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THE STUDY OF EFFECT OF GENOTYPES FOR DNA MARKER ON REPRODUCTIVE QUALITIES OF SOWS OF LARGE WHITE AND LANDRACE BREEDS

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Abstract

The genetic progress by low-inherited reproduction traits in pigs can be increased by integrating into breeding programs the DNA markers, which are associated with quantitative trait loci (QTL) of reproductive qualities (marker selection, MAS). The aim of the present study was to assess the effect of DNA markers *IGF2* (insulin-like growth factor 2), *ECR F18/FUT1* (*Escherichia coli* F18 receptor), *ESR* (estrogen receptor) and *MUC4* (mucin 4) on the fertility traits of Large White and Landrace sows. The studied traits included the total number of piglets born per litter (TNB); number of piglets born alive per litter (NBA); average birth weight (BW) and adjusted birth weight (BW_{adj}); weight at weaning at 21 days (WW) and adjusted weight at weaning at 21 days (WW_{adj}). The genotypes frequencies of the analyzed markers were determined. Besides we identified significant deviations of the genotype frequencies from the population equilibrium for Large White breed by the *IGF2* gene ($p < 0.01$) and Landrace breed by the *IGF*2 ($p < 0.01$), *ECR F18/FUT1* ($p < 0.01$) and *MUC4* ($p < 0.001$). The homozygosity coefficient according to Robertson (Ca) was the highest for genotypes for *IGF2* and *ECR F18/FUT1*. The values of this parameters reached 0.76 and 0.65 for Large White breed against 0.60 and 0.72 for Landrace breed, respectively. We calculated the heritability coefficients for the analyzed traits, which were 0.165-0.179 for TNB, 0.100-0.155 for NBA, 0.232-0.338 for BW, and 0.010-0.115 for WW. Based on the developed equations, breeding values of pigs were determined using the BLUP AM method. The *IGF2* marker showed a significant effect on the weight at weaning for Landrace sows (PHE_{WW}, PHE_{WWadj}, EBV_{WW}); individuals with genotypes *AA* and *AG* were the best. The genotype for *ECR F18/FUT1* significantly influenced the phenotype and breeding value of sows for the number of piglets born and for the birth weight of piglets. Sows with the *AA* genotype were characterized by a lower number of piglets born (by 8.0-8.5 %), and by a higher average birth weight (by 2.0-3.0 %). The significant effects of the *ESR* on TNB and NBA and on EBV values for birth weight were revealed: the sows of both breeds with *CC* genotype for *ESR* were characterized by highest average piglet weight at birth. We found the significant effect of *MUC4* on birth weight of piglets for both breeds. Sows with *CC* and *CG* genotypes were superior comparing to individuals, which are homozygous for the *G* allele. Thus, using the marker assisted selection along with traditional methods for assessing the genetic potential of pigs (BLUP AM) will significantly improve the efficiency of breeding measures on the fertility traits.

Keywords: pigs, Large White breed, Landrace, *IGF2, ECR F18/FUT1, ESR, MUC4*, linear regression, fertility traits, estimated breeding values, marker assisted selection

Improving reproduction traits is one of the key goals of improving ma-

ternal breeds [1]. However, the low inheritance, significant variability, and sex-limited manifestation of such reproduction traits in sows as prolificacy, the number and weight of live piglets upon birth and at weaning, and the milk yield [2] limit the effectiveness of traditional breeding. Thus, the heritability coefficients of fertility traits in Large White sows vary from 0.02 to 0.21 [3]. In this regard, it would be interesting to use DNA markers associated with quantitative trait loci (QTLs) of reproduction traits in the selection programs, i.e. to perform the so-called marker-assisted selection, or MAS [4, 5]. MAS facilitates reproducing the existing genetic diversity in the breeding populations and can be used to improve the desirable traits [6].

ESR was one of the first DNA markers of reproduction traits (the number born alive) recommended for use in breeding programs [7]. The association of this marker with reproduction traits has been confirmed by numerous studies both abroad [8-10] and in Russia [11-13]. Such DNA markers as *ECR F18/FUT1* (*Escherichia coli F18/FUT1* receptor), the genetic variants whereof are associated with resistance to post-weaning diarrhea [14, 15], and *MUC4* (mucin 4) [16], the genetic variants whereof are associated with resistance to colibacteriosis [17, 18], do have an indirect effect on the reproduction traits of sows. Besides, today's genetic engineering programs for pigs seek to improve not only the reproduction traits but also the meat and feedlot productivity. This is where breeders apply a number of DNA markers, including the insulin-like growth factor 2 (*IGF2*) gene. Using *IGF2* is primarily related to its paternalistic properties [19], as well as its effects on pig meatiness [20-22].

