Effect of Proportion of Recorded Cows Inseminated by Young A. I. Bulls on Genetic Improvement in Japanese Holstein Population

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ABSTRACT : The effects of the proprotion of cows inseminated by young A. I. bulls on genetic improvement in the Japanese Holstein population were examined using a simulation technique. The proportion of recorded cows inseminated by young A. I. bulls was assumed to be from 10% to 100% of the total number of recorded cows. The expected total genetic improvement was estimated for all cows and recorded and non recorded cows. The effects of the above were remarkable in the schemes that proven sires were used to produce recorded and non recorded cows for a limited time. Also the increase in the rates for - the expected total genetic improvement was larger when the proportion of recorded cows that were inseminated by young A. I. bulls was about 10% to 40%. When the expected total genetic improvement was estimated for the entire population, we found that the highest values were in a range of about 40 to 60% recorded cows that were inseminated by young A. I. bulls. On the other hand, the expected total genetic improvement that was only estimated in recorded cows dramatically decreased for more than 40% of the recorded cows. The results of this study showed that the optimal proportion of recorded cows inseminated with young A. I. bulls should be about 30% in the Japanese Holstein population.
(**Key Words**: Proportion, Young Bull, Genetic Progress, Japanese Holstein)

INTRODUCTION

There has been little research on breeding strategies for the Holstein population in Japan. Akabori and Mitsumoto (1977) analyzed an optimum breeding program for the Holstein population in Hokkaido Prefecture. Terawaki et al. (1996) studied breeding programs for the Holstein population in Japan, and indicated that the breeding length (the period when proven sires are used to produce recorded and non recorded cows) of 3 or 5 years resulted in the most significant genetic progress in the Japanese Holstein population.

Terawaki et al. (1996) fixed the proportion of recorded cows inseminated with young A. I. bulls at 10 percent, which was about the practical value for the current Japanese Holstein population. The proportion of recorded cows that were inseminated with young A. I. bulls is a significant factor which affects the genetic progress of dairy cattle. A larger proportion of recorded cows being inseminated with young A. I. bulls would result in the two possibilities. One would be more progeny tested young bulls per year, assuming a fixed number of recorded cows being inseminated per young A. I. bull. This increase the selection intensity for young A. I. bulls. The other would be a more accurate of evaluation of young A. I. bulls, assuming a fixed number of progeny tested young bulls per year.

In this study, effects of the proportion of recorded cows that were inseminated by young A. I. bulls on the genetic progress of the Japanese Holstein population were examined.

MATERIALS AND METHODS

The structure of the simulating population of Japanese Holstein cattle was described in detail by Terawaki et al. (1996). Also, the simulation was the same as that done by Terawaki et al. (1996) except for the proportion of recorded cows that were inseminated by young A. I. bulls. The proportion of recorded cows bred to young bulls varied from 10 to 100% by 10% of the total number of recorded cows. The total number of cows and the proportion of recorded cows were assumed to be 2,000,000 cows and 40%, respectively. Selection paths include those from sires to bulls, from sires to recorded cows, from dams to bulls, from dams to recorded cows and from

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Received Jun 7, 1997; Accepted January 13, 1998

sires to non recorded cows. Corresponding animals are called bull's sire, recorded cow's sire, bull's dam, recorded cow's dam and non recored cow's sire. There were five breeding length of recorded and non recorded cow's sire 1, 3, 5, 7 or 10 years. The number of daughter's records used for progeny testing per young bull was fixed at 40 records. Cumulative expression and expected genetic improvement were estimated according to Terawaki et al. (1996) using the gene flow method (Brascamp, 1978; Hill, 1974; McClintoc and Cunningham, 1974). Table 1 shows the genetic superiority of bull's sire (sire to breed bull), recorded cow's sire (sire to breed recorded cow) and non recorded cow's sire (sire to breed non recorded cow).

