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# Genetic Parameters for Number of Piglets Born Alive Using a Random Regression Model

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## Abstract

Genetic parameters for number of piglets born alive (NBA) were estimated using random regression model. Litter records data from three large Slovenian pig farms from the first to the tenth parity were used for analyses. Fixed part of the model included genotype of sow, mating season, parity and weaning to conception interval as class effects. The age at farrowing was adjusted as quadratic regression nested within parity. Previous lactation length was fitted as linear regression. Random regressions on Legendre polynomials of standardized parity were included for direct additive genetic, permanent environmental and common litter environmental effect. Legendre polynomials from the linear power to cubic power were fitted. Heritabilities on all three farms ranged from 0.09 to 0.14. Permanent environmental effect as ratio increased along trajectory from 0.03 to 0.12. Magnitudes of common litter effect were generally small (0.01 to 0.02). The eigenvalues of covariance functions showed that between 10 and 20 % of genetic variability was explained by individual genetic curve of sows. This proportion was mainly covered by linear and quadratic coefficients. The solutions for the random regression coefficients of animals were used to compute breeding value for NBA along trajectory.

**Keywords**: random regression, genetic parameters, litter size, pigs

## Introduction

Litter size in pigs is measured more than once in a sow lifetime and could be considered as a longitudinal trait. Both repeatability and multiple-trait models have been applied to analyze traits that are measured more than once in lifetime of an animal. A repeatability model assumes complete genetic correlations between subsequent observations and a constant variance along trajectory. A multiple-trait analysis supposes subsequent observations to be different traits. Use of multiple-trait model in genetic evaluation of litter size is generally not clearly justified. The main reason often lies in numerical problems and high computational demands. More appropriate way of dealing with longitudinal traits is to fit a set of random regression coefficients describing production over time for each animal (Meyer, 1998). Main advantages of the random regression models (RRMs) in comparison to multiple-trait models are: requirement of fewer parameters to describe longitudinal data, smoother (co)variance estimates, as well as possibility to predict covariance components and breeding values of animal at any point along trajectory. In pigs, RRMs were mainly used for growth and feed intake. In the last decade, litter size has become a major component of selection goals in maternal lines and in some populations significant annual genetic trends have been obtained (Rothchild and Bidanel, 1998). Although litter size differs from fattening traits, some authors suggest that RRMs could be applied in selection on this trait. Possible genetic differences in litter size along the trajectory could be identified with RRMs and persistency in litter size could be used to select breeding sows (Huisman, 2002).

The aim of this paper was to estimate genetic and environmental dispersion parameters using RRM with Legendre (LG) polynomials of different power for number of piglets born alive (NBA) and compare results between three farms.

## Material and methods

The litter records data from three large Slovenian pig farms (A, B, C) from the first to the tenth parity, collected between September 1989 and December 2002, were analyzed separately. Individual records were excluded from the analysis if explanatory variables were outside expected range (interval) obtained by examination of the data. The previous lactation length and the weaning to conception interval were limited within 1-60 days and 1-80 days, respectively. Approximately 5% of the records were eliminated. After data editing, 118079, 99411 and 70034 litter records were analyzed for farm A, B and C, respectively (Table 1).

Table 1. Data and pedigree structure

| Farm | A | B | C |
|---|---|---|---|
| No. of litter records | 118079 | 99411 | 70034 |
| No. of breeding females | 28364 | 27912 | 19170 |
| Litters per female | 4.16 | 3.56 | 3.65 |
| Females per common litter | 1.46 | 1.49 | 1.40 |
| Progenies per sire | 30.79 | 45.01 | 25.59 |
| Progenies per dam | 2.79 | 3.14 | 2.47 |
| No. of animals with records | 28364 | 27912 | 19170 |
| No. of ancestors | 10734 | 4823 | 4367 |
| No. of base animals | 3973 | 1224 | 872 |

Farms B and C had similar data structure regarding the number of litters per female (farm B = 3.56, farm C = 3.65) and smaller in comparison to farm A (4.16). All farms had similar number of animals that shared the same litter environment (farm A = 1.46, farm B = 1.49 and farm C = 1.40). There were some differences in number of progenies per sire (farm A = 30.79, farm B = 45.01 and farm C = 25.59).

For estimation of dispersion parameters for NBA the following RRM presented in scalar notation, was used:

$$
\begin{aligned}
y_{ijklmno} = {} & \mu + G_i + S_j + P_k + W_l + b_{I\,k}\left(x_{ijklmno} - \bar{x}\right) + b_{II\,k}\left(x_{ijklmno} - \bar{x}\right)^2 + b_{III}\left(z_{ijklmno} - \bar{z}\right) + \\
& + \sum_{s=1}^{3}\sum_{m=0}^{k} \alpha_{sm}\Phi_m\left(p^{*}_{ijklmno}\right) + \varepsilon_{ijklmno}
\end{aligned}
$$

where $y_{ijklmno}$ is NBA; $G_i$, $S_j$, $P_k$ and $W_l$ are fixed effects of sow genotype, mating season (year-month interaction), parity and weaning to conception interval, respectively. The weaning to conception interval was defined as effect with classes (1-3, 4, 5, 6, 7, 8, 9, 10-23, 24-33 and 34-70 days). The age at farrowing ($x_{ijklmno}$) was modelled as quadratic regression nested within parity. The previous lactation length ($z_{ijklmno}$) was fitted as linear regression. Statistical package SAS (SAS Institute, 2001) was used in development of fixed part of the model.