One important part of integrating MAS in pig breeding programs is to study the possible antagonistic effects of DNA markers on various productive traits. Scientific literature presents very limited data on how the DNA markers of meat and feedlot traits could negatively affect the reproduction traits of sows, or how the markers of reproduction traits could affect the meat and feedlot productivity traits.

This paper is the first to analyze how a group of genetic markers could affect the determination of reproduction traits in Large White and Landrace sows of Russian reproduction. The results indicate that the *IGF2* gene does not significantly affect sow fertility. The contingency of *ECR F18/FUT1*, *ESR* and *MUC4* genes with the breeding value in terms of sow productivity has proven significant and confirmed the correlation of genetic and physiological mechanisms behind the reproduction traits of sows.

This paper seeks to evaluate how the DNA markers *IGF2*, *ECR F18/FUT1*, *ESR,* and *MUC4* affect the reproduction traits in Large White and Landrace sows.

Techniques. Studies were carried out in 2018 and 2019. Research data comprised the primary records of reproduction traits as observed in the first three litters of *Sus scrofa* Large White (n = 894, 2008 to 2018) and Landrace (n = 513, 2010 to 2018) sows at OOO Selection and Hybrid Center, Voronezh Region. The array of data for Large White sows (born of 66 boars and 291 sows) comprised 2,250 entries (2.52 litters per sow on average); for Landrace sows (born of 63 boars and 503 sows), the data contained 1,360 entries (2.65 litters per sow on average). The authors analyzed the absolute values and adjusted phenotypic indices, as well as the estimated breeding value (EBV) in terms of the total number born (TNB) per litter, the number born alive (NBA) per litter, the average birth weight (BW), the adjusted birth weight (BW_{adj}), sow milk yield (weight at weaning, Day 21) (WW), and adjusted sow milk yield (adjusted weight at weaning, Day 21) (WW_{adj}). Phenotypic data on the studied traits followed a normal distribution.

Adjusted BW and WW phenotypic values were calculated by estimating the significance of the paratypic factor effects per Fisher's *F*-test by linear regression equations. The adjusting factors, presumably influencing the variability of the analyzed traits, included the number born alive, the number after transfer, the number at weaning (NW), and the perinatal and lactation period (PLP). When computing the adjusted milk yield, the researchers considered the factor NW in connection with the more significant coefficient of determination, which characterizes the linearity of trait dependency on the analyzed factor. How factors affected the variability of traits was evaluated by multi-factor analysis of variance (ANOVA).

Linear regression equations for the two breeds for the adjusted BW trait (R^2 is the coefficient of determination):

adjusting factor	Large White pig	Landrace
NBA	$y = -0.03x + 1.83$, $R^2 = 0.23$	$y = -0.03x + 1.84$, $R^2 = 0.19$

Linear regression equations for the two breeds for the adjusted WW trait:

adjusting factor	Large White pig	Landrace
NAT	$y = 2.01x + 51.22$, $R^2 = 0.14$	$y = 1.11x + 60.55$, $R^2 = 0.054$
NW	$y = 7.12x + 0.45$, $R^2 = 0.55$	$y = 6.60x + 5.19$, $R^2 = 0.48$
PLP	$y = 2.89x + 4.41$, $R^2 = 0.42$	$y = 2.46x + 13.22$, $R^2 = 0.41$

Genomic DNA was isolated from tissue samples (earmarks) using a DNA-Extran-2 kit by OOO NPF Sintol, Russia. To evaluate the quality and measure the concentration of DNA, a Qubit 2.0 fluorimeter (Invitrogen/Life Technologies, USA) and a NanoDrop8000 spectrophotometer (Thermo Fisher Scientific, USA) were used.

