

# ANALYSIS OF BACKFAT THICKNESS IN ON-FARM TESTED GILTS IN SLOVENIA USING REACTION NORMS

Martina PLANINC<sup>1</sup>, Milena KOVAČ<sup>2</sup>, Špela MALOVRH<sup>3</sup>

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## *Analysis of backfat thickness in on-farm tested gilts in Slovenia using reaction norms*

Animals have the ability to respond to differences in environment, which can be called phenotypic plasticity or environment sensitivity. Robust animal, that show little variability across environments, are less sensitive. Therefore, the aim of this study was to investigate genotype by environment interaction for backfat thickness using reaction norm. Random regression model have become common for analyzing data on individuals over time. Reaction norms were predicted for 239 sires. Results show how sires differ across environments for backfat thickness.

**Key words:** pigs / gilts / genetics / environment / maternal genotype / backfat thickness / reaction norms / Slovenia

## 1 INTRODUCTION

The ability of living organisms to respond to changes in their environments is called phenotypic plasticity or environmental sensitivity (de Jong and Bijma, 2002). Genotypes with highly variable production across different environments are characterized as 'plastic'. However, genotypes with little variability across environments are called as 'robust'. Population under high selection pressure become more sensitive and as such, robustness has rapidly become a term with high interest in animal production (Knap, 2005; ten Napel *et al.*, 2006). Robustness is not a trait which is easily measured. Thus, there are many definitions for it. Among others, it is defined as the ability of even production potential through a wide range of environments. Robust animals should be less sensitive

## *Reakcijske norme za debelino hrbtne slanine pri testiranih mladica v Sloveniji*

Živali imajo možnost, da se na razlike v okolju odzivajo različno. To imenujemo fenotipska plastičnost ali okoljska občutljivost. Robustne živali, ki kažejo majhno variabilnost med okolji, so manj občutljive. Namen prispevka je z reakcijskimi normami preučiti interakcijo med genotipom in okoljem za debelino hrbtne slanine. Za analizo podatkov smo uporabili model z naključno regresijo, reakcijske norme smo napovedali 239 očetom. Rezultati kažejo, kako se preučevana lastnost za posameznega očeta skozi okolja spreminja.

**Ključne besede:** prašiči / mladice / genetika / okolje / maternalni genotip / debelina hrbtne slanine / reakcijske norme / Slovenija

to stress and are expected to recover more quickly than less robust animals. This indicates that robust animals function well under a wide range of environments.

Phenotypic plasticity is related to genotype by environment interaction. In pig breeding, genotype by environment interaction could reduce genetic improvement if breeding values for any trait used as breeding goal are predicted on records obtained in specific test environments. However, productive animals are raised in different environments. A key problem is to decide under which conditions animals should be tested and how genotype by environment interaction can be included in selection procedure (de Jong and Bijma, 2002). The evaluation of genotypes in only one environment cannot be used to predict the performance of pigs reared in different environments whenever genotype by environment

<sup>1</sup> Univ. of Ljubljana, Biotechnical Fac., Dept. of Animal Science, Groblje 3, SI-1230 Domžale, Slovenia

<sup>2</sup> Same address as 1, e-mail: milena.kovac@bf.uni-lj.si

<sup>3</sup> Same address as 1, e-mail: spela.malovrh@bf.uni-lj.si

interaction exists. Genetic evaluation requires a possibility of sire ranking in each environment.

Kolmodin *et al.* (2002) applied random regression models as reaction norm models to express performance of a genotype as a function of the environment. If different genotypes have different reaction norms, then there is genotype by environment interaction (de Jong and Bijma, 2002). However, these models require definition of environment constraints on a continuous scale. Random regression models have become common for the analysis of longitudinal data or repeated records on individuals over time (Schaeffer, 2004). Some studies on genotype by environment interaction using reaction norm models have been reported for litter size in pigs (Knap and Su, 2008), for growth traits in pigs (Hermesch *et al.*, 2008; Li and Hermesch, 2012), and for milk production in dairy cattle (Kolmodin *et al.*, 2002; Shariati *et al.*, 2007; Logar *et al.*, 2007).

The objective of this study was to apply reaction norm model to evaluate genotype by environment interaction for backfat thickness in gilts in Slovenia.

## 2 MATERIAL AND METHODS

Individual records and pedigree information were collected for 19053 on-farm tested animals. Data comprising Slovenian Landrace – line 11, Slovenian Large White 22 and Hybrids 22x11 (21) and 11x22 (12) gilts

**Table 1:** Descriptive statistics for body weight, daily gain, and backfat thickness ( $N = 18805$ )

**Preglednica 1:** Opisna statistika za telesno maso, dnevni prirast in debelino hrbtnih slanin ( $N = 18805$ )

Variable	Mean	SD	Min.	Max.
Body weight (kg)	108.8	13.8	80	200
Daily gain (g/day)	554	46	375	708
Backfat (mm)	10.5	2.2	4	24

were routinely recorded from 2000 to 2013. Animals were raised on 46 family farms under production conditions. Records were included if body weight was at least 80 kg, and age at the end of the test was at most 300 days. The environmental variable was defined as herd-year average of daily gain. After editing, 18805 records were obtained on gilts weighing on average 108.8 kg at the end of test (Table 1). The average backfat thickness was 10.5 mm ( $\pm 2.2$ ). The observations were spread over 1864 herd-year seasons. The pedigree file contained animals with records and up to five generations of ancestors. There were 239 different sires included. The variable use to characterize

the environment of animal was defined as deviation of herd-year daily gain on test and backfat thickness.