Table 1. Genetic superiority[a] of selected animals

Selected animal	Breeding length (years)	Proportion of the recorded cows inseminated by young A. I. bulls (%)									
		10	20	30	40	50	60	70	80	90	100
Recorded and non recorded cow's sire	1	0.406	0.730	0.891	0.996	1.075	1.140	1.196	1.245	1.290	1.331
	3	0.844	1.069	1.203	1.294	1.345	1.408	1.456	1.490	1.530	1.560
	5	1.000	1.208	1.331	1.412	1.479	1.516	1.562	1.605	1.644	1.682
	7	1.180	1.283	1.391	1.479	1.545	1.577	1.637	1.660	1.687	1.752
	10	1.187	1.361	1.490	1.552	1.637	1.660	1.690	1.742	1.765	1.816
Bull's sire	1	1.172	1.416	1.560	1.655	1.733	1.777	1.831	1.881	1.927	1.971
	3	1.492	1.685	1.848	1.919	1.977	2.012	2.104	2.104	2.166	2.166
	5	1.634	1.807	1.946	2.012	2.064	2.104	2.200	2.226	2.251	2.280
	7	1.701	1.876	2.012	2.104	2.104	2.166	2.200	2.251	2.350	2.364
	10	1.785	1.984	2.103	2.168	2.217	2.251	2.294	2.322	2.350	2.364

[a] Genetic superiority is relative values on recorded and non recorded cow's sire with breeding length of 5 years in the scheme in which the proportion of recorded cows inseminated by young A. I. bulls was 10%.

RESULTS

The cumulative expression of the genes from each selected animal for cows older than 36 months are shown in figure 1. The cumulative expression of bull's sire increased during the course of the selection progress. It was larger in the schemes with higher proportion of recorded cows bred to young bulls. This was also observed in the cumulative expression of genes from bull's dam (dam to breed bull) and recorded cow's dam (dam to breed recorded cow). On the other hand, the cumulative expression of genes from recorded cow's sire was larger as proportion of recorded cows bred to young bulls was small. The effects of the proportion of recored cows bred to young bulls was more significant on cumulative expression of genes from recorded cow's sire than from bull's sire, bull's dam and recorded cow's dam. The three lines for non recorded cow's sire overlapped. This indicated that the cumulative expression of genes from non recorded cow's dam (dam to breed non recorded cow) was not affected by the proportion of recorded cows bred to young bulls in any way.

Figure 2 shows the expected total genetic improvement in the whole cow population after 20 and 50 years. After breeding programs have been done for 20 years, the largest expected total genetic improvement was estimated in the schemes that used proven sires to produce recorded and non recorded cows for 3 or 5 years (the breeding length was 3 or 5 years). Increase rate of expected total genetic improvement with increasing proportion of recorded cows bred to young bulls was the largest in the scheme where the breeding length was one year. After 50 years, the differences in the expected total genetic improvement among the schemes (except for the scheme where proven sire were available for 1 year) were smaller than those after 20 years. Limited expected total genetic improvement was estimated for the above scheme (the breeding length was one year) as compared with other schemes. When the proportion of recorded cows bred to young bulls increased from 10% to 40%, the expected total genetic improvement increased dramatically regardless of the breeding length. The increases were the largest in schemes with a limited breeding length.

Figure 3 shows the expected total genetic improvement only in recorded cows after 20 and 50 years. This peaked at 30 or 40% of recorded cows bred to young bulls after 20 years and at 40 or 50% after 50 years.

