GENETIC AND POPULATION ANALYSIS

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Bekenev V.A.[1] *, **Deeva V.S.**[1], **Bolshakova I.V.**[1], **Aitnazarov R.B.**[2], **Khoroshilova T.S.**[1], **Frolova Y.V.**[1]
[1]Academy of Sciences (SFSCA RAS), Krasnoobsk vill., Russia;
[2] Siberian Federal Scientific Centre of Agro-Bio Technologies of the Russian nstitution "Federal Research Center, Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences", Novosibirsk, Russia

* Correspodning author (bekenev[at]ngs.ru)

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GENETIC FEATURES OF PIGS OF DIFFERENT BREEDS SIBERIA

Research article

Abstract

In pig breeding, along with the assessment of breeding value by statistical methods, the use and search for genetic markers responsible for fertility, intramuscular fat content, stress, and other diseases is becoming increasingly important. In their studies carried out on pigs of different breeds of Siberia, such as Large White (LW), Kemerovo (K), Pietrain (P), Duroc (D), Landrace (L), Canadian Yorkshire (Y) and various hybrids, the authors identified certain relationships. The authors found such relationships between growth rate, fat thickness, stress resistance, fatty acid composition, palatability of meat and back fat on the one hand, and the frequency of occurrence of erythrocyte antigen (EA) genotypes - blood groups, erythrocyte enzymes (*EsD, Gpi, 6 -pgd, Ada*), genes of ryanodine (*RYR-1*), estrogen (*ESR*) receptors, genes of the fatty acid binding protein family (*H-FABP*), genes associated with the susceptibility of piglets to diarrhea (*ECR F18/FUT1*), markers of efficacy growth and obesity (*LEP*), meat productivity (*MC4R*) and others - on the other hand. The frequency of occurrence of genotypes of DNA markers in pigs with different stress sensitivity was studied. The change in the frequencies of some markers in the process of absorption crossing and subsequent selection over several generations was determined.

Keywords: Agriculture breeds, blood groups, erythrocyte enzymes, genetic markers, fatty acids, growth rate.

Бекенев В.А.[1] *, **Деева В.С.**[1], **Большакова И.В.**[1], **Аитназаров Р.Б.**[2], **Хорошилова Т.С.**[1], **Фролова Ю.В.**[1]
[1] Сибирский федеральный научный центр агробиотехнологий Российской академии наук (СФНЦА РАН), Краснообск, Россия;
[2] Институт цитологии и генетики, Сибирское отделение Российской академии наук, Новосибирск, Россия

* Корреспондирующий автора (bekenev[at]ngs.ru)

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ГЕНЕТИЧЕСКИЕ ОСОБЕННОСТИ СВИНЕЙ РАЗНЫХ ПОРОД СИБИРИ

Научная статья

Аннотация

В селекции свиней наряду с оценкой племенной ценности статистическими методами, все большее значение приобретает использование и поиск генетических маркеров, ответственных за плодовитость, содержание внутримышечного жира, стрессам и другим заболеваниям. В наших исследованиях, проводившихся на свиньях разных пород Сибири: крупной белой (КБ), кемеровской (К), пьетрен (П), дюрок (Д), ландрас (Л), канадский йоркшир (Й) и различных гибридов, найдены определённые взаимосвязи между скороспелостью, толщиной шпика, стресс устойчивостью, составом жирных кислот, вкусовых качеств мяса и спинного жира с одной стороны, и частотой встречаемости генотипов системы эритроцитарных антигенов (*EA*) - групп крови, эритроцитарных ферментов (*EsD, Gpi, 6-pgd, Ad*a), генов рианодинового (*RYR-1*), эстрогенового (*ESR*) рецепторов, генов семейства белков, связывающих жирные кислоты *(H-FABR),* ген связанный с восприимчивостью поросят к диарее (*ECR F18/FUT1*), маркеров эффективности роста и ожирения (*LEP*), мясной продуктивности (*MC4N*) и др. Изучена частота встречаемости генотипов ДНК-маркёров у свиней с разной стресс чувствительностью. Определено изменение частот некоторых маркеров в процессе поглотительного скрещивания и последующей селекции в течение нескольких поколений.

Ключевые слова: породы, группы крови, эритроцитарные ферменты, генетические маркеры, жирные кислоты, скороспелость, плодовитость.

1. Introduction

One of the essential critical factors for the innovative development of agricultural production is improving of the genetic potential of animals and plants' productivity. Currently, many breeders - geneticists use statistical methods used in many farms,

which are quite useful. However, even these methods have some disadvantages. These disadvantages are due to the low heritability of the traits, their relatively late manifestation, the presence of hidden carriers of undesirable characteristics, diseases, etc. Therefore, every year new methods are used to control the selection, which seem to be the most effective, but then are replaced or enriched by even more progressive ones.

The current level of science development makes it possible to control breeding at the genomic level [1]. This level is the development of marker selection, which allows the determination of genotypes with the desired manifestation of productive traits by single nucleotide markers - snips (SNPs) associated with quantitative trait loci (QTL). Marker selection allows you to accurately and reliably determine animals' genotype at birth and thereby accelerate the selection process. Nevertheless, the genetic assessment established a similar nature of the evaluation for blood groups (BG) and DNA microsatellites (DNA-MS) in pigs of different breeds, interbreed genealogical groups, and relative differences in the degree of polymorphism [2]. Therefore, scientists recommend considering the degree of heterogeneity calculated by BG or DNA-MS when selecting parental pairs.

The purpose of this work is to review long-term experimental data on the search for associative relationships between clearly inherited genetic blood factors and productive traits to increase the genetic potential of pig productivity in the process of creating new breeding achievements, when assessing the effectiveness of crossing different breeds and studying the adaptation of animals to industrial technology in special natural and economic conditions of Siberia.

The task of the work is to describe the genetically characteristics of pigs of different breeds in the breeding process, the influence of genetic factors, such as blood groups, erythrocyte enzymes, DNA markers, the level of their heterozygosity, on the adaptation of animals to environmental conditions, productivity, chemical composition of tissues and resistance to stress.