Genotypes by the DNA marker *IGF2* (G→A at 16144, Accession No. AY242112, GenBank, https://www.ncbi.nlm.nih.gov/genbank/) were determined as described by Melnikova et al. [22]. Genotypes by the DNA Markers *ESR* (GG→AT at 65-68, Accession No. HF947272.1, No. AY242112), *ECR* (G→A at 915, Accession No. AY242112), *ECR* (G→A at 915, Accession No. DQ848681) were detected by multiplexed PCR with fluorescent amplification-based specific hybridization (FLASH) on the endpoint using a Fluidigm EP1 high-performance genotyping system (Fluidigm Corporation, USA).

The authors have developed and tested models that evaluate how DNA marker genotypes could affect the variability of absolute and adjusted phenotypic pig reproduction indices; the models use least square means (LSM) and the following equation:

$$y = \mu + YMCG + b_1Par + G_l + e, \quad (1)$$

where y are the considered phenotypic indices of the traits TNB and NBA, μ is the population mean, YMCG is the factor of temporary environmental conditions (year, month, and comparison group), b_1Par is the coefficient of regression and the regression factor (sow litter No.), G_l is the genotype effect for each of the markers *IGF2, ECR F18/FUT1, ESR, MUC4*, e is the residual (unaccounted for) model effects. The factor YMCG must be made part of the model equation as this factor significantly affects the variability of all the analyzed traits in both breeds (*F*-test returns significance at $p < 0.01$), which proves that paratypic effects significantly influence the variability of reproduction traits in pigs. White Large sows were grouped into 115 groups by the factor YMCG (19.6 entries per group on average); Landrace sows were grouped into 163 groups (8.3 entries per group).

The breeding value (EBV) was estimated by the BLUP Animal Model, which takes into accounts kinships and uses an additive kinship matrix.

The model contained the following equations:

$$\text{for TNB and NBA: } y = \mu + YMCG + b_1Par + animal + e, \quad (2)$$

for BW: $y = \mu + YMCG + b_1Par + b_2NBA + animal + e$, (3)
for WW: $y = \mu + YMCG + b_1Par + b_2PLP + animal + e$, (4)

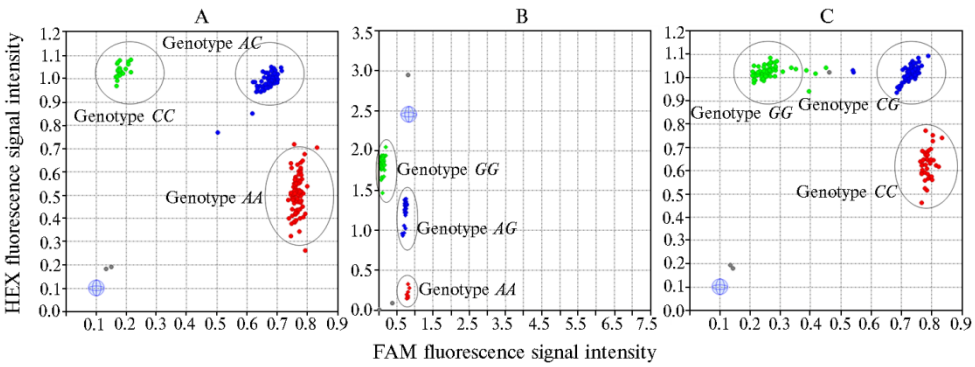
where y is the absolute phenotypic indices, μ is the population mean for TNB and NBA (2), BW (3), WW (4), YMCG is the factor of temporary environmental conditions (year, month, and comparison group), b_1Par is the coefficient of regression and regression factor (sow litter No.), b_2NBA is the coefficient of regression and regression factor (the number born alive), b_2PLP is the coefficient of regression and regression factor (perinatal and lactation period), animal is the animal's additive genetic effect, e is the residual (unaccounted for) model effects.

Heritability coefficients were calculated by restricted maximum likelihood (REML): $h^2 = varA/(varA + varE)$, where varA is the variance of the additive effects of the entire animal genotype, varE is the variance of the residual (unaccounted for) model effects.

ANOVA and LSM calculations were run in STATISTICA 10 (StatSoft, USA). For EBV and ANOVA calculations, BLUPF90 software was used [23]. To characterize the input data arrays, the researchers determined the arithmetic mean of the phenotype in terms of the trait in the sample (μ), the error of the mean ($\pm m_\mu$), and the standard deviation of the trait in the sample (σ).

Results. The figure below shows the results of genotype detection.

