

GENETIC RELATIONSHIP AMONG TRAITS OF TESTING PROGRAM AND THE PROSPECT FOR THE BREEDING PLAN IN WAGYU (JAPANESE BLACK) CATTLE

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SUMMARY

Derivative-free REML analysis was carried out for joint estimation of (co)variance components for traits of performance test and progeny test. Data were test records; 639 bulls in the performance test (PERM) and 493 steers in the progeny test (PROG). Traits in study were concentrate intake (CONC), roughage intake (ROU), TDN conversion (TDN) in PERM, rib eye area (REA), marbling score (MARB) and dressing percentage (DRES) in PROG, and body weight at start (BWS), body weight at finish (BWF) and average daily gain (ADG) in the both tests. The estimation was carried out by two-trait model for the traits in PERM or three-trait model for the traits in PROG. Heritability estimates were .38 (BWS), .35 (BWF), .17 (ADG), .20 (CONC), .60 (ROU) and .12 (TDN) for PERM traits, and .37 (BWS), .41 (BWF), .28 (ADG), .01 (REA), .57 (MARB) and .12 (DRES) for PROG traits. Genetic correlation between CONC and ROU was estimated to be unity. The correlations of CONC and ROU showed positive genetic relationship with ADG and body weights. On the contrary, CONC had positive relationship with TDN and DRES and null relationship with MARB, whereas ROU had negative relationship with TDN and DRES, positive relationship with MARB. MARB showed positive genetic relationship with ADG, whereas null relationship was estimated between MARB and TDN. These results suggested the usefulness of roughage intake for a selection criterion, the possibility of efficient improvement of marbling score without loss of genetic progress in weight gain and the potentiality of a joint evaluation system.

Keywords: Progeny test, performance test, genetic parameter, Japanese Black cattle, breeding program.

INTRODUCTION

Breeding program of Wagyu cattle is traditionally undertaken through the selection of sires by performance test and consecutive progeny test at test stations which are located in each prefecture. There are 23 prefectural testing stations and three national test stations with similar structure of breeding population; approximately 20 sires and 400-800 cows in the nucleus population. The BLUP procedure with animal model allows us a possibility to initiate a refinement of this traditional breeding scheme. Due to the breeding program where selection intensity is higher in the performance test, joint evaluation of the performance test and progeny test seems to bring more efficient breeding program. Especially it is expected on the improvement of meat quality traits because they are evaluated only in the progeny test. For this purpose, the estimation of covariances among traits recorded in the both tests is important because the estimates in literatures are scarce

for the covariances such as feed conversion and marbling score, feed intake and marbling score. The objectives of this study are to estimate genetic parameters by the joint estimation in Okayama and to illustrate the present and proposed breeding program.

MATERIALS AND METHODS

Source of data. The data set was records of performance test and progeny test for Japanese Black bulls at Okayama Prefecture Animal Industry Center. The number of animals was 4251 including pedigree animals. The data structure is described in Table 1. These tests were carried out according to the Wagyu sires' performance testing procedure.

Performance test. The lengths of the testing period were 140 days before 1974 and 112 days afterwards. Bulls were housed individually in box stalls. They were given ad libitum access to roughage (hay), whereas feeding of concentrate was restricted by time; 1 hour for each feeding time that is twice a day. Traits in study were body weight at start (**BWS**, kg), body weight at finish (**BWF**, kg), average daily gain during the test period (**ADG**, kg), concentrate intake (**CONC**, kg), roughage intake (**ROU**, kg) and TDN conversion (**TDN**) expressed as consumption per kilogram gain based on tabular value.

Table 1. Description of data structure

Data set	No. animals	No. sires	No. dams	Years	YS
Performance test	639	51	510	24	138
Progeny test	493	63	478	23	64

Progeny test. The lengths of the testing period were 329 days before 1970, 301 days before 1977 and 364 days afterwards. A group of the steers (8 to 10 animals) sired by the same bull were housed together in loose barn. Unlike the performance test, the animals were given ad libitum access to concentrate, roughage and water. Traits in study were **BWS**, **BWF**, **ADG**, rib eye area (**REA**, cm²), marbling grade (**MARB**) and dressing percentage (**DRES**, %). The REA was measured on the 6th to 7th rib section of the left side of the carcass. The MARB was measured according to the Beef Marbling Standard (Japan Meat Grading Association). Means, SDs and CVs of the traits in study are presented in Table 2 together with age at start (**AGES**, day) and age at finish (**AGEF**, day).