2. Materials and Methods

The work used material obtained in breeding factories and sizeable commercial pig breeding complexes in Siberia during the creation and improvement of several breeds: Large White (LW), Siberian Northern (SN), Kemerovo (K), as well as breeding animals of imported species: Duroc (D), Pietrain (P), Landrace (L), Yorkshire (Y), etc., as well as their hybrids [3,4]. Evaluation of animals for reproductive, fattening, and meat qualities in the breeding process the authors accompanied by a search for their relationships with genetic factors: blood groups, erythrocyte enzymes, proteins, DNA markers and other genes associated with fat content, chemical composition, the taste of meat and back fat.

The authors tested the main pig population in the laboratory of immune genetics of the Siberian Research Institute of Animal Husbandry (SRIAH). They carried out the testing using monoreceptor reagent sera to 20 antigens of 7 blood group systems (A, G, E, F, D, L, H) according to the generally accepted method [5]. As specific reagents, the authors used sera manufactured in the laboratory of Siberian Research Institute of Animal Husbandry (SRIAH) and passed several international comparative tests. The coefficients of similarity in the frequency of occurrence of blood antigens were calculated by the authors using the method of Meshcheryakov V.Ya. [6].

In one of the experiments, the genetic characteristics of pigs of five breeds (LW, K, L, D, P) were studied, which were kept in a sizeable pig-breeding farm "Chistogorsky" of the Kemerovo region in the same conditions of feeding and housing, received feed following the norms. In all animals, blood sampling for research the authors carried out simultaneously. For comparison, they present a study of the frequency of blood antigenic factors in the Siberian Northern breed pigs, conducted earlier in another breeding farm.

In other experiments, the authors paid special attention to the genetic structure of LW pigs in the process of 40 years of selection in the breeding farm and the creation of a new breeding type (micro-breed) "Novosibirsk". Against the background of breeding a new type and constant testing of boar offspring for fattening and meat qualities of the offspring by the method of control feeding of young animals, their genetic characteristics were also studied according to the above criteria. The one of the authors of this work carried out all studies his direct supervision and personal participation. He participated in the assessment and analysis of each individual and each carcass. In one of the farms, the authors studied the absorption crossbreeding of pigs of this species with boars of the Yorkshire breed of Canadian selection. At the same time, the dynamics of changes in the frequency of occurrence of genetic markers and their relationship with the productive qualities of animals were studied.

Statistics. The authors performed statistical processing of the results using the Statistics 6.1 software package for Windows. They presented the results as means with their standard error (M ± SE). Differences were considered statistically significant at $p \leq 0.05$. The authors performed the calculations using one-way analysis of variance using Tukey's test of significance for differences.

3. Results

3.1 Genetic structure of pigs of different breeds of Siberia by blood groups and biochemical parameters

The genotypic composition of blood groups of pigs of five breeds is presented in Table 1. Breed K was characterized by a low frequency of $EAE^{bdg/edf}$ genotypes (0.07) and a high frequency of $EAE^{edg/edg}$ genotypes, equal to 0.17 [7]. In this breed, in the E system of the *EAE* locus, the frequency of the $E^{aeg/bdg}$ genotype was 0.13, compared to 0.06, 0.00 and 0.02, respectively, in L ($P<0.01$) with D ($P<0.001$) and P ($P<0.001$). The $E^{aeg/edg}$ genotype frequency is 0.16, which is significantly higher compared to other breeds ($P <0.001$). The authors identified the $B^{a/b}$ genotype in the *EAB* locus with a frequency of 0.94 ($P <0.001$) compared with a frequency of 0.00 - 0.28 in other breeds. The B^b allele is specific to the Berkshire breed (B), from which the K breed is derived.

In the G system of the *EAG* locus, the $G^{a/a}$ marker is significantly more common in 0.31 ($P<0.001$), in K-breed pigs, than in L, D, and P. The authors note a high frequency of 0.60 ($P<0.001$) of the $L^{bcgi/bdfi}$ genotype of the L – system of the *EAL* locus in sows of the K breed, versus 0.00 – 0.15 in comparison with other breeds.

The frequency of the $E^{bdg/edg}$ genotype of the *EAE* locus E – system in L pigs was 0.49.The differences are significant in comparison with sows of the breeds LW, K and D (P<0.001) - P (P< 0.05).This breed has a higher frequency of occurrence of the $L^{adhi/bcgi}$ genotype in the *EAL* locus system (P<0.001) in comparison with sows of LW and K breeds.

Breed D differs from the compared breeds in the frequency of blood genotypes D, E, F, L - systems.

The authors detected at the *EAD* locus, the $D^{a/b}$ genotype of the *D* system in carriers seen with a frequency of 0.39, which is significantly higher (P <0.001) than in sows of LW and K breeds, as well as L and P (P <0.01). The authors found that the $E^{edg/edf}$ genotype of the *E* system of the *EAE* locus is found more often in D - 0.50 (P <0.01) than in the LW breed and (P <0.001) in K and L.

The frequency of the genotype $F^{a/b}$ 0.39 *F* - the *EAF* locus system in the D breed exceeded (P <0.001) the frequency indices of sows of other breeds. In sows of the D breed, the $L^{adhi/bdfi}$ *L* genotype - the *EAL* locus system - occurs more often (0.83) P <0.001 than in other breeds.

Animals of breed P differ in the frequency of occurrence of genotypes $E^{edg/edg}$ - 0.19 (P <0.001) from other breeds, $G^{b/b}$ - 0.19 (P <0.01), and $L^{bcgi/bcgi}$ - 0.63 (P <0.001) - from K and D.

