International Journal of Agricultural Technology 2020 Vol. 16(1): 97-108
Available online http://www.ijat-aatsea.com
ISSN 2630-0192 (Online)

Effects of heart fatty acid biding protein (H-FABP) gene, housing system and sex on carcass and meat quality of commercial crossbred pigs

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Patthararangsarith, P. (2020). Effects of heart fatty acid binding protein (H-FABP) gene, housing system and sex on carcass and meat quality of commercial crossbred pigs. International Journal of Agricultural Technology 16(1): 97-108.

Abstract The results showed three H-FABP *Hae*III genotypes (DD, Dd, and dd), three H-FABP *Msp*I genotypes (AA, Aa, and aa) and the H-FABP *Hinf*I (HH). The allele Frequency of *Hae*III, *Msp*I and *Hinf*I polymorphism were shown as follows: D=0.55 and d=0.45; A=0.68 and a=0.32, while H=1. There was no effect (p> 0.5) of H-FABP genotypes on carcass quality. It was shown that no significant effect of H-FABP genotypes on meat quality traits T_1, T_{24}, pH_1, color (L, a*, b*), and drip loss. However, it was found that the pH_{24} of both genotypes Dd and dd had lower than genotype DD. Similarly, the pH_{24} of both genotypes Aa and aa had lower than AA. Whereas sex (gilts and barrows), gilts had muscle temperature which lower than the barrows. The pH_1 of the carcasses from closed house had lower than those in opened house. Whereas, the pH_{24} of the carcasses from opened house had lower than those in closed house.

Keywords: H-FABP Gene, Carcass Quality, Meat Quality, Crossbred Pig

Introduction

In the past decade, pig production in Thailand has been emphasized to increase carcass lean content and to decrease fat content. Therefore, the eating quality may have suffered. Eating quality is one of the important aspects of meat quality. This characteristic is affected by both genetic and environmental factors. Concerning eating quality of meat, intramuscular fat (IMF) level has become an intensively parameter, therefore intramuscular fat percentage has been found to be positively associated with sensory quality of pig meat.

As we know, genetic selection has been proven to be the most powerful tool for the improvement of livestock over the past several years. Until recently, the producers and consumers have become sophisticately focused on traits associated with carcass and meat quality. Such traits can be more difficult to improve by selection because heritability is low. Moreover, such traits may be

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expensive to measure (Cameron, 1990). For carcass and meat quality traits, the selection is based on recording the trait on slaughtered littermates. Therefore, it takes a long time to improve carcass and meat quality by selection. Studying candidate gene of known biological action is a useful method to identify genes controlling traits of interest. Heart fatty acid-binding protein (H-FABP), the product of FABP3 gene located on the chromosome 6 (Gerben *et al*., 1997), is an association of the fatty lipid-biding protein (FABP) which is involved in fatty acid transport from the cell membrane to the intracellular sites of fatty acid utilization (Qain *et al*., 1999). From this physiological role, H-FABP has been a candidate gene for intramuscular fat and backfat in pigs. Gerben *et al*. (1997) had detected three polymorphisms of the H-FABP gene which is defined as H, A, and D alleles, map to chromosome 6 in Duroc breed.

Carcass and meat quality of pigs are influenced by both genetic and environmental factors. The pig rearing environment will dictate the level which can express its genetic potential. The interest in meat quality has led to investigate into genetic and environmental controls of these carcass and meat quality traits. Therefore, this research aimed to 1) find the genetic polymorphism and frequency of H-FABP gene genotypes in commercial crossbred pigs and 2) investigate the effect of H-FABP genotypes, housing system and sex on carcass and meat quality traits in commercial crossbred pigs.