Table 2. Means, SDs and CVs for variables in the performance test and progeny test

	AGES	AGEF	BWS	BWF	ADG	CONC	ROU	TDN	REA	MARB	DRES
Performance Test											
Mean	230.9	346.3	270.8	410.9	1.218	689.1	370.5	4.815	-	-	-
SD	14.8	15.5	33.5	40.6	.158	132.3	97.5	.580	-	-	-
CV (%)	6.4	4.5	12.4	9.9	13.0	19.2	26.3	12.0			
Progeny test											
Mean	258.3	612.9	253.1	551.3	.842	-	-	-	46.62	2.521	63.63
SD	15.7	23.0	25.8	60.8	.115	-	-	-	5.96	1.019	1.8
CV (%)	6.1	3.8	10.2	11.0	13.7				12.8	40.4	2.9

Statistical procedure. Statistical analyses were carried out using the 2.2 version of REML VCE program (Groeneveld, 1993) for (co)variance component estimation. Optimization of log likelihood applied in these analyses used a quasi-Newton algorithm. As the data set including both the performance and progeny test records has weak connectedness each other, we first undertook a search for a common trait among BWS, BWF and ADG. According to our preliminary results, we treated BWS of the both tests as a common trait (BWSc). A statistical model used in this analysis was as follows;

$$Y_{ij} = F_{i(j)} + a_{ij} + e_{ij}$$

with $F_i = YS_i$ for TDN, REA, MARB, or $F_{ij} = YS_i + b_1(AGES_{ij} - AGES)$ for BWS or $F_{ij} = YS_i + b_1(AGEF_{ij} - AGEF)$ for BWF, CONC, ROU, DRES, where Y_{ij} : the BWS, BWF, ADG, CONC, ROU, TDN, REA, MARB or DRES for j th animal, a_{ij} : the additive genetic effect for j th animal, e_{ij} : the random residual, YS_i : the fixed effect of i th year-set of the test, b_1 : the linear regression coefficient of the observations on age, $AGEX_{ij}$: the age of j th animals in i th year-set at either the start of the test (X for S) or the finish of the test (X for F), $AGEX$: the mean age of the animals. The estimates of (co)variances for the performance test traits were undertaken by two-trait analyses with records of performance test, while the estimates including progeny test traits were all undertaken by three-trait analyses, BWSc and two other traits being interested in.

RESULTS AND DISCUSSION

Table 3. Means and SDs of heritability estimates

	BWS	BWF	ADG	CONC	ROU	TDN	REA	MARB	DRES
Performance test									
Mean	.38	.35	.17	.20	.60	.12	-	-	-
SD	.02	.01	.08	.06	.03	.01	-	-	-
Progeny test									
Mean	.37	.41	.28	-	-	-	.01	.57	.12
SD	.03	.00	.01	-	-	-	.01	.02	.03

Table 3 presents the estimates of heritabilities. The heritabilities of BWS and BWF in the both tests showed moderate value. The heritability of ROU was higher than a reviewed average of feed intake (.41) by Koots *et al.* (1994a), but the heritability of CONC was lower than it. The low

heritability of ADG in this analysis seems to be affected by the length of the testing period, because the ADG in the progeny traits was not as low as this estimate. Comparing these with the previous estimates by Sasaki *et al.* (1982), BWF and ROU in this study were higher than their estimates, however CONC and TDN were lower than them. The heritability of ADG was almost consistent with their estimates. The heritabilities of REA and DRES were low, whereas the heritability of MARB was high with small SD.

In Table 4, the genetic correlations among growth traits of the performance test showed high estimates. The genetic correlation between CONC and ROU was also very high. The genetic correlation between ROU and BWS was low, whereas the genetic correlation between ROU and ADG was unity. The latter high correlation confirms that ability to intake more roughage is closely related with rate of gain under the feeding regime of restricted concentrate intake. The former low genetic correlation may be related to the different feeding regime before test (less restriction on access to concentrate) and on test. The genetic correlations of TDN showed negative relationship with ADG and ROU. The contrasted results between ROU vs. TDN and CONC vs. TDN suggested a possibility about the favorable role of roughage consumption for the efficiency of growth. As a possible explanation for this result, enlargement in capacity of rumen that is stimulated by the intake of more roughage seems to favorably influence animal's appetite (or vice versa).

Table 4. Estimates^A of genetic correlations and (co)variances of the performance test traits

Trait	BWS	BWF	ADG	CONC	ROU	TDN
BWS	<u>218.4</u>	1.00	.94	.70	.17	-.11
BWF	264.4	<u>354.8</u>	.93	.61	.59	-.22
ADG	.579	.751	<u>.0032</u>	.47	1.00	-.43
CONC	258.7	298.5	.680	<u>821.6</u>	.99	.58
ROU	68.71	291.6	1.976	914.8	<u>676.8</u>	-.51
TDN	-.240	-.673	-.0041	2.551	-2.234	<u>.0260</u>

^ACorrelations above diagonals, variances on diagonals (underlined) and covariances below diagonals.

Among the genetic correlations in the progeny test (Table 5), genetic relationships of REA with MARB and DRES were highly positive, whereas the relationship between REA and the body weights or the gain were negative. The genetic relationship between MARB and DRES was highly negative. According to the reviewed average by Koots *et al.* (1994b), low genetic correlation was reported between MARB and DRES, whereas, Dikeman (1994) indicated that there are genetic antagonisms between meat quality traits and carcass composition.

