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Genetic parameters for fatty acid composition and feed efficiency traits in Japanese Black Cattle

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Abstract

Genetic parameters were estimated for feed efficiency traits (feed intakes (FI), feed conversion ratios (FCR) and residual feed intakes (RFI) of DCP and TDN), beef marbling score (BMS), melting point of fat (MP) and fatty acid composition. Fat and meat (*M. trapezius*) samples were taken from the carcasses of 863 Japanese Black steers derived from 65 sires for determination of MP and fatty acid composition of total lipid of intra-muscular adipose tissue. Genetic parameters were estimated using uni- and bivariate animal models. In addition, the pedigree information for 4,841 animals was used. Heritability estimates for BMS, MP, each fatty acid, monounsaturated fatty acids (MUFA), the ratio of saturated fatty acids to MUFA (MUS) and the ratio of elongation (ELONG) were high (0.63 to 0.86) except C18:2(0.34). Those for FIs were also high (0.70) but FCRs and RFIs were low (0.09 to 0.23) in this study. Genetic correlations of BMS with MP was -0.34 (favorable) and with C18:1, MUFA, MUS and ELONG were 0.40, 0.28, 0.29 and 0.37, respectively (favorable). Those of MP with C18:1, MUFA, MUS and ELONG were negative (also favorable) and high (-0.85, -0.98, -1.00 and -0.66, respectively). The correlation estimates for feed efficiency traits of DCP were quite similar to those of TDN. The estimates for FIs and RFIs also showed a similar trend. Genetic correlations of BMS with FIs, FCRs and RFIs were all positive (unfavorable) (0.19 to 0.51), in particular, with RFIs were high. Those of C18:1, MUFA, MUS and ELONG with FIs and RFIs were positive (unfavorable) but all low (0.06 to 0.17), while those with FCRs were all negative (favorable) (-0.38 to -0.10). These results suggest that it is possible to improve simultaneously both the quantity and quality of beef fat and to improve the quality of beef fat (fatty acid composition) directly or indirectly with MP; furthermore, selecting MP or fatty acid traits does not affect feed efficiency significantly.

Introduction

In the Japanese market, beef marbling score (BMS), the index of the quantity of fat in beef, is the biggest factor in determining the market price of a carcass. Therefore, we have been carrying out breeding Japanese beef cattle with focusing on BMS. However, beef consists of not only lipids (quantity and quality) but also various chemical components. Among these components, fatty acid composition is related to the taste and flavor of beef (Westerling and Hedrick, 1979; Melton *et al.*, 1982; Mandell *et al.*, 1998). Therefore, the quality of fat, such as fatty acid composition and fat melting point (MP), which has a high correlation with fatty acid composition, is one of the most important factors affecting beef quality.

It is reported that fatty acid composition is influenced by sex (Yoshimura and Namikawa, 1985; Zembayashi *et al.*, 1995), diet (Melton *et al.*, 1982; Mandell *et al.*, 1998) and age (Huerta-Leidenz *et al.*, 1996). Genetic influences, such as breed (Yoshimura and Namikawa, 1985; May *et al.*, 1993) and sire (Xie *et al.*, 1996), are also reported, including differentiation by sire in Japanese Black cattle (Oka *et al.*, 2002). However, to improve

genetically for MP and fatty acid composition, it is necessary to confirm the relationship between these traits and BMS by estimating for genetic parameters. There are few reports that have estimated for genetic parameters in the same breed. Of those ones, we reported that it is possible to improve genetically and simultaneously both the BMS (quantity) and fatty acid composition (quality) in our previous study (Inoue *et al.*, 2008).

In addition, it is important to improve not only the quantity or quality of beef fat but also feed efficiency, which affects farmers' operating costs. The Wagyu Registry Association (2000), which regulates performance and progeny tests for Japanese Black bulls, had revised performance test protocol for feed efficiency traits in 2006, and Okanishi *et al.* (2008) reported the details. The association had changed conventional feed conversion ratios (FCR) for residual feed intakes (RFI) which is an alternative indicator of feed utilization by Koch *et al.* (1963).

Therefore, the objective of this study was to estimate genetic parameters of MP, fatty acid composition and feed efficiency traits, and to evaluate their relationships using Japanese Black steers that were fattened for the same period, under the same conditions and slaughtered at similar ages.

