ASSOCIATION OF SNP MARKERS AND MEAT QUALITY CHARACTERISTICS OF DUROC BREEDING STOCKS IN KOREA

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Abstract – This study was conducted to investigate the association between five SNP markers(*PRKAG3, FASN, CAST, HMGA1 and MC4R*) and meat quality characteristics of Duroc breeding stocks in Korea. A total of 200 purebred Duroc gilts reached market weight (110kg) were slaughtered and then chilled overnight. *Longissimus dorsi* (LD) muscles were removed from the carcasses 24 hr after slaughter and used to determine meat quality traits. The *PRKAG3, FASN, CAST* and *MC4R* genes were significantly associated with the quality traits of meat. The meats from pigs with *PRKAG3* AA genotype showed higher pH, redness and texture than those from *PRKAG3* GG genotype. Meats from Duroc with *FASN* AA genotype showed higher texture than *FASN* CC genotype. While the pigs with *CAST* AA genotype showed lower shear force than those from the *CAST* GG genotype. The *MC4R* AA genotypes were involved in higher moisture content in Duroc meat. However, *HMGA1* SNP did not show any significance in quality traits of meat. These results indicated that the five SNP markers tested can be used to screen Duroc breeds to improve meat quality traits in commercial pigs.

Key Words – Duroc, Meat quality, SNP markers

I. INTRODUCTION

Duroc breed is used as a terminal sire when commercial pigs are produced. Also, this breed has an excellent growth rate and higher intramuscular fat content than other breeds [1]. Recently, due to the advances in genetic technology, new livestock sectors such as breeder management, traceability systems, transgenic animal technology, and livestock disease control, which helped improve meat quality, have been developed. Meat quality parameters are the most important factor that influences the purchase decision of consumers in the market. So, extensive researches were conducted to improve meat quality, and to identify the genes associated with various economic traits in livestock. Therefore, the objective of this study was to determine the relationships between the five SNP markers (*PRKAG3, FASN, CAST, HMGA1 and MC4R*) and the quality traits of Duroc meat.

II. MATERIALS AND METHODS

A total of 200 purebred Duroc gilts raised by Korean Feeding Standard for Swine (KFSS) and reached market weight (110kg) were conventionally slaughtered and then chilled overnight. At 24 h postmortem, the LD muscle from the left side of carcass between 5th and 13th rib was removed for meat quality traits (moisture, crude protein, intramuscular fat, crude ash, water holding capacity, pH-24 hr, shear force, color values and texture) and five genomic DNA(*PRKAG3, FASN, CAST, HMGA1 and MC4R*) analyses at Chungbuk National University.

III. RESULTS AND DISCUSSION

Table 1 shows genotype and allele frequency analyses of five polymorphisms in the candidate genes of the Duroc breeding stock population. The associations of five SNP genotypes with the chemical composition of LD muscle in Duroc breeding stock population are described in Table 2. The *MC4R* and *FASN* genes showed significant effects: GG genotype of *MC4R* gene increased moisture content, while AA genotype lowered moisture content in LD muscle of Duroc population. Meats from pigs with the AA genotype of *FASN* gene had significantly higher intramuscular fat than the CC genotype. Kim *et al*. [2] indicated that the *MC4R* genotypes affected lean meat growth in Duroc pigs. Also, Kim *et al*. [3] reported that intramuscular fat content was

associated with the *FASN* gene from the native Korean pigs crossed with Yorkshire or Landlace breeds.

