

Genetic parameters for uniformity of fattening pigs' growth traits

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Summary

In livestock, uniformity of optimum traits is highly desirable because of its advantages throughout the production chain, such as an improved animal welfare, quality of the end product and automation of the process. Recent evidence in different livestock species confirms the existence of a genetic basis for environmental variance (V_E). This implies the possibility to genetically select breeding animals towards an increased uniformity of their offspring. In this study, genetic parameters of V_E were estimated using the double hierarchical generalized linear model (DHGLM) framework in R. This was done in pigs for the traits average daily gain from birth until a test period (ADG_0) and during the test period (ADG_{test}) and age at slaughter (AGE). Results show GCV_E values of 24-27%, meaning that one generation of selection can reduce the V_E of these traits with 24-27%. However, low h_v^2 values (0.006-0.008) indicate that a large dataset is needed to obtain accurate estimated breeding values for V_E . For application in practice the accuracies need to be increased significantly. Furthermore, the use of adequate data transformation techniques for the estimation of the genetic correlation between mean and environmental variance appears necessary to counter scale effects.

Keywords: heritability, environmental variance, uniformity, growth traits, pigs, double hierarchical generalized linear model

Introduction

The past decades, intensive and accurate selection on the mean of (re)production traits has resulted in trait levels which are challenging biological limits. For these traits, increasing uniformity while maintaining the optimal mean trait value is the way to cope with the increasing demands on animal welfare and robustness, reducing environmental impact, rising quality requirements and increasing automation (Merks et al., 2012; Mulder et al., 2008). Recent analysis indicated existence of a genetic basis for environmental variance (V_E), making it possible to select animals for increased uniformity (Blasco et al., 2017; Khaw et al., 2016; Hill & Mulder, 2010; Sell-Kubiak et al., 2015). Uniformity in pigs presents several benefits to the pork chain. It can reduce the necessity to regroup piglets after weaning, avoiding stress and fights associated with a new social hierarchy. Uniform growing pigs will utilize their feed – which is based on an ‘average’ pig – more efficiently, decreasing emissions and as such providing an environmental benefit (Merks et al., 2012). Furthermore, it facilitates all-in all out systems, and on top of that, a farmer gets paid premiums for carcasses within certain weight ranges, leading to a direct economic benefit (Mulder et al., 2008).

The main objective of this study is to estimate genetic parameters of V_E (h_v^2 and GCV_E), as well as vEBVs for growth traits in pigs by using double hierarchical generalized linear models (DHGLM). Furthermore, the genetic correlation between mean and V_E (r_{Amv}) is estimated.

Material and methods

Pig Dataset and growth traits

The dataset contained 30,602 records from the period 2007-2016 of the crossbred offspring of 1,446 Pietrain sires. Approximately 20 - 30 offspring were tested per sire, originating from at least 3 litters. Growth traits were average daily gain (ADG_0) from birth to 70d, from 70d until slaughter (ADG_{test}) and age at slaughter (AGE; in days). Pigs were transported to the slaughter house at an intended end weight of about 115 kg which makes ADG_{test} and AGE in essence a measure for lifetime growth.

Genetic parameters

The estimated genetic parameters were the heritability of environmental variance (h_v^2) and the genetic coefficient of variation for environmental variance (GCV_E) based on the formulae of Mulder et al. (2007). The potential response of selection on the phenotypic variation (GCV_P) was calculated as $GCV_P = GCV_E * \frac{\sigma_E^2}{\sigma_p^2}$. Standard errors for h_v^2 , GCV_E and GCV_P were estimated based on Mulder et al. (2016). Genetic correlations between mean and V_E (r_{Amv}) were estimated using the method of Calo (1973) and using Pearson correlation.

Double hierarchical generalized linear model and model selection

Genetic parameters were estimated using a sire model via the double hierarchical generalized linear models (DHGLM) framework using the extension of Felleki et al. (2012). The DHGLM is a bivariate linear mixed model consisting of a mean part with observations y and a dispersion part (residual variance, denoted with the subscript d) with response variables ψ . The used DHGLM was:

$$\begin{bmatrix} y \\ \psi \end{bmatrix} = \begin{bmatrix} X & 0 \\ 0 & X_d \end{bmatrix} \begin{bmatrix} b \\ b_d \end{bmatrix} + \begin{bmatrix} Z & 0 \\ 0 & Z_d \end{bmatrix} \begin{bmatrix} a_{sire} \\ a_{d_{sire}} \end{bmatrix} + \begin{bmatrix} V & 0 \\ 0 & V_d \end{bmatrix} \begin{bmatrix} a_{dam} \\ a_{d_{dam}} \end{bmatrix} + \begin{bmatrix} U & 0 \\ 0 & U_d \end{bmatrix} \begin{bmatrix} pe \\ pe_d \end{bmatrix} + \begin{bmatrix} e \\ e_d \end{bmatrix} \quad (1)$$