Materials and Methods

Animals and Samples

863 Japanese Black steers derived from 65 sires were progeny tested. These steers were fattened beginning at an average age of 9.1mo (8.0 to 9.6mo) for 364d and weighed their body weight (BW) at the beginning and at the end of the test at stations of the Livestock Improvement Association of Japan Inc. in Hokkaido and Hiroshima prefectures. These steers were born over a 2 year period. Therefore, the progeny tests were carried out in 2 groups, 1 per year. In order to arrange the beginning ages, the progeny tests were begun in 10 steps in the 1st year and in 8 steps in the 2nd year. All steers had *ad libitum* access to the identical concentrate diet (73.3% TDN, 10.3% DCP) and roughage (hay) (54.0% TDN, 5.0% DCP) per herd unit.

All steers were slaughtered after fattening. BMS, which is scored from 1 (poor) to 12 (very abundant), was evaluated between the 6th and 7th rib in accordance with the Japan Meat Grading Association (1988).

Fat and meat (*M. trapezius*) samples were taken from the carcasses of these fattened cattle. Total lipids of intra-muscular adipose tissue were extracted from these samples according to the method of Folch *et al.* (1957).

Melting Point Determination

MP was determined using Method 2 according to The Japanese Pharmacopoeia published by the Ministry of Health, Labour and Welfare (2001). The samples were drawn into capillary tubes to a depth of about 10mm. The charged tubes were allowed to stand for 24 hours at a temperature below 10℃. Then, they were placed in a beaker filled with water. The water temperature was raised by 1℃/min from 10℃. The temperature at which the sample is observed to rise in the capillary tube is taken as the MP.

Fatty Acid Analysis

The fatty acid composition was determined by gas liquid chromatography (Hitachi G-3000, Tokyo, Japan) using a 3mm×2m glass column packed with Thermon-3000 (SHIMADZU). The gas pressures were 0.8kg/cm^2 for the carrier gas (nitrogen), 1.0kg/cm^2 for the hydrogen and 1.1kg/cm^2 for the air. Every peak was determined on the retention times compared with those of authentic samples. The percentage of major fatty acids was calculated from peak area. Total monounsaturated fatty acids (MUFA) were calculated by summing appropriate components. In addition, the ratio of saturated fatty acids to MUFA (MUS) as index of desaturation, and the ratio of elongation (ELONG) were calculated as follows:

Total monounsaturated fatty acids = C14:1+C16:1+C18:1
The ratio of saturated fatty acids to MUFA = (C14:1+C16:1+C18:1) / (C14:0+C16:0 +C18:0)

Table 1. Partial regression coefficients and intercepts of multiple regressions to calculate RFIs

	MWT	WTG	Intercept
RFI_{TDN}	10.08	1.99	622.02
RFI_{DCP}	1.35	0.28	73.43

The ratio of elongation = (C18:0+C18:1) / (C16:0+C16:1)

Calculation of Feed Efficiency Traits

Feed intake of TDN (FI_{TDN}) and DCP (FI_{DCP}) were estimated as total intakes of concentrate diet and roughage multiplied by their TDN and DCP content, respectively. Roughage intake per head was calculated as the total intake of roughage per herd unit divided by head in the unit. Feed conversion ratio of TDN (FCR_{TDN}) and DCP (FCR_{DCP}) were values of FI_{TDN} and FI_{DCP} par unit of weight gain (WTG) during the testing period, respectively. RFI of TDN (RFI_{TDN}) and DCP (RFI_{DCP}) were derived as follows:

$$RFI = FI - (b_1 \times MWT + b_2 \times WTG + intercept)$$

where, MWT is metabolic weight which was calculated as the mean BW during the test, raised to the 0.75 power (mean $BW^{0.75}$), b_1 and b_2 are partial regression coefficients of MWT and WTG, respectively. Coefficients and intercepts of TDN and DCP obtained by multiple regression analysis are presented in Table 1.

