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Estimation of genetic parameters for carcass grading traits, image analysis traits, and monounsaturated fatty acids in Japanese Black cattle from Hyogo Prefecture

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Abstract

Genetic parameters for carcass grading traits, image analysis traits, and monounsaturated fatty acid (MUFA) percentages were estimated in 29,942 Japanese Black cattle from Hyogo Prefecture. The analyzed traits included five carcass grading traits, two image analysis traits, fat area ratio and fineness index, and two MUFA traits, one measured in intermuscular fat using near-infrared spectroscopy (NIRS) and the other in intramuscular fat using gas chromatography (GC). The heritability estimates of image analysis traits and MUFA were moderate to high, ranging from 0.395 to 0.740, and it was considered that they could be improved simultaneously with carcass grading traits because no severe genetic antagonism was observed. Although the heritability of the NIRS-based intermuscular MUFA was slightly lower than that of the GC-based intramuscular MUFA, the genetic correlation between the two methods was as high as 0.804. These results indicate that the NIRS method can be used as an alternative evaluation procedure to predict MUFA in intramuscular fat in the *longissimus* muscle.

KEYWORDS

fineness of marbling, gas chromatography, genetic correlation, heritability, near-infrared spectroscopy.

1 INTRODUCTION

In Japan, beef carcasses are graded by trained graders in accordance with the Japanese Beef Carcass Grading Standards (JMGA, 1988). Among the multiple carcass traits, the beef marbling standard number (BMS No.), in particular, has been shown to play a significant role in the price of beef carcasses (Ibi et al., 2006) and affect the palatability of beef (Corbin et al., 2015; Iida et al., 2015).

In contrast, a method has been developed to analyze digital images of carcass cut surfaces (Kuchida et al., 2006). This method enables quantification of not only the percentage of fat in the *longissimus* muscle, but also the shape of fat (shape of marbling), which is difficult to evaluate under the current grading method. Subsequent studies have also reported the relationship between traits representing the shape of marbling and eating quality (Asa et al., 2017). As the degree of marbling increases, the importance of its shape becomes increasingly significant.

Oleic acid, a monounsaturated fatty acid (MUFA), is well known for its involvement in beef flavor (Dryden & Marchello, 1970; Westerling & Hedrick, 1979), and has been shown to enhance the sweet aroma (Sakuma et al., 2012) and flavor (Suzuki et al., 2013; Tsuyuki et al., 2016) in Japanese Black cattle. These studies have led to increased interest in oleic acid or MUFA as a target trait for sensory characteristics. Generally, MUFA percentage is measured by gas chromatography (GC), but it

is difficult to collect sample data on a large scale because of the time required and labor cost for measurement. However, measurement by a lipid analyzer using near-infrared spectroscopy (NIRS) is now being used in many carcass markets in Japan because it can predict MUFA nondestructively and quickly (Irie et al., 2003; Piao et al., 2018).

Future improvements in beef production ability should be more diverse, including not only the current grading traits, but also those involved in eating quality. Thus, the genetic relationships among these target traits must be carefully examined. Some studies have reported such relationships between carcass grading traits and fatty acids (Nogi et al., 2011; Inoue et al., 2017) or image analysis traits (Osawa et al., 2008). However, only one report by Yamamoto et al. (2020) used MUFA, image analysis traits, and carcass grading traits simultaneously for analysis.

In addition, although the NIRS method is adopted for the intermuscular fat surface, the tissue to be consumed is muscle, and most of the reports that have examined sensory evaluations have used the MUFA ratio of intramuscular fat. In this respect, Nishioka et al. (2008) reported a significant correlation between inter- and intra-muscular fat. However, to the best of our knowledge, no study has investigated the genetic relationship between these two types of fat.

Therefore, in this study, we estimated genetic parameters for image analysis traits, MUFA percentages, and carcass

grading traits of Japanese Black cattle from Hyogo Prefecture and evaluated the potential for genetic improvement in these traits. In addition, we compared the genetic parameters of MUFA percentages obtained by NIRS and GC methods and examined the effectiveness of using NIRS-based MUFA for improvement.

2 MATERIALS AND METHODS

2.1 Animals

All samples and data used in this study were obtained from carcasses processed at the slaughterhouse and existing databases; therefore, approval from the Animal Care and Use Committee was not required.

