

## Phenotypic and Genetic Parameters for Inosine Acid in Relation to Carcass and Meat Quality Traits in Pigs

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**ABSTRACT** : A total of 135 F<sub>2</sub> finishing pigs (65 barrows and 69 gilts) from resource population (Large White×Meishan) were slaughtered at about 87.8 kg BW. Contents of inosine acid (IMP) and carnine (HR) in muscle were assayed by HPLC and genetic parameters for IMP content and HR content were estimated using full sibs model. There was significant sex effect on IMP content ( $p < 0.05$ ), 3.561±0.077 mg/g for gilt and 3.287±0.085 mg/g for barrow. Heritability estimates for IMP and HR content were 0.127 and 0.357, respectively. The phenotypic correlation between IMP content and HR was 0.335, pH (A) 0.024, water lose rate (WLR) -0.069, intramuscular fat (IMF) -0.214, average marbling score (MARB) -0.143, average backfat measurements (AVBF) -0.084 and average color value (CV) -0.156, respectively. The result indicated that inosine acid content in meat might be retained or slightly improved by reducing backfat depth in pig breeding. (*Asian-Aust. J. Anim. Sci. 2003, Vol 16, No. 2 : 257-260*)

**Key Words** : Heritability, Phenotypic Correlation, IMP, Meat Quality, Carcass Quality

### INTRODUCTION

Delicate flavor of meat comes from contents of nucleotide acids, amino acids, small peptides and other components. Inosine acid (IMP) is one of the delicate flavor materials in meat; its effect on flavor is more than 50 times stronger than that of glutamine (Shette, 1995). At the same time, it has synergic effect on glutamine flavor and inhibiting effects on sourness and bitterness. IMP in the meat of mammal comes from adenosine triphosphate (ATP) decomposed in turn by ATP enzyme, adenylate kinase and adenosine monophosphate deaminase. Individual animal with different genetic background has different inosinate cycle rate, so the inosine acid accumulative content in muscle is different and the meat flavor has some difference (Heath, 1986; Lawrie, 1991; Shun et al., 1991; Su, 1997). The IMP content and its affected factors were studied in swine (Su, 1987), chicken (Davidek, 1967; Khan, 1968; Chow, 1968), quail (Su, 1991), fish (Ye, 1999) and other animals. These researches indicated that breed, sex, age, feedstuff and environment of meat storage could affect IMP content in meat significantly. Muscle fiber type and AMPD1 genotype are also factors affecting IMP content (Tullson et al., 1999; Norman et al., 2001). To our knowledge, genetic and phenotypic parameter estimates for the traits of IMP and carnine in pig has not been published before. As the development of China pig industry, knowledge of the genetic control of meat delicate flavor and relationships among pork quality and carcass characteristics

is required for China swine populations to implement selection programs that emphasize meat product quality (Yen et al., 2001). The objectives of this study were (1) to estimate heritability for IMP and HR and (2) to estimate phenotypic correlations between IMP and pork quality measurements and carcass characteristics.

### MATERIALS AND METHODS

#### Animals

The study included data on 135 F<sub>2</sub> finishing pigs (65 barrows and 69 gilts) from resource population. For the resource population 1 male Large White boar was mated with 9 Meishan sows, and 2 F<sub>1</sub> males and 26 females were subsequently used to produce 292 offspring (L×M). The number of progeny per sire varied between 1 and 13, with a mean value of 11.5. The animals were born and raised in Swine Breeding Center of China (Wuhan). They were given twice daily diets formulated according to age under a standardized feeding regimen and freed access to water. The finishing animals were slaughtered and measured based on National Standard for Chinese Pig Industry (GB8467-87, 1988). The mean slaughter weight was 87.8 (s.d. 7.91) kg and mean weight gain of finishing pigs, calculated over the period from birth to slaughter, was 384 (s.d. 45) g/day.

#### Carcass traits

The day after slaughter, backfat thickness was measured on the midline of the half carcass at four levels (shoulder region, 6-7 vertebra, vertebra-lumbar and buttocks). The mean of these four measurements was retained as the average backfat thickness (AVBF). The marbling score was investigated at longissimus muscle and musculus biceps femoris and the mean of the two measurements was

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retained as average marbling score. The color value was measured at two levels (longissimus muscle and musculus biceps femoris) and the mean of the two measurements was kept as average of color value.

### Meat quality traits

At 24 h postmortem, pH was measured directly on the three kinds of muscle (longissimus muscle, musculus biceps femoris and complexus), using a portable pH meter. The means of the three measurements was retained as average of pH. Intramuscular fat (IMF) was assayed by the protocol described by Folch (Folch et al., 1957; Miller et al., 1968). Water-loss-rate (WLR) and water-holding capacity (WHC) were measured by the method described in literature (Xiong, 1999).