Figure 4 shows the expected total genetic improvement

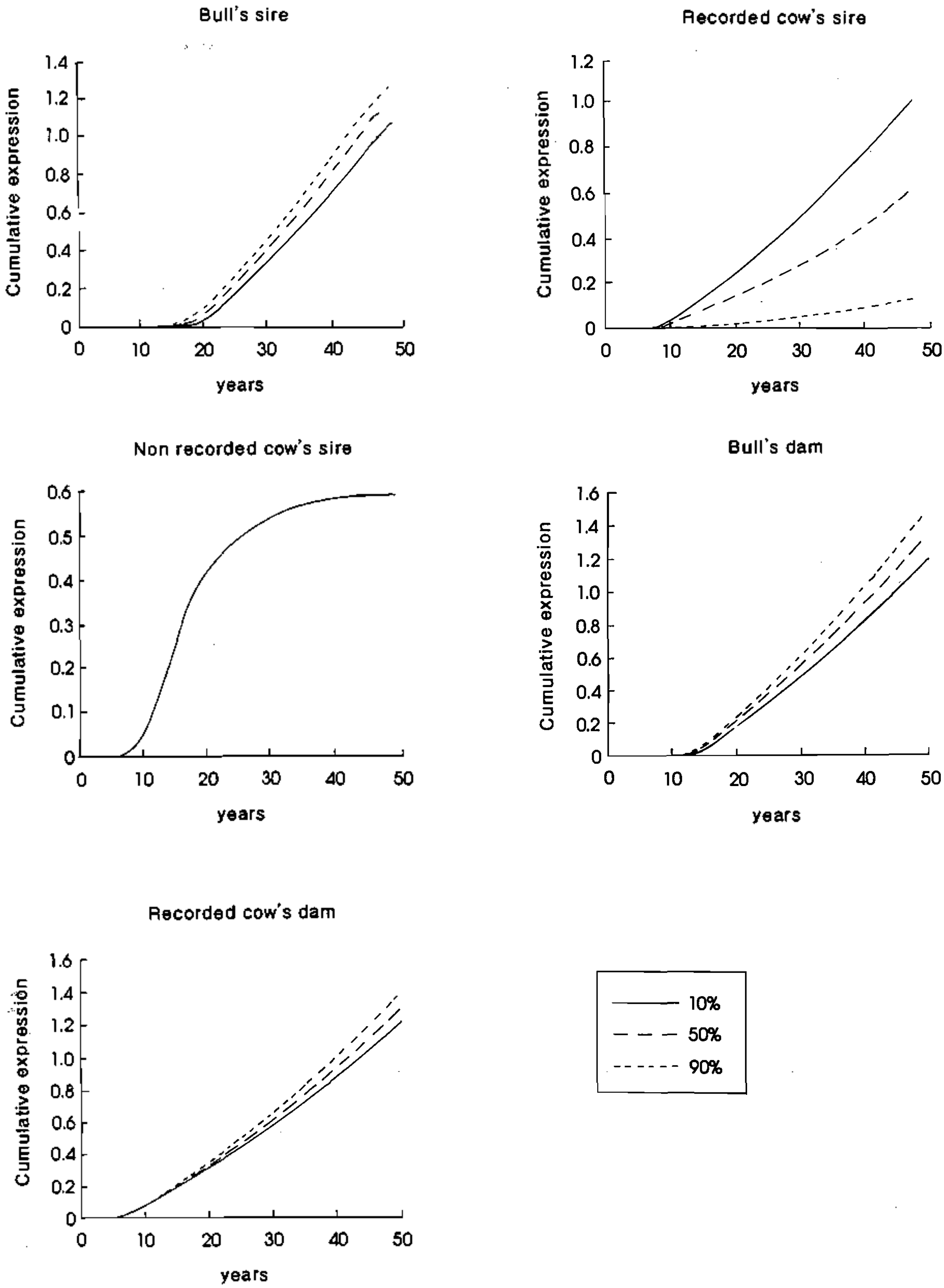

Figure 1. Cumulative expression of genes from all selected animals in cows who were more than 36 months old. (10, 50 and 90% indicate the proportion of recorded cows inseminated by young A. I. bulls. Breeding length of cow's sire is 5 years.).