Random regressions on orthogonal LG polynomials of standardized parity ( $p^*$ ) were included for direct additive genetic, permanent environmental and common litter environmental effect. A standardized parity ( $p^*$ ), with range from -1 to +1, was derived as $p^* = \frac{2*(p - p_{\min})}{(p_{\max} - p_{\min})} - 1$, where $p_{\min}$ is the first parity and $p_{\max}$ is the last (tenth) parity in the data.

Legendre polynomials from the linear power (LG1) with two terms to cubic power (LG3) with four terms were fitted. Estimation of (co)variance components from RRM was based on Residual Maximum Likelihood (REML) method using the VCE-5 software package (Kovač and Groeneveld, 2002). Additionally, modul SAS/IML (SAS Institute, 2001) was used for computation of eigenvalues for covariance matrices of regression coefficients to quantify contribution of higher orders of LG polynomials. Dispersion parameters estimated by REML were used to obtain solutions for fixed and random effects in model. Predicted random regression coefficients for additive genetic effect were used for calculation of breeding value for NBA along trajectory.

## Results and discussion

The estimated phenotypic variances and ratios were presented in Figure 1. The estimates of phenotypic variance showed small increase from first to tenth parity.

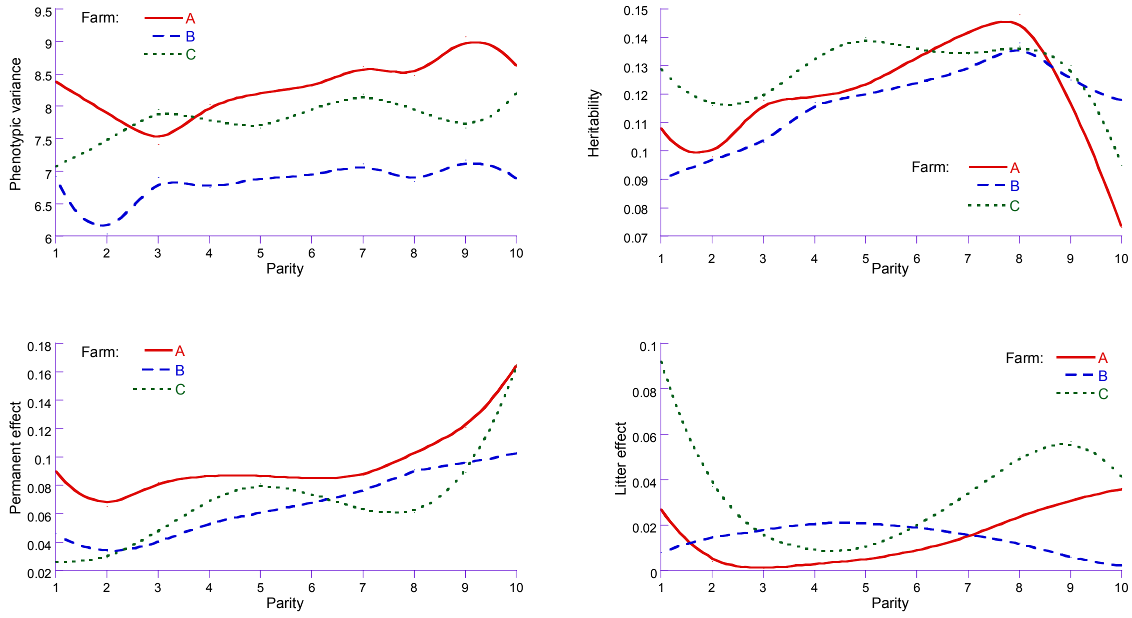

Figure 1. Phenotypic variances and proportions of the phenotypic variance over parities with Legendre polynomials of the cubic power for number of piglets born alive

