Effects of *GH*, *FASN* and *SCD* gene polymorphisms on fatty acid composition in Japanese Black cattle

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INTRODUCTION

The meat of Japanese Black cattle is famously known to have high marbling. Not only the marbling, but also the fat quality itself influence the eating quality of beef. For example, monounsaturated fatty acids (MUFA), e.g. oleic acid (C18:1), are known to positively enhance beef flavor and tenderness. Moreover, heritability of fatty acid composition is considered to be high. *Fatty acid synthase* (*FASN*), *stearoyl-CoA desaturase* (*SCD*) and *growth hormone* (*GH*) were reported to affect fatty acid composition in meat. **This study evaluated the effects of these gene polymorphisms in intramuscular fatty acid composition in *longissimus thoracis muscle* in Japanese Black cattle.**

MATERIALS AND METHODS

Animals and fatty acid analysis

Intramuscular adipose tissues were collected from *longissimus thoracis muscle* of 1189 Japanese Black cattle (798 steers and 391 heifers; 30.5±1.98 mo). Fatty acid composition was analyzed using gas chromatography.

DNA genotyping

SNPs of g.16039T>C in *FASN* and g.702G>A in *SCD* genes were identified by PCR-RFLP method. Two SNPs in *GH* gene, g.1496 C>G (GH^{L127V}) and g.1632 C>T (GH^{T172M}) were identified by sequencing method.

Statistical analysis

To evaluate the genotypic effects on fatty acids, the snp_ad option of Qxpak software was used for individual SNP. The assumed multi trait animal model used in this analysis was

$$\mathbf{y_{ij} = sex_i + year_j + bx_{ij} + SNP + u_{ij} + e_{ij}}$$

where y_{ij} was the observation i_j for the traits, sex_i was the fixed effect of sex i., $year_j$ was the fixed effect of slaughter year j, b was a covariate coefficient with x_{ij} being slaughter age, u_{ij} was the infinitesimal genetic effect of $animal_{ij}$ and e_{ij} was the residual effect. Pedigrees of the base population animals were traced back for 3 generations and 4455 animals were included in the pedigree analysis. Likelihood ratio tests were performed by removing the single locus SNP genotypic effects in the model, and nominal P-values were obtained assuming a χ^2 distribution of the likelihood ratio test.

The proportions of additive genetic variance accounted for by the single locus SNP genotypic effect to additive genetic variance (V_{SNP}/V_A) and phenotypic variance (V_{SNP}/V_P) were calculated as

$$\mathbf{V_{SNP}/V_A = \{2pq[a + d(q - p)]^2\} / V_A}$$

$$\mathbf{V_{SNP}/V_P = \{2pq[a + d(q - p)]^2\} / V_P}$$

where p and q were the allelic frequencies at the SNP locus, a was additive genetic effect, d was dominance effect, V_A was the additive genetic variance of the fatty acid obtained from an animal model analysis ignoring the single locus SNP genotypic effects and V_P was the phenotypic variance.

RESULTS

Fatty acid composition and heritability

Fatty acid	Abbrev.	Mean	SD	Heritability ± SD
Myristic acid (%)	C14:0	2.5	0.51	0.49 ± 0.08
Palmitic acid (%)	C16:0	26.1	2.02	0.40 ± 0.10
Palmitoleic acid (%)	C16:1	4.1	0.85	0.67 ± 0.12
Stearic acid (%)	C18:0	11.6	1.83	0.55 ± 0.11
Oleic acid (%)	C18:1	53.5	2.93	0.42 ± 0.10
Linoeic acid (%)	C18:2	2.2	0.50	0.14 ± 0.06
Total saturated fatty acid (%)[1]	SFA	40.2	3.20	0.35 ± 0.11
Total monounsaturated fatty acid (%)[2]	MUFA	57.6	3.12	0.35 ± 0.11

[1]SFA = C14:0 + C16:0 + C18:0. [2]MUFA = C16:1 + C18:1.

