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ORIGINAL ARTICLE

Investigation of Gibbs sampling conditions to estimate variance components from Japanese Black carcass field data

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ABSTRACT

The genetic evaluation using the carcass field data in Japanese Black cattle has been carried out employing an animal model, implementing the restricted maximum likelihood (REML) estimation of additive genetic and residual variances. Because of rapidly increasing volumes of the official data sets and therefore larger memory spaces required, an alternative approach like the REML estimation could be useful. The purpose of this study was to investigate Gibbs sampling conditions for the single-trait variance component estimation using the carcass field data. As prior distributions, uniform and normal distributions and independent scaled inverted chi-square distributions were used for macro-environmental effects, breeding values, and the variance components, respectively. Using the data sets of different sizes, the influences of Gibbs chain length and thinning interval were investigated, after the burn-in period was determined using the coupling method. As would be expected, the chain lengths had obviously larger effects on the posterior means than those of thinning intervals. The posterior means calculated using every 10th sample from 90 000 of samples after 10 000 samples discarded as burn-in period were all considered to be reasonably comparable to the corresponding estimates by REML.

Key words: *carcass field data, Gibbs sampling condition, Japanese Black cattle, variance component estimation.*

INTRODUCTION

The genetic evaluation using the carcass field data in Japanese Black cattle has been carried out employing an animal model in 42 prefectures. The method used is a two-stage one that first employs the restricted maximum likelihood (REML) estimation of variance components (VCs) (Patterson & Thompson 1971) mainly using the average information (AI) algorithm (Gilmour *et al*. 1995; Johnson & Thompson 1995) and then implements the empirical best linear unbiased prediction. The REML estimation here, as reported by Iwaisaki and Ashida (2004), uses an integrated computational scheme of the AI algorithm as described by Ashida and Iwaisaki (1998, 1999) and the expectation-maximization (EM) algorithm (Dempster *et al*. 1977).

While the REML procedure has several desirable properties (Harville 1977), in recent years the volumes of the official data sets in certain prefectures are increasing rapidly (Wagyu Registry Association 2008), and consequently the REML procedure applied is requiring a (very) large memory space, that could be a possible limiting factor in the future for the use of REML.

An alternative approach that is able to overcome such a setting may be to use Markov chain Monte Carlo methods such as Gibbs sampling (GS) (Geman & Geman 1984; Gelfand & Smith 1990). The GS has

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recently been often used for estimating VCs in animal breeding researches and applications (Sorensen *et al*. 1994; Wang *et al*. 1994; van Tassell *et al*. 1995; Magnabosco *et al*. 2000; Schenkel & Schaeffer 2000; Luo *et al*. 2001; López-Romero *et al*. 2003; Jamrozik 2004). The GS has some advantages over REML (Gianola & Foulley 1990; Wang *et al*. 1993; van Tassell *et al*. 1995). Especially, implementation of GS is known to necessitate a small memory space relative to that of REML. The GS is also relatively easy to be applied for inferences of genetic parameters and for genetic evaluation. Exact confidence interval of the estimate can be obtained very easily. However, the GS techniques require careful consideration to determine the conditions for implementation such as Gibbs chain length, burn-in period, and thinning interval.

The objective of this study was to investigate the influences of Gibbs chain length and thinning interval, in addition to that of burn-in period, on the means of estimated marginal posterior distributions of the VCs, describing a GS scheme like REML to be possibly used, if necessary, to analyze the official carcass data sets of Japanese Black cattle.

MATERIALS AND METHODS

We considered an animal model as used in the official genetic evaluation for the Japanese Black carcass traits, as follows:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}, \tag{1}$$

where $\mathbf{y}$ is the vector of records, $\mathbf{b}$ is the vector of macro-environmental effects, $\mathbf{a}$ is the vector of breeding values, $\mathbf{e}$ is the vector of residuals, and $\mathbf{X}$ and $\mathbf{Z}$ are the known incidence matrices relating elements of $\mathbf{y}$ to those of $\mathbf{b}$ and $\mathbf{a}$, respectively.

Then, in this Bayesian analysis using GS, nuisance parameters (macro-environmental effects), breeding values, and the VCs involved in the model were considered to be unknown. Data were assumed to be generated from a multivariate normal distribution (*MVN*) according to the stochastic process:

$$\mathbf{y}|\mathbf{b},\mathbf{a},\mathbf{R} \sim MVN(\mathbf{Xb} + \mathbf{Za}, \mathbf{R}) \tag{2}$$

with $\mathbf{R} = \mathbf{I}\sigma_e^2$, where $\mathbf{I}$ is an identity matrix, and σ_e^2 is the residual variance.