Statistical Analysis

Genetic parameters were estimated using the following univariate animal model containing fixed effects of tested year-step-station-herd, prefecture of birth and regressions for beginning age. In addition, the pedigree information for 4,841 animals was used.

$$y_{ijk} = CKGP_i + L_j + a1t_{ijk} + u_k + e_{ijk}$$

where, y_{ijk} is observation of traits, $CKGP_i$ is fixed effect of i*th* tested year-step-station-herd, L_j is fixed effect of j*th* prefecture of birth of tested steers, $a1$ is linear regression coefficient for beginning age, t_{ijk} is age of the animal at the beginning of the test, u_{ijk} is random additive genetic effect of ijk*th* animal and e_{ijk} is random residual. Program AIREMLF90 (Misztal *et al.*, 2002) was used for this analysis. Bivariate animal models with the same effects were used for estimations of phenotypic and genetic correlations.

Results and Discussion

Basic statistics

The average of BMS (Table 2) was higher than the value (4.0) using Japanese Black steers fattened in a similar fattening test reported by Oka *et al.* (2002) but almost the same value (7.1) using steers and heifers reported by Inoue *et al.* (2008). On the other hand, fatty acid composition and MUFA averages were similar to those of intra-muscular adipose tissue of *M. longisimms* reported by Oka *et al.* (2002), although the percentages of saturated fatty acids in their report were slightly higher and those of unsaturated fatty acids and MUFA were slightly lower than in this study.

MP was slightly higher than the value (22.8) reported by Inoue *et al.* (2008) but extremely lower than that one (39.1) reported by Pitchford *et al.* (2002). MP has a high correlation with fatty acid composition and there are some reports that fatty acid composition is influenced by sex and age; heifers' fats are more desaturated than those of steers (Yoshimura and Namikawa, 1985; Zembayashi *et al.*, 1995) and aging increases MUFA (Huerta-Leidenz *et al.*, 1996). Furthermore, effects of breed differences are also reported; purebred Wagyu or the other breeds containing Wagyu generally tend to have higher proportions of unsaturated fatty acids than other breeds (Yoshimura and Namikawa, 1985; May *et al.*, 1993). Inoue *et al.* (2008) used field data from heifers and steers with 31.6mo of average slaughter age. On the

Table 2. Basic statistics of fatty traits and feed efficiency traits

Trait	Abbreviation	Mean	SD	Minimum	Maximum
Beef marbling score, No.	BMS	7.8	1.9	3	12
Melting point, °C	MP	26.0	3.4	16.0	35.4
Myristic acid, %	C14:0	2.9	0.5	1.7	5.0
Myristoleic acid, %	C14:1	1.5	0.4	0.9	3.1
Palmitic acid, %	C16:0	24.2	1.7	19.4	30.0
Palmitoleic acid, %	C16:1	6.6	1.0	3.6	9.7
Stearic acid, %	C18:0	8.5	1.2	5.3	16.8
Oleic acid, %	C18:1	50.2	2.5	42.3	57.0
Linoleic acid, %	C18:2	2.5	0.6	1.0	6.5
Total monounsaturated fatty acids, %	MUFA	58.3	2.4	48.6	65.2
Ratio of saturated fatty acids to MUFA	MUS[a]	1.7	0.2	1.1	2.3
Ratio of elongation	ELONG[b]	19.2	2.0	12.9	25.2
Feed intake of TDN, kg	FI_{TDN}	2213.3	197.7	1652.1	2817.1
Feed intake of DCP, kg	FI_{DCP}	292.6	27.1	215.4	374.9
Feed conversion ratio of TDN, kg	FCR_{TDN}	6.79	0.64	5.01	9.76
Feed conversion ratio of DCP, kg	FCR_{DCP}	0.90	0.08	0.66	1.30
Residual feed intake of TDN, kg	RFI_{TDN}	0.6	151.6	–493.9	578.6
Residual feed intake of DCP, kg	RFI_{DCP}	1.7	20.6	–67.2	80.6

[a]MUS = MUFA (sum of C14:1, C16:1 and C18:1) per saturated fatty acids (sum of C14:0, C16:0 and C18:0)

[b]ELONG = (sum of C18:0 and C18:1) per (sum of C16:0 and C16:1)

other hand, Pitchford *et al.* (2002) analyzed data from heifers and steers of Hereford cows mated to sires from seven breeds (Jersey, Wagyu, Angus, Hereford, South Devon, Limousin and Belgian Blue). Thus, MP values among those reports might show a difference.

FCR_{TDN} and FCR_{DCP} were 6.79 and 0.90, respectively and these values were almost the same as the national averages on the progeny tests of Japanese Black in 2007 (Statistics in Japan).