Materials and methods

This research was carried out on eighty-seven commercial crossbred pigs (Landrace x Large White) x (Duroc or commercial New Line) including the castrated males and females. The animals were divided into two groups and then raised in two different housing systems: evaporative cooling system (closed house), using cooling pad in closed house with controlled temperature at 25-28 ℃ and 80 RH; Thai conventional housing system (opened-house) open air house with the concrete block build up to 1 meter height from the floor with separate cages and had the carved tile roof as shade. The temperature of this kind of housing system was dependent on the environmental temperature which the mean minimum and maximum temperatures were about 17 to 37 ℃, respectively. The maintenance and the feeding of both groups were similar for all animals. The animals were slaughtered at a live body weight of about 100 kg at the standard slaughterhouse. The average transportation time from farms to slaughterhouse was approximately 4 hours and the lairage time was about 3 hours. Animals were stunned by Electric stunning and using the horizontal bleeding technique.

DNA extraction

Blood samples were collected from the jugular vein of the pigs into 1.5 micro centrifuged tubes containing 30 µl 10% EDTA. Blood DNA extraction was adapted from Helms (2006).

Genomic analysis

The PCR amplifications were performed in reaction volume of 25 µl, containing dH_2O, 10X buffer, 25 mM $MgCl_2$, 10 mM dNTP, 10 µM primer with sequence according to Gerben *et al*. (1997) as shown on Table 1. The 5 U Taq polymerase and 10 µl extraction solution of genomic DNA were added. The PCR cycling conditions are 94 ℃ (3 min), then 94 ℃ (0.5 min), 65 ℃ (0.5 min), and 72 ℃ (0.5 min) for 8 cycles, then followed by 94 ℃ (0.5 min), 57 ℃ (0.5 min), and 72 ℃ (0.5 min) for 27 cycles and finally 72 ℃ (7 min). PCR products were digested with restriction enzymes in 12 µl solution including dH_2O, 10X buffer, enzyme *Hae*III, *MspI*, and *Hinf*I . The 7 µl PCR product solution and the products were separated by electrophoresis through 1% gel, visualized with an UV transilluminator and photographed (Gene Genius).

Table 1. Primer sequences, corresponding PCR product sizes and positions for each PCR-RFLP

PCR-RFLP	Primer	PCR product size (bp)
*Hinf*I	5'-GGACCCAAGATGCCTACGCCG-3' 5'-CTGCAGCTTTGACCAAGAGG-3'	693
*Hae*III / *Msp*I	5'-ATTGCTTCGGTGTGTTGAG-3' 5'-TCAGGAATGGGAGTTATTGG-3'	816

Carcass quality traits

The animals were slaughtered at the live body weight of about 90-100 kg. At slaughter, pigs were weighted, stunned, and killed by exsanguination. The gastrointestinal tract was removed. The carcasses were splitted into two identical longitudinal halves, weighted and chilled for 18-24 hr at 2-4 ℃ chilling room. Carcasses were dissected according to Thai style by separating the carcasses into boneless lean, fat, bone, skin, and miscellaneous part. All the separated parts were weighed.

Lean percentage (LP) and fat percentage (FP): These were calculated as the percentage of carcass weight.

LSQ: the ratio of backfat thickness and the loin width by Pfeffeer and Falkenberg (1972).

Loin Eye Area (LEA): LEA of *M. longissimus dorsi* was traced on an acetate film between the 13^{th} -14^{th} ribs and determined by planimeter.

Intramuscular fat (IMF): Intramuscular fat (IMF) was determined by the muscle samples from *M. longissimus dorsi* muscle using Soxhlet extraction method and expressed as the weight percentage of wet muscle tissue.

Meat quality traits

Tested muscle samples from *M. longissimus dorsi* were taken for collecting the meat quality traits as follow:

pH: At 45 min (pH_1) and 24 hr (pH_{24}) post mortem, pH_1 and pH_{24} were measured at the loin around 13th rib, using pH-meter (WTW).

Temperature: Temperature was measured at 45 min (T_1) and 24 hr (T_{24}) post mortem at the same point as pH measurement using Sekunden-Thermometer 1103.

Color: CIE L*, a* and b* light reflectance coordinates was measured at room temperature (20 ℃), Loin samples were taken at 24 hr post mortem and bloomed for 30 min prior to measurement using the Minolta Chroma Meter CR 300 (Minolta co. Ltd. Japan). The meter was calibrated using a Minolta calibration plate, A white tile (L* = 97.59), a* = -5.00, b* = +6.76) was used as a standard.

