

INFLUENCE OF THE FOLLICLE STIMULATING HORMONE GENE ON LITTER SIZE IN LARGE WHITE SOWS

VLIV GENU FOLIKULY STIMULUJÍCÍHO HORMONU NA VELIKOST VRHU PRASNIC PLEMENE BÍLÉ UŠLECHTILÉ

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ABSTRACT

The effects of the candidate genes for reproduction the Follicle-stimulating hormone beta subunit gene (*FSHB*) on the litter size of Large White sows have been examined. A total number of 171 sows in *FSHB* gene were genotyped by PCR-RFLP and analysed to determine whether the gene polymorphisms influence the litter size of Large White sows. The sows originated from three nucleus herd of Czech Large White pigs. The influence of these genes in the first, the first to the fourth and the second to the fourth litter was investigated. To discover the gene association with reproduction traits, mixed linear models in SAS for windows 8.2 were used. The influence of the *FSHB* genes in the studied populations was not very conclusive. Since the low number of sows included in the analysis is it not possible to state the final conclusion about the application of the *FSHB* gene.

Key words: Litter size, *FSHB* gene, Large White

ABSTRAKT

Cílem studie bylo stanovení vlivu genu pro folikuly stimulující hormon (*FSHB*) na velikost vrhu prasnic plemene České bílé ušlechtilé. Genotyp ve vybraných genech byl stanoven pomocí metody PCR-RFLP u 171 prasnic plemene Bílé ušlechtilé pocházejících ze 3 nukleových šlechtitelských chovů. Vliv vybraného genu na počet všech, živě a dochovaných selat byl stanoven pomocí smíšeného lineárního modelu programem SAS for windows 8.2. Sledován byl vliv na prvním, prvním až čtvrtém a druhém až čtvrtém vrhu. Přesto, že byly nalezeny průkazné rozdíly v počtu dochovaných selat, je vzhledem k nízkému počtu prasnic zahrnutých do této studie brzo na stanovení konečného verdiktu ohledně aplikace tohoto genu v praktickém šlechtění.

Klíčová slova: Velikost vrhu, gen *FSHB*, Bílé ušlechtilé

INTRODUCTION

One of the factors influencing economic efficiency of pig breed is a number of piglets per sows. Improvement of the litter size is not as efficiency as possible, by the way because the reproduction traits have a low coefficient of heritability. One of the means of increasing

the development of these traits is to use knowledge of the gene markers and candidate genes in animal breeding. The follicle-stimulating hormone gene (*FSHB*) is candidate gene for reproduction. Results of previous studies show that this gene can influence the level of reproduction traits. The objective of our research was to determine the influence of these gene on the litter size in Large White herd.

Follicle-stimulating hormone consists of two subunits α and β coded by different genes. The subunit β is specific for every animal genus and it is coded by the *FSHB* gene (Mellink *et al.*, 1995). The *FSHB* gene is considered as a candidate gene because of its function in maturation of small and medium follicles into ovulating large follicles (Wang and Greenwald, 1993; Mannaertz *et al.*, 1994). Ellegren *et al.* (1994) mapped the *FSHB* gene on the porcine chromosome 2. In the *FSHB* gene, two alleles *A* and *B* are detectable by PCR-RFLP methods. Li *et al.* (1998) found large effects of the *FSHB* gene on pig litter size in the population of Landrace, Yorkshire and Yorkshire hybrids crossed with the Erhualian breed. The positive genetic effect of favourable *FSHB* genotypes appeared in all sow parities and was estimated to approximately one piglet. Rohrer *et al.* (1999) did not detect any QTL effects in the region of the *FSHB* locus, based on the QTL genome scan for reproductive traits.

MATERIAL AND METHODS

The genotypes in *FSHB* genes were determined in 86 sows in herd I; 63 sows in herd II and 22 sows in herd III, respectively. The genotypes were detected by means of PCR-RFLP methods as described by Rohrer *et al.* (1999), for *FSHB* gene.

