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THE EFFECT OF PARENTAL GENOTYPE AND PARITY NUMBER ON PIGS LITTER SIZE

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Abstract: The aim of this study was to investigate the effect of parental genotype and parity number on the litter size properties of sows (number of live born, stillborn and weaned piglets). The investigation was conducted on a farm in Vojvodina. The analysis included 65535 litters that originated from five genotypes of dams (sows with unknown origin, n = 20980; Yorkshire, n = 3189; Landrace, n = 22426; $F1_{(YxL)}$, n = 14251; $F1_{(LxY)}$, n = 4689) and five genotypes of sires (Yorkshire, n = 21641; Landrace, n = 26623; Pietrain, n = 485; Duroc, n = 13463; Hampshire, n = 3323). Based on the obtained results it can be concluded that the genotypes of the dams had statistically significant ($p<0.01$) influence on the observed litters properties. Landrace sows achieved the highest average number of born alive piglets (10.12) with a statistically significant difference ($p<0.01$) compared with sows of other genotypes. The observed effect of sire genotype on litter size properties was statistically significant ($p<0.01$), where the terminal genotypes were superior when it comes to the number of live born and weaned piglets. Regression analysis of dependence between parity and litter size recorded positive regression coefficients: number of live born (b = 0.007), stillborn (b = 0.09) and weaned piglets (b = 0.07). Influence of parity on the observed traits of litter size was highly statistically significant ($p<0.01$).

Key words: genotype, sire, dam, liter size, piglets

Introduction

The aim of contemporary pig production is to improve the most important economic traits. The most important economic trait in swine production represents reproductive traits such as litter size, litter weight at birth and survival rates of piglets to weaning. The reason for this is the fact that the annual productivity of sows depends solely on litter size and number of parity during the year. Annual productivity of sows and economic efficient of piglets production could be increased with increases of any of these parameters (*Vidović et al., 2012*). The objective of modern pig breeding is to exhaust the genetic potential in reproduction performance of sows regarding to litter size and number of weaned piglets per litter (*Stella et al., 2003*). Litter size is one of the most important reproductive traits which present a low heritable trait and the influence of environmental factors on its expression is significantly expressed, because it is necessary 8 to 10 generations of selection to increase litter size by one piglet (*Wähner and Brüssow, 2009*). Knowledge of parent genotype and genetic parameters of reproductive traits is an essential requirement in estimating the breeding value, selection, implementation and select the best method of breeding, because only in this way can the right to genetic improvement of the herd (*Irgang et al., 1994*). Litter size is a quantitative character of considerable complexity and improvement is likely to be slow since it is influenced to a large degree by environmental factors. The normal assumption is that the size of litter produced is primarily dependent on the female (*Roehe and Kennedy, 1993; Vidović, 2009*). The influence of the sire on litter size has been the subject of numerous studies (*Van der Lende et al., 1999; Klindt, 2003)*. Litter size at weaning is one of the most important traits in pig production. Direct selection for this trait is generally restricted in practice due to cross-fostering, which also makes it difficult to adequately estimate genetic parameters for litter size at weaning.

The aim of this study was to investigate the effect of parental genotype and parity number on the litter size properties of sows such as number of live born, stillborn and weaned piglets.

Materials and Methods

This paper analyses 65.535 pig litters, obtained by mating purebred Landrace and Yorkshire sows and F1 hybrid sows ($F1_{(Y\times L)}$ and $F1_{(L\times Y)}$) and sows with unknown origin, with Landrace and Yorkshire and terminal boars such as Pietrain, Duroc and Hampshire sire breeds. The animals originate from one commercial farm in Vojvodina, which has the entire cycle of production, where the collected data between January 2000 and December 2009 was analyzed. During data processing, all sows were distributed in the order of farrowing, and after that analysis of litter size traits (number of live births, stillbirths and weaned piglets) was performed.

