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FREQUENCY OF ESR, FSHB, HAL, MYF-4 AND PRUM GENES BY ANALYSIS OF REPRODUCTION TRAITS OF WHITE MEATY SOWS AND THEIR CROSSES[1]

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Abstract: The frequency of various markers alleles of the White Meaty (WM) sows and their two- or three breed crosses of sows were as follows: ESR, alleles C 0.78 and D 0.22; FSHB, alleles A 0.05 and B 0.95; HAL, alleles N 0.92 and n 0.08; Myf-4, alleles A 0.75 and B 0.25 and PRUM, alleles P 0.66 and M 0.34. Analyses of reproduction traits of various sow genotypes and followed marker genotypes mentioned the necessity of detailed and planned investigations of animal genetic experiments for detection of significant relations of reproduction traits with markers for purposed selection of sows on adequate reproduction parameters at optimal environmental conditions in swine farming.

Key words: pig breeding, reproduction traits, markers

Introduction

Genetic markers are polymorphic traits, of variants which show mendelistic heredity and can be in association with various important production traits in animal breeding.

Legault et al. (1996) were dealing with polymorphism of gene for oestrogen receptor for example. They found out, that in hyper fertile line the frequency of "more beneficial" B allele was higher than in check line (0.52 > 0.46).

Gene FSHB shows extreme asymmetric distribution of genotypes. In commercial breeds the frequent occurrence of BB genotype was determined, while by Chinese breeds it occurred only rarely (*Chen et al.,* 2001).

Following the raising animal selection on meat utility and association of RYR1 gene with greater muscles the recessive n allele occurs in general more often in sire-breeds of pigs (Yorkshire, Landrace, Duroc, Hampshire, Pietrain), higher tendencies are noticeable also in boar population. Regulation factors of muscles development (myogenesis) are genes from so called MyoD family. MyoD family consists of four structural genes: MyoD called also Myf-3 (*Davis et al.,* 1987), myogenin Myf-4 (*Edmondson* and *Olson,* 1989), Myf-5 (*Braun et al.,* 1989) a MRF4 Myf-6, herculin (*Miner* and *Wold,* 1990; *Braun et al.,* 1990).

One of the markers for gain is marked PRUM (gain, utility, meat). Marker has two codominant alleles: P and M, each pig has one of these genotypes: PP, PM or MM (*Dvořák et al.,* 2003).

Material and Methods

The aim of this paper was to study following genes: ESR (gene of oestrogen receptor), FSHB (gene of follicular stimulative hormone), HAL (halothane gene), Myf-4 (myogenin gene) and PRUM (genetic marker of pig gains) with regard to single alleles. The sows reproduction utility of White Meaty breed (WM) and two- or three-breed cross, in which breeds Landrace (L), Duroc (D) and Dutch crossbred Dalland (DA) shared.

For comparison of genotypes presence independence by single sow markers and genotypes, as well as between the combinations of single markers, i. e. regardless of sow genotypes, method of *r x c* contingency tables with determination of χ^2 Pearson´s coefficient, Mantel´s method of maximum likelihood (MML) and contingency coefficient (CC) were used. Furthermore the relative frequency, i. e. probability of single alleles presence of studied genotypes (*p* and *q*), was also defined in whole material. The mathematico-statistical methods were used following *Grofik* and *Fľak* (1990) work, and statistical program package SPSS for Windows, Release 6.0, 1986-1993 was used.

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[1] Original scientific paper –Originalni naučni rad

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Results and Discussion

In table 1 the presence of genotypes frequency and studied markers alleles are presented together in whole (total) sow population.

In population of studied sows we found out by ESR genotypes C allele frequency 0.78 and D allele frequency 0.22. Genotypes representations were: CC 59.3 %, CD 37.2 % and DD 3.5 %. *Tothová et al.* (2002) made analysis of ESR gene polymorphism in sows of Slovak population of White Improved (WI) breed using the restrict enzyme MspI and determined frequencies of genotypes CC 26.81 %, CD 50.32 % and DD 22.87 %. These results show markedly higher frequency of CD and DD genotypes in comparison with our investigations (CD 37.2 % and DD 3.5 %). Higher frequency of CD and DD genotypes mentioned also *Dvořák* and *Vrtková* (1999) in their work. By testing of ESR genotypes by WI breed they found out the allele frequency C 0.63, D 0.37 and genotypes CC 40.8 %, CD 45.4 % and DD 14.0 %. By Landrace breed they found out the allele frequency C 0.89, D 0.11 and genotypes CC 79.9 %, CD 18.6 % a DD 1.6 %.

Table 1. The frequencies of alleles genotypes of followed markers together in whole sow population

Marker	*P*	*H*	*Q*	*n*	*p*	*q*
ESR	CC	CD	DD		C	D
	51	32	3	86	0.78	0.22
	59.3 %	37.2 %	3.5 %	100 %		
FSHB	AA	AB	BB		A	B
	0	8	78	86	0.05	0.95
	0 %	9.3 %	90.7 %	100 %		
HAL	NN	Nn	nn		N	n
	74	11	1	86	0.92	0.08
	86.0 %	12.8 %	1.2 %	100 %		
Myf-4	AA	AB	BB		A	B
	45	39	2	86	0.75	0.25
	52.3 %	45.4 %	2.3 %	100 %		
PRUM	PP	PM	MM		P	M
	38	38	10	86	0.66	0.34
	44.2 %	44.2 %	11.6 %	100 %		

By evaluation of FSHB gene allele frequency we found out frequency of allele A 0.05 and allele B 0.95. The genotypes frequencies were: AA 0 %, AB 9.3 % and BB 90.7 %.