Table 1 – Frequency of blood genotypes of pigs of different breeds (S ± x)

Systems	Genotype	Large White	Kemerovo	Landrace	Duroc	Pietrain
		n=518	n=180	n=164	n=18	n=41
A	*cp/*	0.45±0.09	0.76±0.03	0.62±0.04	0.83±0.09	0.56±0.08
	-/	0.54±0.09	0.24±0.03	0.38±0.04	0.17±0.09	0.44±0.08
B	*a/a*	1.00±0.00	0.06±0.02	0.81±0.03	0.72±0.11	0.98±0.02
	a/b	0	0.94±0.02	0.19±0.03	0.28±0.11	0.02±0.02
D	*a/b*	0	0.04±0.01	0.05±0.02	0.39±0.11	0.07±0.04
	b/b	1.00±0.00	0.96±0.01	0.94±0.02	0.61±0.11	0.93±0.04
	aeg/aeg	0.01±0.07	0	0	0	0
E	*aeg/bdg*	0.10±0.02	0.13±0.03	0.06±0.02	0	0.02±0.02
	aeg/bdf	0.12±0.02	0.04±0.01	0.08±0.02	0	0.02±0.02
	aeg/edg	0.08±0.02	0.16±0.03	0	0.06±0.05	0
	aeg/edf	0.08±0.02	0.05±0.02	0.01±0.01	0	0.05±0.03
	aeg/aef	0.01±0.01	0	0	0	0
	bdg/bdg	0.02±0.01	0.07±0.02	0.06±0.02	0	0
	bdg/edg	0.25±0.03	0.26±0.03	0.49±0.04	0.06±0.05	0.32±0.07
	bdg/edf	0.14±0.02	0.07±0.02	0.23±0.03	0.28±0.11	0.07±0.04
	edg/edg	0.08±0.02	0.17±0.03	0.04±0.02	0.11±0.07	0.19±0.06
	edg/edf	0.11±0.02	0.06±0.02	0.04±0.02	0.50±0.12	0.32±0.07
F	*a/b*	0	0.05±0.02	0.20±0.03	0.39±0.11	0.02±0.02
	b/b	1.00±0.00	0.95±0.02	0.80±0.03	0.61±0.11	0.98±0.02
G	*a/a*	0.12±0.02	0.31±0.03	0.13±0.03	0.11±0.07	0.05±0.03
	a/b	0.66±0.03	0.68±0.03	0.74±0.03	0.78±0.10	0.76±0.07
	b/b	0.22±0.03	0.01±0.01	0.13±0.03	0.11±0.07	0.19±0.06
L	*adhi/bcgi*	0.06±0.04	0.06±0.02	0.29±0.04	0.17±0.09	0.19±0.06
	adhi/bdfi	0.24±0.07	0.17±0.03	0.07±0.02	0.83±0.09	0.15±0.06
	bcgi/bcgi	0.51±0.09	0.17±0.03	0.50±0.04	0	0.63±0.07
	bcgi/bdfi	0.15±0.06	0.60±0.04	0.13±0.03	0	0.02±0.02

	bdfi/bdfi	0.03±0.03	0	0.01±0.01	0	0

For interest, the authors present the data on the frequency of occurrence of the *EA* genotypes *E- EAF-* and *EAG* - blood group systems of SN pigs, bred in the 40s of the 20th century to improve adaptability to cold conditions and thickness back fat [8].

In 350 breeding pigs of this breed, there was an advantage in the frequency of occurrence of the $EAE^{bdg/edf}$ (0.32) and $EAE^{edf/edf}$ (0.16) genotypes and a high level of heterozygous genotypes (0.66) according to the EAG system compared to other breeds.

Pig breeds K and P have significant differences in blood antigenic factors and fatty acids' composition. The frequency of occurrence of the $EAE^{aeg/edg}$ genotype is 0.16 in the K breed; 0.0 in the P breed; $EAE^{edg/edf}$ 0.06 and 0.32, respectively; $E^{aeg/bdg}$ - 0.13 and 0.02 (Table 1). The frequency of the genotype $G^{a/a}$ in pigs of breed K is 0.31, in breed P - 0.05.

These breeds also differ the most in the composition of fatty acids in their meat and lard. According to the composition of fatty acids of intramuscular fat, the K breed, P and D can be distinguished from all the studied breeds. So, in terms of the amount of SFA the animals of the D breed have the advantage. Their meat contains 40.06% SFA versus 37.56 - in the P breed ($P < 0.1$), but MUFA, on the contrary, in the flesh of D pigs is less (49.16%) than in the P breed (52.46%), and it is statistically significant ($P < 0.05$). The authors noted the insignificant superiority of the D breed over other breeds for PUFA. The Kemerovo breed surpasses others and, especially, the D breed in palmitic fatty acid ($P < 0.05$). The least of this acid in the meat of animals of the breed P. This breed is reliably superior to other species ($P < 0.01$) and, especially, the D breed, in terms of the content of oleic fatty acid in intramuscular fat (49.55 versus 45.98%).

Genetic differences between the breeds of LW, L, D, Y pigs were established using the developed multilocus system of analysis based on DNA microsatellites, including 6 markers. In all groups of breeds, a deficiency of heterozygotes was revealed. It is established that the main part of the variability is due to intragroup diversity [9].

A study of Berkshire pigs' complete genomes, based on which the K breed was created, revealed several genes undergoing targeted selection associated with the regulation of lipid metabolism, the distribution of intramuscular fat, and the type of muscle fibres [10]. It can be assumed that a similar relationship exists in pigs of breed K.

3.2. Genetic structure and productivity of Large White pigs

The most widespread breed of pigs in the Siberian region is LW. Breeders have been improving and acclimatizing this breed for several decades, and in the last 20 years they have carried out intensive breeding in the direction of improving the growth rate and reducing the thickness of subcutaneous fat. Over the last 4-5 generations of pigs, the age at which the live weight reaches 100 kg has decreased from 199 days to 162 days, the fat thickness in 6-7 ribs has decreased from 33 mm to 30 mm [11]. Interestingly, over 14 years (1973-1987) of selection, the frequency of occurrence of the alleles of blood groups of the *EAE* and *EAG* systems has undergone significant changes (Table 2). The number of alleles *aeg* and *bdg* increased, but the number of allele *edf* decreased significantly. Over the next 13 years (1987-2000), bdg allele number fell slightly, the rest remained at the 1987 level. Simultaneously, the frequency of genotypes $EAE^{bdg/edg}$ increased from 0.17 to 0.25, and $EAE^{bdg/edf}$ - from 0.10 to 0.14. [12].

Table 2 – Dynamics of the frequency of occurrence of blood group alleles in a herd of Large White pigs of the breed livestock factory farm "Bolshevik."

