

Estimation of genetic variation in residual variance in female and male broiler chickens

Han Mulder, W.G. Hill, A. Vereijken, R. F. Veerkamp
(herman.mulder@wur.nl)

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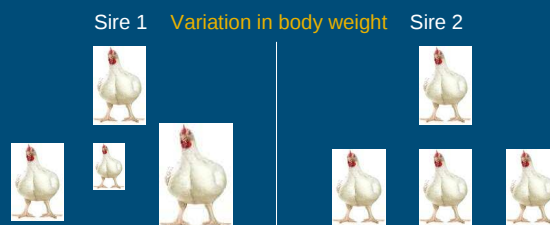
Animal Breeding & Genomics Centre



Introduction

What are genetic differences in residual variance?

- Genotypes differ in environmental/ residual variance



Introduction

Existence

- Analysis of large data sets
 - Litter size in sheep (SanCristobal-Gaudy et al., 2001)
 - Litter size in pigs (Sorensen and Waagepetersen, 2003)
 - Body weight in snails (Ros et al., 2004)
 - Body weight in broilers (Rowe et al., 2006)
 - Carcass weight in pigs (Ibanez-Escriche et al., 2008a)
 - Body weight in mice (Ibanez-Escriche et al., 2008b)
- Analysis of laboratory species
 - Bristle number in Drosophila (Mackay and Lyman, 2005)

Introduction

Relevance

- Slaughterhouses penalize excessive variability
 - Penalty when too many animals are outside preferred range
- To increase robustness against unknown environmental disturbances
- Even though heritability of residual variance is low, large responses are possible (Mulder et al., 2007, 2008)

Objective

- To estimate genetic variability in residual variance for body weight in broilers
- To estimate genetic correlation between mean body weight and residual variance
- To estimate genetic correlation between female and male residual variance

Material and methods

Data

- Data set broilers: body weight at 6 weeks
 - At least 50 offspring of one sex per sire
 - Five animals per joint effect of hatch week of individual and its dam
 - 26,972 records females; 24,407 records males
 - 402 sire families for females; 369 sire families for males
 - 123,328 animals in pedigree file

Material and methods

Analysis

- Use of ASREML
- First stage: body weight
 - Heterogeneous residual variance per sire family
- Second stage: residuals of first stage (e)
 - Log-transformed squared residuals ($\ln(e^2)$)

$$y_{ijklmn} = \mu + h + age + hwihwd + A_m + D + e$$

$$\ln(e^2_{ijklmn}) = \mu + h^* + age^* + hwihwd^* + A_{res} + e_{res}$$

Material and methods

Analysis

- Bivariate analysis of body weight and $\ln(e^2)$
 - 20 Iterations – updating $\ln(e^2)$ every iteration

$$\begin{bmatrix} y \\ \ln(e^2) \end{bmatrix} = \begin{bmatrix} X_y & 0 \\ 0 & X_{\ln(e^2)} \end{bmatrix} \begin{bmatrix} b \\ b^* \end{bmatrix} + \begin{bmatrix} Z_y & 0 \\ 0 & Z_{\ln(e^2)} \end{bmatrix} \begin{bmatrix} a_m \\ a_{res} \end{bmatrix} + W_y d_y + \begin{bmatrix} e_y \\ e_{res} \end{bmatrix}$$

Results

Heritabilities

Sex	Method	h_m^2	Parameter h_v^2	GCV_E
Females	Univariate	0.324 (0.026)	0.022 (0.002)	0.352
	Bivariate	0.400 (0.024)	0.037 (0.003)	0.502
Males	Univariate	0.248 (0.026)	0.012 (0.001)	0.215
	Bivariate	0.320 (0.027)	0.032 (0.003)	0.404

Results

Genetic correlation

- Genetic correlation between mean and residual variance
 - Females: -0.41 (se = 0.03)
 - Males: -0.45 (se = 0.04)
- What is the biological meaning of a negative genetic correlation between mean and residual variance?
 - Disease susceptibility?

Results

Genetic correlation

- Genetic correlation between female and male residual variance
 - 0.11 (se = 0.09)
- Why are females and males so different in variability?
 - Heritabilities and variances are also different for both sexes

Discussion

- Current method can be used in standard software packages for REML and BLUP
- Selection response after one generation of selection in sib testing scheme:
 - Reduction of residual variance: 10-24%

Conclusion

- Heritability for residual variance is between 0.012 and 0.037
 - Large genetic coefficient of variation
- Genetic correlation between mean and residual variance is -0.41 and -0.45 in females and males, respectively
- Genetic correlation between female and male residual variance is 0.11
- Final conclusion:
Selection for uniformity seems possible



Acknowledgement

Hendrix Genetics: providing data

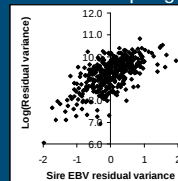
Thank you for your attention!!!!

Questions?????

Extra results

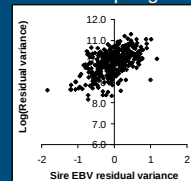
Relationship between EBV and observed residual variance

Female offspring



Correlation = 0.65

Male offspring



Correlation = 0.54

Material and methods

Analysis

- Bivariate analysis of body weight and $\ln(e^2)$
 - 20 Iterations – updating $\ln(e^2)$ every iteration

$$\begin{bmatrix} y \\ \ln(e^2) \end{bmatrix} = \begin{bmatrix} X_y & 0 \\ 0 & X_{\ln(e^2)} \end{bmatrix} \begin{bmatrix} b \\ b^* \end{bmatrix} + \begin{bmatrix} Z_y & 0 \\ 0 & Z_{\ln(e^2)} \end{bmatrix} \begin{bmatrix} a_m \\ a_{res} \end{bmatrix} + W_y d_y + \begin{bmatrix} e_y \\ e_{res} \end{bmatrix}$$

$$\begin{bmatrix} a_m \\ a_{res} \end{bmatrix} \sim MVN(0, A \otimes G_m) \quad \begin{bmatrix} e_y \\ e_{res} \end{bmatrix} \sim MVN(0, I \otimes R)$$

$$G_m = \begin{bmatrix} \sigma_{A_m}^2 & r_{A_m, A_{res}} \sigma_{A_m} \sigma_{A_{res}} \\ r_{A_m, A_{res}} \sigma_{A_m} \sigma_{A_{res}} & \sigma_{A_{res}}^2 \end{bmatrix} \quad R = \begin{bmatrix} \sigma_{e_p}^2 & 0 \\ 0 & \sigma_{e_{res}}^2 \end{bmatrix}$$