To check the significance of the impact of parental genotypes and parity, general linear model (GLM) were used:

$$Y_{ijklm}=\mu+ S_i + D_j + P_k + E_{ijkl}$$

Where is:

Y_{ijkl} - observed traits

μ - mean of observed traits

S_i - sire effect

D_j - dam's effect
P_k – parity effect
E_{ijkl} - random error

For the traits adjusted mean (LSM - Least Square Means) were calculated and Fisher LSD post-hoc test for significance determination between the genotypes of sires and dams were performed. To test the dependence between parity and the observed reproductive traits, multiple linear regression were used with the statistical software XLSTAT 2013.

Results and Discussion

Tables 1 and 2, shows the average number of live births, stillbirths and weaned piglets according to dams and sires genotypes with the adjusted mean (LSM), standard error of the adjusted mean (SE_{Lsm}), and the effect of the parental genotype on the observed properties of litter sizes.

From the data in Table 1, it can be seen that the dams genotype had highly significant (p<0.01) influence on the observed properties. In the studied population, between the genotypes of pure sows breeds and hybrid sows statistically significant differences (p<0.01) in the number of live born and weaned piglets was observed, while the number of weaned piglets showed no significant differences (p>0.05). Greater variability was observed in litter sizes of pure sows breed (9.44; 10.12), while the hybrid sows have almost uniform litter sizes (9.79; 9.78 and 9.72). Almost the same number of weaned piglets in all observed genotypes can be explained by inadequate farm management in the growth process of suckling piglets, where maximum attention should be paid, because this phase is the most critical and most difficult phase of piglet production.

Table 1. Influence of dam genotype on litter size

Dam genotype	Number of litters	Live born piglets		Stillborn piglets		Weaned piglets	
		LSM	SE_{Lsm}	LSM	SE_{Lsm}	LSM	SE_{Lsm}
Hybrid	20980	9.79^{A}	0.02	1.29^{A}	0.01	8.30^{A}	0.02
Yorkshire	3189	9.44^{aB}	0.05	0.59^{aB}	0.02	8.40^{B}	0.06
Landrace	22426	10.12^{abC}	0.02	0.74^{ab}	0.01	8.34^{C}	0.02
$F_{1(YxL)}$	14251	9.78^{bc}	0.02	0.71^{abC}	0.01	8.45^{acD}	0.03
$F_{1(LxY)}$	4689	9.72^{bc}	0.04	0.54^{ac}	0.02	8.67^{abcd}	0.05
p value		*0.000*		*0.000*		*0.000*	
F value		*75.494*		*646.79*		*11.42*	

The same upper and lower case letters – statistically high significant differences p<0.01

The same lower and different upper case letters – no statistically significant differences p>0.05

The genotype of the sire had highly significant (p<0.01) effect on all observed characteristics what can be seen from the results given in Table 2. In addition, the sires genotypes was found to be statistically significant different (p<0.01) in the number of live born and stillborn piglets, where the largest number of live born piglets was found in Pietrain sires (10.55), while the lowest number was recorded in Hampshire sires line (9.65). Differences in the number of weaned piglets within the sires of all breed lines genotype found no significant (p>0.05) differences.

Table 2. Influence of sire genotype on litter size

Sire genotype	Number of litters	Live born piglets		Stillborn piglets		Weaned piglets	
		LSM	SE_{Lsm}	LSM	SE_{Lsm}	LSM	SE_{Lsm}
Yorkshire	21641	9.73^{A}	0.02	1.09^{A}	0.01	8.30^{A}	0.03
Landrace	26623	10.00^{aB}	0.01	0.86^{aB}	0.01	8.27^{B}	0.02
Pietrain	485	10.55^{abC}	0.12	0.84^{aC}	0.06	8.92^{ab}	0.17
Duroc	13463	9.95^{acD}	0.02	0.74^{abD}	0.01	8.62^{ab}	0.03
Hampshire	3323	9.65^{bcd}	0.04	0.43^{abcd}	0.02	8.58^{ab}	0.08
p value		*0.000*		*0.000*		*0.000*	
F value		*39.107*		*230.79*		*25.317*	

The same upper and lower case letters – statistically high significant differences p<0.01
The same lower and different upper case letters – no statistically significant differences p>0.05