Table 1. Genotypes and allele frequencies analysis of five polymorphisms in the candidate genes of Duroc breeding stock population

Marker	*PRKAG3*	*FASN*	*CAST*	*HMGA1*	*MC4R*
Allele "1"	A	C	A	T	G
Allele"1" frequency	0.224	0.301	0.373	0.296	0.208
Allele "2"	G	A	G	C	A
Genotype Count (Head)	AA:4 AG:81 GG:114	CC:19 CA:85 AA:100	AA:31 AG:90 GG:83	TT:8 TC:100 CC:88	GG:11 GA:59 AA:125

The associations of five SNP genotypes with meat quality characteristics from LD muscle of Duroc breeding stock population are shown in Table 3. *PRKAG3* and *CAST* genes had significant effects on the pH_{24h}, shear force, redness and texture of LD muscle of Duroc population. The AA genotype of *PRKAG3* gene was associated with significantly higher pH_{24h} value than the AG and GG genotypes. The animals with an A allele in the *CAST* gene had significantly lower shear force values than those with a C allele. The associations between meat quality and the *PRKAG3* gene that regulates the glycogen content of intramuscular tissue are well established [4]. Furthermore, meat quality was influenced considerably by *PRKAG3* genotypes. On the other hand, Ciobanu *et al*.[5] reported that *CAST* genotypes significantly affected the shear force, cooking loss, and juiciness values of pork from Berkshire x Yorkshire crossbred. Texture score is evaluated by the firmness and springiness of meat surface. The pH of meat is an indicator for determining normal, DFD (Dark firm dry) or PSE (Pale soft exudative) meat. Therefore, the *PRKAG3* gene is significantly associated with the texture of meat. Furthermore, the *FASN* gene is known to be involved in the saturated/unsaturated ratio of fatty acids [6].

Table 2. Association of five SNP genotypes with proximate analysis in Duroc breeding stock population

Traits	Marker	-log10 P-value[1]	Minor Allele	Average for DD[2]	Average for Dd[2]	Average for dd[2]
Moisture (%)	*PRKAG3*	0.18	A	73.24±0.49	73.05±1.03	73.14±1.07
	FASN	0.24	C	73.33±0.91	73.05±1.12	73.08±1.04
	CAST	0.62	A	72.88±1.12	73.11±0.95	73.17±1.14
	HMGA1	0.36	T	73.45±1.28	73.08±1.11	73.03±0.97
	MC4R	4.75	G	74.32±0.22	73.45±0.89	72.91±1.06
Crude protein (%)	*PRKAG3*	0.55	A	22.43±0.43	22.90±0.81	22.72±0.76
	FASN	0.82	C	22.51±0.70	22.80±0.79	22.85±0.77
	CAST	0.48	A	22.88±0.92	22.82±0.81	22.73±0.69
	HMGA1	0.59	T	22.39±0.99	22.81±0.81	22.86±0.71
	MC4R	2.08	G	22.21±0.58	22.66±0.88	22.90±0.71
Intramuscular fat (%)	*PRKAG3*	0.12	A	2.97±0.17	2.99±0.93	3.03±1.01
	FASN	2.93	C	2.92±0.89	3.05±1.04	3.08±0.91
	CAST	0.40	A	3.20±1.26	2.94±0.89	2.97±0.91
	HMGA1	0.15	T	3.01±0.57	3.03±1.02	2.97±0.92
	MC4R	2.14	G	2.29±0.59	2.76±0.76	3.06±0.98
Crude ash (%)	*PRKAG3*	0.13	A	1.37±0.31	1.06±0.16	1.11±0.33
	FASN	0.31	C	1.11±0.21	1.07±0.20	1.12±0.34
	CAST	0.81	A	1.05±0.23	1.09±0.28	1.13±0.29
	HMGA1	0.08	T	1.15±0.22	1.08±0.23	1.11±0.32
	MC4R	0.38	G	1.17±0.29	1.12±0.31	1.09±0.27

[1] Significant when -log10 *P*-values are > 2.50
[2] Minor allele= "D", Major allele= "d"

IV. CONCLUSION

All five SNP marker (*PRKAG3, FASN, CAST, HMGA1 and MC4R*) genes, except for *HMGA1*, were significantly associated with the meat quality traits of Duroc population. *PRKAG3* AA genotype increased pH, redness and texture values of pork LD muscle. *FASN* gene AA genotype increased texture values, while *CAST* AA genotype decreased shear force. *MC4R* AA genotype increased moisture content of pork LD muscle. Therefore, the genetic information from Duroc breeding stocks can be utilized effectively by swine industry to improve pork quality characteristics and to meet the changing consumer demands.