System groups blood	Allele	1973^{D} n=558		1987 n=632		2000 n=518	
		number of individuals	frequency	number of individuals	frequency	number of individuals	frequency
EAE	*aeg*	90	0,16	145	0,23**	109	0,21**
	aef	17	0,03	-	-	5	0,01
	bdg	156	0,28	219	0,35**	135	0,26
	edg	142	0,25	178	0,28*	155	0,30*
	edf	153	0,27	90	0,14***	82	0,16***
	bdf	-	-	-	-	32	0,06
EAG	*a*	201	0,36	250	0,36	233	0,45
	b	357	0,64	436	0,64	285	0,55

Note: ^{D} - according to T.F. Degtyareva (1982) [13].
*The difference in comparison with 1973 is reliable when *- (P <0,05), ** - (P <0,01), ***(P <0,001) and further.*

Such changes can be explained by the selective advantage of animals carrying the *aeg* and *bdg* alleles in terms of growth rate and simultaneous selection by this indicator of productivity. The animals with the $EAE^{aeg/edf}$ and $EAE^{bdg/bdg}$ genotypes had the best growth rate, and the $EAE^{edg/edg}$ genotypes had the worst growth rate (Table.5), the difference in the age of reaching a live weight of 100 kg between them was 6.4-6.8 days ($P<0.05$). In our work, the authors carried out a controlled feeding of a LW breed. Heterozygous pigs according to the *EAG* system tended to achieve a faster live weight of 100 kg over homozygous pigs by 1.7-2.2 days (Table 3). The authors obtained similar results in previous studies [**13,14**]. The authors observed a tendency for heterozygotes' superiority over homozygotes for the age of reaching a live weight of 100 kg and according to the *EAE* system. The tendency of the superiority of heterozygotes over homozygotes by the age of reaching a live weight of 100 kg was also

observed in the *EAE* system, and this is typical for most heterozygous genotypes: $EAE^{aeg/edg}$, $EAE^{aeg/edf}$, $EAE^{bdg/edg}$ compared to the original homozygotes.

Of all the pigs subjected to control fattening, the fastest growing ones were selected, containing simultaneously the best genotypes for four systems, i.e. $EAA^{o/-}$, $EAG^{a/b}$, $EAN^{a/-}$ and one of the best genotypes of the *EAE* system: $EAE^{bdg/bdg}$, $EAE^{bdg/edf}$, $EAE^{aeg/edg}$, or $EAE^{aeg/edf}$. The age at which they reached a mass of 100 kg was 181±1.5 days, which is significantly higher than the average of all the other sub-pigs studied (184.3±0.64 days), as well as any other genotypes taken for individual systems (P<0.05). The genotype of Large White breed pigs of the herd, and maybe other packs, having the form: $EAA^{-/o}$, $EAE^{bdg/bdg}$, *aeg/edf* $EAG^{a/b}$, $H^{a/-}$ can be considered the best for selection by age at which weight reaches 100 kg. The authors found no differences between different genotypes of the *EAA, EAE* and *EAH* systems in the thickness back fat and carcass length. Only $G^{b/b}$ homozygotes were inferior in thickness back fat (P <0.05) to heterozygotes. There was a significant difference in the age at which a weight of 100 kg was reached between the $EAE^{edg/edg}$ genotype and the $EAE^{bdg/bdg}$, $EAE^{aeg/edg}$, $EAE^{edg/edg}$ genotypes, and in the meat color - between the $EAE^{edg/edg}$ and $EAE^{aeg/edg}$ genotypes.

The existing differences between different genotypes in muscle color, which characterizes the predisposition of animals to PSE syndrome, were revealed.Thus, paler meat had *EAE* heterozygotes (P <0.05).

Table 3 – Age at which live weight is 100 kg and meat qualities of Large White pigs of different genotypes by blood group

System	Genotype	Number of individuals	Age at which live weight is 100 kg, days	Thickness back fat, cm	Carcass length, cm	Meat colour, points
EAA	*o/-*	342	183,3±0,6 ^{a}	3,18±0,02 ^{a}	94,2±0,2 ^{a}	3,06±0,05 ^{a}
	cp/-	142	185,1±1,0 ^{a}	3,21±0,06 ^{a}	94,6±0,4 ^{a}	3,18±0,07 ^{a}
EAE	*edg/edg*	32	188,7±2,4^{a}	3,14±0,08 ^{ab}	94,2±0,8 ^{a}	3,29±0,13 ^{a}
	bdg/edg	83	183,7±1,1 ^{ab}	3,20±0,05 ^{ab}	94,2±0,6 ^{a}	3,00±0,11 ^{ab}
	bdg/bdg	62	182,3±1,4 ^{ab}	3,18±0,06 ^{ab}	93,7±0,5 ^{a}	3,28±0,13 ^{a}
	aeg/aeg	19	185,7±2,5 ^{ab}	3,12±0,12 ^{ab}	94,7±0,7 ^{a}	3,12±0,18 ^{ab}
	aeg/edg	103	183,2±1,1^{b}	3,24±0,04^{b}	94,5±0,4 ^{a}	2,96±0,08 ^{b}
	aeg/bdg	57	184,0±1,5 ^{ab}	3,11±0,07 ^{ab}	93,5±0,7 ^{a}	3,02±0,09 ^{ab}
	edf/edf	10	187,5±3,4 ^{ab}	3,27±0,16 ^{ab}	93,2±1,2 ^{a}	2,70±0,30 ^{ab}
	edg/edf	35	184,6±1,8 ^{ab}	3,13±0,07 ^{ab}	94,8±0,8 ^{a}	3,09±0,18 ^{ab}
	aeg/edf	42	181,9±1,8^{b}	3,27±0,08 ^{ab}	93,8±0,5 ^{a}	3,11±0,09 ^{ab}
	bdg/edf	51	183,3±1,6 ^{ab}	3,07±0,07 ^{a}	95,1±0,5 ^{a}	3,15±0,12 ^{ab}
	including					
	homozygotes	123	184,9±1,6^{a}	3,17±0,04^{a}	93,9±0,3^{a}	3,21±0,08^{a}
	heterozygotes	371	183,4±1,2^{a}	3,18±0,02^{a}	94,3±0,2^{a}	3,03±0,04^{b}
EAG	*a/a*	57	185,2±1,5 ^{a}	3,17±0,04 ^{a}	94,5±1,0 ^{a}	2,97±0,07 ^{a}
	a/b	251	182,9±0,7 ^{a}	3,18±0,02 ^{a}	94,7±0,4 ^{a}	3,06±0,07 $^{a\,b}$
	b/b	205	184,6±0,8 ^{a}	3,13±0,05 ^{a}	93,9±0,4 ^{a}	3,16±0,05 ^{b}
EAH	*-/-*	127	185,1±1,0 ^{a}	3,15±0,04 ^{a}	93,6±0,4 ^{a}	3,26±0,08 ^{a}
	a/-	355	183,4±0,6 ^{a}	3,17±0,02 ^{a}	94,5±0,2 ^{a}	3,02±0,04 ^{b}

Note: $^{a.b}$ Superscripts within each column means values differ at (P < .05).