Heritability

Heritability estimates of MP, each fatty acid, MUFA, MUS and ELONG were high (0.63 to 0.86) except for C18:2 (0.34) as presented in Table 3. These results showed that characteristics of station progeny tests, or heritabilities estimated using the data obtained from station tests are higher than the field ones in general. Not to synthesize only C18:2 *in vivo* may cause lower heritability of C18:2 than the other fatty acids. In addition, these results of estimating may evidence the propriety of the sampling data, the analysis method and the model. Heritabilities of MP and fatty acids in this study were high compared not only with the other breeds (MP and fatty acids were 0.28 and 0.14 to 0.21) estimated by Pitchford *et al.* (2002) but also within the same breeds (MP and fatty acids were 0.41 and 0.38 to 0.73) estimated by Inoue *et al.* (2008). The difference in the same breed might be caused by variation of characteristics between data from station progeny tests and from field progeny. However, the estimates of Japanese Black were higher than those of the other breeds. Therefore, it is likely that the difference between the breeds may be caused by the difference of enzyme activities related to desaturation. Abe *et al.* (2009) detected that the difference of the allele frequency of fatty acid synthase (FASN), which affects the proportions of fatty acid composition, was among breeds.

Heritabilities of MP, each fatty acid, MUFA, MUS and ELONG were high. The advantages to improve genetically proportion of unsaturated fatty acids were found from these results.

On the other hand, heritability estimates of feed efficiency traits were low to high. The estimates of FIs were high (0.70) and similar to fatty traits but those of FCRs and RFIs were low (0.09 to 0.23) in this study.

Hoque *et al.* (2006) reported that heritability estimates of FCR and phenotypic RFI in the study of individual performance tests (Wagyu Registry Association, 2000) on Japanese Black bulls were 0.15 and 0.24, respectively. These estimates were

Table 3. Estimated heritability, genetic variances and residual variances

Trait	Heritability	Standard errors	Genetic variance	Residual Variance
BMS[a]	0.64	0.10	2.31	1.32
MP	0.63	0.09	6.64	3.84
C14:0	0.82	0.10	0.18	0.04
C14:1	0.86	0.10	0.13	0.02
C16:0	0.65	0.09	1.78	0.96
C16:1	0.66	0.10	0.59	0.30
C18:0	0.71	0.10	1.02	0.42
C18:1	0.73	0.09	4.02	1.50
C18:2	0.34	0.08	0.13	0.25
MUFA	0.66	0.09	3.47	1.76
MUS	0.75	0.10	0.02	0.01
ELONG	0.67	0.10	0.03	0.01
FI_{TDN}	0.70	0.11	21557	9221
FI_{DCP}	0.70	0.11	423.4	182.3
FCR_{TDN}	0.11	0.05	0.03	0.28
FCR_{DCP}	0.09	0.05	0.00	0.01
RFI_{TDN}	0.22	0.07	0.35	1.21
RFI_{DCP}	0.23	0.07	0.01	0.02

[a]See Table 2 for abbreviations.

similar to FCRs and RFIs in this study. However, Hoque *et al.* (2009) also reported slightly higher estimates of the two traits (FCR and RFI were 0.38 and 0.49) and of FI_{TDN} (0.35) and FCR_{TDN} (0.46) in another Japanese Black population. Heritability estimates for FCRs of TDN and DCP were 0.14 and 0.03, and RFIs of those were 0.10 and 0.12, respectively in performance tests on Japanese Black bulls reported by Okanishi *et al.* (2008). They also reported that the estimates for FIs of TDN and DCP were 0.27 and 0.25, respectively. Our results were almost the same or slightly higher than those except for FIs.

Relationships between fatty traits

The phenotypic correlations between each fatty acid and BMS, which is an index of the amount of fat within beef, were low and the range of these was about ±0.15 between C14:0 and C18:1 (Table 4). Although the genetic correlations between them were higher overall than the phenotypic ones, these were -0.42 (C14:1) to 0.40 (C18:1). The negative genetic correlation between BMS and MP (-0.34), and the positive ones of BMS with C18:1 (0.40), MUFA (0.28), MUS (0.29) and ELONG (0.37) suggest that these relationships are favorable to enhancing desaturation and elongation, and that it is possible to improve both quantity and quality of fat in beef.