Large White sows had 3% to 7% greater values than their Landrace counterparts by all the traits except BW. Attention should be paid to the phenotypic standard deviations, which indicated that the studied populations were promising in terms of genetic progress in fertility. Thus, the observable variability of the analyzed traits indicated that the bred population was likely to demonstrate the theoretical effects of selection, see Table 1. The inheritance of the analyzed traits did not vary too much: 0.115 to 0.232 for Large White sows and 0.010 to 0.338 for Landrace sows. Heritability coefficients were the highest for birth weight ($h^2 = 0.232$ for Large White piglets and $h^2 = 0.338$ for Landrace piglets) due to lower phenotypic variability, which in its turn was due to taking into account the effects of NBA, see Table 1.



Detection of Large White and Landrace pigs (*Sus scrofa*) by the DNA markers *ESR* (A), ***ECR F18/FUT1*** (B) **and *MUC4*** (C)**.** Method: **PCR,** FLASH**,** endpoint detection (Fluidigm EP1, Fluidigm Corporation, USA) (OOO Selection and Hybrid Center, Voronezh Region, 2017-2018).

The population was χ^2-tested to find significant deviations of genotypic occurrences from the population equilibrium for Large White sows in terms of the *IGF2* ($p < 0.01$) gene, as well as for Landrace sows in terms of the *IGF2* ($p < 0.01$), *ECR F18/FUT1* ($p < 0.01$), and *MUC4* ($p < 0.001$) genes, see Table 2. The Robertson homozygosity coefficient (Ca) was the highest for *IGF2* and *ECR F18/FUT1* genotypes: 0.76 and 0.65 for Large White sows vs 0.60 and 0.72 for Landrace sows. At the same time, the distribution of allele frequencies for *IGF2* and *ESR* genes differed radically in the studied samples, which might indicate

breed-specific phenotype manifestations.

1. Reproduction traits in the studied population of Large White and Landrace pigs (*Sus scrofa*) (OOO Selection and Hybrid Center, Voronezh Region, 2017-2018)

Breed	Trait	Values				
		n, sows	*n*, litters	$\mu \pm m_\mu$	σ	h^2
Large White	TNB	894	2250	14.6±0.1	4.1	0.179
	NBA			13.5±0.1	3.8	0.155
	BW			1.45±0.01	0.22	0.232
	WW			76.6±0.3	13.5	0.115
Landrace	TNB	513	1360	13.7±0.1	3.5	0.165
	NBA			12.6±0.1	3.2	0.100
	BW			1.45±0.01	0.23	0.338
	WW			74.6±0.3	12.6	0.010

N o t e. TNB is the total number born; NBA is the number born alive (both values per litter); BW is the average birth weight; WW is the weight at weaning, Day 21; μ is the phenotypic arithmetic mean of the trait in the sample, m_μ is error of the mean, σ is the standard deviation of the trait in the sample, h^2 is the trait heritability coefficient.

2. Distribution of genotype and allele frequencies for *IGF2*, *ECR F18/FUT1*, *ESR*, and *MUC4* genes in Large White and Landrace sows (*Sus scrofa*) ($\mu \pm m_\mu$, OOO Selection and Hybrid Center, Voronezh Region, 2017-2018)

DNA marker	GFD	Genotype			Allele frequency		χ^2	Ca
		11	12	22	1	2		
				Large White				
IGF2	O	0.73±0.01	0.26±0.01	0.01±0.00	0.86±0.01	0.14±0.01	10.7	0.76
	E	0.74	0.24	0.02				
ECR F18/FUT1	O	0.06±0.00	0.34±0.01	0.60±0.01	0.23±0.01	0.77±0.01	2.7	0.65
	E	0.05	0.35	0.60				
ESR	O	0.06±0.00	0.36±0.01	0.58±0.01	0.24±0.01	0.76±0.01	0.0	0.64
	E	0.06	0.36	0.58				
MUC4	O	0.39±0.01	0.46±0.01	0.15±0.01	0.62±0.01	0.38±0.01	1.1	0.53
	E	0.39	0.47	0.14				
				Landrace				
IGF2	O	0.06±0.01	0.44±0.01	0.50±0.01	0.28±0.01	0.72±0.01	7.6	0.60
	E	0.08	0.40	0.52				
ECR F18/FUT1	O	0.02±0.00	0.30±0.01	0.68±0.01	0.17±0.01	0.73±0.01	8.3	0.72
	E	0.03	0.28	0.69				
ESR	O	0.56±0.01	0.36±0.01	0.08±0.01	0.74±0.01	0.26±0.01	3.6	0.62
	E	0.55	0.38	0.07				
MUC4	O	0.38±0.01	0.53±0.01	0.09±0.01	0.64±0.01	0.36±0.01	28.7	0.54
	E	0.41	0.46	0.13				