HAL gene allele frequencies in studied sow population were N 0.92 and allele n 0.08 and frequencies of genotypes NN 86.0 %, Nn 12.8 % and nn 1.2 %. Our investigations of allele frequencies are different from results, published by *Bauerová* (1996) in Landrace population in Slovakia. In her work she found out the frequencies of allele N 0.36 and n 0.64. Analysing the frequencies of single HAL genotypes she did not find out the presence of NN genotype, by Nn she found out 71.8 % and nn 28.2 %. Our results are similar to those, published by *Russo* (1994) in Landrace population in Italy. He found out the frequencies of allele N 0.89 and n 0.11. Analysing the frequency of single HAL genotypes he found out the presence of genotype NN 80.1 %, Nn 18.4 % and nn 1.5 %.

By evaluation of Myf-4 gene allele frequency we found out the frequency of allele A 0.75 and allele B 0.25 and frequencies of genotypes AA 52.3 %, AB 45.4 % and BB 2.3 %. Allele frequency of Myf-4 marker in Landrace population published by *Soumillion et al.* (1997) in their work. They found out by A allele presence 50.0 % and by B allele also 50.0 %. Within the frame of single genotypes they present by AA 30 %, by AB 40 % and by BB 30 %. *Ernst* and *Davis* (1995) found out the presence of A allele 0.31 and B allele 0.69. In AA genotype they found out presence 8 %, by AB 46 % and by BB 46 %.

The effect and frequency of PRUM marker *Dvořak et al*. (2003) verified by pigs of WI breed and crossbreed White Fatherly BO (boars) x White Generous WI (sows) in one of the cooperative company in Moravia. They found out following representation of PRUM genotypes by fattening pigs: PP 34.2 %, PM 56. 2 % and MM 6.6 % in WI breed. Analysing allele frequency of PRUM gene we found out by P allele 0.66 and by M allele 0.34. In frame of single genotypes we found out the representation of genotype PP 44.2 %, PM 44.2 % and MM 11.6 %.

Table 2. Results of contingency tables of comparison of markers and sow genotypes

Marker	*Pearson* χ^2	*f*	*MMV*	*f*	*Mantel*	*f*	*CC*	% $y_{ij} < 5$
ESR	14.230	14	15.609	14	0.223	1	0.377	75.0
FSHB	12.354	7	10.567	7	1.653	1	0.354	68.8
HAL	7.500	14	7.737	14	0.501	1	0.283	79.2
Myf-4	11.097	14	11.345	14	0.146	1	0.338	79.2
PRUM	11.712	14	13.245	14	0.769	1	0.346	83.3

χ^2 - Pearson´s chi-squared test of *r* x *c* contingency table
y_{ij} – expected frequency in cell *i* x *j*

The comparisons of observations of single marker genotypes, binomial equation $(p_A + q_a)^2 = p^2AA + 2pqAa + q^2aa$, over sow genotypes showed (Table 2), that Pearson´s χ^2 - tests were not statistical significant, what shows on the fact, that the observations of single genotypes of either evaluated marker by comparison of sow genotypes are identical. However, it is necessary to verify this conclusion in future experiments, because expected frequencies $y_{ij} < 5$ ranged in single marker genotypes from 68.8 % by FSHB to 83.3 % by PRUM. From the above mentioned it follows that the presence of single alleles or genotypes of analysed markers it is possible to evaluate together, regardless of single sow genotypes.

Conclusion

The analyses of contingency tables of sow and marker genotypes showed no significant differences in distribution of marker genotypes by comparison through sow genotypes. Analysis of independence between marker genotypes showed only on significant relation between FSHB and HAL markers. Determined dependence of FSHB and HAL markers shows the necessity to use relation between reproduction and meat traits. It is therefore necessary in selection on reproduction parameters to evaluate the markers association with fattening and meat production traits.

FREKVENCIJA ESR, FSHB, HAL, MYF-4 I PRUM GENA ANALIZOM REPRODUKTIVNIH OSOBINA BELE MESNATE SVINJE I NJENIH MELEZA

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Frekvencije različitih markera alela bele mesnate krmače (WM) i njena dva ili tri meleza su bile sledeće: ESR, aleli C 0.78 i D 0.22; FSHB, aleli A 0.05 i B 0.95; HAL, aleli N 0.92 i n 0.08; Myf-4, aleli A 0.75 i B 0.25 i PRUM, aleli P 0.66 i M 0.34. Analiza reproduktivnih osobina različitih genotipova krmača i markera genotipova pokazuje neophodnost detaljnog i planskog ispitivanja u genetskim ogledima sa životinjama za otkrivanje signifikantnih odnosa reproduktivnih osobina i markera za predloženu selekciju krmača na adekvatne reproduktivne parameter pri optimalnim uslovima sredine u svinjarstvu.

Ključne reči: svinjarstvo, reproduktivne osobine, markeri

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