Table 3. Association of five SNP genotypes with meat quality characteristics of the *Longissimus dorsi* muscle in Duroc breeding stock population

Traits	Marker	-log10 P-value[1]	Minor Allele	Average for DD[2]	Average for Dd[2]	Average for dd[2]
Water holding capacity (%)	*PRKAG3*	0.19	A	57.96±2.77	58.89±4.48	58.49±3.88
	FASN	0.09	C	58.89±4.89	58.68±4.41	58.61±3.69
	CAST	0.86	A	58.82±3.43	59.28±4.19	57.98±4.17
	HMGA	0.0	T	60.39±6.	58.36±4.	58.95±3.

	1	8		61	45	39
	MC4R	2.16	G	54.98±2.46	58.09±4.89	59.24±3.63
pH_{24h}	*PRKAG3*	3.05	A	5.85±0.10	5.77±0.17	5.70±0.13
	FASN	1.13	C	5.79±0.21	5.74±0.16	5.72±0.13
	CAST	0.53	A	5.70±0.11	5.77±0.17	5.70±0.13
	HMGA1	0.70	T	5.71±0.14	5.75±0.15	5.71±0.15
	MC4R	0.36	G	5.80±0.13	5.73±0.13	5.73±0.15
Shear force (g)	*PRKAG3*	0.09	A	1474.59 ±119.56	1499.53 ±276.34	1485.30 ±365.79
	FASN	1.81	C	1405.19 ±360.69	1444.85 ±330.63	1553.43 ±313.81
	CAST	2.59	A	1415.02 ±323.78	1534.25 ±346.18	1604.89 ±295.04
	HMGA1	0.65	T	1301.04 ±203.98	1502.95 ±330.56	1520.27 ±332.93
	MC4R	1.05	G	1433.00 ±279.74	1434.35 ±339.38	1525.30 ±327.21
Lightness	*PRKAG3*	1.27	A	54.89±1.65	55.34±2.73	56.07±2.64
	FASN	0.01	C	55.36±2.47	56.03±2.74	55.71±2.82
	CAST	0.54	A	56.25±2.94	55.83±2.58	55.62±2.86
	HMGA1	0.59	T	56.25±2.25	55.96±2.53	55.53±3.10
	MC4R	0.02	G	54.26±1.88	56.10±2.54	55.69±2.88
Redness	*PRKAG3*	4.03	A	5.12±0.86	4.52±0.92	4.52±1.00
	FASN	2.39	C	5.47±1.11	4.90±1.04	4.70±0.89
	CAST	0.45	A	4.97±0.81	4.67±1.03	5.01±1.00
	HMGA1	0.05	T	5.50±1.00	4.75±0.85	4.94±1.15
	MC4R	0.71	G	5.68±1.36	4.87±1.08	4.83±0.92
Yellowness	*PRKAG3*	2.25	A	7.63±0.49	8.03±0.90	8.37±0.93
	FASN	0.23	C	8.18±0.64	8.29±0.85	8.16±1.03
	CAST	0.15	A	8.28±1.11	8.13±0.89	8.28±0.90
	HMGA1	0.07	T	8.96±0.98	8.12±0.92	8.28±0.94
	MC4R	0.04	G	8.01±0.53	8.26±0.87	8.19±0.98
Texture	*PRKAG3*	3.33	*PRKAG3*	3.38±0.29	3.15±0.30	3.02±0.28
	FASN	2.57	*FASN*	2.90±0.23	3.05±0.32	3.13±0.28
	CAST	0.12	*CAST*	3.05±0.22	3.08±0.32	3.07±0.31
	HMGA1	0.42	*HMGA1*	3.06±0.34	3.05±0.32	3.10±0.28
	MC4R	0.29	*MC4R*	3.03±0.20	3.05±0.29	3.08±0.31

[1] Significant when -log10 *P*-values are > 2.50
[2] Minor allele= "D", Major allele= "d"

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