### Content of IMP in meat

1 g muscle sample was homogenated with 6% perchloric acid buffer in homogenator at 5-10°C. Every homogenating sample was centrifuged and filtrated with 0.45 µm film to obtain inosine acid mixture solution (pH 6.5), which was analyzed using Waters chromatography equipped with a Symmetry C<sub>18</sub> column (3.9 mm×150 mm, 5 µm). The mobile phase was 0.05 M phosphoric acid and triethylamine buffer (pH 3.2)/ acetonitrile (95/5, v/v) at a constant flow of 0.8 ml/min. The column temperature was 25°C and the wavelength was 254 nm. The washing time of each sample was 15 min. Identification was made by comparison with retention times of the corresponding contrast standard. At the same time, the content of carmine (HR) in the sample was assayed.

### Statistical analysis

Least square means and their standard errors and phenotypic standard deviation for all the traits were analyzed using the GLM procedure of SAS (1995). The genetic parameters were estimated using Least Square and Maximum Likelihood Computer Program (Harvey, 1990). Data from full sibs were analyzed using the following model (model 4).

$$Y_{ijk} = \mu + S_i + D_j(S_i) + e_{ij}$$

Where,  $Y_{ijk}$ =the  $k_{th}$  progeny observations on  $i_{th}$  sire  $j_{th}$  dam;  $\mu$ =overall mean,  $S_i$ =sire effect,  $D_j(S_i)$ = $i_{th}$  sire  $j_{th}$  dam effect and  $e_{ij}$ =random error.

## RESULTS AND DISCUSSION

### The values of IMP, HR, carcass compositions and meat quality traits

Least square means and their standard errors for IMP, HR, carcass compositions and meat quality traits were

presented in Table 1. The present study indicated that sex had significant effect on IMP content: females had higher IMP content than males (3.561 vs 3.287,  $p < 0.05$ ). The result highly agreed to previous studies in pig (Su, 1987) and in chicken (Cheng et al., 2000).

A higher IMF content was found in barrows than in gilts (2.598 vs 2.371%,  $p < 0.05$ ), in complete agreement with other literatures (Barton-Grade, 1987; Larzul et al., 1997). The IMF content in this study was higher than those in literatures (Gandemer et al., 1992; Larzul et al., 1997). Maybe it's because the animals in this study had half Meishan pigs' blood. Higher IMF content would be one of the reasons for the reputation of remarkable palatability for the meat of Chinese native pigs. MARB (L) of barrows was higher than that of gilt significantly (3.289 vs 3.220,  $p < 0.05$ ).

**Table 1.** Least square means and their standard errors for carcass compositions and meat quality traits

Trait <sup>b</sup>	Average	Sex		Sig <sup>a</sup>
		Gilt	Barrow	
IMP, mg/g	3.433±0.737	3.561±0.077	3.287±0.085	*
HR, mg/g	0.402±0.036	0.390±0.028	0.415±0.030	NS
Pork quality traits				
pH (A)	6.423±0.011	6.430±0.014	6.414±0.016	NS
pH (B)	6.421±0.016	6.413±0.020	6.430±0.019	NS
pH (L)	6.332±0.027	6.333±0.027	6.330±0.027	NS
pH (C)	6.449±0.014	6.456±0.018	6.441±0.020	NS
WLR, %	5.659±0.097	5.809±0.129	5.527±0.083	NS
WHC, %	91.922±0.201	92.241±0.187	91.559±0.366	NS
IMF, %	2.477±0.139	2.371±0.068	2.598±0.090	*
Carcass characteristic				
MARB (A)	3.703±0.033	3.680±0.019	3.729±0.026	NS
MARB (B)	4.153±0.044	4.139±0.019	4.168±0.025	NS
MARB (L)	3.253±0.021	3.220±0.022	3.289±0.026	*
AVBF, mm	2.213±0.071	2.143±0.059	2.294±0.068	NS
BB, mm	1.515±0.075	1.430±0.060	1.611±0.076	NS
BVL, mm	1.795±0.074	1.745±0.061	1.853±0.065	NS
BV, mm	2.456±0.077	2.381±0.070	2.540±0.077	NS
BS, mm	3.049±0.081	2.989±0.078	3.118±0.082	NS
CV (A)	21.349±0.252	21.135±0.306	21.592±0.309	NS
CV (B)	20.601±0.181	20.385±0.166	20.846±0.190	NS
CV (L)	22.097±0.357	21.885±0.484	22.338±0.480	NS

<sup>a</sup> Levels of significance of sex effect; \*  $p < 0.05$ ; NS=Not significant.

<sup>b</sup> IMP, content of Inosine acid; HR, content of carmine; pH (L), pH of longissimus muscle; pH (B), pH of musculus biceps femoris; pH (C), pH of complexus; pH (A)=average of pH (L), pH (B) and pH (C); WLR, water-loss-rate; WHC, water-holding capacity; IMF, intramuscular fat, percentage of extractable lipid from the longissimus muscle; MARB (L), longissimus muscle marbling score; MARB (B), musculus biceps femoris marbling score; MARB (A)=average of MARB (L) and MARB (B); BS, backfat at shoulder region; BV, backfat at 6-7 vertebra; BVL, backfat at vertebra-lumbar; BB, backfat at buttocks; AVBF= average of shoulder region, 6-7 vertebra, vertebra-lumbar and buttock backfat measurements, millimeter; CV (L), longissimus muscle color value; CV (B), musculus biceps femoris color value; CV (A)=average of CV (L) and CV (B).