To perform the Bayesian analysis, it is necessary to assign prior distributions to the unknown parameters. Then, in this study, a flat improper prior distribution was used for $\mathbf{b}$, as follows:

$$p(\mathbf{b}) \propto constant. \tag{3}$$

Also, a MVN distribution was used for $\mathbf{a}$:

$$\mathbf{a}|\mathbf{A}, \sigma_a^2 \sim MVN(0, \mathbf{A}\sigma_a^2), \tag{4}$$

where $\mathbf{A}$ is the additive relationship matrix among all animals in the pedigree file, and σ_a^2 is the unknown additive genetic variance.

As for the VCs, independent scaled inverted chi-square distributions were used, so that we assumed:

$$\sigma_a^2|\upsilon_a, S_a^2 \sim \chi_a^{-2}(\upsilon_a, \upsilon_a S_a^2) \tag{5}$$

and

$$\sigma_e^2|\upsilon_e, S_e^2 \sim \chi_e^{-2}(\upsilon_e, \upsilon_e S_e^2), \tag{6}$$

where υ_i and $S_i^2(i = a, e)$ are degrees of belief and scale parameters interpreted as *a priori* values, respectively. Then, to derive the Bayesian framework via GS like REML, these prior distributions for the VCs were assumed to be non-informative, and therefore, according to Wang *et al*. (1994) and Sorensen and Gianola (2002), we here set $\upsilon_i = -2$ and $S_i = 0$.

The joint posterior distribution of the unknowns is proportional to the product of the likelihood function and the prior distributions. Then we had the joint posterior distribution as

$$\begin{aligned} p(\mathbf{b}, \mathbf{a}, \sigma_a^2, \sigma_e^2|\mathbf{y}) \propto\; & p(\mathbf{y}|\mathbf{b}, \mathbf{a}, \sigma_e^2)p(\mathbf{b})p(\mathbf{a}|\mathbf{A}, \sigma_a^2) \\ & p(\sigma_e^2|\upsilon_e, S_e^2)p(\sigma_a^2|\upsilon_a, S_a^2). \end{aligned} \tag{7}$$

Posterior marginal inferences on the parameters of our interest were drawn from their corresponding conditional posterior distributions through the single-site Gibbs sampler (Wang *et al*. 1994; Sorensen & Gianola 2002). Shariati and Sorensen (2008) pointed out that this sampler can lead to a slow mixing problem, but is more efficient in terms of total cost such as computing time.

Data used were from 3 prefectures (denoted as data sets A, B and C). Carcass traits analyzed were carcass weight, ribeye area, rib thickness, subcutaneous fat thickness, estimated yield percent, and marbling score that were measured by official graders to the carcass grading standards (JMGA 1988). For detail about the definitions of the 6 traits, see, e.g. Oyama *et al*. (2004). The numbers of records and some descriptive statistics of the traits in the data sets are given in Table 1.

The GS was run at differing total chain lengths (20 000, 50 000, 100 000, 200 000, and 1000 000) and thinning intervals (0, 5, 10, 20 and 100) to investigate their influences on the estimated marginal distributions. The length of burn-in period was determined by assessing convergence using the coupling method (Johnson 1996; García-Cortés *et al*. 1998) which uses several chains with different starting values and the same sequence of random numbers. According to the criteria of García-Cortés *et al*. (1998), when the absolute maximum difference between variances of 2 coupled chains neared a given tolerance (10^{-3}), the 2 chains were defined as convergence. Posterior means rather than modes were

Table 1 Number of records and descriptive statistics (mean ± SD) for carcass traits in 3 data sets

Item	Data set A	Data set B	Data set C
No. of records	4 412	10 080	18 550
No. of sires	101	249	197
No. of dams	3 935	8 406	14 672
No. of animals in the pedigree file	12 204	26,129	42 295
Age at carcass market, m	28.7 ± 2.9	29.0 ± 2.5	28.9 ± 1.9
Inbreeding coefficient, %	1.0 ± 2.7	1.0 ± 3.0	0.8 ± 2.4
Trait†			
CW, kg	422.4 ± 47.8	395.4 ± 47.8	413.0 ± 42.4
RA, cm^2	50.3 ± 6.6	45.3 ± 6.2	48.5 ± 6.4
RT, cm	7.3 ± 0.9	6.8 ± 0.8	7.1 ± 0.8
SFT, cm	2.4 ± 0.9	2.5 ± 0.8	2.5 ± 0.8
EYP, %	73.4 ± 1.3	72.7 ± 1.2	73.0 ± 1.2
MS, 0 to 5	1.7 ± 0.9	1.1 ± 0.6	1.4 ± 0.7