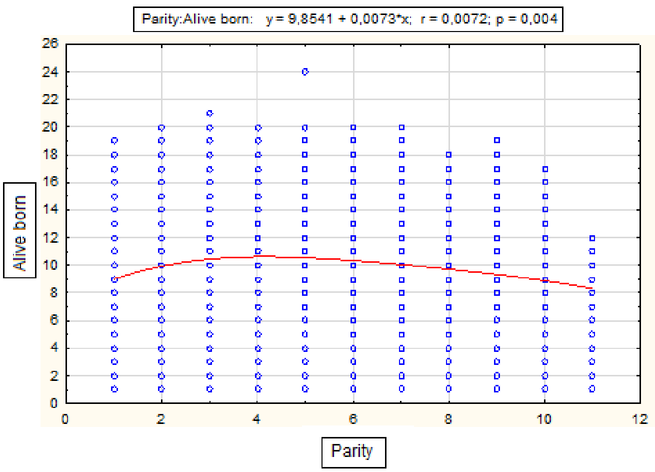
The Table 3 shows the parity structure of the herd on the farm, on the basis of which can be seen very good parity structure of the population, where the number of litters till fifth farrowing is around 72%. The highest percentage of litters was in a first parity which was around 21.56%, and then in the second 15.81%, 13.39% in the third, fourth 11.41% and 9.57% in the fifth, respectively. According *Vidović and Šubara (2011)* the preferred structure of the sows herd parity is, when a number of zero-parity sows is around 20%, in the first 18%, in the second 15%, in the third 14%, in the fourth 12%, in the fifth10%, sixth 6%, and more than seven is around 7%. A similar parity structure was proposed by *Tretinjak et al. (2009), Chen et al. (2003).*

Farrowing parity as expected, had statistically significant (p<0.01) effect on the number of live births, stillbirths and weaned piglets. Once again the hypothesis that the first farrowing sows have smaller litters, and later with increasing the sows parity, the number of live born and weaned piglets was increased till the sixth farrowing, which after was gradually decreased, while the number of stillborn piglets was increased is confirmed. The similar results was obtained by *Lukač (2013), Vidović et al. (2011a, 2011b), Tretinjak et al. (2009), Lucia et al. (2002)* and *Vincek (2005)* in their investigations.

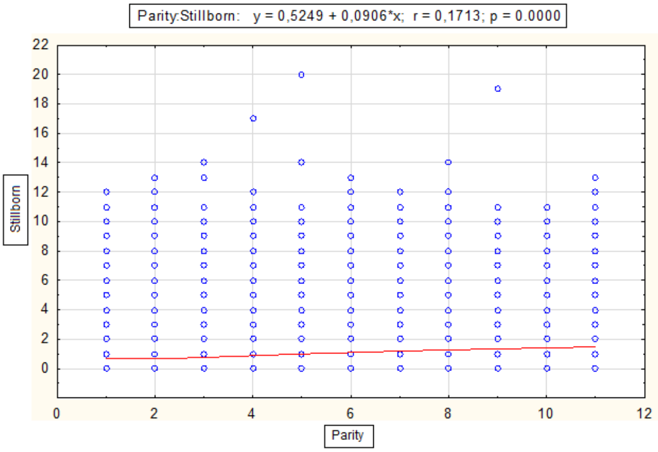
Table 3. Influence of parity on litter size

