Genetic Variation and Genetic Relationship of Seventeen Chinese Indigenous Pig Breeds Using Ten Serum Protein Loci*

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ABSTRACT : Seventeen Chinese indigenous pig breeds and three introduced pig breeds had been carried out by means of vertical polyacrylamide gel electrophoresis (PAGE). According to the results, eight serum protein loci were highly polymorphic except Pi-2 and Cp. The polymorphism information content (PIC) of Hpx was the highest (0.5268), while that of Cp was the lowest (0.0257). The population genetic variation index showed that about 84% genetic variation existed in the population, and the rest of 16% distributed between the populations. The genetic variation of Yimeng black pig and Duroc were the highest and the lowest, respectively. The genetic variation of Chinese indigenous pig breeds was much more than that of exotic groups. Genetic distance results showed that Chinese indigenous pig breeds were classified into four groups with the three introduced pig breeds clustered into another group. The results also supported the geographic distribution of Chinese indigenous pig breeds in certain extent. *(Asian-Aust. J. Anim. Sci. 2003. Vol 16, No. 7 : 939-945)*

Key Words : Chinese Indigenous Pig, Serum Protein Polymorphism, Genetic Variation, Genetic Relationship

INTRODUCTION

Serum protein polymorphism has the characteristics of genetic stability and lifetime constancy, which are usually controlled by autosomal codominant alleles. Therefore serum protein polymorphism is significant in studying the origin, differentiation and genetic distances between animal populations (Li et al., 1993). With massive land and complex natural environment, China has abundant resources of pig breeds. Additionally, in the domestic animal diversity information system (DAD-IS) of the FAO, 128 Chinese pig breeds have been reported, which take up almost one-third of the total pig breeds in the world. The Chinese indigenous pig breeds are known for their strong adaptability, high reproductive capacity and excellent taste. The reproductive capability of Taihu pig is the highest in the world (Zhang et al., 1986); Wuzhishan pig is one of the special and rare small pig breeds in the world and can be used as experimental animals. Much work has been devoted to the study on domestic animal serum proteins and enzymes after the introduction of molecular silver electrophoresis. Especially, zone electrophoresis in starch gels described by Smithes (1955a, b) provided a great impetus to the study of polymorphic proteins (Hesselhol, 1969; Zuozuomu, 1982); But in China, the study on indigenous pig breeds using serum protein loci has not been performed systematically, and their work was restricted in a few provinces (Huang et al., 1989; Lin et al., 1998). Analysis of 17 indigenous pig breeds and three introduced pig breeds has been carried out using 10 serum protein polymorphisms in the present study in order to study revealing present genetic variation and relationships among breeds.

MATERIALS AND METHODS

Samples collection

Serum samples were obtained from 922 Chinese indigenous pig individuals and 175 introduced pig individuals. Chinese pigs came from 17 breeds in the 12 provinces of western China and its surrounding areas such as Inner Mongolia, Sichuan province, Guangdong province. According to the book of Pig Breeds in China (Zhang et al., 1986), they belong to 5 types: North China type (6), South China type (6), Central China type (3), and Southwest China type (2). All samples were collected randomly from breeding farm and the villages without affinity records. More details about the type of each breed, sample location, sample size, the numbers of males and females were shown in Table 1.

Table 1. 17 Chinese indigenous pig breeds and 3 introduced pig breed included in the study and their type, sampling location, sample size, number of males and females

Type	Breed (abbreviation)	Sampling location	Total	Males	Females
North China type	Min pig (MZ)	Lanxi county breeding farm in Heilongjiang province	59	4	55
	Hanjiang black pig (HJ)	Hanjiang black pig breeding farm in Yueyang city	60	7	53
	Mashen pig (MS)	Breeding farm in Datong city	59	15	44
	Hetao large-ear pig (HT)	Breeding farm in Wuyuan city	53	8	45
	Laiwu pig (LWZ)	Laiwu city breeding farm in Shandong province	59	2	57
	Yimeng black pig (YM)	Linyi city breeding farm in Shandong province	60	5	55
Southwest Type	Guanling pig (GL	Pingzhai village of gaozhai town in kaiyang city	32	5	27
	Chenghua pig (CH)	Chengdu city livestock breeding farm	60	4	56
Central China type	Dongshan pig (DS)	Dongshan town of Quanzhou county in Guangxi Autonomous Region	58	9	49
	Large black-white pig (LBW)	Dongguan city livestock breeding farm	56	2	54
	Putian pig (PT)	Changtai town of Putian county in Fujian province	57	7	50
South China type	Longlin pig (LL)	De town of Longlin county in Guangxi Autonomous Region	59	6	53
	Donglan pig (DL)	Wuzhuan town of Donglan county in Guangxi Autonomous Region	48	2	46
	Wuzhishan pig (WZ)	CAAS Wuzhishan pig breeding farm in Hainan province	60	5	55
	Baixiang pig (BX)	Biologic Technical College of Guizhou university	23	5	18
	Lantang pig (LT)	Dongguan city livestock breeding farm	57	4	53
	Huai pig (HZ)	Taihua town of Datian county in Fujian province	60	8	52
Out-group	Large white (LW)	Purebreed farm of pig breeding center in Beijing	66	12	54
	Landrace (LD)	Purebreed farm of pig breeding center in Beijing	66	8	58
	Doruc (DR)	Purebreed farm of Doruc in Beijing	62	11	51