†CW, carcass weight; RA, ribeye area; RT, rib thickness; SFT, subcutaneous fat thickness; EYP, estimated yield percent; MS, marbling score.

chosen here as point estimates, since in previous studies the means were found to be closer to the true values (van Tassell *et al*. 1995; Luo *et al*. 2001). Monte Carlo errors and effective sample sizes of estimates of the VCs were computed using the time-series procedure described by Geyer (1992) and Sorensen and Gianola (2002). The Monte Carlo error is the error of a Monte Carlo estimate based on a run of the chain of a given length from the true value. The effective sample size means the amount of information available for parameter estimation, depending on the degree of autocorrelation between Gibbs chains, and therefore higher values are desirable. The computer program was written using DIGITAL Visual Fortran.

For comparison, REML estimation was also implemented using an integrated computational scheme of the AI and the EM algorithms as used in the official genetic evaluation (Iwaisaki & Ashida 2004). In both the GS and REML analyses, the single-trait operational model considered included discrete effects of fattening farms, year at slaughter, places of slaughter (carcass markets), and gender, continuous effects of age of slaughter and degrees of inbreeding (both as a covariate), animal effects (breeding values), and residuals. With the REML estimation, the convergence criterion was that changes in the ratios of the corresponding estimates between two consecutive rounds were all less than 10^{-8}.

Computation was carried out on a personal computer with a Pentium 4, 3.0 GHz processor under Windows XP (1.5 Gb of RAM).

RESULTS AND DISCUSSION

Table 2 shows the results for iterations up to convergence obtained by the coupling method for the VCs in 3 data sets. For the estimation of the burn-in period, Raftery and Lewis's (1992) convergence diagnosis is often applied to the outputs from GS. However, García-Cortés *et al*. (1998) and López-Romero *et al*. (2003) reported that the number of iterations to be discarded in accordance with the Raftery and Lewis criterion, which was based on a single chain, was smaller than that as indicated by the coupling method, suggesting that the Raftery and Lewis's method is likely to produce less reliable results than the multiple chain methods with respect to burn-in period estimation.

Table 2 Number of coupling iterations with different starting values for additive genetic ($\hat{\sigma}_a^2$) and residual variances ($\hat{\sigma}_e^2$) by trait

Trait†	Data set A		Data set B		Data set C	
	$\hat{\sigma}_a^2$	$\hat{\sigma}_e^2$	$\hat{\sigma}_a^2$	$\hat{\sigma}_e^2$	$\hat{\sigma}_a^2$	$\hat{\sigma}_e^2$
CW, kg	4909	4726	7607	7423	5036	4797
RA, cm^2	4646	4427	3772	3684	4164	4056
RT, cm	3100	3034	2875	2666	2593	2443
SFT, cm	2789	2700	3110	2927	2864	2712
EYP, %	2653	2622	2544	2344	2823	2688
MS, 0 to 5	2762	2671	2522	2267	2437	2290

†CW, carcass weight; RA, ribeye area; RT, rib thickness; SFT, subcutaneous fat thickness; EYP, estimated yield percent; MS, marbling score.

With the coupling method, under the given criterion, convergence rates were obviously different among the traits. The number of iterations to be discarded in accordance with the coupling method for additive genetic variance ranged from 2653 to 4909, from 2522 to 7607, and from 2437 to 5036 for data sets A, B, and C, respectively. Convergence for additive genetic variance was slightly, but consistently slower, than that of residual variance, agreeing with a previous finding of Jamrozik (2004). Also, it was observed that convergence for traits with higher VC values like carcass weight was obviously slower than that for those with lower ones. The trace plot of iterations of coupled chains for additive genetic variance for carcass weight in data set B is presented in Figure 1 as an illustration, which was the most demanding case to satisfy the given criterion. Since more than 7000 iterations were required to satisfy the criterion for all the traits, the first 10 000 iterations would be considered to be sufficient enough for the overlapped two chains, so that the burn-in was set to this length for all the traits.