Thus, paler meat had *EAE* heterozygotes (P <0.05) versus homozygotes, and in the homozygote $EAG^{a/a}$ differed in paler meat from the homozygote $EAG^{b/b}$ (P <0.05). The authors observed a similar trend in carriers of the $A^{o/-}$ blood groups compared to $A^{cp/-}$. Carriers of the $EAH^{a/-}$ allele had paler meat (P <0.01) compared to $EAH^{-/-}$, which confirms the data obtained by other researchers [15], [16] the higher frequency of animals with PSE syndrome in carriers of $EAH^{a/-}$.

It can be assumed that animals with the complex genotype $EAN^{a/-}$, $EAA^{o/-}$, $EAG^{a/a}$ and heterozygous according to the *EAE* system are less desirable due to the poorer quality of production and stress sensitivity.

Apparently, the genotype of pigs of the Large White breed of the herd, and maybe the whole breed: $EAA^{cp/-}$; $EAE^{edg/edg}$ or $EAE^{bdg/bdg}$ or $EAE^{aeg/aeg}$; $EAG^{b/b}$; $EAH^{/-}$ can be considered a model for selection for meat quality and stress resistance. However, the authors draw attention to the fact that complex genotypes can reflect objective reality, indicating a connection with meat qualities or early maturity only in a given closed population with long-term selection under the same conditions.

Many scientists believe that meat quality is genetically determined and associate it with blood groups of some systems. Of particular interest is the *EAH* blood group system, which turns out to be related to the adaptability of pigs to powerful influences, with stress sensitivity and meat quality (PSE syndrome). In studies [**17-19**], the authors found that the $EAH^{a/-}$ antigen is more common in stress-sensitive pigs. It is believed that this is due to the location of the *EAH* system locus - in chromosome 15 near the halothane sensitivity locus [20], [21].

However, the EAH system's close relationship with stress sensitivity is not natural for all pigs' populations. So, in experiments on a LW breed [22], on pigs of the Swedish Landrace and Swedish Yorkshire breeds [23], on the German Landrace breed [24], this system did not affect the performance indicators of pigs, and according to [25], the animals with the *EAH a / a* blood group had a higher growth rate and a darker meat color than those not carrying this genotype.

Heterozygosity of genotypes for the *EAE*- and *EAG*- systems of blood groups also affects boar sperm production (Table 4) [26].

Table 4 – Effect of Large White boar heterozygosity on sperm quality

Blood group system	Homozygosity	Number of boars	Ejaculate volume, ml	Sperm concentration	
				In 1 ml, million	In ejaculate, billion
EAE	homozygotes	26	191,5±17,9	187,3±15,9	35,9±11,9
	heterozygotes	70	299,4±14,9***	191,1±8,5	57,7±3,5*
EAG	homozygotes	39	221,3±19,4	187,8±13,1	41,5±9,2
	heterozygotes	57	303,7±16,5**	199,5±9,2	61,4±6,1**

*Note: *- (P <0,05), ** - (P <0,01), ***(P <0,001) and further.*

According to the *EAE* and *EAG* systems, heterozygous boars significantly exceeded the homozygous boars in terms of the volume of ejaculate and spermatozoa concentration in it. Authors Goncharenko G.M. et al. [.27], Timofeev L.V., in own researches, obtained similar indicators for the superiority of ejaculate volume in Large White boars heterozygous according to the EAG system. And the author Shkatov M.A. received a similar result in boars of the Duroc and Landrace breeds [28].

3.3 Dynamics of the frequency of occurrence of pig blood groups during absorption crossbreeding

To improve the pigs of the LW breed of Siberia in order to improve the quality of pork, animals of foreign selection were used, in particular the Yorkshire (Y) breed of Canadian selection. Analysis of the genetic structure by blood group showed that each generation has a specific frequency of genotypes of erythrocyte antigen (EA) loci of seven genetic systems (Table 5). We carried out this analysis in three breeds of pigs, such as the LW breed of the Novosibirsk type, the Y breed and their descendants of the first (F_1) and third (F_3) generations.

Table 5 – Frequency of blood genotypes of sows and boars Yorkshire, Large White breed and their crosses (X ± sx)

Systems	Genotype	Large White	Yorkshire	F_1	F_3
		n=97	n=26	n=31	n=349
A	*cp/-*	0,42±0,05	0,58±0,13	0,64±0,09*	0,51±0,03
	-/-	0,58±0,05	0,42±0,13	0,35±0,09*	0,49±0,03
B	*a/a*	1,00±0,00	0,92±0,07	0,88±0,06***	0,85±0,02***
	a/b	-	0,08±0,07	0,12±0,06	0,15±0,02
D	*a/b*	0,70±0,05	0,50±0,13	0,39±0,09**	0,44±0,03***
	b/b	0,30±0,05	0,50±0,13	0,61±0,09**	0,56±0,03***
E	*aeg/bdg*	0,13±0,03	-	0,10±0,05	0,05±0,01*
	aeg/bdf	0,03±0,02	0,03±0,07	0,03±0,03	0,05±0,01
	aeg/edg	0,08±0,03	-	-	0,10±0,02
	aeg/edf	0,04±0,02	0.07±0.08	-	0,04±0,01
	bdg/edg	0,32±0,05	0,26±0,12	0,23±0,07	0,18±0,02
	bdg/edf	0,08±0,03	0,61±0,13	0,64±0,09***	0,56±0,03***
	bdg/bdf	-	0,04±0,07	-	-
	edg/edg	0,11±0,03	-	-	0,02±0,01**
	edg/edf	0,20±0,04	-	-	0,01±0,00***
F	*a/a*	-	0,04±0,07	-	-
	a/b	0,04±0,02	0,08±0,08	0,03±0,03	0,04±0,01
	b/b	0,96±0,02	0,88±0,11	0,97±0,03	0,96±0,01
G	*a/a*	0,07±0,03	0,04±0,08	0,03±0,03	0,03±0,01
	a/b	0,64±0,05	0,27±0,09****)	0,52±0,09	0,51±0,03*
	b/b	0,29±0,05	0,69±0,09*****)	0,45±0,09	0,46±0,03**
L	*adhi/bcgi*	0,02±0,01	0,08±0,07	0,12±0,06	0,08±0,02**
	adhi/bdfi	0,05±0,02	-	-	0,01±0,01
	bcgi/bcgi	0,41±0,05	0,84±0,09	0,76±0,08***	0,78±0,03**

	bcgi/bdfi	0,52±0,05	0,08±0,07	0,12±0,06***	0,13±0,02*

Note: **, **, *** - P <0.05, P <0.01, P <0.001 - the reliability of the difference in the frequencies of the genotypes of pigs of the LW breed with Y and crossbred animals.*
- genotype not identified