A total of 29,942 carcasses of Japanese Black cattle from Hyogo Prefecture (Tajima cattle) were used in this study. They were slaughtered at an average age of 32.0 ± 1.8 months between 2006 to 2020 at three carcass markets in Hyogo. Among these, image analysis traits were recorded in 24,704 carcasses, NIRS MUFA in 18,570 carcasses, and GC MUFA in 2,952 carcasses. Furthermore, image analysis traits and NIRS MUFA were measured in 13,686 animals, image analysis traits and GC MUFA in 2,511 animals, both NIRS and GC MUFAs in 356 animals, and all traits were recorded in 269 animals.

2.2 Image analysis traits

Digital images of the sixth and seventh intercostal incision surfaces of the left side carcass were acquired using a beef

carcass imaging system (HK-333, Hayasaka Riko Co., Ltd., Sapporo, Japan). The images were taken at a resolution of 169 pixels per cm and automatically analyzed by Beef Analyzer II (Hayasaka Riko Co., Ltd.), a software program for analyzing beef carcass images. The traits evaluated were fat area ratio (FAR), which is the percentage of fat pixels to total pixels of the *longissimus* muscle, and fineness index (FI), which is calculated as the total number of fine fat particles in the range of 0.01 to 0.5 cm^2 in the *longissimus* muscle divided by *longissimus* muscle area (LMA). A high FI indicates the presence of an increased number of fine particles. Detailed procedures for the FAR and FI measurements are provided in Kuchida et al. (2006) and Nakahashi et al. (2008).

2.3 NIRS-based MUFA

Using NIRS, MUFA was measured in the intermuscular fat area of the cut surface bounded by the *vastus lateralis*, *serratus anterior*, *serratus abdominis*, and *rhomboid* muscles between the sixth and seventh ribs using a meat lipid measuring device (S-7040, Soma Optics, Tokyo, Japan). Each sample was measured three times, and the average was used for analysis.

2.4 GC-based MUFA

Approximately 1 g of sample was collected by scraping the entire surface of the *longissimus* muscle between the sixth and seventh ribs and stored at -30 °C until analysis. The composition of

13 fatty acids was measured according to the method described by Oka et al. (2002). Briefly, methylated lipid samples were analyzed using a hydrogen flame ionization detector on a gas chromatograph (GC-2014; Shimadzu Corporation, Kyoto, Japan) equipped with a capillary column (Famewax; Restek, Bellefonte, PA, USA). The column was programmed to warm from 120 °C to 240 °C at a rate of 3 °C/min and then maintained at 240 °C for 3 min. The sample fatty acids were identified by comparison with the relative retention times of standard fatty acid methyl esters (G.L. Science, Tokyo, Japan). The relative ratio was determined as a percentage of the total peak area, and MUFA percentage was calculated as the sum of myristoleic (C14:1), palmitoleic (C16:1), heptadecenoic (C17:1), oleic (C18:1), and eicosenoic (C20:1) acids.

2.5 Genetic parameters

Genetic parameters were estimated for nine traits belonging to four categories, namely five carcass grading traits, two image analysis traits (FAR and FI), NIRS MUFA, and GC MUFA. The carcass grading traits were carcass weight (CW), LMA, rib thickness (RT), subcutaneous fat thickness (SFT), and BMS No.

The same analytical models were used for all categories of data, with slaughter year, slaughter month, sex, and carcass market considered as the fixed effects, and age at slaughter (linear and quadratic) and inbreeding coefficient (linear) included as covariates. Animals, fattening farms, and residuals

were treated as random effects. Data from fattening farms with fewer than five records were deleted. The number of levels differed in each category: 15, 12, 2, 3, and 150 for carcass grading traits; 13, 12, 2, 3, and 147 for image analysis traits; 8, 12, 2, 3, and 132 for NIRS MUFA; and 15, 12, 2, 3, and 81 for GC MUFA, in the order of slaughter year, slaughter month, sex, carcass market, and fattening farm, respectively. Pedigrees were traced back to animals born in 1965, and 29,030 ancestors were added. Thus, 58,972 animals were used to construct an additive relationship matrix.

A multi-trait animal model was applied, and all nine traits were analyzed simultaneously. The analysis was performed using the AIREMLF90 program (Misztal et al., 2018). The REML (Patterson & Thompson, 1971) under the EM algorithm (Dempster et al., 1977) was used for the first 20 iterations to obtain appropriate initial (co)variance components for the AI algorithm (Johnson & Thompson, 1995; Ashida & Iwaisaki, 1999) because of the convergence problem with AI alone.