Table 3 gives posterior means, posterior standard deviations, Monte Carlo errors, and effective sample sizes for the VCs of carcass weight, which were simulated using chains of different length, holding burn-in period and thinning interval constant at 10 000 and 10, respectively. When changed from 20 000 to 1 000 000, chain length had smaller effect on the posterior means and the posterior standard deviations for both the additive genetic and the residual variances. The Monte Carlo errors were reduced with the increased chain length and could be made arbitrarily small, given large enough chain size. Percentages of the Monte Carlo errors to the posterior means were varied here approximately from 5 to below 1%. The effective sample size had the lowest value of about 10 and increased in an almost linear manner, as chain length became higher. Several animal breeders suggested 100 as the minimum effective sample size for reliable statistical inference (e.g. Uimari *et al*. 1996; Bink *et al*. 1998).

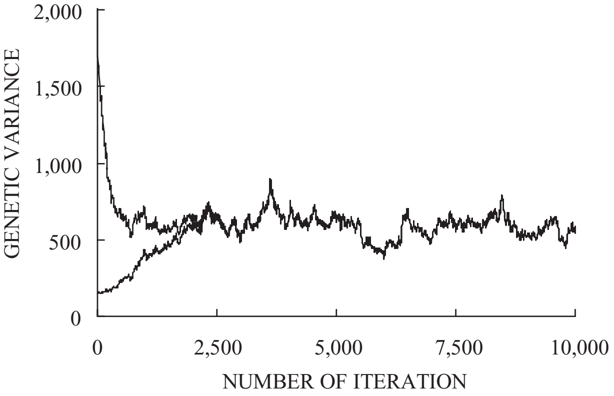

Figure 1 Trace plots of coupled chains for the additive genetic variance of carcass weight in data set B.

The length of the chain determines the precision of the posterior moment estimates, though for practical purposes, posterior mean obtained from a valid, but possibly short chain would be reasonable. When chain length was 100 000, effective sample size higher than 100 were observed for all the cases, and Monte Carlo errors with this setting were found to be very small (all lower than 2% of the corresponding posterior means). These findings for carcass weight were true for the remaining traits, even at differing thinning intervals (data not shown). Hence, the estimates obtained with the Gibbs chain length of 100 000 with a burn-in period of 10 000 cycles could be accurate enough, and these settings are likely to be a reasonable standard specification.

Table 4 presents posterior means, posterior standard deviations, Monte Carlo errors, and effective sample size for the VCs of carcass weight using the different

Table 3 Posterior means (PM), posterior standard deviations (PSD), Monte Carlo errors (MCE), and effective sample sizes (ESS) for the variance components of carcass weight, holding burn-in period and thinning interval constant at 10 000 and 10, respectively

CL†	Data set A				Data set B				Data set C			
	PM	PSD	MCE	ESS	PM	PSD	MCE	ESS	PM	PSD	MCE	ESS
$\hat{\sigma}_a^2$‡												
2	1301.4	176.6	36.0	24.1	635.9	94.4	27.5	11.8	596.2	49.6	9.6	26.7
5	1222.8	183.3	24.3	56.7	621.5	101.9	13.5	56.6	613.0	53.0	5.5	93.5
10	1225.1	190.6	15.9	143.9	626.5	100.2	8.0	157.1	613.1	54.3	3.9	197.4
20	1236.3	189.6	11.6	268.3	621.2	101.4	6.8	221.6	613.3	60.2	3.5	295.1
100	1250.4	194.6	5.1	1467.6	609.0	102.1	3.5	857.8	615.2	60.6	1.5	1600.8
$\hat{\sigma}_e^2$												
2	530.4	120.5	24.8	23.6	1134.7	68.9	19.0	13.2	828.0	34.8	6.3	30.4
5	582.3	125.4	16.5	57.7	1144.7	72.2	9.3	60.7	816.6	36.8	3.6	103.6
10	581.2	130.4	10.8	144.6	1141.2	71.0	5.4	171.8	816.4	37.5	2.5	216.0
20	573.9	129.1	7.8	271.1	1144.8	71.9	4.7	238.8	816.7	41.2	2.3	318.5
100	564.5	132.2	3.4	1485.7	1153.1	72.5	2.4	933.5	815.5	41.4	1.0	1718.5

†CL, Gibbs chain length (×10^4). ‡$\hat{\sigma}_a^2$, additive genetic variance; $\hat{\sigma}_e^2$, residual variance.