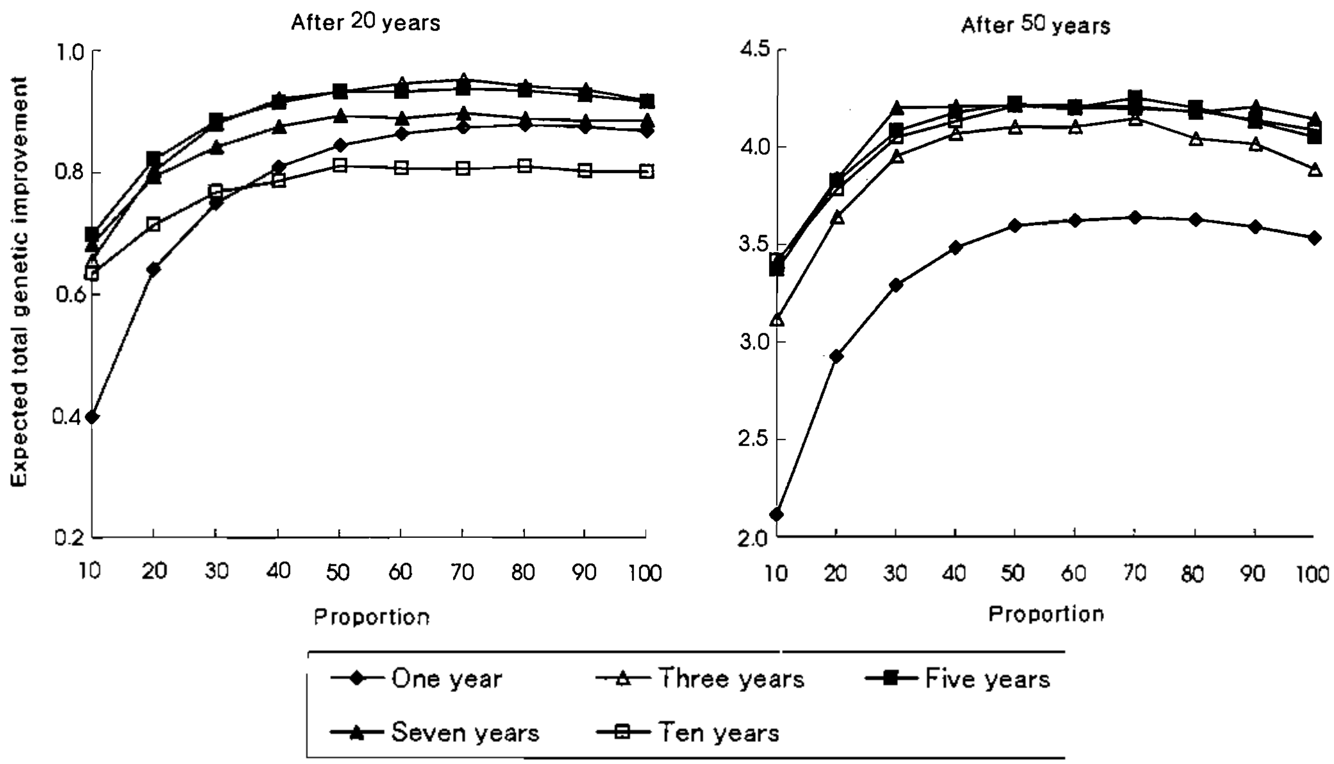

Figure 2. Expected total genetic improvement in the whole cow population after 20 and 50 years. (Each line indicates breeding length of cow's sire.)