Genetic and residual covariances were assumed for all the trait categories. However, although fattening farm covariances within each category were assumed, those between different categories (e.g., between carcass grading and image analysis traits) were ignored because the fattening farms of each category were not identical. Genetic trends were expressed as the average predicted breeding values of breeding cows by birth year divided by the estimated genetic standard deviation.

3 RESULTS AND DISCUSSION

3.1 Basic statistics

The basic statistics of the data are listed in Table 1. The mean values of CW, LMA, RT, SFT, and BMS No. were 404.6 kg, 55.0 cm^2, 6.9 cm, 2.5 cm, and 6.8, respectively. Osawa et al. (2008) reported the means of the same traits for Japanese Black steers slaughtered at the Hokkaido Meat Center as 445.0 kg, 56.8 cm^2, 7.6 cm, 2.3 cm, and 5.5, respectively. Compared to the values obtained in this study, differences were observed, especially for CW and RT. This is because our data included both steers and heifers of Tajima cattle, which are known for their small body size. The size of the Hyogo population has been kept small because there is an upper limit of 499.9 kg for CW to be certified as Kobe Beef (Kobe Beef Marketing & Distribution Promotion Association, 2021).

A mean value of 47.1% for the FAR was obtained in this study. It was approximately 8 percentage points higher than the 39.3% reported by Osawa et al. (2008). BMS No. was also 1.3 higher than that reported by Osawa et al. (2008). In addition to genetic background, improvement in BMS No. in Japanese Black cattle was evident in the difference in FAR values between the two studies.

[Table 1]

The mean value of the GC MUFA measured in intramuscular fat

was 59.2%. Nogi et al. (2011) reported a mean MUFA of 57.1% measured in the same fat tissue of Japanese Black cattle from the Tottori Meat Center. The animals used in their study were approximately 3 months younger than the animals in our study. Because MUFA is known to be affected by age (Honda et al., 2016), it was suggested that age at slaughter largely contributed to the difference in MUFA between the two studies.

The mean value of NIRS MUFA measured in intermuscular fat was 63.2%, which was approximately 4 percentage points higher than that obtained with the GC method for intramuscular fat. Although the difference included the effects of both measurement method and tissue site, Nishioka et al. (2008) also showed that the GC MUFA percentage of intermuscular fat was 2.5 percentage points higher than that of fat in the *longissimus* muscle.

3.2 Genetic parameters

The heritability estimates of the five carcass grading traits in this study were high, ranging from 0.432 to 0.691 (Table 2). A review by Oyama (2011) reported on the heritability of carcass grading traits of Japanese Black cattle throughout Japan, and the unweighted means for CW, LMA, RT, and BMS No. were similar to those of our study. However, the estimate of SFT was 0.559, whereas these values were 0.22, 0.39, and 0.34 in the studies by Osawa et al. (2008), Oyama (2011), and Nogi et al. (2011), respectively. Using the same Hyogo population, Shojo et al.

(2006) reported a high heritability estimate for SFT (0.52) similar to that in our study. A study by Arakawa et al. (2009), using animals from all over Japan, also reported a high heritability of 0.53 for SFT. Tajima cattle are well known to be maintained in a closed breeding system (Kobe Beef Marketing & Distribution Promotion Association, 2021) and be highly inbred (Shojo et al., 2006). In general, genetic variation tends to decrease in such a system. Alternatively, it can be large when several subpopulations and genetic distances among these populations are properly maintained. In this case, a high heritability estimate is not surprising, even in a highly inbred population. However, it is not clear whether this is the reason for the high estimate of SFT in our study.

[Table 2]

In the image analysis traits, heritability was estimated to be moderate to high, with 0.740 for FAR and 0.395 for FI. These values were consistent with the values of 0.79 and 0.49, respectively, reported by Kato et al. (2014).

A few studies have reported the relatively high heritability of GC MUFAs in Japanese Black cattle. The values were 0.71 for intermuscular fat in Yamagata Prefecture (Komatsu et al., 2021), 0.68 for intramuscular fat in Tottori Prefecture (Nogi et al., 2011), and 0.63 for intramuscular fat in Yamagata Prefecture (Inoue et al., 2017). In contrast, the heritability of 0.542 estimated in the present study was somewhat lower than the reported values.