Genotypes and allele frequencies

Marker	Genotype	Frequency (%)	Allele	Frequency (%)
FASN	RR	0.13	R	0.36
	RW	0.47	W	0.64
	WW	0.40		
SCD	AA	0.31	A	0.57
	AV	0.53	V	0.43
	VV	0.16		
GH^{L127V}	LL	0.13	L	0.36
	LV	0.47	V	0.64
	VV	0.40		
GH^{T172M}	TT	0.60	T	0.78
	TM	0.36	M	0.22
	MM	0.04		

Effects of gene polymorphisms on fatty acid

	FASN					*SCD*					GH^{L127V}					GH^{T172M}				
Fatty acid	V_{SNP}/V_A(%)[3]	V_{SNP}/V_P(%)[4]	Average effect Allele R	Allele W	P-value[5]	V_{SNP}/V_A(%)	V_{SNP}/V_P(%)	Average effect Allele A	Allele V	P-value	V_{SNP}/V_A(%)	V_{SNP}/V_P(%)	Average effect Allele L	Allele V	P-value	V_{SNP}/V_A(%)	V_{SNP}/V_P(%)	Average effect Allele T	Allele M	P-value
C14:0	14.74	5.98	0.12	-0.07	<0.001	4.45	1.81	-0.03	0.05	<0.001	10.00	4.06	0.11	-0.06	<0.001	1.25	0.51	0.00	0.00	0.52
C16:0	2.62	1.06	0.19	-0.11	0.01	0.33	0.13	-0.03	0.04	0.36	5.59	2.26	0.34	-0.19	<0.001	6.44	2.60	0.05	-0.16	0.04
C16:1	10.96	4.41	0.17	-0.09	<0.001	0.31	0.12	-0.01	0.02	0.57	3.66	1.47	0.11	-0.06	<0.001	0.12	0.05	-0.01	0.04	0.28
C18:0	0.36	0.15	-0.08	0.05	0.29	7.76	3.14	-0.20	0.27	<0.001	0.65	0.26	-0.08	0.04	0.32	0.17	0.07	0.00	-0.01	0.84
C18:1	5.85	2.37	-0.40	0.23	<0.001	7.61	3.08	0.29	-0.39	<0.001	4.70	1.90	-0.47	0.27	<0.001	3.30	1.34	-0.04	0.14	0.23
C18:2	0.10	0.04	0.01	0.00	0.84	0.34	0.13	-0.01	0.02	0.49	0.12	0.05	-0.01	0.01	0.72	0.06	0.03	0.00	0.00	0.92
SFA	1.67	0.67	0.23	-0.13	0.04	5.28	2.12	-0.26	0.35	<0.001	2.37	0.95	0.37	-0.21	<0.001	2.39	0.96	0.05	-0.18	0.28
MUFA	1.89	0.76	-0.23	0.13	0.03	5.97	2.40	0.28	-0.37	<0.001	2.31	0.93	-0.36	0.21	<0.001	2.65	1.06	-0.05	0.17	0.26

[1]V_A = total additive genetic variance. [2]V_P = phenotypic variance. [3]V_{SNP}/V_A(%) = proportion accounted for by the single locus SNP genotypic effect to total additive genetic variance. [4]V_{SNP}/V_P(%) = proportion accounted for by the single locus SNP genotypic effect to phenotypic variance. [5]P-value = significance of each gene polymorphism for each trait.

CONCLUSIONS

- The respective contributions of *FASN*, *SCD* and GH^{L127V} gene polymorphisms to genetic variance and phenotypic variance were low. However, the total contribution of these gene polymorphisms for C18:1 was estimated as 18.17% to genetic variance and 7.35% to phenotypic variance.

  ⇒*FASN*, *SCD* and GH^{L127V} gene could be a good genetic marker to improve C18:1 genetically.

- Average effects of each allele were small, i.e. less than 1%. However, when the genotypes of markers that have significant effect on C18:1 were substituted from the lesser effect allele to the greater effect allele, it was estimated that the proportion of C18:1 increased by 2.05%

  ⇒Because standard deviation of C18:1 was 2.93, 2.05% change in proportion of C18:1 with the substitution of genotype could become a large change.

To use *FASN*, *SCD* and GH^{L127V} gene polymorphisms for the improvement of fatty acid composition effectively, it is necessary to improve not single but multiple genotypes at the same time. Further researches, such as panel test, are needed to reveal association between fatty acid composition and eating quality of beef.