Comparing the frequency of the *EA* genotypes of the A-blood system locus, we observed a difference in the distribution of the $EAA^{cp/-}$ and $EAA^{-/-}$ genotypes between the original breeding stock of the Large White breed and the F_1 generation of offspring. There is an increase in the $EAA^{cp/-}$ genotype frequency from 0.42 to 0.64 and decreased the $EAA^{-/-}$ genotype from 0.58 to 0.35.

The carriers of the $B^{a/a}$ genotypes of the *EAB* locus in the group of sows of the LW breed turned out to be 100%, in animals Y- 0.92-0.93. In the first and third generations, it decreased to 0.88–0.85. The $B^{a/b}$ genotype - the *EAB* blood system was absent in the LW breed, but we detected it in Y boars and sows and their offspring (F_1, F_3), its frequency increases from 0.07 (Y) to 0.15 (F_3).

The frequency distribution of the $D^{a/b}$ and $D^{b/b}$ genotypes of the *EAD* locus in hybrids are intermediate between their frequency in the LW and Y breeds. Locus *EAE* is the most informative of the systems under consideration. The authors observed a wide distribution of the genotypes $E^{aeg/bdg}$, $E^{edg/edg}$, $E^{edg/edf}$ in sows of the LW breed, which we not detected in Y. However, in F_1 hybrids, genotypes $E^{aeg/bdg}$ and $E^{aeg/bdf}$ appear, and in F_3 hybrids, genotypes $E^{aeg/edg}$ and $E^{aeg/edf}$ also appear. The blood genotype $E^{bdg/edf}$ is more common (0.56-0.64) (P <0.001) in Y and offspring of the first and third generations than in sows of the LW breed - 0.08.

Yorkshire sows the heterozygous $F^{a/b}$ genotype of the *EAF* locus - blood system was detected with a frequency of 0.14, while in other breeding groups its frequency varied from 0.03 to 0.04. The authors found the homozygous $F^{b/b}$ genotype in LW sows and offspring F_1, F_3 with a frequency close to 0.96-0.97. We identified this $F^{b/b}$ genotype in boars of breed Y with a frequency of 1.00, which is higher than in LW. In hybrid pigs, the frequency of this genotype is intermediate. The frequencies of the homozygous $G^{b/b}$ genotype and the heterozygous $G^{a/b}$ locus *EAG* in the F_1 and F_3 hybrids are media between the LW and Y breeds, deviating towards Y. When comparing the frequencies *EAL* of the *L* locus of the pig blood system, we observed the $L^{bcgi/bdfi}$ genotype frequency in sows of the LW breed than the $L^{bcgi/bcgi}$ genotype in breed Y (P <0.001). In the offspring of F_1, F_3, the frequency of these genotypes is intermediate, approaching Y's breed.

Immunogenetic analysis of the distribution of pig blood genotypes made it possible to reveal the degree of difference in frequencies in the offspring of the first and third generations with LW and Y breeds and to determine the trend of their frequency in the course of absorptive crossing.

The authors calculated the indices of immunogenetic similarity (r) between breeds and crossbred groups of animals according to the frequency of the genotypes of blood groups The smallest genetic similarity was found between LW pigs of breed Y and F_3 (from 0.74 to 0.72). Indices of immunogenetic similarity allow us to conclude that the gene pool of the resulting population of F_3 offspring deviates towards the improving Yorkshire breed.

Thus, pigs of the original breeds LW and Y differ significantly in the frequency of genotypes of erythrocyte blood antigens. In hybrids of the first - third generations, all studied systems' antigens' frequency is intermediate, deviating as absorptive crossing towards the Y breed. Indices of genetic similarity confirm this pattern. Hybrid F_1 and F_3 inherited genotypes of the EAE system from the LW breed's pigs: $E^{aeg/bdg}$, $E^{aeg/edg}$, $E^{aeg/edf}$, $E^{edg/edg}$, $E^{edg/edf}$, which breed Y did not have. Perhaps they are playing a specific role in the life support systems or productivity of animals.

3.4 Polymorphic systems of porcine erythrocyte enzymes

Four polymorphic biochemical systems of blood erythrocytes have been studied: esterase *D* (*EsD*), glucose phosphate isomerase (*Gpi)*, 6-phosphogluconate dehydrogenase (*6Pgd*), adenosine deaminase (*Ada*) [29], [30].

There was no relationship between the genotype for polymorphic biochemical traits and meat and fattening traits in most cases (Table 6). However, in the LW population, a significant relationship between the EsD genotype and the fat thickness was found (animals with a heterozygous $EsD^{a\alpha}$ genotype are characterized by a smaller fat thickness); LW is characterized by a relationship between the genotype according to the Ada system and the growth rate. (animals with the Ada^{AA} genotype reach a weight of 100 kg on average eight days faster than animals with the Ada^{BB} genotype). Animals with genotype Ada^{00} have the most intensely colored meat.