Table 5. Estimates^A of genetic correlations, (co)variances of the progeny test traits

Traits	BWSc	BWF	ADG	REA	MARB	DRES
BWSc	<u>219.4</u>	.90	.75	-.54	.40	.06
BWF	421.5	<u>970.1</u>	.96	-.66	.43	-.01
ADG	611	1.540	<u>.0029</u>	-.41	.38	.05
REA	-2.530	-5.358	-.0065	<u>.280</u>	.92	.96
MARB	3.489	7.751	.0120	.439	<u>.353</u>	-.96
DRES	1.109	-.0190	.0011	.3003	-.335	<u>.263</u>

^ACorrelations above diagonals, variances on diagonals (underlined) and covariances below diagonals.

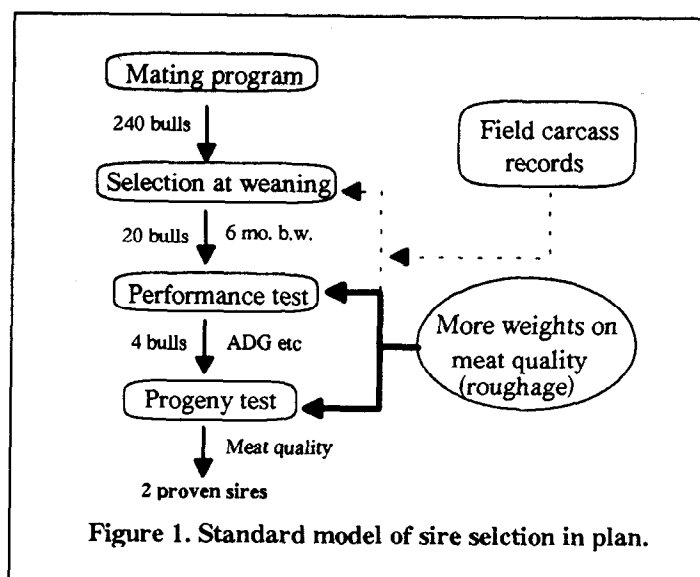
Table 6 presents the genetic correlations between the traits of the performance test and progeny test. The genetic correlations of BWF and ADG between the tests seem to be slightly lower than the value for which no genotype by environment interaction is indicated. The possible causality of this low genetic correlations is the differences in length of testing period, feeding regime for concentrate, effect of sex and housing procedure. Very low genetic relationship was found between TDN and MARB. The genetic correlation between TDN and DRES was higher than the estimate (.21) referred by Koots *et al.* (1994b). CONC showed moderate positive genetic relationship with the progeny test traits except for the very low correlation with MARB. The correlations of CONC and ROU, which showed the correlation of unity between them, showed contrary tendency for their relationship with TDN, MARB, DRES and REA but similar tendency for the traits of body weights and weight gain. The genetic correlations of MARB were low with BWSc, BWF, CONC or TDN, whereas MARB had positive correlations with ADG and ROU.

Table 6. Estimates of genetic correlations between performance test traits and progeny test traits

	Performance test					
	BWSc	BWF	ADG	CONC	ROU	TDN
Progeny test						
BWSc	-	1.00	.96	.81	.20	-.10
BWF	.92	.73	.92	.65	.76	-.10
ADG	.79	.42	.70	.52	.81	-.03
REA	-.19	-.67	-.67	.65	-.97	1.00
MARB	.33	.08	.63	-.08	.43	.08
DRES	.07	-.00	-.51	.60	-.57	.97

APPLICATION

Figure 1 presents the outline of the current standard model of sire selection and some future evaluation prospects (in right side of the figure). Assiming 600 cows in a nucleus population, then approximately 240 bulls are born every year. Out of this 240 bulls, 4 animals are selected mostly by growth performance; body weight or weight gain, via the selection at weaning and the performance test. Thus selection pressure on meat quality in this standard model is low in spite of great requirement from breeders and market side. The result of this study suggests that joint evaluation (with the records of both tests being included) would be potentially effective for improvement of meat quality as well as meat quantity, although exact advantage of the new system need be investigated by simulation study for the sire evaluation system. As the similar system is take by most of prefectures in Japan, accumulation of the estimates can be expected, which will contribute to the advancement of beef cattle improvement. More unified evaluation system, includes weaning records and field carcass records, would have a further possibility in future.



REFERENCES

Dikeman, M.E. (1994) *5th World Cong. on Genet. Appl. to Livest. Prod.*, 19:437.
 Groeneveld, E. (1993) REML VCE - a multivariate multimodel restricted maximum likelihood (co)variance component estimation package. In: E. Groeneveld (Ed.), Mariensee.
 Koots, K.R., J.P.Gibson, C.Smith, and J.W.Wilton. (1994a) *Anim. Breed. Abstr.* 62:309.
 Koots, K.R., J.P.Gibson, and J.W.Wilton. (1994b) *Anim. Breed. Abstr.* 62:825.
 Sasaki, Y., H.Iwaisaki, T.Masuno, and S.Asoh. (1982) *J.Anim. Sci.* 55:771.