Drip loss: At 24 hr post-mortem, 25 cm slices of *M. longissimus dorsi* (LD) muscle was taken for the water holding capacity evaluation. It was estimated as the drip loss from slices of muscle suspended inside polyethylene bags and held at 1 ℃ for 24 hr. Drip loss was expressed as a percentage of the initial sample weight.

Allele frequency represented the abundance of each genotype within a population as a fraction of population size. Least squares procedures were used to analyse data for the carcass traits. The General Linear Model (GLM) was used in the analysis of this characteristics. The H-FABP genotypes with each restriction enzyme (*Hae*III, *Msp*I, and *Hinf*I), housing system, and sex were defined as the fixed effect in linear model. The option PDIFF was used for calculating significant differences between least squares means.

The statistical model used was:

$$Y_{ijkl} = \mu + G_i + H_j + S_k + \varepsilon_{ijkl}$$

where:

Y = the dependent variable
μ = mean of the observation
G_i = genotype effect with enzyme *Hae*III, *Msp*I, and *Hinf*I
(1=DD, 2=Dd, 3=dd)
(1=AA, 2=Aa, 3=aa)
(1=HH, 2=Hh, 3=hh)
H_j = housing system effect
(1=evaporative housing system)
(2=Thai conventional housing system)
S_k = sex effect
(1=barrow, 2=gilt)
ε_{ijkl} = residual error

A pre-analysis showed that the interaction was not significant, so it was excluded out of the model.

Results

The genetic variation of H-FABP gene, RFLPs were detected as follow: three H-FABP *Hae*III genotypes (DD, Dd, dd); three H-FABP *Msp*I genotypes (AA, Aa, aa); the H-FABP *Hinf*I genotype (HH) were found. Genotype frequency of *Hae*III were; DD=29.07%, Dd=52.33%, and dd=18.60%; *Msp*I were AA=51.16%, Aa=34.88%, and aa=13.95%; *Hinf*I was HH=100%).

Table 2. Least Squares means and standard error of carcass quality traits according to genotypes in each PCR-RFLP restriction enzyme (*Hae*III, and *Msp*I)

Genotype	LEA	Lean (LP)	Fat (FP)	LSQ	IMF
*Hae*III					
DD	53.96±2.18	44.68±1.21	8.71±1.22	0.30±0.01	2.52±0.36
Dd	52.11±1.53	44.65±0.55	9.07±0.56	0.31±0.01	2.38±0.22
dd	53.33±2.69	45.81±1.13	6.95±1.13	0.29±0.02	2.40±0.44
p-value	0.75	0.65	0.26	0.37	0.94
*Msp*I					
AA	51.82±1.51	44.94±0.57	8.73±0.60	0.30±0.01	2.27±0.21
Aa	53.06±1.81	44.71±0.71	8.54±0.75	0.31±0.01	2.72±0.28
aa	57.27±3.22	NA	NA	0.31±0.02	1.96±0.73
p-value	0.30	0.79	0.83	0.85	0.35

NA = not available

Table 3. Least Squares Means and standard error of carcass quality traits according to sex in each PCR-RFLP restriction enzyme (*Hae*III, *Msp*I, and *Hinf*I)

Traits	*Hae*III			*Msp*I			*Hinf*I		
	Female	Male	p-value	Female	Male	p-value	Female	Male	p-value
LEA	54.23±1.75	52.03±1.61	0.32	55.28±1.88	52.82±1.60	0.26	53.96±1.67	51.74±1.45	0.31
LP	45.02±0.81	45.07±0.66	0.95	44.81±0.76	44.83±0.56	0.97	44.85±0.72	44.85±0.54	0.99
FP	7.90±0.81	8.58±0.67	0.48	8.23±0.80	9.04±0.59	0.43	8.27±0.76	9.05±0.57	0.43
LSQ	0.29±0.01	0.31±0.01	0.05	0.29±0.01	0.32±0.01	0.09	0.29±0.01	0.32±0.01	0.07
IMF	2.38±0.33	2.49±0.23	0.77	2.22±0.38	2.41±0.28	0.58	2.34±0.26	2.49±0.21	0.67