Table 2. Electrophoretically detectable variants of protein loci in the pig

Protein	Locus	Number of alleles	Allele sign
Alkaline phosphatase	Akp	4	Akp^A Akp^B Akp^C Akp^D
Albumin	Alb	2	Alb^A Alb^B
Amylase	Am	4	Am^A Am^{BF} Am^B Am^C
Ceruloplasmin	Cp	3	Cp^A Cp^B Cp^C
Hemopexin	Hpx	6	$Hpx^0, Hpx^{1F}, Hpx^1, Hpx^2, Hpx^3, Hpx^4$
Protease inhibitor-1	Pi-1	2	$Pi\text{-}1^A$ $Pi\text{-}1^B$
Protease inhibitor-2	Pi-2	2	$Pi\text{-}2^A$ $Pi\text{-}2^B$
Postalbumin-1	Po-1	2	$Po\text{-}1^A$ $Po\text{-}1^B$
Postalbumin-2	Po-2	3	$Po\text{-}2^A$ $Po\text{-}2^B$ $Po\text{-}2^C$
Transferrin	Tf	3	Tf^A Tf^B Tf^C

Serum protein electrophoresis

Serum protein was measured by means of vertical discontinuous PAGE in this study. Ten proteins loci for examination, the number of observed alleles and their sign were listed in the Table 2. Gel concentration, buffer system component and other electrophoresis conditions concerned were listed in the Table 3.

Data analysis

Genotype was judged according to the opposite migration rate of protein. Gene frequency, Number of the effective alleles (Ne), PIC and genetic similarity coefficient were obtained by programming in Microsoft Excel. GENEPOP ver. 3.3 (Raymond et al., 1995) computer package was employed in the calculations of the expected heterozygosity, observed heterozygosity of each population,

Wright's Fst static in each locus and the test of Hardy-Weinberg equilibrium. The D_A distance (Nei's et al., 1983), gene diversity (Ht) and their associated parameters such as Hs and Gst were performed by the DISPAN program (Ota, 1993). Phylogenetic trees were constructed by using the unweighted pair group-method with arithmetic mean (UPGMA) (Sneath and Sokal, 1973) from matrix of D_A distances.

RESULTS AND DISCUSSION

Serum protein polymorphism in swine

The allele frequencies showed that Pi-2 in all breeds was monomorphic and the other 9 loci were polymorphic, in which Cp allele represented a homozygote almost, too. The very low frequencies of Cp^A and Cp^C were later

Table 3. Gel concentration, buffer system and other electrophoresis conditions concerned

Electrophoresis condition	Protein locus									
	Pi-1	Pi-2	Po-1	Po-2	Tf	Alb	Akp	Hpx	Cp	Am
Separating gel concertration	14%	-	-	-	-	-	12%	8%	-	-
Stacking gel concentration	4%	-	-	-	-	-		-		-
Separating gel buffer	Tris-HCl pH 8.9	-	-	-	-	-	-	Tris-HCl pH8.8	Tris-citrate pH8.9	-
Stacking gel buffer	Tris-HCl PH 6.7	-	-	-	-	-	-	Tris-HCl pH6.8	Tris-citrate pH6.8	-
Electrode buffer	Tris-Gly pH 8.3	-	-	-	-	-	-	-	Tris-Gly pH8.7	-
Voltage in stacking gel	130V pass line	-	-	-	-	-	80V pass line	-	-	-
Voltage in separating gel	370V 7h	-	-	-	540V 7h	-	120V 12h	140V 12h	160V 12h	200V 12h

-: Predicates the condition is same as that ahead of it in the same row.