The positive phenotypic and genetic correlations between MP and each saturated fatty acid were 0.53 to 0.69 for phenotypic and 0.72 to 0.91 for genetic, the negative ones between MP and each unsaturated fatty acid were -0.05 to -0.66 for phenotypic and -0.11 to -0.85 for genetic except for C14:1 (0.05 for genetic). Furthermore, the genetic correlations of MP with MUFA, MUS and ELONG were also negative and high (-0.98, -1.00 and -0.66, respectively). These results show that a higher percentage of (un)saturated fatty acid raises (lowers) MP.

It is known that C16:0 synthesizes C16:1 via stearoyl-CoA-desaturase (SCD) and C18:0 via fatty acid elongase, after that, to desaturate C18:0 via SCD synthesizes C18:1 *in vivo*. Thus, it is considered that the equilibriums between C16:0 and C16:1, and between C18:0 and C18:1 are maintained. Therefore, the phenotypic and genetic correlations between them might be low. The phenotypic and genetic correlations between C16:1 and C18:0 were moderately negative (-0.63 and -0.51, respectively). This relationship between them seems to be contrary because both are synthesized from C16:0. There are several reports that the relationship between the percentages of C16:1 and C18:0 might show a negative correlation where, as the percentage of C16:1 increases, that of C18:0 decreases, and *vice versa*. Our results corresponded with their reports. There was a high negative genetic correlation between C16:0 and C18:1.

Table 4. Estimated genetic (above diagonal) and phenotypic (below diagonal) correlations between fatty traits

Trait	BMS[a]	MP	C14:0	C14:1	C16:0	C16:1	C18:0	C18:1	C18:2	MUFA	MUS	ELONG
BMS		–0.34	–0.35	–0.42	–0.31	–0.22	–0.04	0.40	0.05	0.28	0.29	0.37
MP	–0.12		0.74	0.05	0.91	–0.11	0.72	–0.85	–0.53	–0.98	–1.00	–0.66
C14:0	–0.14	0.53		0.51	0.70	0.37	0.16	–0.91	–0.09	–0.74	–0.72	–0.81
C14:1	–0.09	–0.05	0.48		0.22	0.64	–0.38	–0.43	0.07	–0.01	–0.03	–0.54
C16:0	–0.11	0.69	0.68	0.20		0.10	0.28	–0.88	–0.26	–0.89	–0.90	–0.86
C16:1	–0.04	–0.20	0.40	0.69	0.11		–0.51	–0.34	0.23	0.17	0.13	–0.56
C18:0	–0.06	0.57	0.02	–0.49	0.19	–0.63		–0.29	–0.64	–0.60	–0.64	0.08
C18:1	0.17	–0.66	–0.84	–0.36	–0.85	–0.27	–0.22		0.15	0.86	0.87	0.92
C18:2	–0.07	–0.29	–0.14	–0.05	–0.24	0.00	–0.27	0.04		0.26	0.36	–0.02
MUFA	0.15	–0.77	–0.62	0.08	–0.80	0.25	–0.57	0.86	0.03		0.99	0.67
MUS	0.14	–0.81	–0.64	0.04	–0.87	0.20	–0.60	0.85	0.22	0.96		0.67
ELONG	0.12	–0.45	–0.79	–0.53	–0.85	–0.57	0.20	0.87	0.08	0.57	0.61	

[a]See Table 2 for abbreviations. Standard errors of genetic correlations were 0.00 to 0.16.

Although C18:1 is synthesized from C16:0 via C18:0 *in vivo*, their relationship might be opposite, because C16:0 and C18:1 occupy the largest proportions of unsaturated fatty acids and saturated fatty acids, respectively and C18:1 is the last phase of unsaturated fatty acid synthesized from C16:0. The correlation between C14:0 and C18:1 was also negative and high. It is reported that mutations of the FASN gene affect the percentages of C14:0 and C18:1 oppositely (Abe *et al.*, 2009; Morris *et al.*, 2007). The results in this study supported their reports.