Table 6 – Relationship of genotypes of polymorphic biochemical systems with economically useful traits in pigs of the LW breed

Traits	System	Genotype			
		AA	*AB*	*BB*	*00*
Thickness back fat, cm	*EsD*	3.50±0,03 n=78	3.30±0,02*** n=88	3.70±0,04 n=39	-
Meat colour, score	*Gpi*	3.07±0,06 n=58	3.33±0,06** n=93	3.36±0,05 n=53	-
Ham weight, kg	*Gpi*	10.40±0,03 n=54	10.60±0,04*** n=86	10.40±0,03 n=85	-

Meat colour, score	*Ada*	2.73±0,04 n=131	2.86±0,03* n=21	2.78±0,10 n=18	2.98+0,09* n=51
Age at which live weight is 100 kg	*Ada*	169.0± 0,9 n=137	174.0±2,1* n=22	176.6±2,7** n=18	171.1±1,7 n=51

Note: ** difference between genotypes EsD^{AA}, Gpi^{AA} , Ada^{AA} and alternative genotypes of the same systems is significant at * P <0.05, ** P <0.01, *** P <0.001 *, n - number of animals.*

Thus, the research shows that the adenosine deaminase system, which is polymorphic in all studied populations of wild and domestic pigs, has the most significant degree of variability.

The use of immunogenetic and biochemical markers makes it possible to monitor the correspondence of the genotypes of the offspring to the genotypes of their best ancestors and, on this basis, choose the successor of the lineage, related group, family. For example, the boar Samson 7053 is the best in the herd in terms of many offspring productivity indicators. The age at which a weight of 100 kg was reached was 167 days, the consumption of feed per 1 kg of gain was 3.67 conventional feed units, the half-carcass length was 96.6 cm, the back fat was 30 mm thick, and the weight of the rear third of the half-carcass was 10.9 kg. The following allelic variants represented this boar's genotype: *$EAA^{cp/-}$; $EAE^{edg/edf}$; $EAG^{a/b}$; $EAB^{a/b}$; $EAD^{a/b}$; EAL^{adfb} $EAK^{ac/-}$; $EAH^{a/-}$; EsD^{AA} , Ada^{AA}; $6Pgd^{AB}$; Gpi^{BB}* .

3.5 DNA markers and their relationship with reproductive qualities and stress resistance in animals

As genetic markers allowing to improve the indicators of milk production of sows associated with reproductive qualities, we used: genes of the ryanodine receptor *(RYR-1),* the gene for the estrogen receptor *(ESR)*, the gene related to the susceptibility of piglets to diarrhoea *(ECR F18/FUT1),* the protein gene binding fatty acids *(H-FABP) (FABP-D),* leptin *(LEP),* melanocortin receptor gene *(MC4R)* [31], [32], [33].

The frequency of genotypes' occurrence for the *ESR* gene of sows was: *AA* - 21%, *AB* - 19%, *BB* - 60%. In the research of Tolokontsev A.I. [34] the frequency of these genotypes in the Yorkshire breed of Canadian selection was 19, respectively; 52 and 29%, in the L breed 94; 6 and 0%, in the D breed only the homozygous ESR^{AA} genotype was present.

Homozygous ESR^{AA} sows had less, in comparison with heterozygous ESR^{AG}, nest weight at birth by 1.2 kg, milking capacity (weight litter in 21 day) by 6.9 kg, litter weight at two months, by 14 kg, and less, respectively, by 0.5; 4.4; 17.8 and 0.8 kg, compared with homozygous ESR^{GG} (Table 7).

Table 7 – Large White sows' productivity considers the genotypes of genes *ESR* and *H-FABP* (for two or more farrows)

Indicator	Genotype *ESR*		
	ESR^{AA}	ESR^{AG}	ESR^{GG}
Number of registered farrowing	59	52	169
Number of piglets at birth, individuals	11.1±0.37	11.3±0.26	11.3±0.21
Litter weight at birth, kg	11.9±0.39	13.1±0.43*	12.4±0.24
Milking capacity, kg (weight litter in 21 days)	45.9±1.64	52.8±1.21***	50.3±0.78*
The number of piglets at weaning, individuals	8.9±0.23	9.9±0.20**	10.0±0.12***
Litter weight in 2 months, kg	157.3±5.97	171.3±5.55	175.1±3.18**
Body weight of one pig in 2 months, kg	16.5±0.77	17.3±0.39	16.6±0.35
Indicator	Genotype *H-FABP*		
	$H\text{-}FABP^{DD}$	$H\text{-}FABP^{Dd}$	$H\text{-}FABP^{dd}$
Number of registered farrowing	62	156	61
Number of piglets at birth, individuals	11.5±0.29	11.0±0.21	11.7±0.34
Litter weight at birth, kg	12.2±0.33	12.5±0.25	12.2±0.42
Milking capacity, kg (weight litter in 21 days)	47.6±1.40	51.0±0.86*	48.9±1.26
The number of piglets at weaning, individuals	9.6±0.23	9.7±0.13	9.9±0.21

Litter weight in 2 months, kg	166.2±5.10	174.1±3.42	165.1±5.50
Bodyweight of one pig in 2 months, kg	17.5±0.43	18.0±0.29*	16.7±0.44

*Note: * the difference in productivity indicators between ESR^{AA} and $H\text{-}FABP^{DD}$ genotypes and alternative genotypes, significant at * P <0.05, ** P <0.01, *** P <0.001 **

The works of Kostyunina O.V. evidence the relationship of the *ESR* gene genotype with the milk production of sows and the number of piglets at 21 days of age. and others [35], [36]. In Konovalova E.N. et al., shows [37] that piglets with the ECR^{GG} genotype are more susceptible to diarrhoea than ECR^{AA} genotypes. In heterozygous $H\text{-}FABP^{Dd}$ sows, the nest's weight at two months of age was higher than in the homozygous of both alternative genotypes by 7.9 - 9.0 kg, the weight of the piglet - by 0.5 - 1.3 kg.

The authors used the same genetic markers to study their relationship with pigs' stress resistance during the fattening period (Table 8).