Research on fatty acid-related genes has been conducted intensively. Their representatives include stearoyl-CoA desaturase (SCD) (Taniguchi et al., 2004) and fatty acid synthase (FASN) (Abe et al., 2009). In the Hyogo population, the frequencies of the major allele were 0.96 for SCD and 0.91 for FASN, which were considerably higher than those in other Japanese Black populations (Ookura et al., 2013). Such extreme bias in allele frequencies may have reduced the genetic variance in MUFA in Hyogo, resulting in a low heritability.

However, the heritability of NIRS MUFA was lower than that of GC and was estimated to be 0.450. A similar tendency was reported by Komatsu et al. (2021). They compared the heritability estimates of MUFA, saturated fatty acid, and oleic acid percentages obtained using different methods; for example, the estimates for MUFA were 0.441 by NIRS and 0.714 by GC. In addition to the estimation error with the NIRS method, a large environmental variation, such as the refrigeration temperature at the time of measurement and individual differences in equipment, were cited as reasons for the lower estimates with NIRS. Thus, to improve MUFA, it is highly desirable to take measurements under similar environmental conditions when the NIRS method is employed.

Table 3 shows the phenotypic and genetic correlations among the traits analyzed. Except for a negative estimate between LMA and SFT (-0.289), the genetic correlations among carcass grading traits were similar to those previously reported (Oyama,

2011).

Similar to Osawa et al. (2008), we also obtained high phenotypic and genetic correlations of 0.814 and 0.959, respectively, between FAR and BMS No. In recent years, the identification of FAR-related genes has progressed (Nakajima et al., 2018; Sasazaki et al., 2020), and expectations for marker-assisted selection have received increased attention. Because FAR is an objective evaluation index purely calculated from digital images of carcass cross-sections, the influence of external factors can be reduced, and FAR seems to be more compatible with such a selection. When the use of image analysis equipment becomes common, FAR may be used as an alternative indicator of BMS No. to control the amount of marbling.

[Table 3]

Although FI generally showed unfavorable genetic correlations with other traits, the estimate with the highest absolute value was -0.219 with FAR and not a large value. A similar tendency was observed for MUFA. The highest unfavorable genetic correlation of MUFA was found between NIRS MUFA and SFT (0.300); however, genetic antagonism was not severe, indicating that image analysis traits and MUFA can be improved simultaneously with carcass grading traits.

The genetic correlation between the two MUFAs in this study was estimated to be 0.804. Using intermuscular fat tissue, Komatsu et al. (2021) reported a higher genetic correlation of 0.962 between NIRS and GC MUFAs. As our estimate was obtained

between inter- and intra-muscular fat, the correlation did not seem to be low. However, the Pearson's correlation coefficient was calculated as 0.503 (n = 356), which might include measurement errors in the NIRS method. Maintaining the NIRS equipment under proper conditions, and as previously stated, a uniform environment for measurement is important, especially when NIRS MUFA is used as a sales promotion tool.

Compared with the direct selection for GC MUFA, the efficiency of indirect selection for NIRS MUFA to improve GC MUFA is expected to be 0.73 ($=\sqrt{0.450}\times 0.804/\sqrt{0.542}$). This efficiency assumes that both methods have equal selection intensity. When we consider the time required and labor cost for GC, the NIRS method seems to be more efficient and practical, the only way to improve MUFA. However, the standard errors involved in GC MUFA were larger than those in the other traits. Although the average additive relationships among animals in the Hyogo population are expected to be high, and this fact contributes to estimation accuracy, we still encountered the problem of divergence by the AI algorithm. Because this is practically due to the small number of samples, further data accumulation for GC MUFA is required to compare the relationship accurately.

3.3 Genetic trends

The genetic trends expressed by the standardized average predicted breeding values of females showed a drastic positive

change in FAR (Figure 1) compared with that in MUFAs and FI. The trend of FAR was almost identical to that of BMS No. and was due to genetic improvement, mainly in BMS No., over the last few decades. However, FI has been slowly declining since 1965. Although it has turned upward in recent years, the shape of marbling is expected to become coarse if insufficient attention is paid to FI.

Although the two MUFAs showed a gradual upward trend, the amount of improvement was less than one sigma unit, reflecting the fact that little attention has been paid to this characteristic in the past. Considering the recent decreasing trend in MUFA values, it is necessary to place increased emphasis on MUFA as well as FI immediately to achieve beef production according to consumer demand.