N o t e. GFD stands for genotype frequency distribution; O stands for observed; E stands for expected. Alleles 1 and 2, and genotypes 11, 12, 22 correspond to alleles *A, G* and genotypes *AA, AG, GG* for *IGF2* and *ECR F18/FUT1*; to alleles *A, C* and genotypes *AA, AC, CC* for *ESR*; and to alleles *C, G* and genotypes *CC, CG, GG* for *MUC4*.

3. Significance of the marker genotypes of Large White and Landrace sows (*Sus scrofa*) for the variability of phenotypic and genetic reproduction traits (OOO Selection and Hybrid Center, Voronezh Region, 2017-2018)

Index	*F*-test							
	Large White (n = 894)				Landrace (n = 513)			
	IGF2	*ECR F18*	*ESR*	*MUC4*	*IGF2*	*ECR F18*	*ESR*	*MUC4*
PHE_{TNB}	0.24	5.79*	6.27*	0.43	1.78	3.08	0.54	0.49
PHE_{NBA}	0.16	10.79*	6.80*	0.23	0.78	1.24	1.85	0.46
PHE_{BW}	1.13	4.28*	2.62	8.75*	0.72	2.10	2.00	3.21*
PHE_{BWadi}	1.44	2.79	1.20	12.59*	1.51	2.63	2.44	4.75*
PHE_{WW}	1.18	0.21	1.84	0.36	6.01*	0.21	0.68	1.47
PHE_{WWadi}	0.30	0.30	1.80	1.00	5.31*	1.14	0.10	0.30
EBV_{TNB}	1.04	2.95	5.30*	3.70*	1.65	3.01	0.87	0.44
EBV_{NBA}	0.02	8.96*	7.90*	4.93*	0.85	0.47	4.51*	0.02
EBV_{BW}	1.44	3.46*	10.90*	22.84*	1.00	2.80	10.69*	3.19*
EBV_{WW}	2.05	3.58*	0.32	2.43	14.99*	2.86	2.30	2.76

N o t e. PHE stands for the phenotypic index, EBV stands for the estimated breeding value; TNB stands for the total number born; NBA stands for the number born alive (both per litter); BW stands for the birth weight, BW_{adj} stands for the mean adjusted birth weight, WW stands for milk yield (weight at weaning, Day 21), WW_{adj} stands for adjusted milk yield (weight at weaning, Day 21).
* The *F*-value is significant at $p < 0.05$ for the corresponding number of degrees of freedom.

Testing the significance of genetic factors (*F*-testing) for each of the ana-

lyzed markers identified marker genotypes, each of which significantly affected the phenotypic manifestations of reproduction traits as well as the variability of EBV, see Table 3.

Thus, F-test returned significance for the marker *IGF2* when applied to the phenotypic and genetic milk-yield indices (PHE_{WW}, PHE_{WWadj}, EBV_{WW}) of Landrace sows. The authors believe that this correlation could be due to the better milk yield of sows featuring the preferable genotype in terms of this marker, see Table 4. Earlier studies [22] found that specimens featuring *IGF2* alleles *A* had the thinnest speck and matured faster. At the same time, sows of this genotype had better milk yield than their alternative-allele heterozygous and homozygous counterparts. Notably, the milk yield measured as the piglet weight at weaning (Day 21) could be affected by the piglet growth rate, i.e. animals carrying the desirable alleles of this marker had greater growth rate, resulting in greater weight at weaning. No significant difference in this marker was identified for Large White sows.