Table 4 Posterior means (PM), posterior standard deviations (PSD), Monte Carlo errors (MCE), and effective sample sizes (ESS) for the variance components of carcass weight, holding Gibbs chain length and burn-in period constant at 100 000 and 10,000, respectively

TI†	Data set A				Data set B				Data set C			
	PM	PSD	MCE	ESS	PM	PSD	MCE	ESS	PM	PSD	MCE	ESS
$\hat{\sigma}_a^2$‡												
0	1225.2	190.7	15.7	146.7	626.6	100.2	7.9	159.5	613.0	54.2	3.8	201.1
5	1225.2	190.8	15.8	145.3	626.5	100.3	8.0	158.5	613.0	54.2	3.8	199.2
10	1225.1	190.6	15.9	143.9	626.5	100.2	8.0	157.1	613.1	54.3	3.9	197.4
20	1224.8	191.1	16.0	141.9	626.6	100.3	8.1	154.3	613.2	54.2	3.9	193.8
100	1224.7	192.3	17.4	121.5	625.6	99.9	8.6	134.0	613.5	54.2	4.3	160.2
$\hat{\sigma}_e^2$												
0	581.1	130.1	10.7	146.8	1141.4	71.1	5.4	174.1	816.6	37.4	2.5	221.8
5	581.2	130.1	10.8	146.2	1141.3	71.1	5.4	172.4	816.5	37.5	2.5	220.8
10	581.2	130.4	10.8	144.6	1141.2	71.0	5.4	171.8	816.4	37.5	2.5	216.0
20	581.4	130.1	10.9	141.8	1141.5	71.4	5.5	169.9	816.4	37.6	2.6	206.7
100	580.9	130.1	11.8	122.2	1140.8	70.5	5.9	141.3	816.2	37.6	2.9	165.9

†TI, thinning interval. ‡$\hat{\sigma}_a^2$, additive genetic variance; $\hat{\sigma}_e^2$, residual variance.

thinning intervals, holding Gibbs chain length and burn-in period constant at 100 000 and 10 000, respectively. Thinning interval was found to have no substantial effect on the posterior means and on the posterior standard deviations. Accordingly, increasing the interval between samples only very slightly changed the effective sample size and also the Monte Carlo errors. These results on the effect of thinning interval were very similar for the cases of different chain lengths and among the other analyzed carcass traits.

Thinning interval influences the autocorrelation among the samples, and consecutive samples with no lags would be expected to be almost perfectly correlated (e.g. Jamrozik 2004). In theory, according to the ergodic theorem, if we had an infinite number of samples, all samples should be included in moment's calculations (Gilks *et al*. 1996). However, the length of a chain produced by GS with the long-chain scheme is practically limited. Therefore, intermediate cycles must be eliminated or thinned, and some distance between samples is necessary. On the other hand, since a very low frequency of retaining sampled values reduces the number of samples available, a thinning interval of 10 could be one possible decision for a reasonable specification.

The posterior means and the posterior standard deviations of the VCs for the all carcass traits are shown in Table 5 in comparison with the corresponding REML estimates, which were simulated using every 10th sample from 90 000 of Gibbs chain after 10 000 samples discarded as burn-in period. The REML estimates in these data sets were actually obtained only with the implemented AI algorithm of the integrated procedure of the AI and the EM ones. Then their standard errors were calculated using the information on the inverse of the AI matrix. The posterior means and posterior standard deviations obtained by the current GS procedure and the estimates by the REML method were totally reasonably comparable to each other, indicating that the current GS procedure with the sampling conditions determined here performs well for the Japanese Black carcass field data.

A few of the GS estimates for carcass weight and ribeye area may be slightly different from the corresponding REML estimates, although the differences were very small taking into consideration the sampling variances. For data sets A and B with relatively small numbers of records, the posterior means of the additive genetic variance for these traits appeared to be very slightly higher than the estimates obtained by REML, while the corresponding means for the residual variance were slightly lower than the REML estimates. Similar differences were found in the previous study using field data of Nelore cattle (Magnabosco *et al.* 2000). On the other hand, for results from simulated data, such a difference between the posterior mean by GS and the corresponding estimate by REML was not observed (van Tassell *et al*. 1995; Schenkel & Schaeffer 2000; Duangjinda *et al*. 2001). From a Bayesian viewpoint, the REML estimates are the elements of the mode of the joint posterior density of all VCs, when flat priors are employed for all parameters in the model (Harville 1974). Magnabosco *et al.* (2000) indicated

