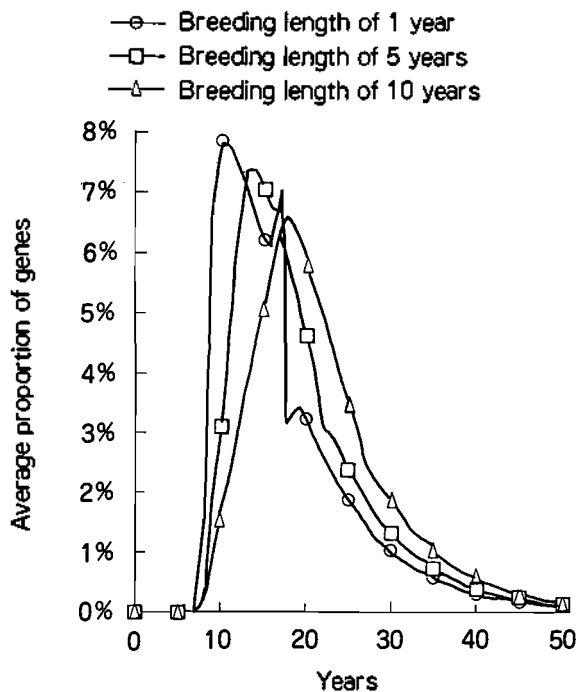


Figure 4. Proportions of genes transmitted from Ncow-sire into non-recorded cows.

to non-recorded cows because young bulls were directly mated to the group of recorded cows. The yearly pattern of gene transmission from Bull-dam were similar to that from Bull-sire.

The proportions of genes in recorded cows transmitted from Rcow-sire (figure 3) peak of about 6 to 7% after 10-15 years and then decreased by 22-25 years to about 3 to

4% where they remained. There was little if any transmission of genes into non-recorded cows until 20 years after which there was a moderate increase to asymptotic values of about 3% after 50 years.

Transmission of genes to non recorded cows had a peak of about 7-8% after 10-23 years. As breeding length of sires decreased, the proportion was high in early year and decreased rapidly (figure 4). These phenomena resulted in rapid transmission of the genes from Ncow-sire for short term and after then occupation of non-recorded cows by new Ncow-sire's genes. No genes from Ncow-sire were transmitted to recorded cows.

Transmission of genes to recorded cows increased rapidly after 5 years to a peak of about 7% in all breeding length groups at about 15 years, wherefore there was an abrupt decrease to levels between 3 and 4% which were maintained from about 20 years (figure 5). Genes from Rcow-dam were observed in non-recorded cows after about 15 years and the proportions gradually approached asymptotic values of about 3-4%. Figures 2-5 indicated that changes of sire's breeding length influenced not only the aspects of transmission of their genes but also those of genes deriving from all other selected animals.

Figure 6 and 7 shows expected total genetic improvements from three paths of selection after 10, 20 30 40 and 50 years when sires were used for 1, 3, 5, 7, 10 years. The total genetic improvements arising from the three selection paths for sires are given. Assuming discount rate of 0% (figure 6), expected total genetic improvements after 10 years were maximized with a breeding length of 3 years and after 20 years with a