Linear regression was applied to describe random sire effect over environments. The following mixed model was used:

$$y_{ijklmno} = \mu + G_i + S_j + R_k + b(x_{ijklmn} - \bar{x}) + h_k + s_{0im} + s_{1im} + w_{ijklmn} + l_{ijklmn} + e_{ijklmno} \quad (1)$$

where  $y_{ijklmno}$  is a trait,  $\mu$  is overall mean for trait. The fixed part of model included genotype  $G_i$  ( $i = 1, 2, 3, 4$ ), season  $S_j$  ( $j = 1, 2, \dots, 160$ ) and herd  $R_k$  ( $k = 1, 2, \dots, 46$ ). Animal weight at the end of test ( $x_{ijklmn}$ ) was described by linear regression with  $b$  as linear regression coefficient. Random part of model included common herd-year environment ( $h_{ki}$ ), common litter environment ( $l_{ijklmn}$ ), intercept (level) of reaction norm for sire ( $s_{0im}$ ), random regression coefficient (slope) for sire ( $s_{1im}$ ) with environmental variable ( $w_{ijklmn}$ ) expressed as deviation of herd-year average of daily gain. Variable ( $e_{ijklmno}$ ) is random residual.

Sire effect  $s_0$  and  $s_1$  were assumed to be normally distributed with mean zero and covariance structure:

$$\text{var} \begin{bmatrix} s_0 \\ s_1 \end{bmatrix} = \begin{bmatrix} \sigma_{s_0}^2 & \sigma_{s_{01}} \\ \sigma_{s_{01}} & \sigma_{s_1}^2 \end{bmatrix} \otimes \mathbf{A} = \mathbf{S}_0 \otimes \mathbf{A} = \frac{1}{4} \begin{bmatrix} \sigma_{\alpha_0}^2 & \sigma_{\alpha_{01}} \\ \sigma_{\alpha_{01}} & \sigma_{\alpha_1}^2 \end{bmatrix} \otimes \mathbf{A} \quad (2)$$

where  $s_0$  and  $s_1$  are vectors of unknown parameters for intercept and slope in random regression for sire effect. Genetic variance was partitioned into three components: variance for level ( $\sigma_{\alpha_0}^2$ ), for slope ( $\sigma_{\alpha_1}^2$ ), and covariance between the two ( $\sigma_{\alpha_{01}}$ ). Matrix  $\mathbf{A}$  is the additive relationship matrix for sire and the matrix  $\mathbf{S}_0$  is equal to one quarter of the genetic variance matrix for level and slope.

The environmental variable herd-year averages were grouped into six classes allowing for heterogeneous residual variances across environments. The observations were assigned to classes by their environment value. The lowest values formed first class and the highest values formed the sixth class. The classes had equal range of environmental variables. The residuals were assumed to be independently distributed with mean zero and variance  $\sigma_{te}^2$  within environmental class  $t$ .

In the reaction norm models, breeding values are described by linear regression with level and slope as parameters. Predicted breeding values within environment  $w_t$  could be expressed as predicted offspring performance  $POP_{im/wt}$ ; Kolmodin *et al.*, 2002) calculated as:

$$POP_{im/wt} = s_{0im} + s_{1im}w_t \quad (3)$$

SAS software (SAS Inst. Inc., 2008) was used for data editing and finalization of the results. Dispersion parameters were estimated using residual maximum likelihood methodology as applied in VCE-5 (Groeneveld *et al.*, 2010).

### 3 RESULTS AND DISCUSSION

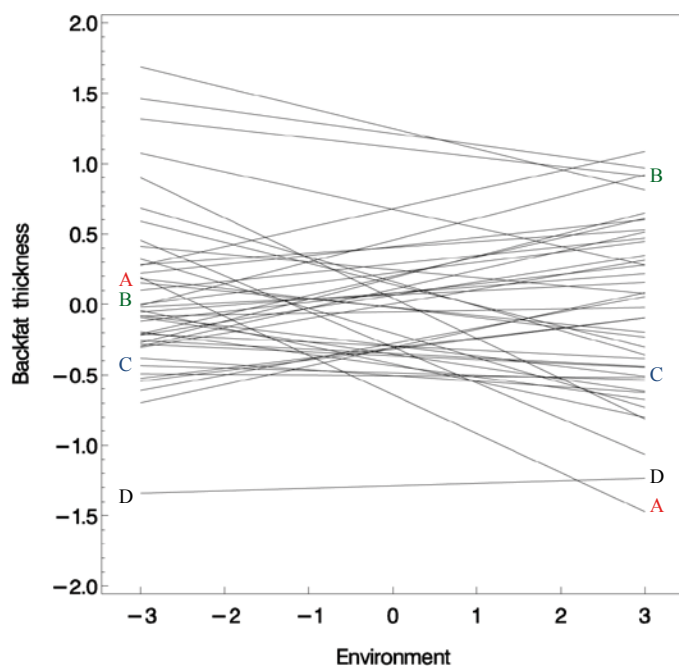
Estimates of genetic (co)variances and correlations together with residual variance estimates in the reaction norm model are shown in table 2.