4. Phenotypic means of the studied traits in Large White and Landrace sows (*Sus scrofa*) as a function of marker genotypes ($\mu \pm m_\mu$, OOO Selection and Hybrid Center, Voronezh Region, 2017-2018)

Marker genotype		*n*, farrows	Mean phenotypic indices (LS) for traits					
			TNB	NBA	BW	BW_{adj}	WW	WW_{adj}
Large White (*n* = 2250 farrows)								
IGF2	*AA*	1649	14.9±0.2	13.6±0.1	1.47±0.01	1.46±0.01	76.8±0.5	60.2±0.1
	AG	576	14.8±0.2	13.7±0.2	1.47±0.01	1.46±0.01	76.4±0.7	60.2±0.1
	GG	25	15.2±0.8	13.7±0.8	1.40±0.05	1.39±0.04	73.2±2.6	59.9±0.4
ECR F18/FUT1	*AA*	128	13.8±0.4*	12.2±0.3*	1.50±0.02*	1.45±0.02	76.5±1.2	60.3±0.2
	AG	759	15.0±0.2	13.7±0.2	1.45±0.01	1.44±0.01	76.8±0.6	60.2±0.1
	GG	1363	15.0±0.2	13.8±0.2	1.47±0.01	1.47±0.01	76.5±0.5	60.2±0.1
ESR	*AA*	129	14.7±0.4	13.4±0.3	1.44±0.02	1.42±0.01	75.0±1.2	60.3±0.2
	AC	817	14.6±0.2	13.3±0.2	1.48±0.01	1.46±0.01	77.1±0.6	60.2±0.1
	CC	1304	15.2±0.2*	13.9±0.2*	1.45±0.01	1.45±0.01	76.6±0.5	60.1±0.1
MUC4	*CC*	884	14.9±0.2	13.6±0.2	1.49±0.01	1.48±0.01	75.9±0.6	60.2±0.1
	CG	1034	14.7±0.2	13.5±0.2	1.46±0.01	1.44±0.01	76.3±0.6	60.3±0.1
	GG	332	15.0±0.3	13.6±0.3	1.43±0.01*	1.41±0.01*	76.6±0.8	60.1±0.1
Landrace (*n* = 1360 farrows)								
IGF2	*AA*	87	14.0±0.4	13.0±0.4	1.51±0.03	1.51±0.02	79.5±1.5*	62.3±0.3*
	AG	591	14.0±0.2	12.8±0.2	1.46±0.01	1.46±0.01	75.4±0.7	61.8±0.1
	GG	682	13.6±0.1	12.6±0.2	1.47±0.01	1.46±0.01	74.1±0.7	61.5±0.1
ECR F18/FUT1	*AA*	23	14.3±0.8	13.0±0.7	1.46±0.05	1.46±0.04	73.6±2.7	61.0±0.6
	AG	407	14.2±0.2	12.9±0.2	1.44±0.01	1.44±0.01	75.1±0.8	61.7±0.2
	GG	930	13.7±0.2	12.6±0.2	1.48±0.01	1.47±0.01	75.3±0.6	61.7±0.1
ESR	*AA*	759	13.8±0.2	12.6±0.2	1.46±0.01	1.45±0.01	75.1±0.7	61.7±0.1
	AC	496	14.0±0.2	12.9±0.2	1.48±0.01	1.47±0.01	75.6±0.7	61.7±0.2
	CC	105	13.9±0.4	12.9±0.3	1.51±0.02	1.51±0.02	74.0±1.3	61.7±0.3
MUC4	*CC*	517	13.8±0.2	12.7±0.2	1.49±0.01	1.48±0.01	74.4±0.8	61.7±0.2
	CG	715	13.9±0.2	12.8±0.2	1.47±0.01	1.46±0.01	75.7±0.7	61.8±0.1
	GG	128	13.6±0.3	12.5±0.3	1.43±0.02*	1.42±0.02*	75.0±1.2	61.6±0.2

Note. TNB stands for the total number born; NBA stands for the number born alive (both per litter); BW stands for the birth weight, BW_{adj} stands for the mean adjusted birth weight, WW stands for milk yield (weight at weaning, Day 21), WW_{adj} stands for adjusted milk yield (weight at weaning, Day 21).
* Difference in relation to the alternative homozygous genotype group deemed significant at $p < 0.05$.

ECR F18/FUT1 genotype was found to significantly affect the phenotype in terms of the total number born, the mean birth weight, and the number born alive. The impact of the DNA marker on the genetic value of specimens was confirmed for such indices as prolificacy and mean birth weight. Thus, *AA* (*ECR F18/FUT1*) sows had significantly lower TNB per litter (8.0% to 8.5% negative), but the mean birth weight was significantly larger by 2.0% to 3.0% at $p < 0.05$. According to the mean estimated genetic value in terms of TNB and NBA, AA sows were significantly inferior to heterozygous and homozygous animals with the alternative allele ($X_{EBV(AA)} = -0.50$ and -0.55). This pattern was not confirmed in Landrace sows, as no significant difference in terms of these traits was identified between genotypes.