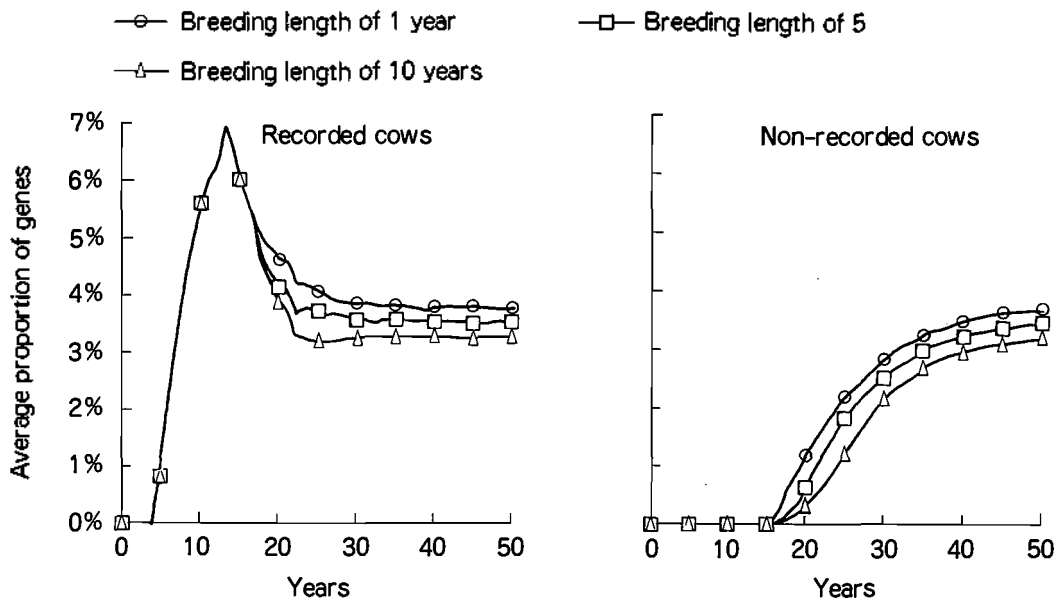


Figure 5. Proportions of genes transmitted from Rcow-dam into recorded and non-recorded cows.