Table 4. Number of the effective alleles (Ne), polymorphism information content (PIC), mean (expected, observed) heterozygosity

Beeds	Ne	PIC	Mean heterozygosity	
			Expected	Observed
Donalan pig	1.7923	0.3091	0.3565	0.3521
Longlin pig	1.8934	0.3419	0.3976	0.3580
Dongshan pig	1.9542	0.3336	0.3859	0.4318
Min pig	1.8580	0.2945	0.3603	0.4254
Wuzhishan pig	2.0459	0.3788	0.4423	0.4174
Chenhua pig	1.8462	0.3162	0.3780	0.4128
Guanling pig	1.8307	0.3306	0.3900	0.4094
Baixiang pig	1.7599	0.3033	0.3611	0.3581
Large black-white pig	1.7902	0.3038	0.3689	0.3518
Lantang pig	1.6467	0.2728	0.3222	0.3930
Putian pig	1.6412	0.2814	0.3418	0.4386
Huai pig	2.0373	0.3686	0.4293	0.4346
Hetao large-ear pig	1.7863	0.3126	0.3731	0.3755
Laiwu pig	1.8787	0.3537	0.4231	0.4525
Yimeng black pig	2.0161	0.3660	0.4415	0.4891
Mashen pig	1.8185	0.3368	0.4056	0.4780
Hanjiang black pig	1.6586	0.2889	0.3402	0.4044
Large white	1.6382	0.2776	0.3356	0.4363
Landrace	1.7571	0.3043	0.3737	0.4322
Duroc	1.5707	0.2496	0.3084	0.3765

ascertained in the breeds of Wuzhishan pig, Huai pig, Laiwu pig, Mashen pig, large white and Landrace. It indicated that Cp was homozygotic and was losing its practical significance in studying consanguineous relationship among pig breeds, which was similar as Pi-2.

On basis of the phenotypic heterozygosity of locus Tf in these populations, it was reasonable to suggest that the variations observed were controlled by three codominant alleles: Tf^A, Tf^B and Tf^C, which were consistent with the results of other studies in China (Huang and Zhou, 1989; Lin et al., 1998). These three alleles were observed in all the breeds studied except Duroc, in which the allele of Tf^A was

not observed. Resulted from the comparison 3 alleles' frequencies of Po-2, it was concluded that $Po-2^C$ and $Po-2^A$ were the dominant alleles in Chinese indigenous pig breeds whereas the allele of $Po-2^B$ was dominant in the introduced three pig breeds. In the three protein loci (Po-1, Alb, Pi-1), the frequency of allele A was higher in the examined pig breeds except Laiwu pig, Yimeng pig, large white and Landrace. In addition, we observed the existence of Po-1 monomorphism in large black-white pig, Lantang pig and the introduced three pig breeds.

It's found that the allele Am^B was primary in most breeds, and the result of study on polymorphism of Am was consistent with Hesselhol (1969) and Zuozuomu (1982). The allele Am^{BF}, which was very rare, occurred in Dongshan pig, Chenhua pig, Baixiang pig and Hetao large-ear pig. In this investigation, four alleles of Akp^A, Akp^B, Akp^C and Akp^D were observed in Akp loci. It was easy to discover that the primary allele of Akp^C was in Chinese indigenous pig breeds and Akp^D was in most of the introduced pig breeds. The Hpx components occured in these populations suggested that the polymorphism was under genetic control of six alleles of Hpx^0, Hpx^{1F}, Hpx^1, Hpx^2, Hpx^3 and Hpx^4 with a codominant mode of inheritance. Among these alleles, Hpx^2 was possessed in all pig breeds studied, but allele Hpx^1 was not observed in Chenghua pig and Hpx^3 lacked in Huai pig and Mashen pig.

