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Genetic parameters and trends for litter size in Black Slavonian pigs

Z. Luković*, D. Karolyi*, V. Klišanić, Ž. Mahnet**, V. Gantner*** and D. Škorput***

*Department of Animal Science, Faculty of Agriculture, University of Zagreb,
Svetosimunska 25, 10000 Zagreb (Croatia)
**Croatian Agricultural Agency, Zagreb (Croatia)
***Zootechnical Department, Faculty of Agriculture, Josip Juraj Strossmayer University,
Osijek, (Croatia)

Abstract. Genetic progress in litter size in local pig breeds is limited mainly due to low heritability and inbreeding depression. After increase of population size of Black Slavonian (BS) pig breed in recent years, there is opportunity to renew a breeding programme including some new breeding goals related to litter size. Aim of study was to determine genetic parameters for litter size in BS pigs. Litter size was presented as number of piglets born alive (NBA) and number of piglets weaned (NW). Genetic parameters were estimated using a univariate repeatability models. Fixed part of the model included breeding organization, birth number, farrowing season and service sire as class effects. Random part of the model included direct additive genetic effect and permanent environmental effect. Litter size records proceeded from 5792 litters from 1817 sows. The complete pedigree file contained 1862 triads (animal-sire-dam). Heritability estimates for NBA and NW were lower than average values of 0.10 - 0.20, and ranged for both traits between 0.04 and 0.08. Implementation of some others models in breeding scheme (particularly multivariate and random regression models) requires availability of large set of reproductive traits for this local breed.

Keywords. Pigs – Local breed – Genetic parameters – Litter size.

Paramètres génétiques et tendances de la taille de la portée chez le porc slavonien noir

Résumé. *Le progrès génétique de la taille de la portée chez les races locales est limité essentiellement en raison de la faible héritabilité et de la dépression de consanguinité. Après l'augmentation de la taille de la population du porc slavonien noir (SN) au cours des dernières années, il est maintenant possible de renouveler les programmes d'amélioration en y incluant de nouveaux objectifs relatifs à la taille de la portée. L'étude avait pour but de déterminer les paramètres génétiques de la taille de la portée des porcs SN. Cette taille a été présentée sous la forme du nombre de porcelets nés vivants (NNV) et du nombre de porcelets sevrés (NS). Les paramètres génétiques ont été estimés en utilisant le modèle univarié de répétabilité. La partie fixe du modèle est composée de l'organisation de l'amélioration, du numéro de mise bas, de la saison de la mise bas, du reproducteur mâle comme effets liés à la classe. La partie aléatoire du modèle est composée de l'effet génétique additif direct et de l'effet environnemental permanent. Les dossiers sur la taille de la portée sont basés sur l'analyse de 5792 portées de 1817 truies. Le dossier complet des pedigrees contenait 1862 triades (animal-père-mère). Les estimations d'héritabilité pour les NNV et les NS sont inférieures aux valeurs moyennes de 0,10-0,20, et varient pour les deux caractères entre 0,04 et 0,08. La mise en œuvre d'autres modèles dans le schéma d'amélioration (en particulier des modèles multivariés et de régression aléatoire) exige la disponibilité d'un grand nombre de caractéristiques reproductives pour cette race locale.*

Mots-clés. *Porcs – Race locale – Paramètres génétiques –Taille de la portée.*

I – Introduction

The Black Slavonian (BS) pig is one of two autochthonous pig breeds in Croatia. The breed was developed at the end of the 19th century in the east part of Croatia (Slavonia region). Until middle of 20th century it was the most widespread breed in the country. A period of extinction of these breed lasted until middle 1990s, when number of pigs was reduced to only 60 sows and 5 boars (Uremovic *et al.*, 2001). Since 1996 population of BS pigs increased, primarily due to state protection measures and individual efforts of pig breeders. The breed is kept traditionally in outdoor system and meat from BS pigs is used mainly for production of local meat products (Karolyi *et al*., 2007). In the last few years, population of BS pigs increased to more than 600 sows and 70 boars. The increase of population size opens a possibility to renew the breeding programme of this local breed.

Litter size is one of the economical most important traits in pig production. Litter size of BS pigs is low compared to modern pig genotypes, on average 6 to 7 piglets born alive (Sencic *et al*., 2001). Increase of litter size of BS pigs is crucial for production of sufficient amounts of local meat delicious, like Slavonian kulen sausage). The objective of this study was to determine genetic parameters for litter size of BS pigs and to consider the possibility to increase litter size by selection.

II – Materials and methods

Data were supplied by the Croatian Agricultural Agency. Litter size were presented as number of piglets born alive (NBA) and number of piglets weaned at 21 days (NW). Litter records were collected from sows farrowed between January 1998 and December 2009. In total there were 5792 litter records from 1817 sows (Table 1). Data file contained only litters from the first to the tenth parity. The complete pedigree file contained 1862 triads (animal-sire-dam).

Table 1. Basic statistics for number of piglets born alive (NBA) and number of piglets weaned (NW)

Trait	Min	Max	Mean	SD
NBA	1.0	16.0	6.14	1.75
NW	0.0	15.0	4.76	2.60

Genetic and environmental parameters were analyzed using a univariate repeatability model assuming complete genetic correlations between successive parities, for each trait separately. Fixed part of the model included breeding organization, parity, farrowing season, and service sire effect. Litter records were obtained form eight breeding organization, while farrowing season was defined as month-year interaction. In the twelve year period piglets from litters were descendants from 241 different service boars. The random part of the model included direct additive genetic effect, and permanent environmental effect. Computations were performed using the VCE6 software (Groeneveld *et al*., 2008).

III – Results and discussion

The estimated values of variances and heritabilities for NBA and NW (Table 2) of BS pigs obtained using univariate repeatability models were substantially lower than estimates in genetic analysis of modern pig genotypes with heritabilities ranging mainly between 0.10 and 0.15. Particularly low values of permanent environmental variances indicate possible bad data structure. Phenotypic variance for NW was doubled in comparison to NBA as consequence of a similar increase of the residual error variance. Some similar values of heritabilities for NBA in this study were found in some studies on Iberian pigs (Pérez-Enciso and Gianola, 1992; Fernández *et al*. 2008). Fernández *et al*. (2007) suggested that multiple-trait models should be recommended to estimate breeding values for litter size in Iberian pigs when the first and later parity records are involved. Further, they noted that a model for litter size treating NBA records at the first parity as one trait, and records at the later parities as second trait could be more advisable than the repeatability model.

Table 2. Variance† and heritability (h^2) estimates for number of piglets born alive (NBA) and number of piglets weaned (NW) under the univariate repeatability models

Trait	Var(a)	Var(p)	Var(e)	Var(ph)	h^2
NBA	0.21	0.02	2.27	2.50	0.08
NW	0.22	0.01	5.50	5.73	0.04

†Var(a): direct additive genetic variance; Var(p): permanent environmental variance; Var(e): residual error variance; Var(ph): phenotypic variance.

IV – Conclusions

The values of variances and heritabilites obtained in our analysis using univariate repeatability model were not promising too much for selection purposes. Some other strategies for estimation of genetic and environmental parameters, as multivariate approach and random regression models must be taken into consideration in the future. Additional attention must be also given to data quality, especially to the control of pedigree precision and registration of reproductive data.

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