GENETIC DETERMINISM OF METABOLIC RESOURCE ALLOCATION IN PIGS: A STUDY IN A DUROC POPULATION

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INTRODUCTION

Because feed is the major cost in pork production, optimization of the efficiency in the use of the food resources is an important focus for improvement in pig production.

In the present study we propose to consider the individual variation in the resource allocation pattern and its possible utilization into an index of selection for feed efficiency.

OBJECTIVE

To analyse the variability and genetic determinism of individual metabolic resource allocation for body weight maintenance and growth in pigs, using the procedure described by Piles and Varona (2006)

MATERIAL AND METHODS

Data Collection

- **Animal material:** 370 castrated males, belonging to a Duroc commercial line
- Animals stayed under normal intensive conditions and were fed *ad libitum* on a standard diet
- Daily **feed intake** was recorded automatically by means of an electronic identification system during a period of 106 d (mean of 2.2 kg/day)
- **Weight** was recorded at 5 timepoints (approximately each 20 days) during fattening (until 190 d of age and 120 kg of live weight)
- Individual **weight gain** and **average body weight** were calculated per animal at each 15 days period.

Statistical Analyses

A procedure based on a hierarchical Bayesian analysis has been used.

First Stage of the model

$$y_{ij} = a_i + b_i \times P_{ij}^{0.75} + d_i \times G_{ij} + e_{ij}$$

- y_{ij} cumulative **food intake** of individual i during the 15d-period j
- a_i individual intercept
- $P_{ij}^{0.75}$ average **metabolic body weight** of individual i in the 15d-period j
- G_{ij} cumulative body **weight gain** of individual i during the 15d-period j
- b_i d_i **individual regression coefficients** of food intake on, respectively, metabolic body weight and weight gain
- e_{ij} residual effect

Second Stage of the model

$$(b,d \mid \beta_b,\beta_d,u_b,u_d,p_b,p_d,G,R,P) \sim N\left(\begin{matrix} X\beta_b + Zu_b + Wp_b \\ X\beta_d + Zu_d + Wp_d \end{matrix}, R \otimes I\right)$$

$$\left(\begin{matrix} u_b \\ u_d \end{matrix} \mid G\right) \sim N(0, G \otimes A); \quad \left(\begin{matrix} p_b \\ p_d \end{matrix} \mid P\right) \sim N(0, P \otimes I)$$

- ***b***, ***d*** vectors of individual regression coefficients on, respectively, body weigh and growth
- $\boldsymbol{\beta}_b$, $\boldsymbol{\beta}_d$ vectors of corresponding systematic effects (farm origin and batch of fattening)
- $\mathbf{u}_b$, $\mathbf{u}_d$ vectors of additive genetic effects for ***b*** and ***d***
- $\mathbf{p}_b$, $\mathbf{p}_d$ box effect
- ***G***, ***P***, ***R*** genetic, box and residual (co)variances matrices

RESULTS

Statistics of posterior marginal distributions of **additive genetic (co)variances**, **proportion of additive variance** and **genetic correlation** of / between:

- partial regression coefficients of food intake on metabolic body weight (*b*).
- partial regression coefficients of food intake on body weight gain (*d*).

		Posterior Mean	Posterior standard deviation	Highest posterior interval at 95%	Monte Carlo error
Additive genetic variance of ***b***	$\sigma^2_{A(b)}$	0.016	0.009	0.000, 0.035	0.000048
Additive genetic covariance between ***b*** and ***d***	$\sigma_{A(bd)}$	0.015	0.007	0.001, 0.030	0.000091
Additive genetic variance of ***d***	$\sigma^2_{A(d)}$	0.024	0.014	0.000, 0.061	0.000011
Proportion of additive genetic variance for ***b***	h^2_b	0.431	0.180	0.073, 0.794	0.000421
Proportion of additive genetic variance for ***d***	h^2_d	0.370	0.156	0.068, 0.694	0.000122
Genetic correlation between ***b*** and ***d***	r_{Abd}	0.811	0.266	0.250, 1.000	0.000665

Posterior means for proportion of additive genetic variance of coefficients b and d took medium to high values (0.43 and 0.37), and in both cases the highest posterior intervals at 95% did not include zero.

CONCLUSIONS

Individual metabolic resource allocation for body weight maintenance and growth have an important genetic determinism in our Duroc pigs population

Individual efficiency in the use of food resources for maintenance and growth could be improved by selection

Described model would allow performing genetic evaluation for biological efficiency, and using these breeding values into an index of selection for feed efficiency.