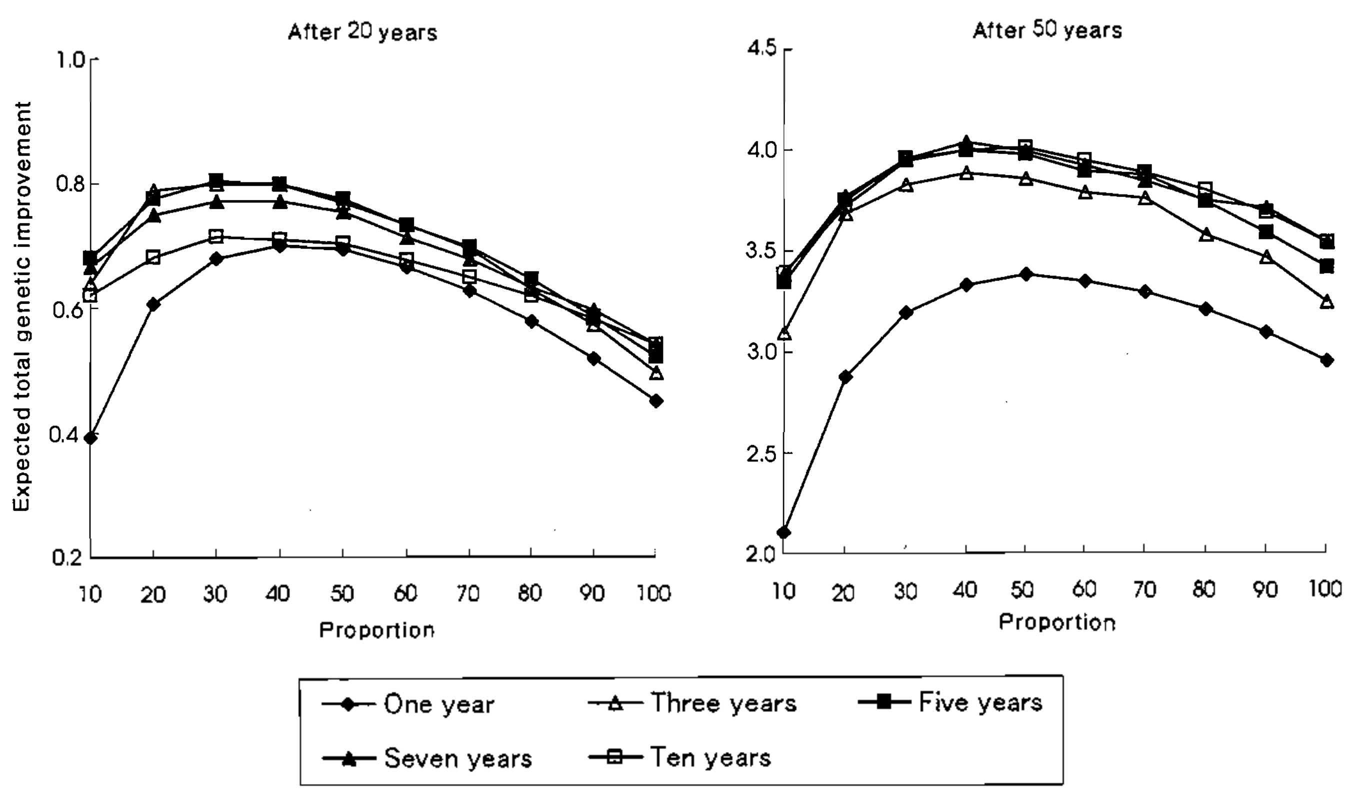

Figure 3. Expected total genetic improvement only in recorded cows after 20 and 50 years. (Each line indicates breeding length of cow's sire.)