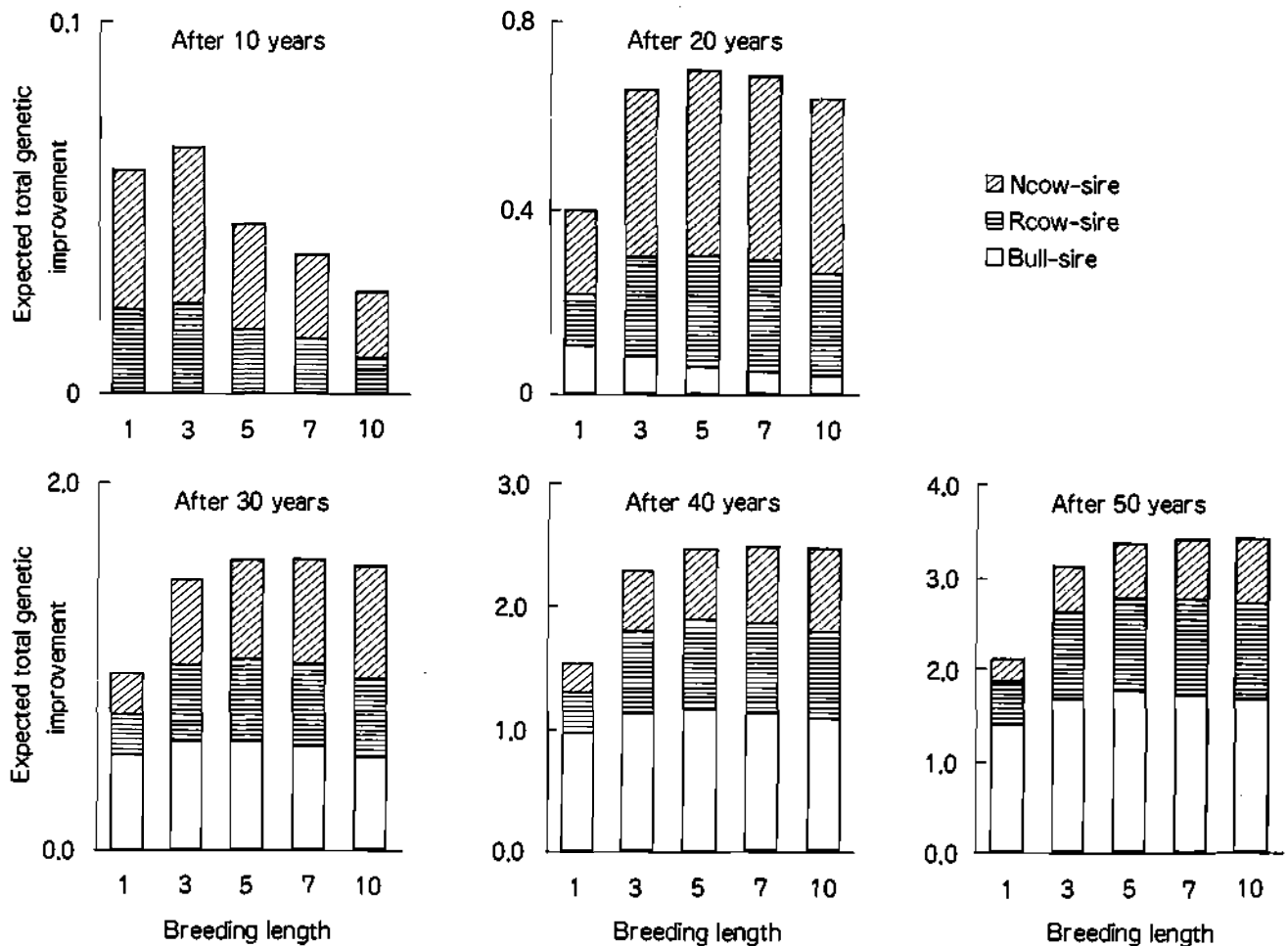


Figure 6. Expected total genetic improvements with discount rate of 0%.

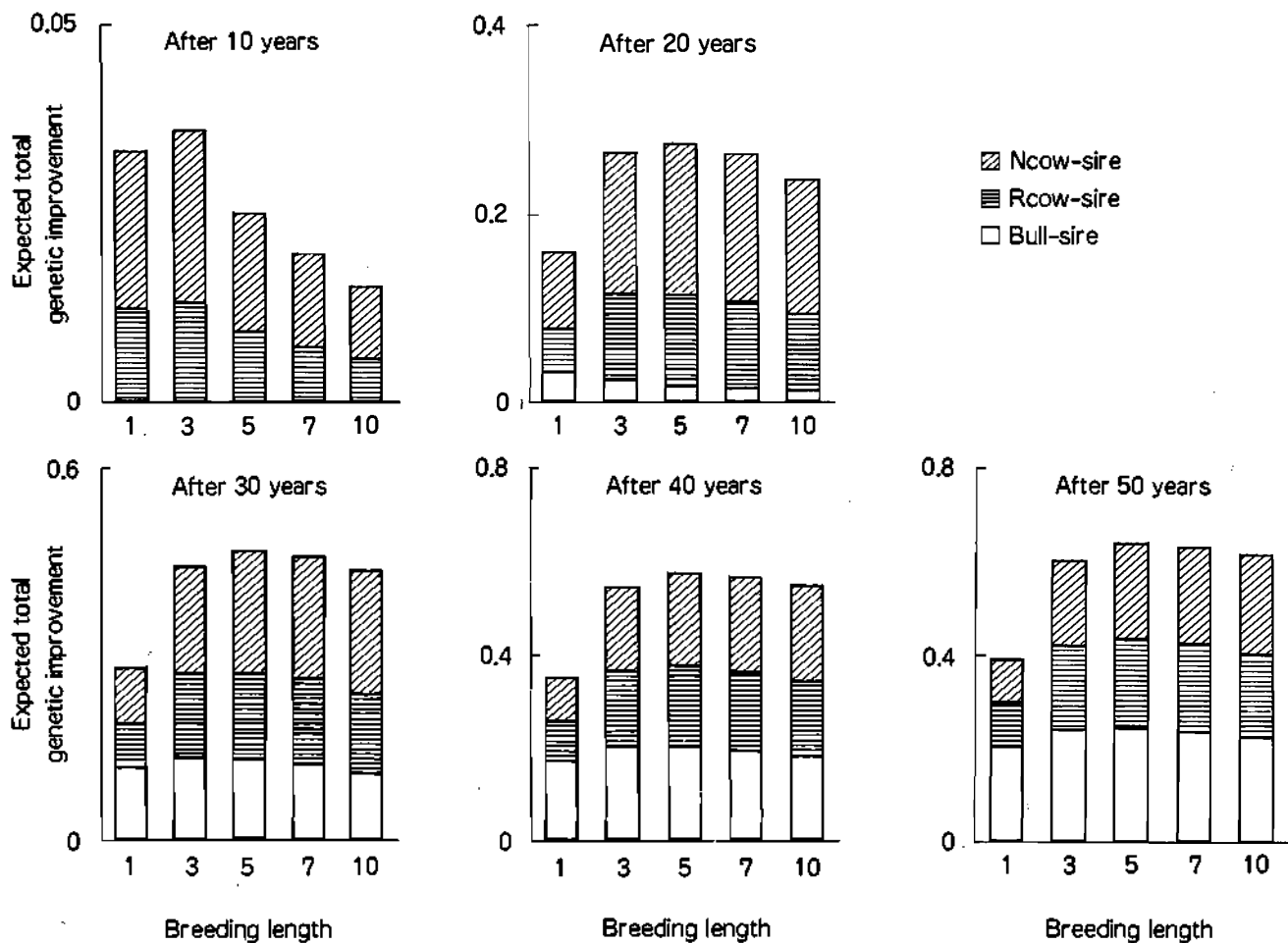


Figure 7. Expected total genetic improvements with discount rate of 6% not 0%.