Estimates of residual variances decrease progressively with increasing environmental variable for backfat thickness suggesting heterogeneous residual variances. In better environments, testing conditions of gilts are

**Table 2:** Variance components and genetic correlations between level and slope for backfat thickness

**Preglednica 2:** Komponente variance in genetska korelacija med stopnjo in naklonom za debelino hrbtne slanine

(Co)variance component		Estimate $\pm$ SEE	Genetic correlation
Sire	level	0.30 $\pm$ 0.04	0.14 $\pm$ 0.13
	slope	23.84 $\pm$ 7.26	
Residual variances in class	1	2.14 $\pm$ 0.04	
	2	2.63 $\pm$ 0.13	
	3	1.63 $\pm$ 0.02	
	4	1.53 $\pm$ 0.02	
	5	1.37 $\pm$ 0.03	
	6	1.20 $\pm$ 0.07	



**Figure 1:** Reaction norms for sample of 43 sires for backfat thickness (mm) in different herd environments (x-axis shows deviation from average environment in SD units of herd-year daily gain average)

**Slika 1:** Reakcijske norme za debelino hrbtne slanine (mm) v različnih okoljih pri 43 očetih (na x-osi je prikazan odklon od povprečnega okolja, ki je definirano kot povprečni dnevni prirast v čredi znotraj leta)

more standardized and the gilts express more uniformity as in barren environments.

Estimated sire variance for slope was 23.84 (mm/(g/day))<sup>2</sup>. Genetic correlation between level and slope was estimated to 0.14, which is an indication of potential re-ranking. As long as the genetic variance of the reaction norm slope is greater than zero and genetic correlation among environments is smaller than one, there is genotype by environment interaction (de Jong and Bijma, 2002). Genetic correlation between the reaction norm of level and slope far from 1 will cause re-ranking of animals among environments (Su *et al.*, 2006).

Reaction norm was used also to describe genetic variability of pig carcass weight as a function of heat stress of crossbreed pigs in North Carolina (Zumbach *et al.*, 2008). They estimated negative correlation between the intercept and slope. This could be due to increased sensitivity of animals to heat stress.

Sire effects for 43 sires are illustrated by linear regression on Figure 1 showing re-ranking of sires across environments. For backfat thickness, the best animals have the most negative breeding values predicted, because selection is for thinner backfat. Sires A and B are very sensitive, in other words not robust to the environmental changes. Sire A is more superior with less backfat thickness in rich environment (Fig. 1, right) and is ranked on the 27<sup>th</sup> place only in the most barren environment (Fig. 1, left), while sire B fits better to barren than rich environment. Both are very specific and not well suited for the whole spectrum of environmental conditions. Nevertheless, sire D performed well and has excellent as well as steady genetic merit across all environments. Sire C has a robust genotype as well. Its breeding values seems to be more or less constant over environments considered, but the level of breeding value is worse than the level for sire D. In general, re-ranking observed was greater than expected in such small population.

Re-ranking of boars in organic and conventional pig production was studied in Swedish Landrace (Wallenbeck *et al.*, 2009) for growth rate and backfat thickness. Wallenbeck *et al.* (2009) found re-ranking of boars between the two production systems. In their study, the best boar in the conventional environment (boar X) was ranked on

place 11th in the organic environment. At the same time, the lowest ranking boar in the conventional environment was almost as good as boar X in the organic environment. But, the positive correlations mean that boars that are ranked highly on conventional breeding value are in many cases ranked highly on organic breeding value. This indicates that interactions GxE are weak.

Reaction norms were used to investigate sire by environment interactions for growth rate and backfat thickness in Australian pigs (Li and Hermesch, 2012). Li and Hermesch (2012) reported, that Large White was the most sensitive breed for growth rate and backfat thickness, while Duroc was the most robust breed across their production systems.

#### 4 CONCLUSIONS

Robustness of gilts in Slovenia was studied using reaction norm model. Analyses were performed using random regression model for backfat thickness. Breeding value as well as ranking of some sires (example sire A and B) changed over environments. There was a group of sires which breeding values and rank did not change much over environments. Overall results proved existence of genotype by environment interaction. This information is useful to setup strategic performance recording procedures for genetic improvement of productivity and robustness.

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