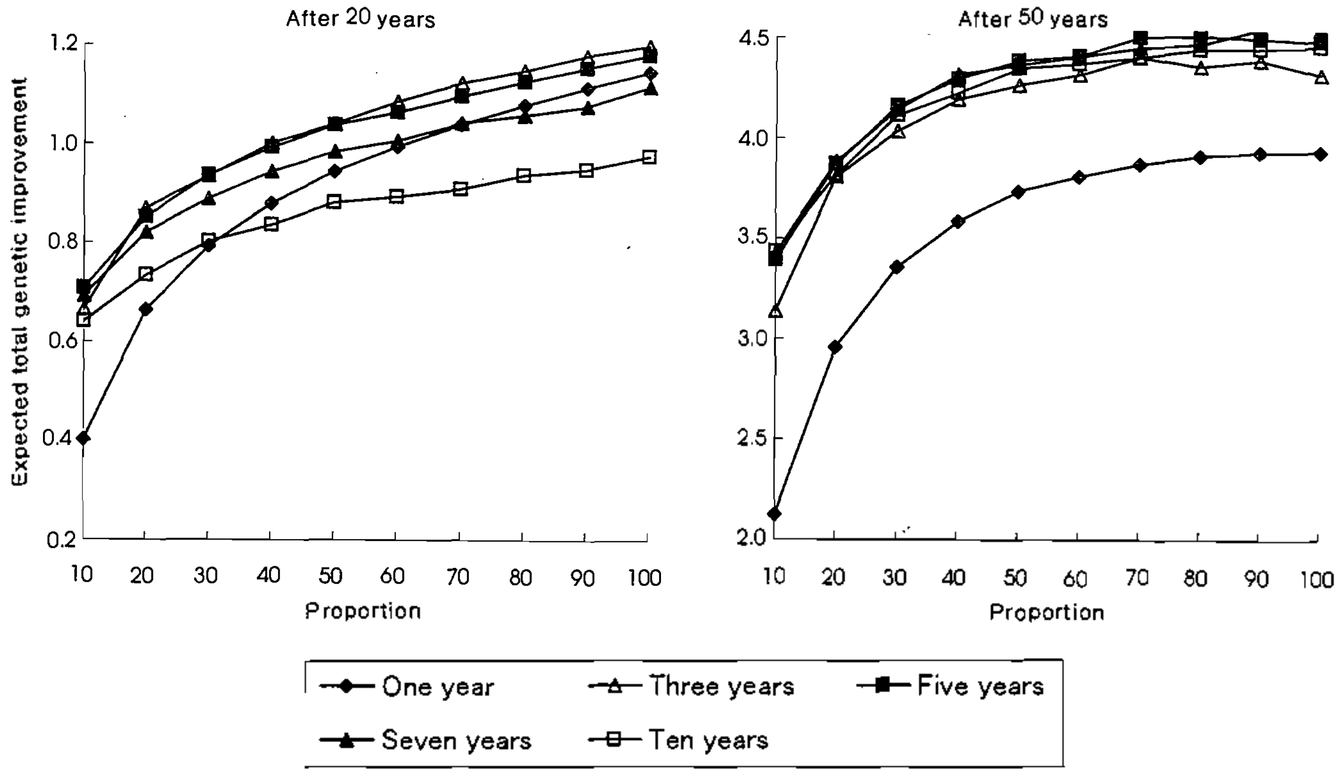

Figure 4. Expected total genetic improvement only in the non recorded cows after 20 and 50 years. (Each line indicates breeding length of cow's sire.)

only in non recorded cows after 20 and 50 years. The increase in the expected total genetic improvement was recognized until 100% of the recorded cows were inseminated with young A. I. bulls.

DISCUSSION

The expected total genetic improvement increased dramatically when the proportion of recorded cows bred to young bulls was small, especially from 10 to 40% (figure 2). The increase in the expected total genetic improvement became small as the proportion of recorded cows bred to young bulls increased. These phenomena was observed by Hunt et al. (1972; 1974). The increase in the superiority of selected animals was larger for a small proportion of recorded cows bred to young bulls (table 1). For example, the superiority of selected animals increased about 1.3 times when the proportion of recorded cows bred to young bulls changed from 10 to 20 percent. On the other hand, when this number changed from 90 to 100%, superiority only increased approximately 1.02 times.

In this study, the number of daughter's records used for progeny testing per young A. I. bulls was fixed. Therefore, an increase in the proportion of recorded cows bred to young bulls resulted in an increase of the selection intensity of the bulls. If the breeding program permitted the number of daughter's records per young bull to vary in addition to the increase of selection intensity of the bulls, there may be the best combination point where the largest improvement was estimated.

The expected total genetic improvement in recorded cows decreased when the proportion of recorded cows that were inseminated with young A. I. bulls was more than 40% (figure 3). This is in contrast to that for non recorded cows (figure 4). This difference between recorded and non recorded cows was because the latter were not inseminated with young A. I. bulls. The cumulative expression of recorded cow's sire (sire to breed recorded cow) decreased with an increase in the proportion of recorded cows that were bred to young bulls. On the other hand, the cumulative expression of non recorded cow's sire (sire to breed non recorded cow) was not affected by the proportion of recorded cows bred to young bulls.

In Finland, 60% of cows were recommended to be inseminated with a young bull's semen (Juga et al., 1987). Hunt et al. (1972) found that 40% of the tested cows should be bred to young bulls when 20% of the cow population is milk recorded. The results for the entire population (figure 2) showed higher expected total genetic improvement in schemes where 40 to 60% of the population of recorded cows was inseminated by young A. I. bulls. These results are similar to Juga et al. (1987) and Hunt et al. (1972). However, only in recorded cows, the largest expected total genetic improvement was estimated in the schemes where 30% recorded cows had been inseminated by young A. I. bulls (fiugre 3). Also, the expected total genetic improvement decreased sharply when the proportion of recorded cows bred to young bulls was more than about 30-40%.

The results from this study indicate that the optimum proportion of recorded cows inseminated with young A. I. bulls should be about 30% for the Japanese Holstein population. However, it is very difficult practically to increase the number of recorded cows that are inseminated with young A. I. bulls. A possible alternative strategy may be a combination of MOET program (Leitch et al., 1994; Leitch et al., 1995; Nicholas and Smith, 1983; Woolliams and Smith, 1988; Woolliams, 1989) and a conventional progeny testing scheme.

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