Also, phenotypic variances for farm B were smaller in comparison to other two farms. Heritabilities for all three farms ranged from 0.09 to 0.14. These estimates are in agreement with the literature (Haley et al., 1988; Rothchild and Bidanel, 1998). In contrast, Hanenberg et al. (2001) and Duc et al. (1998) reported lower heritabilities (0.04 to 0.10). Increasing tendency of heritability estimates by parities was in agreement with other studies (Roehe and Kennedy, 1995). At the end of trajectory decrease in heritability was noticed, probably as a consequence of selection in previous parities and small number of data in the last parities. Permanent environmental effect (expressed as a ratio) generally increased over parities and ranged from 0.02 for farm C in first parity to 0.16 for farm A in tenth parity. These results for permanent environmental effect are consistent with those reported by Ferraz and Johnson (1993), Logar et al. (1999) and Chen et al. (2003). Magnitudes of common litter environmental effect (expressed as ratio) were generally small, ranged from 0.01 to 0.02. There were some differences in shape of curves between farms. Small magnitude of this effect may be because the number of full-sibs is usually relatively small (more than 50% litters had only one sow) and the large amount of cross-fostering was practiced on farms in Slovenia. Nevertheless, the effect of common litter environment is probably decreasing with aging of sow.

Eigenvalues for Legendre polynomials from linear to cubic power for all three farms were computed (Table2). Eigenvalues of covariance functions for the additive genetic effect varied for the different orders of polynomials. They showed that the constant (0th) term accounted between 80 and 90 % of the additive genetic variability for NBA.

Table 2. Eigenvalues (%) for additive genetic effect with different power of LG polynomials

| Farm | | A | | | B | | | C | |
|---|---|---|---|---|---|---|---|---|---|
| Eigenvalues | LG1 | LG2 | LG3 | LG1 | LG2 | LG3 | LG1 | LG2 | LG3 |
| 0th | 90.4 | 86.9 | 86.1 | 91.2 | 88.7 | 87.5 | 84.3 | 83.0 | 80.1 |
| 1st | 9.6 | 10.1 | 11.0 | 8.8 | 8.2 | 8.6 | 15.7 | 14.5 | 14.9 |
| 2nd | | 3.0 | 2.9 | | 3.1 | 3.2 | | 2.5 | 4.4 |
| 3rd | | | 0.0 | | | 0.7 | | | 0.0 |

This means that 10 to 20 % of variability was explained by individual genetic curves of sows. This proportion of variability was mainly covered by linear (8.2 to 15.7 %) and quadratic (2.5 to 4.4 %) coefficients. These values are higher compared to our previous study only for farm

A that included litter records from the first to the sixth parity (Luković et al., 2003). Also, the eigenvalues of covariance functions showed a quadratic Legendre polynomial with three regression coefficients to be sufficient to explain all additive genetic variability. Although, this study considered equal power of Legendre polynomials in order to provide equal opportunity of variation for all random effects, some evidence has been found in favor to a lower order needed for the genetic than for the permanent environmental effect (Van der Werf et al., 1998).

The solutions from RRM with cubic power for the random regression coefficients of animals were used to compute breeding values for NBA along trajectory. The curves for eight boars from the farm A with number of progenies between 500 and 850 showed that genetic merit function varies between individual animals (Figure 2). There were variations in the level and in shape of curves. Choosing boars whose predicted breeding value increases over parities seems possible to change shape of curves for NBA of sows.

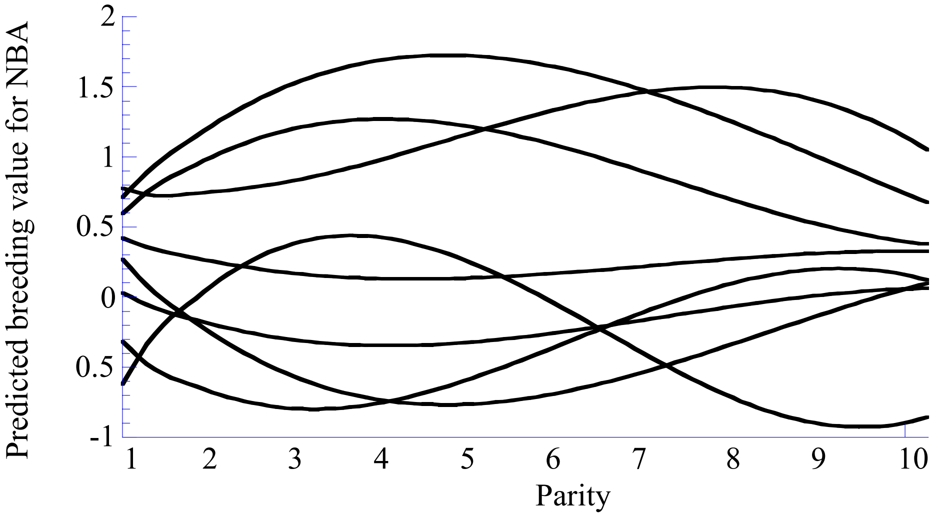

Figure 2. Predicted breeding values for number of piglets born alive over parities for eight boars

## Conclusion

Parameters of dispersion for number of pigs born alive changed over parities and differed between populations. The existence of 10 to 20 % of non-constant additive genetic variation for NBA indicates that RRM could be used for selection on level and possibly on persistency of litter size in pigs.

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