It can be seen from the Table 5 that the increasing/decreasing magnitude order of heterozygosity among populations Dst in the 10 loci was listed as following: Hpx, Po-2, Am, Tf, Akp, Pi-1, Po-1, Alb, Cp, Pi-2 whereas the magnitude order of heterozygosity within population (Hs) is: Hpx, Tf, Pi-2, Po-2, Akp, Alb, Am, Po-1, Pi-1, Cp. From the above, it could be concluded that there was discrepancy of alleles of locus Hpx between breeds as much as within breeds in the constitution and content. As a result, Hpx can be used as an important locus for studying the

Table 5. Loci variation at pig breeds studied including coefficient of gene differentiation (Gst), total genetic heterozygosity (Ht), heterozygosity within population (Hs), heterozygosity between populations (Dst), Polymorphism information content (PIC), fixation indices (Fis, Fit and Fst) in each loci and number of breeds deviated from Hardy-Weinberg equilibrium (H-W) which resulted from X^2

Locus	Gst	Ht	Hs	Dst	PIC	Fis	Fst	Fit	H-W	X^2
Tf	0.1321	0.6553	0.5688	0.0865	0.4922	-0.049	0.1389	0.0967	17	489.3
Cp	0.0531	0.0288	0.0273	0.0015	0.0257	0.4421	0.0415	0.4653	17	46.0
Po-2	0.2122	0.6177	0.4866	0.1311	0.4175	0.3340	0.2146	0.4769	11	315.0
Po-1	0.2416	0.2585	0.1960	0.0625	0.1605	0.1125	0.2508	0.3351	9	96.8
Pi-1	0.2991	0.2110	0.1479	0.0631	0.1228	-0.0334	0.3084	0.2853	7	18.6
Pi-2	0.0000	0.5000	0.5000	0.0000	0.3750	-1	0	-1	20	14.2
Am	0.2213	0.4459	0.3472	0.0987	0.3058	0.0408	0.2283	0.2598	5	47.7
Akp	0.1434	0.5604	0.4800	0.0804	0.4098	0.3643	0.1428	0.4551	16	398.2
Alb	0.0353	0.4300	0.4148	0.0151	0.3260	-0.5148	0.0276	-0.473	16	382.8
Hpx	0.2524	0.7678	0.5740	0.1938	0.5268	-0.0028	0.2589	0.2569	5	Infinity
Mean	0.1637	0.4475	0.3743	0.0733	0.3162	-0.0967	0.1677	0.0872	12.5	

Table 6. The D_A genetic distance (below diagonal) and resemble coefficient in 20 pig breeds (above diagonal)