There was a strong negative genetic correlation between C16:0, which is a major saturated fatty acid, and C18:1, which is a major unsaturated fatty acid. Moreover, MP, which contributes to the softness and flavor of fat, had the strong negative genetic correlations with C18:1, MUFA and MUS, and had a strong positive genetic correlation with C16:0. Therefore, it suggested that it was possible to improve each trait indirectly by improving proportion of unsaturated fatty acids or MP.

Relationships between fatty traits and feed efficiency traits

The ranges of correlation estimates of fatty traits with FI_{TDN} and FI_{DCP} were -0.23 (C16:0 and both) to 0.38 (C18:2 and both), with FCR_{TDN} and FCR_{DCP} were -0.38 (ELONG and FCR_{DCP}) to 0.43 (C14:1 and FCR_{DCP}) and with RFI_{TDN} and RFI_{DCP} were -0.22 (C16:0 and both) to 0.51 (BMS and RFI_{TDN}), respectively (Table 5). The correlation estimates for feed efficiency traits of DCP were quite similar to those of TDN. The estimates for FIs and RFIs also showed a similar trend except C14:1. Genetic correlations of BMS with FIs, FCRs and RFIs were all positive (unfavorable) (0.19 to 0.51), in particular, with RFIs were high. These results suggest that animals having high BMS would be expected to have a low feed efficiency.

Hoque *et al.* (2009) reported that genetic correlations of BMS with FI_{TDN}, FCR_{TDN} and RFI were -0.49, -0.62 and -0.59, respectively. These estimates were derived from a study about relationships between feed efficiency traits (FI_{TDN}, FCR_{TDN} and RFI) (which were the results of

Table 5. Estimated genetic correlations between selected fatty traits and feed efficiency traits

Trait	BMS[a]	MP	C14:0	C14:1	C16:0	C16:1	C18:0	C18:1	C18:2	MUFA	MUS	ELONG
FI_{TDN}	0.19	–0.21	–0.08	–0.08	–0.23	0.00	–0.05	0.10	0.38	0.09	0.17	0.16
FI_{DCP}	0.20	–0.21	–0.08	–0.08	–0.23	0.00	–0.05	0.10	0.38	0.09	0.17	0.16
FCR_{TDN}	0.21	0.13	0.19	0.40	0.28	0.23	–0.29	–0.23	–0.30	–0.11	–0.11	–0.37
FCR_{DCP}	0.26	0.11	0.19	0.43	0.28	0.25	–0.32	–0.23	–0.27	–0.11	–0.10	–0.38
RFI_{TDN}	0.51	–0.20	–0.02	0.05	–0.22	0.00	–0.13	0.06	0.23	0.08	0.16	0.10
RFI_{DCP}	0.50	–0.20	–0.02	0.04	–0.22	0.01	–0.13	0.06	0.24	0.08	0.16	0.10

[a]See Table 2 for abbreviations. Standard errors of genetic correlations were 0.02 to 0.23.

individual performance tests (Wagyu Registry Association, 2000) on candidate bulls before their selection) and BMS of the selected bulls' field progeny. On the other hand, we studied relationship between feed efficiency traits of selected bulls and BMS of their progeny. Their results were quite opposite to ours. Therefore, the populations of bulls and the effects of selection may be the cause of the differences of these results.

Genetic correlations of C18:1, MUFA, MUS and ELONG with FIs and RFIs were positive (unfavorable) but all low (0.06 to 0.17), while those with FCRs were all negative (favorable) (-0.38 to -0.10). Similarly, Genetic correlations of MP with FIs and RFIs were unfavorable, although the sign has changed, and low (-0.21 to -0.20), while those with FCRs were all favorable (0.11 to 0.13).

These results suggest that selecting MP or fatty acid traits does not affect feed efficiency significantly.

Implications

Heritability estimates of fatty traits except C18:2 were high, and there were favorable genetic correlations between BMS and MP, BMS and fatty acid composition, and between fatty acids themselves. These results suggest that it is easy to improve MP and fatty acid composition (fat quality) genetically, and possible to improve simultaneously both the quantity and quality of beef fat and to improve fatty acid composition directly or indirectly with MP.

Genetic correlations of MP, C18:1, MUFA, MUS and ELONG with FIs and RFIs were unfavorable but all low, while those with FCRs were all favorable. These results suggest that selecting MP or fatty acid traits does not affect feed efficiency significantly. We can expect to improve the quality of beef fat without reducing feed utilization efficiency.

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