Table 4. Least Squares means and standard error of carcass quality traits according to housing system in each PCR-RFLP restriction enzyme (*Hae*III, *Msp*I, and *Hinf*I)

Traits	*Hae*III			*Msp*I			*Hinf*I		
	Close	Open	p-value	Close	Open	p-value	Close	Open	p-value
LEA	55.87±1.44[a1/]	50.39±1.97[b]	0.02	56.55±1.48[a]	51.55±2.03[b]	0.03	55.51±1.33[a]	50.19±1.83[b]	0.02
LP	44.99±0.79	45.10±0.73	0.91	44.86 ±0.63	44.78±0.67	0.93	44.88±0.61	44.82±0.64	0.94
FP	7.69±0.79	8.80±0.73	0.28	7.97±0.66	9.29±0.70	0.18	7.99±0.64	9.32±0.67	0.16
LSQ	0.29±0.01	0.31±0.01	0.28	0.30±0.01	0.31±0.01	0.30	0.30±0.01	0.31±0.012	0.25
IMF	2.44±0.21	2.43±0.35	0,96	2.37±0.27	2.27±0.39	0.76	2.43±0.20	2.40±0.28	0.93

1/: Least Squares Means within a row with different superscripts are significantly difference at 5% level

The results showed that there was no effect ($p>0.05$) of H-FABP genotypes on carcass quality traits of the pigs. However, there was a trend for fat percentage (FP) from PCR-RFLP *Hae*III that dd genotype tended to be the smallest. There was no sex effect ($p>0.05$) on all of the carcass quality traits of the pigs (Table 2, 3, and 4). However, there was trend such that LSQ value of the gilts tended to be lower than barrows. Moreover, there was a significant ($p<0.05$) effect of housing system on Loin Eye Area (LEA) of the pig carcasses.

Results showed no significant effect of H-FABP genotypes on meat quality traits (T_1, T_{24}, color, drip loss) as seen in Table 5, 6 and 7. However, it was found that pH_{24} of both genotypes Aa and aa were lower than genotype AA. Whereas Sex (gilts and barrows), the gilts had the muscle temperature (T_1 and T_{24}) which was lower than the barrows. The pH_1 of the carcasses from closed house were lower than in opened house. On the other hand, the pH_{24} of the carcasses from opened house were lower than in closed house.

Table 5. Least Squares Means and standard error of meat quality traits according to genotypes in each PCR-RFLP restriction enzyme (*Hae*III and *Msp*I)

Genotype	T_1	T_{24}	pH_1	pH_{24}	L	a*	b*	DL
*Hae*III								
DD	34.80±0.72	1.30±0.22	6.41±0.07	5.85±0.04	48.89±1.03	5.12±0.39	0.95±0.29	2.52±0.36
Dd	36.02±0.54	1.47±0.16	6.39±0.05	5.75±0.03	50.71±0.71	5.53±0.27	1.52±0.20	2.38±0.22
dd	36.27±0.93	1.48±0.28	6.29±0.09	5.71±0.05	49.64±1.23	5.86±0.46	1.65±0.34	2.40±0.44
p-value	0.31	0.79	0.52	0.04	0.30	0.47	0.20	0.94
*Msp*I								
AA	35.48±0.57	1.32±0.17	6.38±0.05	5.82±0.03	50.10±0.73	5.29±0.27	1.26±0.20	2.27±0.21
Aa	36.29±0.66	1.58±0.20	6.39±0.06	5.73±0.03	50.08±0.89	5.82±0.32	1.68±0.24	2.72±0.28
aa	34.82±1.05	1.39±0.31	6.33±0.09	5.72±0.05	49.29±1.63	5.24±0.60	1.00±0.44	1.96±0.73
p-value	0.43	0.58	0.85	0.06	0.89	0.41	0.26	0.35

Table 6. Least Squares Means and standard error of meat quality traits according to sex in each PCR-RFLP restriction enzyme (*Hae*III, *Msp*I, and *Hinf*I)