	DL[a]	LL	DS	MZ	WZ	CH	GL	BX	LBW	LT	PT	HZ	HT	LWZ	YM	MS	HJ	LW	LD	DR
DL	*	0.9615	0.9427	0.9066	0.9670	0.9014	0.9300	0.9809	0.8576	0.9330	0.8752	0.9531	0.8899	0.8655	0.8709	0.8611	0.9047	0.7952	0.7899	0.7780
LL	0.0393	*	0.8967	0.8894	0.9650	0.9071	0.9062	0.9224	0.8415	0.9010	0.8611	0.9595	0.8851	0.8758	0.8768	0.8856	0.8745	0.7911	0.7829	0.7800
DS	0.0590	0.1090	*	0.8823	0.9513	0.8712	0.9054	0.9410	0.9306	0.9526	0.8761	0.9247	0.8344	0.8073	0.8244	0.8655	0.9143	0.7737	0.7857	0.7617
MZ	0.0981	0.1172	0.1252	*	0.9515	0.9581	0.9728	0.9437	0.8709	0.8996	0.9542	0.9070	0.9277	0.8888	0.9595	0.9110	0.9272	0.8390	0.8700	0.8765
WZ	0.0336	0.0356	0.0499	0.0497	*	0.9658	0.9638	0.9603	0.9430	0.9562	0.9300	0.9807	0.9056	0.9071	0.9234	0.9124	0.9209	0.8293	0.8413	0.8569
CH	0.1038	0.0975	0.1379	0.0428	0.0348	*	0.9468	0.9173	0.9155	0.9029	0.9045	0.9342	0.9008	0.8818	0.9273	0.8891	0.8902	0.8346	0.8544	0.9034
GL	0.0726	0.0985	0.0994	0.0276	0.0369	0.0547	*	0.9392	0.8942	0.9274	0.9691	0.9315	0.8924	0.9181	0.9303	0.9186	0.9549	0.8552	0.8773	0.8756
BX	0.0193	0.0808	0.0608	0.0579	0.0405	0.0863	0.0627	*	0.8820	0.9072	0.8889	0.9373	0.9538	0.8676	0.9029	0.8834	0.9277	0.8624	0.8582	0.8275
LBW	0.1536	0.1726	0.0719	0.1382	0.0587	0.0883	0.1118	0.1256	*	0.9219	0.8582	0.9206	0.8259	0.8125	0.8336	0.8724	0.8514	0.8134	0.8195	0.8323
LT	0.0693	0.1043	0.0486	0.1058	0.0448	0.1021	0.0754	0.0974	0.0813	*	0.9267	0.9379	0.7992	0.7984	0.8399	0.8493	0.8695	0.7410	0.7578	0.7379
PT	0.1333	0.1496	0.1323	0.0469	0.0726	0.1004	0.0314	0.1178	0.1529	0.0761	*	0.8976	0.8452	0.8724	0.9126	0.8396	0.9283	0.7765	0.8151	0.8054
HZ	0.0480	0.0413	0.0783	0.0976	0.0195	0.0681	0.0710	0.0648	0.0827	0.0641	0.1080	*	0.8964	0.8775	0.9042	0.8930	0.8948	0.8206	0.7933	0.7929
HT	0.1167	0.1220	0.1810	0.0751	0.0992	0.1045	0.1138	0.0473	0.1913	0.2242	0.1682	0.1094	*	0.8979	0.9424	0.8745	0.8883	0.9147	0.8838	0.8489
LWZ	0.1445	0.1326	0.2140	0.1179	0.0975	0.1258	0.0855	0.1420	0.2076	0.2252	0.1365	0.1307	0.1077	*	0.9164	0.8540	0.8974	0.8458	0.8351	0.8759
YM	0.1382	0.1315	0.1931	0.0413	0.0797	0.0755	0.0723	0.1021	0.1820	0.1745	0.0915	0.1007	0.0593	0.0873	*	0.8695	0.8836	0.8202	0.8213	0.8286
MS	0.1496	0.1215	0.1444	0.0932	0.0917	0.1175	0.0849	0.1240	0.1365	0.1634	0.1748	0.1132	0.1341	0.1578	0.1398	*	0.8425	0.8747	0.8732	0.8507
HJ	0.1001	0.1341	0.0896	0.0756	0.0824	0.1163	0.0462	0.0751	0.1609	0.1398	0.0744	0.1112	0.1184	0.1082	0.1238	0.1714	*	0.8132	0.8241	0.8336
LW	0.2291	0.2343	0.2566	0.1756	0.1872	0.1808	0.1564	0.1480	0.2065	0.2997	0.2530	0.1977	0.0892	0.1675	0.1982	0.1339	0.2068	*	0.9797	0.9099
LD	0.2359	0.2447	0.2412	0.1393	0.1728	0.1573	0.1309	0.1529	0.1991	0.2773	0.2045	0.2315	0.1235	0.1802	0.1969	0.1356	0.1935	0.0205	*	0.9488
DR	0.2510	0.2484	0.2722	0.1318	0.1544	0.1016	0.1329	0.1894	0.1836	0.3039	0.2164	0.2321	0.1638	0.1325	0.1880	0.1617	0.1820	0.0944	0.0526	*

[a] The abbreviation of pig breeds.

origin and differentiation of breeds and consanguineous relationship between individuals. That was to say, the function of different loci were variable in studying population genetic variation. At the same time, choosing the right loci and number of loci played decisive influence on veracity of experiment results when studying serum protein polymorphism in swine.

Population genetic variations and genetic differentiation

As described in Table 4, it showed that most of PIC are middle polymorphism except Duroc whose is low (0.2496). As for mean expected heterozygosity, it ranged from 0.3084 to 0.4423 and Duroc's was the lowest. The value of mean observed heterozygosity distributed between 0.3518 and 0.4891, and it was higher than that of former. With the three indexes (Ne, PIC, H), it can be directly compared not only genetic polymorphism and selective potential of the same gene loci in different populations, but also variation extent of the same population at different gene loci. The more the

mean genetic heterozygosity is, the more alleles are, and the higher the genetic diversity is. It also results in the higher selection potential and the higher selection pressure.

