

EFFECT OF DATA COLLECTION AND CENSORING METHOD FOR GENETIC EVALUATION OF AGE AT DISPOSAL

O. Sasaki, K. Ishii and H. Takeda

National Institute of Livestock and Grassland Science,
Tsukuba Norindanchi P.O.Box 5, Ibaraki 305-0901, Japan

INTRODUCTION

It is difficult to evaluate the genetic performance for longevity, because the complete information on longevity cannot be obtained until disposal. Since some cows are still alive at the time of genetic evaluation, the information on longevity are censored at earlier stage. To exclude the censored records in the analysis would lead to biased results. Vukasinovic *et al.* (1999) showed that the rank correlations of the estimated transmitting abilities of sires from the data with censored records and from the reference data decreased with increasing proportion of censored records. However, the effect of periods of data collection for genetic evaluation on longevity has not been reported.

The objective of our study was to compare the effect of different periods of data collection for age at disposal and censoring methods for genetic evaluation using computer simulation.

MATERIAL AND METHODS

A stochastic simulation of 100 replicates of random selection for age at disposal with overlapping generations was simulated over 150 years. In the first 100 years, the phenotypic records of age at disposal with heritability (h^2) of 0.0 were assumed to be the mean of 4.07 and variance of 7.38, respectively. When phenotype was less than 2, it was generated again. Then age to give was equal to or more than 2 years old. In the last 50 years, the h^2 of age at disposal was changed to 0.1. The mean and variance of age at disposal used in this study were estimated based on method for the normal distribution when samples were singly truncated (Chohen, 1959) from the data of Livestock Improvement Association of Japan Inc. (2000). The h^2 used in this simulation was referred to h^2 of 0.07 from Japanese Holstein in Hokkaido Region (Kawahara *et al.*, 1996).

The population structure is diagrammed in figure 1. Five breeding herds for sires and 295 commercial herds were assumed. Each herd consisted of 60 females containing calves. Ten newborn males from 5 breeding herds were randomly selected every year. Ten sires at 9 years old were removed. At 6 years old, the males were used for mating until 8 years old. Then 30 sires were constantly used for mating. Any three sires of them were randomly mated with cows over 2 years old in each herd every year. The sex ratio of 1:1 was used. In the commercial herds, all newborn males were disposal at birth. Females were removed when they came to be the age given to them. The females of the same number as the removed females were chosen from the newborn females. The other newborn females were disposal at

birth.

Records for age at disposal were generated using the following model:

$$y_i = \mu + 0.5a_s + 0.5a_d + (\sqrt{0.5} h \times RD) + e_i$$

where y_i is phenotype of the i^{th} cows for age at disposal; μ is overall mean; a_s and a_d are breeding values of the sire and dam, respectively; RD is standard normal deviation; and e_i is residual effect.

Data of the first 100 years were not used in any analysis. Then base animals at the 101th year were assumed. Two sets of data analyzed. One set of data consisted of records from the next 20 years. Records of cows which were still alive at the 20th year were excluded (DAT1). Another set of data consisted of records of cows which were born in next 20 years and alive until the age given to them (DAT2). Each data was treated by five methods: full data (F); censored at 5 years old (C5); truncated at 5 years old (T5); censored at 6 years old (C6); and truncated at 6 years old (T6).

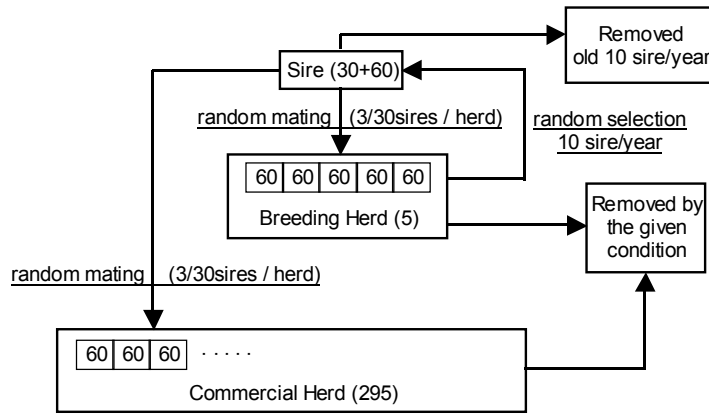


Figure 1. Population structure and breeding strategies for the simulation model. Each herd consists of 60 females containing calves

Real phenotypic and genetic variances for age at disposal were calculated from simulated phenotypes and breeding values and dividing the phenotypic variance by the genetic variance was referred to as real h^2 for age at disposal. The h^2 for age at disposal, referred to as estimated h^2 , was estimated by an animal model, which was composed of additive genetic effect and residual effect, using MTDFREML (Boldman *et al.*, 1993). The breeding values were also estimated at the same time.