Trait	*Hae*III			*Msp*I			*Hinf*I		
	Female	Male	p-value	Female	Male	p-value	Female	Male	p-value
T_1	33.73±0.64$^{x/2}$	37.65±0.56^{y}	0.00	33.57±0.65^{x}	37.50±0.57^{y}	0.00	33.74±0.60^{x}	37.66±0.54^{y}	0.00
T_{24}	1.00±0.19^{x}	1.83±0.17^{y}	0.00	1.02±0.19^{x}	1.83±0.17^{y}	0.00	1.01±0.18^{x}	1.83±0.16^{y}	0.00
pH_1	6.36±0.06	6.37±0.05	0.87	6.36±0.06	6.37±0.05	0.91	6.38±0.06	6.38±0.05	0.94
pH_{24}	5.90±0.03^{y}	5.65±0.03^{x}	0.00	5.88±0.03^{y}	5.64±0.03^{x}	0.00	5.90±0.03^{y}	5.65±0.03^{x}	0.00
L	50.54±0.84	48.95±0.72	0.13	50.63±0.95	49.01±0.78	0.13	50.85±0.82	49.18±0.68	0.11
a*	5.39±0.32	5.61±0.27	0.57	5.36±0.35	5.54±0.29	0.63	5.40±0.30	5.56±0.25	0.67
b*	1.47±0.23	1.28±0.20	0.52	1.42±0.26	1.21±0.21	0.46	1.51±0.23	1.27±0.19	0.41
DL	2.33±0.38	2.14±0.33	0.69	2.19±0.43	1.97±0.35	0.65	2.45±0.37	2.17±0.31	0.56

2/: Least Squares Means within a row with different superscripts are significantly difference 1% Level

Table 7. Least Squares Means and standard error of meat quality traits according to housing system in each PCR-RFLP restriction enzyme (*Hae*III, *Msp*I, and *Hinf*I)

Traits	*Hae*III			*Msp*I			*Hinf*I		
	Closed	Open	p-value	Close	Open	p-value	Close	Open	p-value
T_1	35.97±0.48	35.42±0.73	0.51	35.91±0.51	35.15±0.75	0.37	36.00±0.45	35.40±0.45	0.47
T_{24}	1.48±0.14	1.36±0.22	0.63	1.51±0.15	1.34±0.22	0.52	1.49±0.13	1.36±0.21	0.61
pH_1	6.20±0.04^{x}	6.52±0.07^{y}	0.00	6.20±0.05^{x}	6.53±0.07^{y}	0.00	6.21±0.04^{x}	6.54±0.07^{y}	0.00
pH_{24}	5.83±0.02^{y}	5.71±0.04^{x}	0.00	5.81±0.03^{a}	5.70±0.04^{b}	0.01	5.83±0.02^{x}	5.71±0.04^{y}	0.00
L	49.58±0.65	49.91±0.94	0.75	49.72±0.73	49.93±1.01	0.84	49.88±0.63	50.15±0.88	0.80
a*	5.56±0.25	5.44±0.35	0.77	5.58±0.27	5.32±0.37	0.52	5.59±0.23	5.36±0.33	0.57
b*	1.24±0.18	1.51±0.26	0.37	1.24±0.20	1.38±0.28	0.64	1.30±0.17	1.48±0.25	0.56
DL	2.09±0.21	2.37±0.42	0.57	2.04±0.33	2.11±0.45	0.89	2.24±0.29	2.38±0.40	0.77

1/: Least Squares Means within a row with different superscripts are significantly difference at 5% level
2/: Least Squares Means within a row with different superscripts are significantly difference 1% Level