Taking a comprehensive view of the whole gene frequency, in the protein loci with more alleles such as Am, Akp, Hpx, etc., the number of alleles in Chinese indigenous pig breeds is often more than that of introduced pig breeds. Moreover, much more variation exists within breeds. As it is concerned, this kind of phenomena indicated that many genes in exotic pig breeds had been lost resulted from the long-term natural selection. On the other hand, many indigenous pig breeds still kept relatively higher genetic variations because of the conditional restrictions of the complex survival environments and the relatively lower crossing. In addition, the genetic differentiation coefficient (Gst) and the fixed index (Fst) between the populations indicated that 84% of the total genetic variation was between populations in all the 20 pig breeds. As for genetic differentiation, Hpx is maximal (0.2598) while Pi-2 is
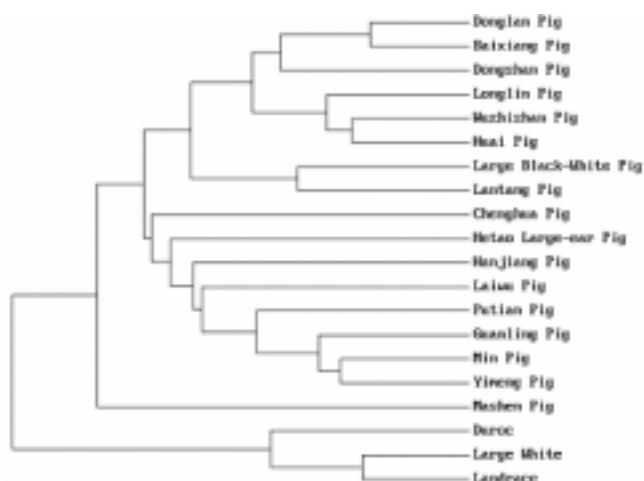
Figure 1. UPGMA phylogenetic tree showing the genetic structure of 17 Chinese indigenous pig breeds and three introduced pig breeds using Nei's D_A distance.

minimal (0.0000). The numbers of pig breeds deviating from equilibrium are different in variant loci. Am and Hpx are the least (5, p<0.05); on the other hand, that of Pi-2 is the most (20, p<0.05), which according to the value of X^2 resulted from fisher's method.

With the advancement of reforming and opening in China, and the continuous improving of artificial insemination and crossing, the genetic variation of many breeds became smaller and some excellent breeds had almost lost their breeding potentiality. So protecting the present breeds should be the important strategic selection in the 21st century for all the countries in the world.

Population genetic relationships and clustering analysis

Table 6 showed that the value of genetic distance ranged from 0.0193 to 0.2773, and the genetic distance between Donglan pig and Baixiang pig was the closest whereas that of Lantang pig and Landrace was the farthest. Figure 1 showed that the Chinese indigenous pig breeds studied in this work were divided into three branches. In the first branch, there are Donglan pig, Baixiang pig, Dongshan pig, Wuzhishan pig, Huai pig and Longlin pig; large black-white pig and Lantang pig grouped the second branch. In the third branch, it contained the North China type pig and Southwest China type pig, which distributed according to the book of pig Breeds in China. In addition, Mashen pig was far away from other breeds. Three introduced pig breeds were used as the out-group.

From above, it was not fully consistent with the previous division. The Donglan pig in Guangxi province and the Baixiang pig in Guizhou province had the near geographic location and there were frequent exchanges, therefore they had the nearest relationship and they formed into a small cluster with the Dongshan pig in Guangxi

province. Then the cluster was merged with the Wuzhishan pig, Huai pig and Longlin pig, which were long distance away, into a larger cluster. This formed the South China type pig. This result was easily comprehended and it simultaneously indicated the geographic isolation had certain influence on genetic differentiation of breeds.

To be surprised, the Guanlin pig in Guizhou province of Southwest type and the Chenhua pig in Sichuan province, Putian pig in Fujian province of Central China type clustered into a branch with North China type pig such as Yimeng pig, Min pig. In fact, they had relatively farther geographic location. We thought the causes might be that the serum samples from the backward of farmers and they might be mixed by the blood of Min pig and exotic pig breeds, which had a good crossing effect with them in recent years. The possibility of gene mixture was larger and might be affected by the genetic erosion. According to the book of pig Breeds in China, the immigrant people from Shanxi province carried the Bamei pig into the Hetao area, so it had large influences on the forming of Hetao large-ear pig in Hetao area of Inner Mongolian autonomous region.

The results of our study indicated that the classification according to body stature, appearance features, producing functions and geographic distribution could not reflect the basic genetic difference of breeds and genetic relationship between them. Mashen pig in Shanxi province existed in the remote mountain areas and had the less exchange with the outer spaces, so it formed a branch itself. Of course the Chinese indigenous pig breeds originated from Asian wild pig had a far relationship with the three exotic pig breeds from Europe and America.

Resulted from the large difference of survival circumstance and social conditions of pig breeds, the genetic differentiation and the diversity of economic characters evolved. Therefore both serum proteins polymorphism and other study methods had their own characteristics and limitations for putting importance on different aspects. We should pay more attention to that in the specific work.