Parity	Number of litters		Live born piglets		Stillborn piglets		Weaned piglets	
	No	%	LSM	SE_{Lsm}	LSM	SE_{Lsm}	LSM	SE_{Lsm}
1	14132	21.56	8.96	0.02	0.67	0.02	7.00	0.03
2	10366	15.81	10.05	0.02	0.63	0.01	9.00	0.04
3	8779	13.39	10.52	0.03	0.74	0.01	9.02	0.04
4	7480	11.41	10.62	0.03	0.89	0.01	8.97	0.04
5	6277	9.57	10.47	0.03	1.02	0.02	8.90	0.05
6	5201	7.93	10.26	0.04	1.07	0.02	8.67	0.05
7	4219	6.43	9.98	0.04	1.19	0.02	8.45	0.06
8	3334	5.08	9.64	0.05	1.28	0.02	8.33	0.07
9	2578	3.93	9.29	0.05	1.32	0.03	8.22	0.07
10	1925	2.93	8.96	0.06	1.39	0.03	7.88	0.09
>10	1244	1.89	8.30	0.08	1.48	0.04	7.93	0.11
p value			*0.000*		*0.000*		*0.000*	
F value			*393.11*		*205.52*		*282.14*	

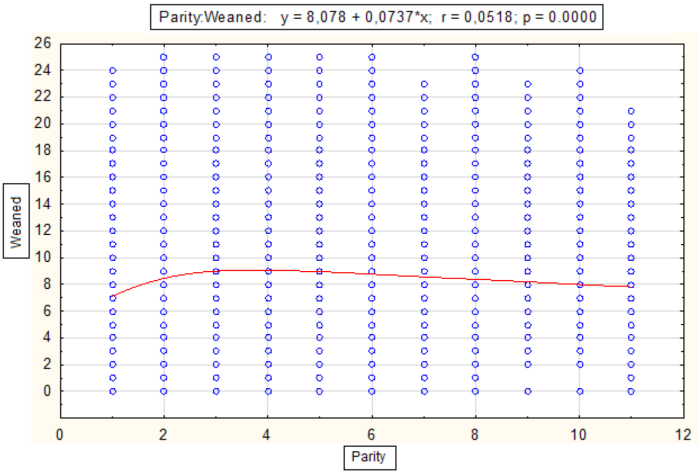
Regression analysis of dependence between parity and litter size recorded positive regression coefficients which can be seen from the results showed at Graphs 1, 2 and 3. With each unit increase in parity, there was an increase in the number of live born (b=0.007), stillborn (b=0.09) and weaned piglets (b=0.07). Observed properties of litter size was significant (p<0.05) and highly statistically significant (p<0.01).



Graph 1. Relation between parity and alive born piglets



Graph 2. Relation between parity and stillborn piglets



Graph 3. Relation between parity and weaned piglets

Conclusion

Based on the gained results, which have the aim to investigate the influence of parental genotype and parity number on the litter size properties of sows it can be concluded that the dams and sires genotype had highly significant influence on the observed properties of number of live born, stillborn and weaned piglets. The same tendency was observed in the influence of parity number on litter size with also high significance. In this regard, the maximum litter size, which is also an indicator of economic production, together with the number of farrowing sow per year, can be achieved by proper selection of genotypes of future parents with properly define production technology and with the optimization of paragenetic factors.

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Uticaj genotipa roditelja i pariteta na veličinu legla svinja

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Rezime

Cilj ovog rada je bio da se ispita uticaj genotipa roditelja i pariteta prašenja na osobine veličine legla krmača (broj živorođene, mrtvorođene i zalučene prasadi). Podaci su sakupljeni sa jeden farme u Vojvodini. Analiza je obuhvatila 65535 legala koja vode poreklo od pet različizih genotipova majki (plotkinje sa nepoznatim poreklom, n= 20980; jorkšir, n= 3189; Landras, n= 22426; $F1_{(YxL)}$, n = 14251; $F1_{(LxY)}$, n = 4689) i pet genotipova očeva (jorkšir, n= 21641; landras, n= 26623; pietren, n= 485; durok, n= 13463; hempšir, n=3323). Na osnovu dobijenih rezultata može se zaključiti da su genotipovi majki imali statistički značajan uticaj ($p<0.01$) na posmatrane osobine veličine legla. Landras krmače su imale prosečno najveći broj živorođene prasadi (10,12) u poređenju sa krmačama druga četiri genotipa, gde je zabeležena statistički značajna razlika ($p<0.01$). Genotip oca je imao statistički značajan uticaj ($p<0.01$) na osobine veličine legla, gde su terminalnih genotipovi bili superiorniju u pogledu broja živorođene i zalučene prasadi. Regresiona analiza zavisnosti između pariteta i osobina veličine legla beleži pozitivne regresione koeficijente: broj živorođene prasadi (b= 0,007), broj mrtvorođene prasadi (b= 0,09) i broj zalučene prasadi (b= 0,07). Uticaj pariteta prašenja na posmatrane osobine veličine legla je bio statistički visoko značajan ($p<0.01$).