The associations of studied polymorphisms with a total number of born piglets (NB); number of piglets born alive (NBA) and number of weaned piglets (NW) were estimated using a mixed linear model in SAS for windows 8.2. The influence of the genes in the first; the first to the fourth and the second to the fourth litter were monitored. The genotypes the *FSHB* gene, year of sow's birth (YB), month of sow's birth (MB), month of litter (ML), year of litter (YL), effect of litter order (OL) and herd of sows (HERD) and whether the sow belonged to the super fertility line (SFL) were included in models as a fixed effect. The effect of the boar (*BOAR*) was used as a random effect. Furthermore, linear regressions on backfat thickness (cm) (BT), lean meat content (%) (LM), average daily gain from birth to test end (g/day) (ADG) and the age of the first conception (AFC) were included.

Model 21 used in the first litter in data set III:

$$y_{ijklmnoqrstu} = \mu + ESRI_i + FSHB_j + YB_k + MB_l + YL_m + ML_n + HERD_o + BOAR_p + SFL_r + BT_s + LM_t + e_{ijklmnoqrst}$$

Model 2 used in the first to the fourth litter and the second to the fourth litter in data sets III:

$$y_{ijklmnoqrstuvw} = \mu + ESRI_i + FSHB_j + YB_k + ML_l + MB_m + YL_n + OL_o + HERD_p + SFL_r + BT_s + LM_t + ADG_u + AFC_v + BOAR_w + e_{ijklmnoqrstuvw}$$

RESULTS

The *BB* genotypes in the *FSHB* gene was the most frequent in all examined herds (Table 1). In the herd II as well as in the herd III, one sow only was detected with *AA* genotype in *FSHB* gene.

The effect of the *FSHB* gene (Table 2) was significant in the second to the fourth litter. There were significant differences between *AB* and *BB* genotypes in total number of piglets born and in number of piglets born alive in data set II and between *AA* and *BB*, *AA* and *AB* genotypes in *FSHB* gene in number of piglets weaned in data set III. In the first and in the first to the fourth litters, no significant differences between *FSHB* gene and litter size were found.

Tab. 1 Absolute and relative frequencies of alleles and genotypes

		<i>FSHB</i>					
Frequencies of genotypes	<i>AA</i>	22	0.26	1	0.02	1	0.05
	<i>AB</i>	28	0.32	7	0.11	9	0.41
	<i>BB</i>	36	0.42	55	0.87	12	0.55
Frequencies of alleles	<i>A</i>	72	0.42±0.04	9	0.07±0.02	11.00	0.25
	<i>B</i>	100	0.58±0.04	117	0.93±0.02	33.00	0.75
H-W (χ^2)		no		A		A	

Note: ^A Population is in gene equilibrium by H-W for P = 0.01; ^{no} population is not in gene equilibrium by H-W

Tab. 2 Sows' efficiency with different genotypes in the *FSHB* gene (LSM ± SE), effects of additive (A) and dominance (D) for allele B

	<i>AA</i>	<i>AB</i>	<i>BB</i>	A	D
the 1 st litters					
NW	/	11.62 ± 0.81	11.31 ± 0.47	/	/
NB	12.83 ± 0.64	13.68 ± 0.47	13.61 ± 0.40	0.39	0.46
NBA	12.36 ± 0.66	13.39 ± 0.49	13.01 ± 0.42	0.33	0.71
NW	11.26 ± 0.60	12.21 ± 0.44	11.76 ± 0.38	0.25	0.70
the 2 nd – 4 th litters					
NB	13.38 ± 1.21	12.69 ± 1.14	12.42 ± 1.17	-0.48	-0.21
NBA	13.00 ± 1.14	12.61 ± 1.07	12.43 ± 1.10	-0.29	-0.11
NW	13.05 ± 1.01 ^{a b}	12.09 ± 0.95 ^a	11.94 ± 0.98 ^b	-0.56	-0.41
the 1 st – 4 th litters					
NB	13.48 ± 0.85	13.23 ± 0.79	13.09 ± 0.80	-0.20	-0.05
NBA	13.06 ± 0.82	13.00 ± 0.77	12.86 ± 0.78	-0.10	0.04
NW	12.69 ± 0.75	12.27 ± 0.70	12.17 ± 0.71	-0.26	-0.16