APPENDIX. The following is allele frequencies of ten serum protein employed in this study

	Tf			Cp			Po-2			Po-1		Pi-1		Pi-2	
	A	B	C	A	B	C	A	B	C	A	B	A	B	A	B
Donglan pig	0.5938	0.2292	0.1771	0.0000	1.0000	0.0000	0.6354	0.0833	0.2813	0.9792	0.0208	0.9583	0.0417	0.5000	0.5000
Longlin pig	0.7869	0.1066	0.1066	0.0000	1.0000	0.0000	0.3361	0.2705	0.3934	0.8934	0.1066	0.9262	0.0738	0.5000	0.5000
Dongshan pig	0.4035	0.3947	0.2018	0.0000	1.0000	0.0000	0.9138	0.0862	0.0000	0.9569	0.0431	0.9569	0.0431	0.5000	0.5000
Min pig	0.0192	0.5769	0.4038	0.0000	1.0000	0.0000	0.5763	0.0932	0.3305	0.8051	0.1949	1.0000	0.0000	0.5000	0.5000
Wuzhishan pig	0.3833	0.3167	0.3000	0.0417	0.9583	0.0000	0.5333	0.2250	0.2417	0.8583	0.1417	0.9750	0.0250	0.5000	0.5000
Chenghua pig	0.0500	0.5417	0.4083	0.0000	1.0000	0.0000	0.2583	0.3083	0.4333	0.9750	0.0250	1.0000	0.0000	0.5000	0.5000
Guanling pig	0.1406	0.4531	0.4063	0.0000	1.0000	0.0000	0.6719	0.2813	0.0469	0.7969	0.2031	0.8281	0.1719	0.5000	0.5000
Baixiang pig	0.3636	0.3409	0.2955	0.0000	1.0000	0.0000	0.6522	0.0435	0.3043	0.9565	0.0435	1.0000	0.0000	0.5000	0.5000
Large black-white pig	0.0357	0.4464	0.5179	0.0000	1.0000	0.0000	0.5982	0.4018	0.0000	1.0000	0.0000	1.0000	0.0000	0.5000	0.5000
Lantang pig	0.2456	0.5614	0.1930	0.0000	1.0000	0.0000	0.8333	0.1667	0.0000	1.0000	0.0000	1.0000	0.0000	0.5000	0.5000
Putian pig	0.0439	0.4737	0.4825	0.0000	1.0000	0.0000	0.8596	0.1404	0.0000	0.5789	0.4211	0.9211	0.0789	0.5000	0.5000
Huai pig	0.4083	0.2750	0.3167	0.0000	0.9750	0.0250	0.3621	0.3362	0.3017	0.8583	0.1417	0.9833	0.0167	0.5000	0.5000
Hetao large-ear pig	0.2340	0.4149	0.3511	0.0000	1.0000	0.0000	0.1887	0.3679	0.4434	0.7264	0.2736	0.9811	0.0189	0.5000	0.5000
Laiwu pig	0.3644	0.1949	0.4407	0.0508	0.9492	0.0000	0.2712	0.7288	0.0000	0.4407	0.5593	0.9153	0.0847	0.5000	0.5000
Yimeng black pig	0.0339	0.5847	0.3814	0.0000	1.0000	0.0000	0.2417	0.2167	0.5417	0.4417	0.5583	0.9000	0.1000	0.5000	0.5000
Mashen pig	0.4407	0.4407	0.1186	0.0000	0.9576	0.0424	0.3475	0.4831	0.1695	0.9576	0.0424	0.7966	0.2034	0.5000	0.5000
Hanjiang black pig	0.1695	0.2373	0.5932	0.0000	1.0000	0.0000	0.7500	0.2500	0.0000	0.7250	0.2750	1.0000	0.0000	0.5000	0.5000
Large white	0.1415	0.4245	0.4340	0.0250	0.9750	0.0000	0.1917	0.8083	0.0000	1.0000	0.0000	0.4750	0.5250	0.5000	0.5000
Landrace	0.0816	0.4388	0.4796	0.1071	0.8929	0.0000	0.4286	0.5536	0.0179	1.0000	0.0000	0.3839	0.6161	0.5000	0.5000
Duroc	0.0000	0.2544	0.7456	0.0000	1.0000	0.0000	0.2458	0.6102	0.1441	1.0000	0.0000	0.6017	0.3983	0.5000	0.5000