References

CHEN P. T., BASS T. J., MABRY J. W., KOEHLER J.C.M., DEKKRES C. M. (2003): Genetic parameters and trends for litter traits in U.S. Yorkshire, Duroc, Hampshire and Landrace pigs. J. Anim. Sci., 81, 46-53.

IRGANG R., FAVERO J. A., KENNEDY B. W. (1994): Genetic parameters for litter size of different parities in Duroc, Landrace, and Large White sows. J. Anim. Sci., 72, 2237-2246.
KLINDT J. (2003): Influence of litter size and creep feeding on preweaning gain and influence of preweaning growth on growth to slaughter in barrows. J. Anim. Sci., 81, 2434-2439.
LUCIA T. J., CORREA N. M., DESCHAMPS C. J., BIANCHI I., DONIN A. M., MACHADO C. A., MEINCKE W., MATHEUS E. M. J (2002): Risk factors for stillbirths in two swine farms in the south of Brazil. Prev. Vet. Med., 53, 285-292.
LUKAČ D. (2013): Reproductive traits in relation to crossbreeding in pigs. Afr. J. Agric. Resh., 8, 2166-2171.
ROEHE R., KENNEDY B. W. (1993): The Influence of Maternal Effects on Accuracy of Evaluation of Litter Size in Swine. J. Anim. Sci., 71, 2353-2364.
STELLA A., STALDER K. J., SAXTON A. M., BOETTCHER P. J. (2003): Estimation of variances for gametic effects on litter size in Yorkshire and Landrace swine. J. Anim. Sci., 81,2171-2178.
TRETINJAK M., ŠKORPUT D., ĐIKIĆ M., LUKOVIĆ L. (2009): Veličina legla u krmača na obiteljskim gospodarstvima u republici Hrvatskoj. Stočarstvo, 63, 175-185.
VAN DER LENDE T., WILLEMSEN M. H. A., VAN ARENDONK J. A. M., VAN HAANDEL E. B. P. G. (1999): Genetic analysis of the service sire effect on litter size in swine. Liv. Produc. Sci., 58, 91-94.
VIDOVIĆ, V., (2009): Principi i metodi oplemenjivanja životinja. Poljoprivredni fakultet, Novi Sad, pp 348.
VIDOVIĆ V., LUKAČ D., ŠTRBAC LJ., STUPAR M. (2011a): Effect of age and weight of Yorkshire gilts at mating on litter size and longevity. Stočarstvo, 65, 3-12.
VIDOVIĆ V., ŠTRBAC LJ., LUKAČ D., STUPAR M.(2011b): Influence of age and weight of Landrace gilts at fertile insemination on litter size and longevity. Biotech. Anim. Husb., 27, 75-85.
VIDOVIĆ V., ŠUBARA V. (2011): Farmski menadžment – ključ uspeha. Poljoprivredni fakultet, Novi Sad, pp 140.
VIDOVIĆ V., LUKAČ D., ŠTRBAC LJ., STUPAR M.,VIŠNJIĆ V., KRNJAIĆ JOVANKA (2012): Heritability and repeatability estimates of reproduction traits in pure breed pigs. Biotec. Anim. Husb., 28, 455-462.
VINCEK D. (2005). Veličina legla majčinskih linija uzgojnog programa u svinjogojstvu. Stočarstvo, 59, 13-21.
XLSTAT (Data analysis and statistics softwer) (2013) (http://www.xlstat.com/)
WÄHNER M., BRÜSSOW P. K. (2009): Biological potential of fecundity of sows. Biotec. Anim. Husb., 25, 523-533.

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