Impact of the *ESR* gene on litter size and litter weight in Czech Large White pigs

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Introduction

The impact of the *Pvu*II polymorphism of the oestrogen receptor gene on litter size has been discussed by many authors since the mid nineties. Nevertheless, the effect of approximately 0.4 piglets born alive per copy of the favourable allele *B* in Large White populations reported in the large studies of Rothschild *et al.* (1995, 1996) and Short *et al.* (1997) was not confirmed in many smaller studies. The aim of the present investigation was to analyze the effect of the *ESR* gene on litter traits using a large data set of Czech Large White sows.

Material and methods

The *ESR-Pvu*II effect on litter size traits and litter weight at weaning was investigated in a data set of nearly 3600 litters from 1030 Czech Large White sows. The following traits were analyzed: number of piglets born, number of piglets born alive, number of piglets weaned and litter weight at weaning. Basic statistical characteristics for all traits are summarized in Table 1.

Table 1 Number of observations (litters), means and standard deviations for traits

Trait	*n*	Mean	Stand. dev.
Number of piglets born	3597	13.10	2.383
Number of piglets born alive	3597	12.38	2.236
Number of piglets weaned	3595	10.86	1.994
Litter weight at weaning (kg)	1514	59.3	13.14

Table 2 Effects included in four-traits animal models (C – covariable, F – fixed effect, R – random effect, A – random effect with relationship matrix)

Effect	Type of effect for	
	litter size traits	litter weight
Additive effect of *ESR*	C	C
Dominance effect of *ESR*	C or -	C or -
Age of litter at weaning	-	C
Age at first farrowing (linear and quadratic, 1st parity only)	C	C
Farrowing interval (linear and quadratic, 2nd and subsequent parities only)	C	C
Mating type (AI or natural mating)	F	F
Boar breed	F	F
Parity	F	F
Herd-year-season of farrowing	R or F	R or F
Permanent effect of sow	R	R
Animal	A	A

Four-trait repeatability animal models were used to estimate the effect of the *ESR* gene. The animal models differed by considering the herd-year-season effect as random or

fixed and by including or not including the dominance effect (see table 2 for model structure). Both the additive and the dominance effects of the *ESR* gene were calculated as regression coefficients of a covariable. The additive effect was defined as *B-A*, where *B* and *A* were the effects of the appropriate alleles. The difference between *BB* and *AA* sows was therefore twice the additive effect. The dominance effect was defined as *AB*-(*AA*+*BB*)/2, where *AA*, *AB* and *BB* were the appropriate genotypes of the *ESR* gene. All calculations were carried out with the PEST program (Groeneveld et *al.*, 1990).

Results and discussion

The *ESR* gene showed a mostly significant effect (P<0.05) on litter size traits in favour of allele *A*. For evaluated litter size traits over all parities, the difference between *AA* and *BB* sows was approximately 0.3 piglets (P<0.05). For litter weight at weaning no significant additive effect was observed (table 3). Although no significant dominance effect was found for litter size traits, a significant negative dominance effect of -1.3 to –1.5 kg was estimated for litter weight at weaning (table 4).

Table 3 Estimates of the additive effect of the *ESR* gene and its standard error for litter size traits and weight at weaning in models with fixed or random herd-year-season of farrowing

Trait	Estimates of the additive effect in models with	
	random herd-year-season	fixed herd-year-season
Number of piglets born	**-0.167±0.063**	-0.129±0.067
Number of piglets born alive	**-0.161±0.059**	**-0.136±0.063**
Number of piglets weaned	**-0.184±0.055**	**-0.137±0.058**
Litter weight at weaning (kg)	-0.60±0.42	-0.35±0.43

Bold letters: Effect differs significantly from zero at least on the level P = 0.05

Table 4 Estimates of the dominance effect of the *ESR* gene and its standard error for litter size traits and weight at weaning in models with fixed or random herd-year-season of farrowing

Trait	Estimates of the dominance effect in models with	
	random herd-year-season	fixed herd-year-season
Number of piglets born	0.086±0.079	0.080±0.082
Number of piglets born alive	0.048±0.074	0.039±0.077
Number of piglets weaned	-0.059±0.069	-0.040±0.072
Litter weight at weaning (kg)	**-1.34±0.52**	**-1.49±0.53**

Bold letters: Effect differs significantly from zero at least on the level P = 0.05

Additive and dominance effects estimates were consistent between all used models. Including or not including the dominance effect into the model did not essentially influence the results for the additive *ESR* effect. Greater differences of estimates were found between models which differed in the type of the herd-year–season effect. The *ESR* effects were higher when estimated from models with a random herd-year-season effect than when estimated from models with herd-year-season fixed. But the differences were small compared with the standard errors of the estimates.

Differently from our investigation, Rothschild *et al.* (1995, 1996) and Short *et al.* (1997) detected a statistically significant favourable effect of the *B* allele on litter size in large data sets of American Large White populations. These authors found additive effects between 0.30 and 0.50 piglets for number born and number born alive. Other studies showed no clear association between the *ESR* polymorphism and litter size traits (Legault et al. 1996).

Nevertheless, there was a tendency to better prolificacy of sows with genotype *BB* compared with *AA* sows. From our results it seems, that the Czech Large White population differs from the previously analysed populations in the state of linkage disequillibrium between the *ESR-Pvu*II polymorphism and a *QTL* influencing litter size. A more detailed presentation of the results in the Czech Large White population was recently published in Animal Genetics (Goliášová and Wolf, 2004).

Conclusions

Apart from Rothschild *et al.* (1996) or Short *et al.* (1997), the present study is the largest study in which the *ESR-Pvu*II effect was evaluated. Differently from these two studies, a better prolificacy of sows carrying allele *A* was found. From this difference in the favourable allele and also from the localization of the *Pvu*II restriction site in an intron (Gibson *et al.*, 2002), it could be concluded that the *Pvu*II polymorphism of *ESR* is only a marker for an unknown QTL for litter size.

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