Discussion

In the study of genetic variation of H-FABP gene, RFLPs were detected in the upstream region 2. Three H-FABP gene *Hae*III genotypes (DD, Dd, and dd), three H-FABP *Msp*I genotypes (AA, Aa, aa), and the H-FABP *Hinf*I (HH) have been investigated. Allele frequencies of alleles in *Hae*III, *Msp*I, and *Hinf*I polymorphism were as following: D=0.53 and d=0.47; A=0.64, and a=0.36, while H=1. The subsequent genotypes show a diverse distribution in the pig samples except the *Hinf*I genotype. Normally, in almost common breed, three H-FABP PCR-RFLP (*Hae*III, *Msp*I, and *Hinf*I) have been described for pigs (Gerben *et al*., 1997). Generally, three H-FABP *Hae*III genotypes were found to be polymorphic in all European pig breeds but except in Chinese pig breeds. From this study, it has been shown that all three H-FABP gene *Hae*III genotypes (DD, Dd, and dd) were found. As known, dam and sire lines of fattening pigs in Thailand are western pig breeds so that is the reason why all genotypes of H-FABP gene *Hae*III-RFLP have been investigated. There was no *Hinf*I polymorphism at the upstream region found in this samples and all were of the HH genotype, while a few aa genotype was found. Generally, genetic characteristic of pig breed was formed by continuous selective breeding. The *Hinf*I and *Msp*I allele frequency distribution was at disequilibrium in Duroc breed, which may suggest selection pressure in favor of H allele (Gerben *et al*., 1997). The pig samples in this study were commercial crossbred (Landrac x Large White) x (Duroc or Commercial New Line) which were disequilibrium at allele frequency distribution so that is why some genotypes (Hh and hh) were not found and a few aa was investigated.

The results of this study indicated that there was no effect ($p>0.05$) of H-FABP gene genotypes on carcass quality of the commercial crossbred pigs. The findings were in accordance with the work of Nechtelberger *et al*. (2001) and Urban *et al*. (2002). They also did not find effect of H-FABP gene genotypes on carcass quality of their pigs. However, other groups of scientists (Gerben *et al*., 1997; Emnett *et al*., 2000) found that the H-FABP gene was a candidate gene for intramuscular fat. Hence, the gene had effect on both carcass and meat quality of the pigs. In this study, it was found that there was no effect of genotypes on intramuscular fat (IMF). Nevertheless, Gerben *et al*. (1997) and Wei-Jun *et al*. (2006) found that the recessive allele had effect on IMF in the pig muscle. Similarly, the results in this study investigated that IMF aa>IMF Aa>IMF AA and IMF dd>IMF Dd>IMF DD. Fiedler *et al*. (2003) had found that muscle fiber of different types would influence IMF in different muscles. Muscle fiber glycolytic would have IMF deposition in the muscle more than muscle oxidative. On the contrary, muscle fiber of glycolytic type would have high glycolysis reaction in the muscle after the pigs had been slaughtered which

resulted to rapid lowering pH of the carcass. The results of this study indicated that there might have muscle fiber of glycolytic type or white muscle fiber type. There was a trend that aa genotype had larger loin eye area (LEA). Veerkamp and Maatman (1995) reported that H-FABP gene had no relationship with back fat thickness. Since, the H-FABP protein was not found in subcutaneous fat which is in agreement with the result of this study that found no significant difference in LSQ among genotypes.

Although the results indicated that sex has no effect ($p>0.05$) on all carcass quality of the crossbred pigs in this study, it was found the trend of LSQ value of gilts tended to be lower than those of the barrows. Generally, the Lenden Speck Quotient (LSQ) is an index used in estimating lean percentage of pig carcasses. It is an accurate index in estimating pig carcass quality. Moreover, it is a very efficient index in grading pig carcasses for lean and fat percentage. The LSQ with the restriction enzyme as following: *Hae*III (gilts, 0.29 ± 0.01), and (barrow, 0.31 ± 0.01); *Msp*I (gilts, 0.29 ± 0.01), and (barrow, 0.32 ± 0.01); *Hinf*I (gilts, 0.29 ± 0.01), and (barrow, 0.32 ± 0.01), respectively. The results were in aggrement with the results of Olsson *et al*. (2003) who found that boars had lean percentage lower than those of gilts. Furthermore, Correa *et al*. (2006) reported that female crossbred pigs, (Landrace x Yorkshire) x Duroc, had lean percentage higher than those of the male counterpart.