[Figure 1]

The genetic trends of the two types of MUFAs closely resembled each other. However, since around 2001, the difference in average breeding value between the NIRS and GC MUFAs has widened. This could be partly attributed to the fact that the genetic variance of the GC MUFA was 42% larger than that of the NIRS MUFA. Because the standard errors involved in the two MUFA measurements are relatively large, it is necessary to continue data collection for both MUFAs and examine the trends more precisely.

These results showed that the heritability of FI, an indicator of fine fat particles, and MUFA, an indicator of

palatability, was comparable to that of the carcass grading traits, and there was no severe genetic antagonism among the analyzed traits. This indicates the possibility of improving FI and MUFA simultaneously with the current target traits for improvement.

FI and MUFA have been reported to be involved in the palatability of Japanese Black beef (Suzuki et al., 2013; Asa et al., 2017), and promoting these improvements will lead to increased productivity of beef with the superior quality desired by consumers. In particular, the complexity of measuring MUFAs based on GC has been a bottleneck in data collection. Our study suggests that the NIRS method is not only a useful tool for such data collection, but also an alternative evaluation procedure for MUFA in the *longissimus* muscle.

However, the widespread use of NIRS has just begun, and the investigation seems insufficient. Continued data collection and analysis are required for both types of MUFAs, considering the relatively high standard error of the estimates in this study. Moreover, MUFA has been suggested to have an optimal value for carcass evaluation (Nishioka et al., 2008) or eating quality (Suzuki et al., 2013) and to have a high positive genetic correlation with beef fat color score (Inoue et al., 2017). Because excessive improvement in MUFA could reduce the taste and strengthen the yellowness of fat, careful attention should be paid to avoid excessive changes, as in the case of BMS No.

CONFLICTS OF INTEREST

The authors declare no conflicts of interest for this article.

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11

Figure legends

FIGURE 1 Genetic trends expressed as average breeding values of breeding cows by birth year in genetic standard deviation units for beef marbling standard number (BMS No.), image analysis traits (FAR, fat area ratio; FI, fineness index) and monounsaturated fatty acid (MUFA) measured by near-infrared spectroscopy (NIRS) and gas chromatography (GC).

Fig. 1

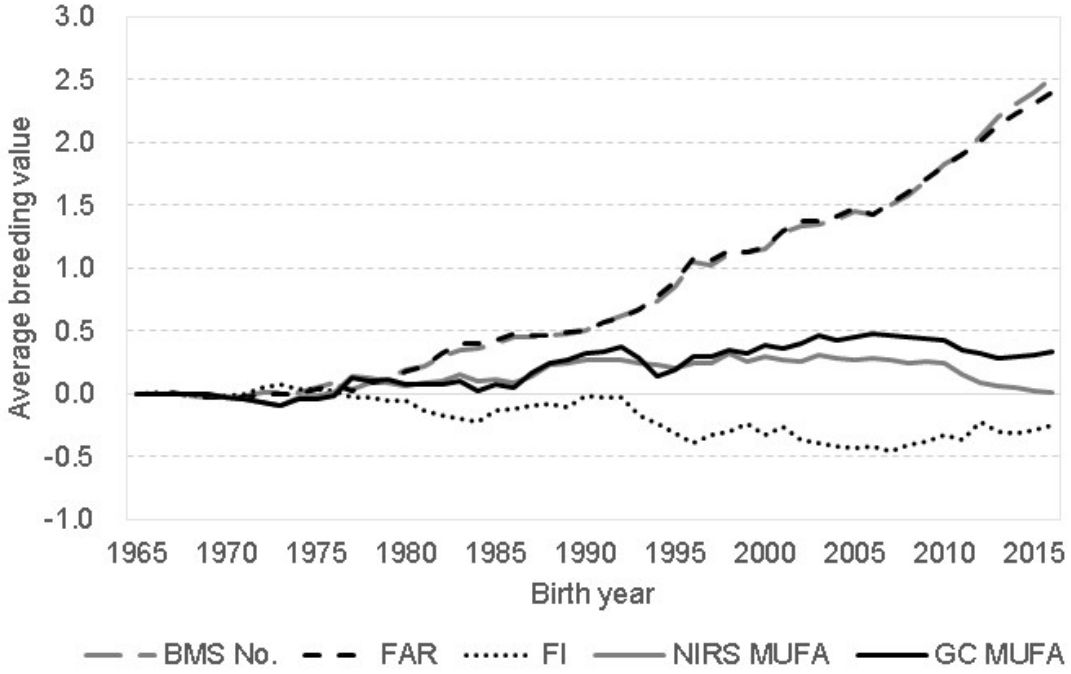

3.0
2.5
2.0
1.5
1.0
0.5
0.0
-0.5
-1.0
Average breeding value
1965
1970
1975
1980
1985
1990
1995
2000
2005
2010
2015
Birth year
BMS No.
FAR
FI
NIRS MUFA
GC MUFA