In this equation X and X_d are design matrices for fixed effects whereas Z , Z_d , V , V_d , U and U_d are design matrices for random effects. The additive genetic sire effects (a_{sire} , $a_{d_{sire}}$) were assumed to be normally distributed

$$\begin{matrix} a_{sire} \\ a_{d_{sire}} \end{matrix} \sim N \begin{pmatrix} 0, A\sigma_{a_{sire}}^2 \\ 0, A\sigma_{a_{d_{sire}}}^2 \end{pmatrix}, \begin{matrix} a_{dam} \\ a_{d_{dam}} \end{matrix} \sim N \begin{pmatrix} 0, A\sigma_{a_{dam}}^2 \\ 0, A\sigma_{a_{d_{dam}}}^2 \end{pmatrix}, \begin{matrix} pe \\ pe_d \end{matrix} \sim N \begin{pmatrix} 0, I\sigma_{pe}^2 \\ 0, I\sigma_{pe_d}^2 \end{pmatrix} \quad (2)$$

where A is the additive genetic relationship matrix and it is assumed that $\sigma_{sire}^2 = \frac{1}{4}\sigma_a^2$ for both the mean as the dispersion part of the model. The additive genetic dam effects (a_{dam} , $a_{d_{dam}}$), the permanent environment effects (pe , pe_d) and residual variances (e , e_d) were respectively assumed to be distributed as follows (where I stands for the identity matrix):

$$\begin{bmatrix} e \\ e_d \end{bmatrix} \sim N \left(0 \begin{bmatrix} W^{-1} \sigma_e^2 & 0 \\ 0 & W_d^{-1} \sigma_{e_d}^2 \end{bmatrix} \right) \quad (5)$$

W and W_d are weight matrices ($W = \Phi^{-1} = \text{diag}(\exp(\hat{\psi})^{-1})$, $W_d = \text{diag}(\frac{1-h}{2})$) which are used in the iterating algorithm of the DHGLM model (Mulder et al., 2016). Different models were tested and compared for each considered growth trait. Model selection was based upon the estimation of the adjusted profile h-likelihood (APHL). To compare models and to consider the number of variance parameters (t), APHL is combined with Akaike's information criterion (AIC): models with a lower AIC value were considered to be more adequate.

$$AIC = APHL + 2t \quad (7)$$

The DHGLM model was run via the *hglm* package in R. Estimation of AIC-values was included in this model and genetic parameters were also calculated using R.

Results and discussion

Moderate to high heritabilities were estimated for the mean part of model (table 1).

Table 1. Variance components for the **mean** part of the model for the different growth traits.

Variance Component	ADG ₀	ADG _{test}	AGE
sire ¹ (se)	489.4 (26.3)	648.3 (36.7)	12.9 (0.7)
dam (se)	595.2 (23.7)	638.9 (27.9)	12.8 (0.6)
Permanent environment (se)	586.6 (49.9)	1741.4 (139.8)	36.5 (2.9)
Residual variance ² (se)	1400.1 (12.6)	2851.2 (25.5)	59.4 (0.5)
Additive genetic (se)	1957.6 (105.1)	2593.2 (146.6)	12.9 (2.9)
h_m^2 (se) ²	0.64 (0.030)	0.44 (0.024)	0.42 (0.024)

¹ Additive genetic variance of the sire component is calculated as $\frac{1}{4} * \sigma_a^2$ (additive genetic)

² Calculated based on the model with the homogenous residual variance

For V_E , genetic coefficients of variation were similar between traits, with a GCV_E of 0.241-0.265 and GCV_P of 0.110-0.129. Hence, changing V_E with one genetic standard deviation can decrease the environmental variance of these traits with 24-27% and the phenotypical variance with 11-13% indicating a great potential to improve the uniformity of growth traits in pigs. However, values of h_v^2 ranged from 0.006-0.008. Consequently, accuracy of mass-selection to improve the uniformity will be low, unless a significant amount of information is available. Ibáñez-Escriche et al. (2008) calculated genetic parameters of V_E in purebred Landrace pigs (weight at slaughter at 175d). Their results (GCV_E of 0.34 and h_v^2 of 0.011) were comparable to our findings.

Table 2. Variance components for the environmental variance part of the model for the different growth traits.

Variance Component	ADG ₀	ADG _{test}	AGE
sire ¹ (se)	0.015 (0.002)	0.017 (0.002)	0.018 (0.002)

dam (se)	0.019 (0.002)	0.010 (0.002)	0.010 (0.002)
Permanent environment (se)	0.024 (0.003)	0.065 (0.006)	0.065 (0.007)
Residual variance ² (se)	1.144 (0.010)	1.185 (0.010)	1.174 (0.010)
Additive genetic (se)	0.058 (0.008)	0.067 (0.009)	0.070 (0.010)
h_v^2 (se)	0.006 (0.001)	0.008 (0.001)	0.008 (0.001)
GCV_E (se)	0.241 (0.017)	0.259 (0.018)	0.265 (0.018)
GCV_P (se)	0.110 (0.008)	0.126 (0.009)	0.129 (0.009)

¹ Additive genetic variance of the sire component is calculated as $\frac{1}{4} * \sigma_a^2$ (additive genetic)

The genetic correlation between mean and environmental variance (r_{Amv}) is a crucial parameter and Pearson correlations (0.12-0.21) and Calo correlations (0.25-0.38) were positive, suggesting that an increase of the mean trait level is genetically correlated with an increased V_E (or decreased uniformity). However, ADG_{test} and AGE presented some conflicting results. The expectation was that r_{Amv} in absolute value would be approximately the same, but the true values should have an opposite sign. The origin for these positive r_{Amv} could lie in scale effects: a larger mean value leading to a greater variance. This needs further investigation and data transformation techniques, e.g. Box-Cox transformation, could be necessary to obtain an adequate estimation of r_{Amv} .

Conclusion

We estimated genetic parameters of V_E for growth traits in a terminal line of pigs and the results show a great potential to improve the uniformity of growth traits in pigs. However, the low accuracy for selection on uniformity is still an obstacle towards its implementation in current breeding programs. Furthermore, possible scale effects need to be investigated to arrive at robust estimation of the genetic correlation between mean and environmental variance.

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