Note: Values with the same exponents show significance level within lines: ^{a b} P = ≤ 0.05; Approaching significance level ^{c d} P = ≤ 0.10

DISCUSSION

All investigated sows were collected from three nucleus herds of Large White pigs, where an intensive selection for reproduction traits is carried out. It can be assumed, that this selection have been performed in favour of sows with the alleles positively influencing reproduction traits. The most frequent genotypes were homozygous genotypes *BB* in *FSHB* gene in all included herds (Table 1). In the *FSHB* gene, the lowest frequencies of genotypes *AA* were found in all herds. These differences were the most evident in herd II and III. Linville *et al.* (2001) described similar frequencies in four synthetic lines.

In the second to the fourth litters, significant differences were detected between sows with *AB* and *BB* genotypes in *FSHB* gene in total number of piglets born and number of piglets born alive and *AA* and *AB*, *AA* and *BB* genotypes in piglets of weaned in data set II and III (Table 3). The influence of the *FSHB* gene on reproductive traits in the first and in the first to the fourth litters was significant in none of the observed data set (Table 3). Li *et al.* (1998) observed that sows with the *BB* genotype achieved the highest total number of piglets born and born alive. Linville *et al.* (2001) reported that the *FSHB* gene did not explain selection response in two pig lines selected for ovulation rate and litter size in comparison with a randomly selected control line.

Our results indicated that the *FSHB* gene can have some influence on the litter size notably on the number of weaned piglets. The results can be rule by the low number of sows, therefore is necessary to continue in the research of this candidate gene.

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REFERENCES

- ELLEGREEN, H., CHOWDHARY, B.P., JOHANSSON, M., MARKLUND, L., FREEDHOLM, M., GUSTAVSSON, I., ANDERSSON, L. (1994): A primary linkage map of the porcine genome reveals a low rate of genetic recombination. *Genetics*. 137. (1994), 1089-1100
- KOWALSKI, A. A., GRADDY, L. G., VALE-CRUZ, D. S., CHOI, I., KATZENELLENBOGEN, B.S., SIMMEN, F.A., SIMMEN, R.C. (2002): Molecular cloning of porcine estrogen receptor- complementary DNAs and developmental expression in periimplantation embryos. *Biology of Reproduction*. 66. 7609
- LI, N., ZHAO, Y. F., XIAO, L., ZHANG, F. J., CHEN, Y. Z., DAI, R. J., ZHANG, J. S., SHEN, S. Q., CHEN, Y. F., WU, C. X. (1998): Candidate gene approach for identification of genetic loci controlling litter size in swine. In: *Proceedings of the 6th World Congress on Genetics Applied to Livestock Production*. Armidale. Australia. January 11-16. vol. 26. 183-186

- LINVILLE, R. C., POMP, D., JOHNSON, R. K., ROTHSCHILD, M. F. (2001): Candidate gene analysis for loci affecting litter size and ovulation rate in swine. *J. Anim. Sci.* 79. 60–67
- MANNAERTZ, B., UILENBROCK, J., SCHOT, P., DE LEEUW, R. (1994): Folliculogenesis in hypophysectomized rats after treatment with recombinant human follicle stimulating hormone. *Biol. Reprod.* 51. 72 – 81
- MELLINK, C., LAHBIB-MANSAIS, Y., YERLE, M., GELLIN, J. (1995): PCR amplification and physical localization of the genes for pig FSH β and LH β . *Cytogenetics and Cell genetics*, 70. 224-227
- ROHRER, G. A., FORD, J. J., WISE, T. H., VALLET, J. L., CHRISTENSON, R. K (1999): Identification of quantitative trait loci affecting female reproductive traits in a multigeneration Meishan-White composite swine population. *J. Anim. Sci.* 77. 1385 – 1391
- WANG, H. N., GREENWALD, G. S. (1993): Hypophysectomy of the cycling mouse. I. Effects of follicle stimulating hormone (FSH) and leuteinizing hormone on folliculogenesis, FSH and human chorionic gonadotropin receptors and steroidogenesis. *Biol. Reprod.*, 48. 595 – 605