TABLE 1 Summary statistics for carcass grading traits, image analysis traits, and monounsaturated fatty acids

Trait	N	Mean	SD	Minimum	Maximum
Carcass trait					
CW (kg)	29,942	404.6	41.8	258.0	562.0
LMA (cm^2)	29,942	55.0	7.7	32.0	92.0
RT (cm)	29,942	6.9	0.7	4.5	10.5
SFT (cm)	29,942	2.5	0.8	0.5	6.6
BMS No.	29,942	6.8	2.0	2.0	12.0
Image analysis trait					
FAR (%)	24,704	47.1	7.3	19.4	74.8
FI (count/cm^2)	24,704	2.6	0.5	0.5	5.4
Monounsaturated fatty acid					
NIRS MUFA (%)	18,570	63.2	3.1	45.8	71.8
GC MUFA (%)	2,952	59.2	3.6	45.8	71.7

Abbreviations: CW, carcass weight; LMA, longissimus muscle area; RT, rib thickness; SFT, subcutaneous fat thickness; BMS No., beef marbling standard number; FAR, fat area ratio; FI, fineness index; NIRS MUFA, monounsaturated fatty acid by near-infrared spectroscopy; GC MUFA, monounsaturated fatty acid by gas chromatography.

TABLE 2 Estimated variances and heritability for carcass grading traits, image analysis traits, and monounsaturated fatty acids

Trait	Farm variance	Genetic variance	Residual variance	Heritability ± SE
Carcass trait				
CW	166.140	685.640	599.630	0.472 ± 0.024
LMA	3.570	36.080	21.241	0.593 ± 0.024
RT	0.047	0.233	0.259	0.432 ± 0.025
SFT	0.047	0.326	0.210	0.559 ± 0.024
BMS No.	0.270	2.809	0.988	0.691 ± 0.023
Image analysis trait				
FAR	3.127	37.106	9.918	0.740 ± 0.024
FI	0.008	0.099	0.143	0.395 ± 0.029
Monounsaturated fatty acid				
NIRS MUFA	0.529	4.090	4.466	0.450 ± 0.033
GC MUFA	0.808	5.802	4.085	0.542 ± 0.071

See TABLE 1 for abbreviations.

TABLE 3 Estimates of genetic (above diagonal) and phenotypic (below diagonal) correlations among carcass grading traits, image analysis traits, and monounsaturated fatty acids

Trait	CW	LMA	RT	SFT	BMS No.	FAR	FI	NIRS MUFA	GC MUFA
CW		0.278	0.535	0.222	0.130	0.106	-0.197	0.070	0.129
		(0.035)	(0.030)	(0.038)	(0.036)	(0.036)	(0.049)	(0.051)	(0.078)
LMA	0.459		0.204	-0.289	0.507	0.369	-0.064	-0.203	-0.039
			(0.039)	(0.036)	(0.026)	(0.029)	(0.047)	(0.047)	(0.076)
RT	0.655	0.384		0.229	0.291	0.274	-0.178	0.091	0.069
				(0.040)	(0.035)	(0.036)	(0.052)	(0.054)	(0.083)
SFT	0.309	-0.096	0.275		-0.090	-0.060	-0.089	0.300	0.178
					(0.034)	(0.034)	(0.048)	(0.047)	(0.078)
BMS No.	0.175	0.463	0.286	-0.041		0.959	-0.065	-0.228	-0.077
						(0.005)	(0.044)	(0.044)	(0.074)
FAR	0.133	0.323	0.232	-0.029	0.814		-0.219	-0.259	-0.168
							(0.042)	(0.044)	(0.073)
FI	-0.196	-0.159	-0.160	-0.056	-0.085	-0.169		-0.158	-0.062
								(0.060)	(0.091)
NIRS MUFA	0.077	-0.063	0.084	0.133	-0.072	-0.113	-0.090		0.804
									(0.062)
GC MUFA	0.124	0.034	0.098	0.085	-0.036	-0.061	-0.145	0.467	

Standard errors of genetic correlations are shown in parentheses.

See TABLE 1 for abbreviations.