Table 5 Posterior means and posterior standard deviations for the variance components of carcass traits obtained with the current GS, and the estimates and approximate standard errors with REML

Trait†	Data set A				Data set B				Data set C			
	$\hat{\sigma}^2_{a(GS)}$ ‡	$\hat{\sigma}^2_{a(REML)}$	$\hat{\sigma}^2_{e(GS)}$	$\hat{\sigma}^2_{e(REML)}$	$\hat{\sigma}^2_{a(GS)}$	$\hat{\sigma}^2_{a(REML)}$	$\hat{\sigma}^2_{e(GS)}$	$\hat{\sigma}^2_{e(REML)}$	$\hat{\sigma}^2_{a(GS)}$	$\hat{\sigma}^2_{a(REML)}$	$\hat{\sigma}^2_{e(GS)}$	$\hat{\sigma}^2_{e(REML)}$
CW, kg	1225.1	1216.1	581.2	585.1	626.5	595.0	1141.2	1161.5	613.1	610.9	816.5	817.8
	(190.6)§	(192.6)	(130.5)	(131.1)	(100.2)	(92.0)	(71.0)	(65.9)	(54.3)	(61.6)	(37.5)	(42.1)
RA, cm^2	17.3	16.9	24.1	24.3	14.1	13.8	21.8	22.0	23.1	23.1	19.4	19.3
	(3.3)	(3.6)	(2.4)	(2.6)	(1.8)	(1.9)	(1.3)	(1.3)	(1.9)	(2.1)	(1.3)	(1.4)
RT, cm	0.19	0.19	0.46	0.46	0.16	0.15	0.40	0.40	0.23	0.23	0.34	0.34
	(0.04)	(0.05)	(0.03)	(0.03)	(0.03)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)
SFT, cm	0.23	0.23	0.36	0.36	0.27	0.26	0.32	0.33	0.30	0.29	0.29	0.29
	(0.05)	(0.05)	(0.03)	(0.03)	(0.04)	(0.04)	(0.03)	(0.02)	(0.03)	(0.03)	(0.02)	(0.02)
EYP, %	0.74	0.72	0.81	0.82	0.67	0.66	0.72	0.72	0.92	0.93	0.65	0.64
	(0.13)	(0.14)	(0.09)	(0.10)	(0.08)	(0.08)	(0.06)	(0.06)	(0.08)	(0.08)	(0.05)	(0.05)
MS, 0 to 5	0.61	0.61	0.21	0.21	0.19	0.19	0.19	0.19	0.25	0.25	0.17	0.17
	(0.08)	(0.09)	(0.06)	(0.06)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)	(0.02)	(0.01)	(0.01)

†CW, carcass weight; RA, ribeye area; RT, rib thickness; SFT, subcutaneous fat thickness; EYP, estimated yield percent; MS, marbling score. ‡$\hat{\sigma}^2_{a(GS)}$ and $\hat{\sigma}^2_{a(REML)}$, additive genetic variance estimated with GS and REML, respectively; $\hat{\sigma}^2_{e(GS)}$ and $\hat{\sigma}^2_{e(REML)}$, residual variance with GS and REML, respectively. §Posterior standard deviation by GS or approximate standard error by REML in parenthesis.

that in a simulated population, the posterior means for VCs by GS and the REML estimates agreed quite well, since the likelihood might be relatively symmetric. In our GS program, flat priors were adopted for all parameters in the model, but the posterior means rather than the posterior modes of VCs were computed as point estimates. This could be one reason for some slight differences between the current GS and the REML estimates, especially in the data sets with smaller numbers of records. Whereas the posterior mode may be a better approximation to the mean, the posterior mean as used in this study is the optimal estimator under quadratic loss (Gianola & Foulley 1990).

As a conclusion, the Gibbs sampling conditions determined in this study could be recommended as a standard specification for estimating VCs using the Bayesian framework via GS from the carcass field data in Japanese Black cattle. The GS scheme requires relatively small memory requirement compared with REML, although GS is more time-consuming than REML. In another paper, we will report that the current specification of the GS sampling conditions has worked very well also in the analysis of a very large data set of carcass traits. However, further investigation may be necessary to check if the current sampling conditions are valid or not in the case of a data set from a population with relatively high degree of inbreeding.

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