Table 8 – Frequency of occurrence of genotypes of DNA markers and average daily gain (gram) depends on animals' stress resistance

DNA marker Genotype	Stress resilience					
	Sustainable n=95			Sensitive n=77		
	Frequency	Average daily gain, g		Frequency	Average daily growth, g	
		Ten days after weaning	For the growing period		Ten days after weaning	For the growing period
$H\text{-}FABP^{HH}$	0.26±0.05	318±10	553±17	0.43±0.06*	165±10	503±18
$H\text{-}FABP^{Hh}$	0.43±0.05	297 ±7	414±19***	0.36±0.05	139±13	369±15***
$H\text{-}FABP^{hh}$	0.31±0.05	294±17	472±16***	0.21±0.05	82±20	369±24***
$H\text{-}FABP^{DD}$	0.16±0.04	309±7	593±23	0.21±0.05	191±9	544±20
$H\text{-}FABP^{Dd}$	0.78±0.05	300±8	436±12**	0.53±0.06***	124±12	358±14***
$H\text{-}FABP^{dd}$	0.30±0.05	302±17	502±18**	0.26±0.05	126±16	463±19**
$MC4R^{AA}$	0.21±0.04	290±13	484±15	0.16±0.04	162±22	430±22
$MC4R^{AG}$	0.47±0.05	297±9	486±22	0.71±0.05***	133±10	443±19
$MC4R^{GG}$	0.32±0.05	315±12	474±19	0.13±0.04**	142±23	421±31
LEP^{TT}	0.80±0.06	302±12	519±18	0.66±0.08	148±14	513±20
LEP^{CC}	-	-	-	0.11±0.05	167±27	-
LEP^{TC}	0.20±0.06	257±22	504±34	0.23±0.07	123±32	426±26**
ECR^{AA}	0.14±0.04	308±22	485±33	0.06±0.03	136±28	424±34
ECR^{AG}	0.30±0.05	289±11	487±23	0.43±0.06	117±15	423±20
ECR^{GG}	0.56±0.05	307±9	478±16	0.51±0.06	157±9	449±22
$RYR\text{-}1^{NN}$	0.60±0.05	306±9	422±21	0.99±0.01***	133±8	438±15
$RYR\text{-}1^{Nn}$	0.40±0.05	296±12	517±17***	0.01±0.01***	100±0.0	444±0.0
$RYR\text{-}1^{nn}$	-	-	-	-	-	-

*Note: * the difference between stress resistance and stress resistance in terms of frequency and average daily gain, respectively, is significant at –0.05; ** P<0.01; *** 0.001*

The criterion for dividing piglets into groups of stress-resistant and stress-sensitive was the method proposed by Kovalenko V.A., which he called the “weaning crisis” method. It consists of assessing the average daily gain of piglets in the first ten days immediately after weaning. Piglets that showed growth over this period above average (within each group) were classified as stress-resistant, below average - as stress-sensitive [38].

Since the selection of pigs for meat productivity and meat quality by traditional methods is difficult due to the low coefficient of heritability (h^2) of these traits, we used the genes of the fatty acid-binding protein family *H-FABP* as candidates for genetic markers.

The authors found the direct relationship between the $H\text{-}FABP^{HH}$ and $H\text{-}FABP^{DD}$ genotypes' presence and the better growth rate of pigs during the rearing period (Table 8). Carriers of homozygous dominant genotypes of the $H\text{-}FABP^{HH}$ system are significantly superior ($P<0.001$) both to carriers of recessive homozygotes $H\text{-}FABP^{hh}$ and heterozygotes $H\text{-}FABP^{Hh}$.

Moreover, this pattern is observed both among stress-resistant and - among stress-sensitive individuals. The same picture is kept in the allele $H\text{-}FABP^{D}$, where carriers of dominant homozygotes $H\text{-}FABP^{DD}$ were significantly better in average daily gain. It should be noted that during the period of determination of stress sensitivity according to the "weaning crisis" method, that is the growth of piglets for ten days after weaning, no difference in the average daily gain during this period was observed between the different genotypes of these two systems *H-FABP* The difference manifested itself later, that is, during the period of rearing young pigs.

We found a difference in the frequency of *MC4R* occurrence between stress-resistant and stress-sensitive genotypes. In stress-sensitive animals, the heterozygous $MC4R^{AG}$ genotype frequency is 0.71 versus 0.47 in stress-resistant animals ($P<0.01$). The number of $MC4R^{GG}$ homozygotes in stress-sensitive animals is less, which is associated with the growth rate. The relationship of the *MC4R* genotypes with the age at which live weight reaches 100 kg and the average daily gain of fattening pigs is confirmed by the work of Kostyunina O.V. at al. [36].

A high frequency of occurrence of the desired *TT* genotype of the LEP^{TT} gene (66-80%), responsible for thinner back fat, was revealed in all breeds combinations. In the leptin system (*LEP*), the lowest gain was shown by stress-sensitive heterozygous LEP^{TC} genotypes ($P<0.01$).

A transition to genome-wide DNA sequencing methods is currently underway to increase the effici ency of the determination of gene and regulatory DNA polymorphisms in genomes, allowing to increase the genetic potential of pigs' productivity and to use them as genetic markers [39], [40], [41], [42]. Thus, in our works, it was found that upon domestication of a pig, there was a change in the frequency of SNP genotypes in the 3-region of the *LTB* gene. Apparently, this SNP can be associated with different levels of mRNA expression of the *LTB* gene. Bioinformatic analysis showed that the region of the 3'-region of the *LTB* gene surrounding the SNP is conservative. A nucleotide substitution at a polymorphic position can affect potential binding sites for transcription factors. Five types of factor binding sites (*Brn-2, AP-1, RFX1, ISRE, USF*) have been identified. According to authors estimates, the site of the *Brn-2* factor was recognized with the least overprediction error. From a biological point of view, the most interesting sites for further research are the *RFX1* and *ISRE* binding sites. It is also possible that the rs340283541 polymorphism is in linkage disequilibrium with another, as yet unknown, functionally significant mutation in the *LTB* gene [43].

Conclusion

To improve genetic programs to improve the productive qualities of pigs, to create new breeding forms in the special climatic conditions of Siberia, along with the use of statistical methods, the study and use of genetic markers was carried out to speed up the breeding process. An assessment of five breeds of pigs was carried out, according to genetic markers of biochemical and productive qualities. This was carried out in the process of improving and creating new types in the LW and K breeds in order to establish the genetic factors of adaptation to the conditions of Siberia, to the conditions of industrial technology. At the same time, the world gene pool of pigs was used in breeding programs, when assessing the effectiveness of crossing different breeds, studying the adaptation of animals to stressful conditions. Connections of genetic markers, such as blood groups, erythrocyte enzymes, DNA markers, were established in terms of their frequency of occurrence, degree of heterozygosity, chemical composition, quality indicators of production, economically useful and adaptive characteristics of pigs. This made it possible to use them in the improvement of these breeds, in the breeding of new types of animals [44], [45], corresponding to the consumer properties of people.

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Conflict of Interest

None declared.

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