### Heritability and phenotypic correlations

Heritability estimates and their standard errors, phenotypic correlations, and genetic (co)variances for IMP and HR from full sibs model are presented in Table 2. The heritability estimate for IMP was very low (0.127) and that for HR was moderate (0.357). To our knowledge, no data about the heritability of IMP and HR in pig skeletal muscle were available in the literature. However, this value for IMP in present study was lower than 0.692 from that in chicken (Li, 2000). Although estimates of genetic parameters for chicken were not comparable to estimates for swine, the difference was too big. As concerning of the standard deviations of the heritability estimates, there might have potentially large error in them. This is probably due to a combination of factors, such as species, data structure, population samples and expression of genes.

In the present study, the phenotypic correlations between IMP and pork quality traits were presented in Table 2. The phenotype correlation for IMP and HR was 0.335. It was positive and the highest one among all the phenotypic correlations, which was in agreement with the fact that IMP and HR are in the same metabolism chain and closely related. The phenotypic correlations between IMP and pH were all very low, range from -0.214 to 0.068. The phenotype correlations between IMP and WLR or IMF

were negative, and the absolute values were very low (0.069 and 0.214, respectively).

At the same time, genetic correlations between IMP and pork quality traits and carcass traits were estimated (results not listed). The estimates ranged from -0.833 to 0.899, while the standard errors of the estimates of genetic correlations were too large, between 0.46 and 1.65, indicating that the estimated value was virtually meaningless.

The phenotypic correlations between IMP and carcass traits were presented in Table 3. The phenotypic correlations were very low and negative (range from -0.059 to -0.215) and none of them was significant ( $p > 0.05$ ). The Genetic correlations between IMP and carcass traits were also estimated (from -0.230 to -0.859). Unfortunately, the standard errors of the genetic correlation estimates were too large, between 0.550 and 0.679, which indicated that the estimated values were somewhat meaningless (results not listed). Even though, we could say that the correlations between IMP and carcass traits were negative.

### IMPLICATION

The expected genetic improvement in a swine population is determined by the heritability of interested

**Table 2.** Heritability and phenotypic correlations between IMP and pork quality traits

Traits <sup>a</sup>		Heritability (SE)	Phenotypic correlation	Environmental correlation	Variance or cov components	
					Among	Within
HR	HR	0.357(0.209)	1.000	1.000	0.013	0.048
IMP	IMP	0.127(0.126)	1.000	1.000	0.032	0.438
IMP	HR		0.335	0.284	0.012	0.042
IMP	pH(A)		0.024	-0.008	0.001	-0.001
IMP	pH(B)		0.030	-0.010	0.002	-0.001
IMP	pH(L)		0.068	-0.004	0.006	-0.000
IMP	pH(C)		0.049	-0.007	0.004	-0.001
IMP	WLR		-0.069	-0.002	-0.022	-0.003
IMP	WHC		0.066	-0.002	-0.021	-0.003
IMP	IMF		-0.214	-0.146	-0.026	-0.061

<sup>a</sup> See footnote of Table 1.

**Table 3.** Phenotypic correlations between IMP and carcass characteristic

Trait <sup>a</sup>		Phenotypic correlation	Environmental correlation	Variance or cov components	
				Among	Within
IMP	MARB(A)	-0.143	-0.034	-0.008	-0.005
IMP	MARB(B)	-0.198	-0.089	-0.009	-0.011
IMP	MARB(L)	-0.215	-0.097	-0.010	-0.012
IMP	AVBF	-0.084	-0.042	-0.010	-0.015
IMP	BB	-0.059	-0.020	-0.009	-0.008
IMP	BVL	-0.116	-0.090	-0.009	-0.030
IMP	BV	-0.073	-0.025	-0.012	-0.011
IMP	BS	-0.087	-0.029	-0.016	-0.014
IMP	CV(A)	-0.156	-0.028	-0.074	-0.034
IMP	CV(B)	-0.161	-0.029	-0.077	-0.034
IMP	CV(L)	-0.154	-0.027	-0.074	-0.033

<sup>a</sup> See footnote of Table 1.

traits, selection differential and genetic correlations among traits. Inosine acid content in meat is a flavor material for the meat delicate flavor, but the heritability estimate in this study was very low. So it is not feasible to account directly for it in breeding for improved meat quality in relatively short period. Fortunately, backfat depth is one of selective traits in most of our pig breeding programs and backfat depth had negative genetic and phenotypic correlations with inosine acid content. So inosine acid content might be retained or slightly improved by reducing backfat depth in pig genetic breeding.

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