breeding length of 5 years. After 30 or more years there was essentially little difference in total genetic improvements between breeding lengths of 5, 7 or 10 years. As such, total genetic improvements is optimized by shorter breeding length in the early years, but as time progresses, optimum total genetic improvement is achieved with the longer breeding lengths. In early years, the contribution of Bull-sire to total improvements is relatively small. However, after about 40 years, the contribution from this pathway is the greatest. Assuming a 6% rate of discount (figure 7), total genetic improvement after 10 years was greatest with a breeding length of 3 years but from 20 years, total genetic improvement was greatest with a breeding length of 5 years. Again, there was relatively little difference in the longer term between breeding lengths of 5, 7 and 10 years. Again the Bull-sire contribution to total genetic improvements increased with time from commencement of selection but such contribution was somewhat reduced in comparison to that assessed assuming a 0% discount rate.

## Discussion

The selection intensity, accuracy of selection and the generation interval, which affect genetic improvement per year, are influenced in practice by breeding length, number of cows mated to young bulls, number of young bulls progeny tested per year, number of daughters used to progeny testing per young bull etc. Breeding length of selection animals, especially Bull-sire, Rcow-sire and Ncow-sire, are easily controlled. If the number of cows mated to young bulls per year is fixed, breeding length of sire influences the generation interval and the selection intensity. Long breeding length could increase the selection intensity by decreasing the number required for annual replacement, but increase the generation interval by increasing the age of parents producing progeny.

In this study, 5 selection paths are assumed. When breeding lengths of Rcow-sire and Ncow-sire varied, the transmitting aspects of genes from not only concerned selected animals but also all other selected animals (Bull-

sire, Bull-dam and Cow-dam) were influenced. Those facts are worthy of notice when breeding strategy is examined. The proportions of genes transmitted into cows from selected animals converged at the asymptotic values equal to the reciprocal of the sum of the mean generation intervals (Hill, 1974). But in this study 10% of recorded cows were mated to young bulls, so that asymptotic values were smaller than ones estimated from average generation intervals.

When breeding length was 5 to 10 years, expected total genetic improvements with discount rate of 0% were largest on and after 30 years. Also, the discounted genetic improvement with the rate of 6% was largest over all most evaluated periods, when the breeding length was 5 years. These results indicated that Rcow-sire's and Ncow-sire's breeding length of 5 years was appropriate for the population structure of this study. The discounted genetic improvements with 1-year breeding length were very small because of very low selection intensity of Rcow-sire and Ncow-sire (table 2). On the other hand, when breeding length was increased as long as 7 and 10 years more intensive selection could be applied. However, the discounted genetic improvements were not so much as the improvement with 5-year breeding length. This result was due to the slow rate of transmission of genes deriving from selected animals to cows in spite of high selection intensities of Rcow-bull and Ncow-bull. Moreover, accounting for 6% discount rate, delay of gene's transmission had large negative effects on total expected genetic improvements.

When the horizon is 20 to 30 years, expected total genetic improvements with the breeding length of 5-year were largest regardless of any discounted rate. But setting up more long evaluation period (for example 50 years), the most appropriate breeding lengths vary with discounted rate. It is difficult to determine the reasonable rate of discount because of instability of economic conditions. Also, Hill (1971) discussed that perhaps evaluation period of 20-year is too long, and period of only 15 years would be justified. In this study, the largest expected total genetic improvements with discount rate of 0% for 15 and 20 years after beginning of selection were obtained when breeding length is 3 and 5 years, respectively. Total expected genetic improvements with the discount rate of 6% indicated the same trend. The generally high total genetic improvements, particularly in the later years of assessment, of the 5 year breeding length in both the 0 and 6% rate of discount, suggests that such replacement rate may be optimal for the population in question. In Japanese dairy population, young bulls with high genetic merit have been imported every year, so that

the optimum breeding length may be shorter than the results of this study.

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