Real h^2 and estimated h^2 were calculated in each replicate. The results are shown as the average of 100 replicates as below. Correlation coefficient between real and estimated breeding values of the cows with own record were calculated in joint data of all replicates (SAS, 1990).

RESULTS AND DISCUSSION

Real h^2 s from full and censored data were similar to given h^2 (table 1). However, real h^2 s from truncated data were significantly higher than given h^2 . This is because the phenotypic and the residual variances of truncated data were reduced by truncation.

Table 1. Real and estimated heritabilities of age at disposal and the standard deviations. Given heritability is 0.10. Data was treated by five methods: full data (F); censored at 5 years old (C5); truncated at 5 years old (T5); censored at 6 years old (C6); and truncated at 6 years old (T6)

Data ¹⁾	F	C5	T5	C6	T6
DAT1 Real	0.118±0.002	0.118±0.002	0.302±0.003	0.118±0.002	0.235±0.003
Estimated	0.177±0.005	0.280±0.018	0.046±0.015	0.271±0.014	0.134±0.018
DAT2 Real	0.118±0.002	0.118±0.002	0.312±0.003	0.118±0.002	0.247±0.003
Estimated	0.029±0.005	0.016±0.005	0.003±0.004	0.020±0.006	0.006±0.005

¹⁾See the text.

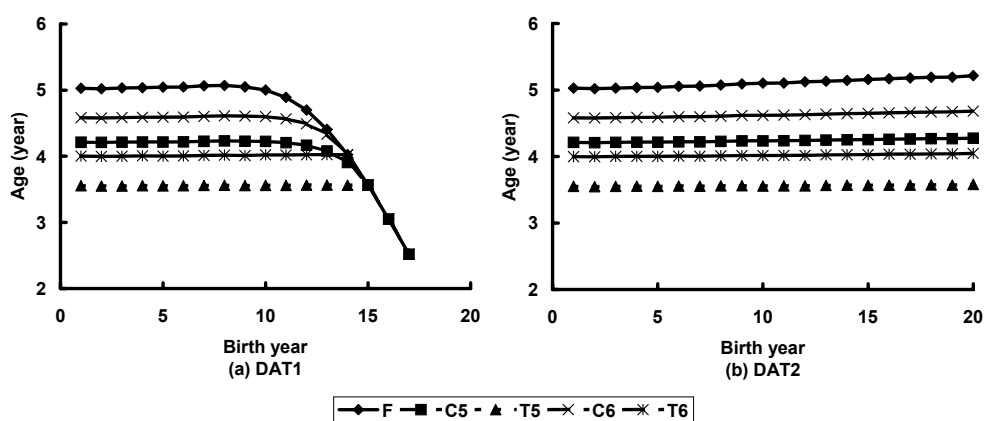


Figure 2. Mean of phenotypic value of age at disposal. Abbreviations are the same as in table 1

Estimated h^2 s from DAT1 except T5 were higher than given h^2 . The means of age at disposal

of DAT1 were decreased with increment of birth year (figure 2). Since the cows with high phenotypic value of age at disposal were still alive at the end of the collecting period, DAT1 include a large number of records of cows with lower performance in the latter period. This is a reason why the h^2 s were overestimated from DAT1.

The estimated h^2 s from DAT2 were lower than both those from DAT1 and given h^2 . Since phenotypic distribution of both DAT1 and DAT2 was basically truncated normal distribution, it is expected that h^2 s of both DAT1 and DAT2 are small. DAT1 was compensated for a part of truncation because DAT1 has a lot of cows with lower performance. The estimated higher h^2 from DAT1 than DAT2 may be attributed to this difference.

The correlation coefficient between real and estimated breeding values from DAT2 was higher than that of DAT1 in each method (table 2). As expected, the correlation coefficient between real and estimated breeding values from full data was high. The correlation coefficients from truncated data were lower than those from censored data and those of C5 and T5 were similar to C6 and T6, respectively.

The correlation coefficient between real and estimated breeding values from F was larger than the others (table 2). In particular, that of DAT2 was high. These results were similar to the results of previous report. Vukasinovic *et al.* (1999) reported that rank correlation between the estimated transmitting abilities of sires from the reference data and from data with censored records showed a slight decrease up to 7 to 9 year after first calving.

Table 2. Correlations between real and estimated breeding values for age at disposal. Abbreviations are the same as in table 1

	F	C5	T5	C6	T6
DAT1	0.14	0.10	0.06	0.10	0.08
DAT2	0.40	0.26	0.07	0.28	0.13

When data of age at disposal were collected based on birth year of cows, the estimated breeding values were more accurate. Our result shows that data of age at disposal should be collected based on birth years of cows rather than on recording year.

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