	Am				Akp				Alb		Hpx					
	A	BF	B	C	A	B	C	D	A	B	0	1F	1	2	3	4
Donglan pig	0.2708	0.0000	0.5938	0.1354	0.0417	0.0417	0.8438	0.0729	0.8229	0.1771	0.0208	0.0208	0.3854	0.2083	0.3125	0.0521
Longlin pig	0.0328	0.0000	0.6311	0.3361	0.0246	0.0492	0.7295	0.1967	0.6167	0.3833	0.0164	0.0574	0.1885	0.4590	0.1557	0.1230
Dongshan pig	0.5086	0.0259	0.2931	0.1724	0.0172	0.0948	0.5259	0.3621	0.6638	0.3362	0.0000	0.0000	0.1897	0.2759	0.1466	0.3879
Min pig	0.0000	0.0000	1.0000	0.0000	0.0000	0.0000	0.5763	0.4237	0.5678	0.4322	0.0000	0.2542	0.1864	0.2966	0.2542	0.0085
Wuzhishan pig	0.2083	0.0000	0.5417	0.2500	0.0508	0.0000	0.5678	0.3814	0.6750	0.3250	0.0667	0.0417	0.1250	0.4500	0.3167	0.0000
Chenghua pig	0.0000	0.1167	0.7167	0.1667	0.0536	0.0982	0.4464	0.4018	0.7083	0.2917	0.0500	0.0000	0.0000	0.4833	0.4667	0.0000
Guanling pig	0.0000	0.0000	0.8906	0.1094	0.0469	0.0000	0.6406	0.3125	0.8438	0.1563	0.0000	0.2813	0.0625	0.3906	0.2344	0.0313
Baixiang pig	0.2391	0.0435	0.7174	0.0000	0.0652	0.0217	0.5652	0.3478	0.8261	0.1739	0.0000	0.0000	0.6304	0.1087	0.1957	0.0652
Large black-white pig	0.4643	0.0000	0.1607	0.3750	0.0446	0.0714	0.2411	0.6429	0.7054	0.2946	0.0000	0.0714	0.1339	0.5893	0.2054	0.0000
Lantang pig	0.4211	0.0000	0.4386	0.1404	0.1140	0.0702	0.7632	0.0526	0.6404	0.3596	0.0000	0.0175	0.0614	0.7807	0.1404	0.0000
Putian pig	0.0263	0.0000	0.9737	0.0000	0.0000	0.1053	0.6579	0.2368	0.6404	0.3596	0.0965	0.0439	0.0351	0.7105	0.1140	0.0000
Huai pig	0.2917	0.0000	0.4417	0.2667	0.0083	0.0500	0.6750	0.2667	0.7672	0.2328	0.3417	0.0333	0.1583	0.4667	0.0000	0.0000
Hetao large-ear pig	0.0189	0.0755	0.8585	0.0472	0.0000	0.0000	0.4608	0.5392	0.6792	0.3208	0.0000	0.0000	0.8113	0.0377	0.0472	0.1038
Laiwu pig	0.0254	0.0000	0.8136	0.1610	0.0678	0.0508	0.5763	0.3051	0.6949	0.3051	0.0169	0.1441	0.2288	0.0593	0.5508	0.0000
Yimeng black pig	0.0833	0.0000	0.7583	0.1583	0.0250	0.0000	0.6083	0.3667	0.6333	0.3667	0.0000	0.2250	0.3000	0.2667	0.2083	0.0000
Mashen pig	0.2458	0.0000	0.7542	0.0000	0.0339	0.0508	0.2881	0.6271	0.6017	0.3983	0.0000	0.6949	0.0678	0.2373	0.0000	0.0000
Hanjiang black pig	0.0250	0.0000	0.9000	0.0750	0.0175	0.0526	0.6140	0.3158	0.8333	0.1667	0.0000	0.0083	0.1250	0.1250	0.1250	0.6167
Large white	0.0917	0.0000	0.9083	0.0000	0.0000	0.0000	0.2895	0.7105	0.6750	0.3250	0.1017	0.0000	0.7712	0.0678	0.0508	0.0085
Landrace	0.0000	0.0000	1.0000	0.0000	0.0446	0.0357	0.1786	0.7411	0.5625	0.4375	0.0000	0.0000	0.5625	0.1607	0.2768	0.0000
Duroc	0.0000	0.0000	1.0000	0.0000	0.0000	0.0000	0.1897	0.8103	0.5847	0.4153	0.0000	0.0000	0.1102	0.1102	0.7797	0.0000

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