The results indicated that there was a significant effect ($p<0.05$) of housing system on Loin Eye Area (LEA) of the pig carcasses. The LEA values of the pigs that were raised in the conventional opened house was smaller than those of the pigs raised in the closed house. Housing system has been shown to greatly influence on performance, voluntary feed intake, muscle and adipose tissue traits. Generally, Thailand has the hot-humid type climate with average temperatures approximately 30-40 ℃ with 50-80 RH which is well above thermo neutral zone of pigs. Therefore, the pigs that were raised in the conventional opened house would be exposed to variation in environmental temperature and humidity. While the pigs that were raised in the closed house were exposed to a relative constant temperature of 28 ℃ at all times. Lefaucheur and Etienne (1991) reported that ambient temperature influence swine production efficiency such that is would reduce feed intake, daily rate of gain, lean meat and lipid compositions of the pigs. Heat stress also reduced DNA, RNA synthesis. Gil *et al*. (2003) found the pigs raised in ambient temperarure of 24-28 ℃, that is well within the thermo neutral zone, would have muscle fiber (white type increased by 10% and myosin (myosin heavy chain, MyHC) increased by 10%, as well.

From this study, it showed no significant effect of H-FABP genotypes on meat quality traits (T_1, T_{24}, pH_1, color, drip loss). However, it was found that

the pH_{24} of both genotypes Dd and dd were lower than those of genotype DD. Similarly, the pH_{24} of both genotype Aa and aa were lower than that of genotype AA. The results indicated that sex has influence on carcass temperarure values. The barrows had T_1 and T_{24} higher than the gilts such that with enzyme *Hae*III, *Msp*I, and *Hinf*I. Carcass temperature at post mortem (T_{24}) depened on room temperature of the chilling room, carcass weight and subcutaneous fat thinkness. It is quite common that mammals including pigs, male would have larger body size, and castrated male would have higher body fat than female conterparts (Swatland, 1994). In this study, it was found that LSQ of gilts tended to be lower than that of barrow. Generally, the LSQ was positively correlated with the backfat thickness. Therefore, pigs with high LSQ tended to have thick subcutaneous fat. This fat acted as an insulator preventing heat loss from the carcasses freely. Hence, the heat from the muscle would accelerate glycolystic reaction which resulted in increased carcass pH.

In this study, there was no statistically significant ($p>0.05$) influence of housing system on carcass temperature of pigs (T_1 and T_{24}), meat color (L, a*, b*), and drip loss. However, the value of pH_1 of the closed house pigs was significantly ($p<0.05$) lower than the conventional opened house pigs because the closed house pigs were raised at a constant ambient temperature of 28 ℃. When they were moved to slaughterhouse, they were exposed to the natural temperature of above 28 ℃. Therefore, the pigs may develop heat stress prior to slaughtering. The stress would accelerate glycolytic reaction which would increase pH of the carcasses. The present study has found that the pH_{24} of the closed house pigs was significantly higher than that the conventional opened house pigs. Since, the closed house pigs tend to have subcutaneous fat thicker than that of opened house pigs. As seen, the LSQ of the closed house pigs was lower than the LSQ of the opened house pigs. This pigs with thicker backfat would expel heat from the body slower than those with less backfat. Thus, this retained heat would accelerate glycolytic process which resulted in more accumulated acids in the carcasses.

The genotype of H-FABP gene was detected by the PCR-RFLP technique using the *Hae*III, *Msp*I, and *Hinf*I as the restriction enzymes. Frequencies of alleles of *Hae*III, *Msp*I, and *Hinf*I were as follow: D=0.55 and d=0.45; A=0.68 amd a=0.32, while H=1. The results of this study conclude that H-FABP genotypes could not be used as a genetic maker for some carcass and meat quality traits in commercial crossbred pigs. However, the non-genetic factors such as housing system and sex had effect on some carcasses and meat quality traits in this study. H-FABP gene cannot be used as a genetic marker due to the fact that the pig samples in this study are the commercial crossbred pigs which do not have the variaton. However, the possible use of the H-FABP genotypes

as a marker gene may require further studies by using the large population of pigs or compared with the variety of pig breeds. Furthermore, this study was carried on the commercial farm and slaughterhouse. Thus, there were processes in the processing line which could not be interfered so insufficient data in some parameters was acquired.

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(Received: 17 August 2019, accepted: 30 December 2019)