Results were ambiguous when it came to *ESR* effects on reproduction traits. In Large White sows, ESR genotype had a significant ($p < 0.05$) effect on TNB, NBA, as well as on EBV in terms of mean birth weight. *CC* sows had better phenotypic and genetic characteristics. *ESR* effects on the reproduction phenotype of Landrace sows were not identified; however, mean EBV in terms of TNB and NBA was significantly higher in heterozygous animals: $\bar{X}_{EBV(AC)} = +0.10$, whereas $\bar{X}_{EBV(CC)} = 0.00$ and $\bar{X}_{EBV(AA)} = -0.10$. *CC* sows were the best in terms of mean birth weight.

MUC4 genotypes proved to be significant factors of variability in terms of mean birth weight in both breeds; genotypic effects were significant for both phenotypic (absolute and adjusted) and genetic estimates ($p < 0.05$) *CC* and *CG* sows were superior to *G*-homozygous sows in terms of the absolute and adjusted phenotypic index of piglet birth weight (2.0% to 5.0% for Large White sows and 4.0% to 4.5% for Landrace sows). EBV was significantly higher in *CC* sows than in heterozygous or *GG* sows: $\bar{X}_{EBV(CC)} = +0.01$ for Large White sows, $\bar{X}_{EBV(CC)} = 0.00$ for Landrace sows at negative values in compared groups.

Earlier studies did not identify any effects of *IGF2* polymorphism on the reproductive traits of Large White sows; *ESR-CC* genotype positively correlated with meat and feedlot qualities [24]. Some papers devoted to finding the correlation of *ESR* variants with productivity traits demonstrated the superiority of allele *C* in Large White sows in terms of reproduction traits [25, 26], which is consistent with the authors' data.

ECR F18/FUT1 polymorphism is associated with resistance to colibacteriosis. Horak et al. [27] studied this polymorphism and reported a far lower prolificacy and TNB in black-motley *AA* sows. In turn, Bao et al. [28, 29] found that in terms of litter size, AA sows were superior to AG or GG sows of Duroc and Sutai pigs. This research has identified that AA carriers had greater TNB and NBA, which is consistent with the reports of Bao et al. Fontanesi et al. [30] studied *MUC4* polymorphism and found that allele *G* associated with susceptibility to ETEC (enterotoxigenic *Escherichia coli* K88) did speed up the maturation of Large White (P = 6.66E–04) and Landrace (P = 7.23E–12) pigs, indicating an antagonistic association of alleles in *MUC4* g.8227C>G in terms of growth and ETEC susceptibility. Bannikova [31] discovered the superiority of Large White pigs of CC genotype in terms of prolificacy; however, this research identified no significant correlation of this trait in either breed.

The obtained data have confirmed that some *IGF2*, *ECR F18/FUT1*, *ESR*, *MUC4* genotypes do affect the variability of phenotypic indices of pig reproduction traits and breeding value. *AG* and *GG* genotypes (*ECR F18/FUT1),* and *CC* genotype (*ESR*, White Large sows only) were the best in terms of prolificacy; *CC* and *CG* sows (*MUC4*, both breeds) had the best mean birth weight; *AA* Landrace sows (*IGF2*) had best milk yield. It should be noted, however, that animal fertility traits are largely attributable to paratypic factors (>90%) and the additive effects of a significant number of genes and their combinations that may both positively and negatively affect the biology of reproduction; any factor can turn out to be dominant in affecting the outcome. Besides, pig reproduction traits feature genetic correlations, including negative ones. For NBA and BW, $r_g = -0.33$. This complicates evaluating the effect of genetic markers on the manifestation of the analyzed traits in selecting animals for reproduction, as specimens that carry the desirable alleles of one marker are not guaranteed to have the desirable alleles of other markers.

Thus, it can be recommended to apply marker-assisted selection in combination with conventional BLUP AM methods to decide on whether to select a specimen for breeding or to cull it; this is applicable to sows and boars alike.

When selecting parental genotypes, data on the animals' genetics in terms of *IGF2*, *ECR F18/FUT1*, *ESR*, *MUC4* will help increase the occurrence rate of the desirable alleles and genotypes to improve the genetics of Large White and Landrace pigs in terms of fertility.

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