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

Animal (2009), **3:12**, pp 1673–1680 © The Animal Consortium 2009
doi:10.1017/S1751731109990668

animal

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

H. A. Mulder[1†], W. G. Hill[2], A. Vereijken[3] and R. F. Veerkamp[1]

[1]*Animal Breeding and Genomics Centre, Animal Sciences Group, PO Box 65, 8200 AB Lelystad, The Netherlands;* [2]*Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Edinburgh EH9 3JT, UK;* [3]*Hendrix Genetics B.V., Breeding Research and Technology Centre, Spoorstraat 49, PO Box 114, 5830 AC Boxmeer, The Netherlands*

(Received 19 December 2008; Accepted 17 July 2009; First published online 11 August 2009)

In breeding programs, robustness of animals and uniformity of end product can be improved by exploiting genetic variation in residual variance. Residual variance can be defined as environmental variance after accounting for all identifiable effects. The aims of this study were to estimate genetic variance in residual variance of body weight, and to estimate genetic correlations between body weight itself and its residual variance and between female and male residual variance for broilers. The data sets comprised 26 972 female and 24 407 male body weight records. Variance components were estimated with ASREML. Estimates of the heritability of residual variance were in the range 0.029 (s.e. = 0.003) to 0.047 (s.e. = 0.004). The genetic coefficients of variation were high, between 0.35 and 0.57. Heritabilities were higher in females than in males. Accounting for heterogeneous residual variance increased the heritabilities for body weight as well. Genetic correlations between body weight and its residual variance were −0.41 (s.e. = 0.032) and −0.45 (s.e. = 0.040), respectively, in females and males. The genetic correlation between female and male residual variance was 0.11 (s.e. = 0.089), indicating that female and male residual variance are different traits. Results indicate good opportunities to simultaneously increase the mean and improve uniformity of body weight of broilers by selection.

Keywords: genetic heterogeneity of residual variance, body weight, broilers, genetic parameters, uniformity

Implications

Robustness of animals and uniformity of end product can be improved by exploiting genetic variation in uniformity in breeding programs. The aim of this study was to estimate genetic variation in uniformity of body weight of broilers. Data from a commercial dam line were used and analyzed with different models. Although heritability of uniformity was low (0.03 to 0.05), a relatively high genetic variation was estimated as indicated by high genetic coefficients of variation (0.35 to 0.57). Surprisingly, uniformity in females and males was not correlated. Nevertheless, results indicate that uniformity can be improved by means of genetic selection.

Introduction

Uniformity of body weight of broilers is of economic interest, because slaughterhouses want to produce homogeneous products. As a consequence, producers get price penalties when too many broilers delivered to the slaughterhouse are outside the preferred range. Management and breeding strategies can be used to improve uniformity (Hohenboken, 1985), but selective breeding for uniformity in livestock breeding programs can be useful only if it varies genetically.

There is some empirical evidence that genetic variation in residual variance exists. SanCristobal-Gaudy *et al*. (2001), Sorensen and Waagepetersen (2003), Ros *et al*. (2004), Gutierrez *et al*. (2006) and Ibanez-Escriche *et al*. (2008a and 2008b) used a structural model for heterogeneous residual variance and found substantial genetic variation in residual variance for litter size in sheep, litter size in pigs, body weight in snails, litter size and weight in mice, body weight traits in mice, and slaughter weight in pigs, respectively. Rowe *et al*. (2006) found substantial genetic heterogeneity of residual variance between sire families in body weight of broilers. Probably the clearest example is by Mackay and Lyman (2005), who derived 300 isofemale lines of *Drosophila melanogaster* and found substantial highly significant genetic variance in residual variance between lines under controlled laboratory conditions.

† E-mail: herman.mulder@wur.nl

If there is genetic variance in residual variance, it should be possible to change it by selection. Phenotypic variance changed in some selection experiments with *Drosophila melanogaster* or *Tribolium*, with stabilizing selection or divergent selection on phenotypic variance (Rendel *et al*., 1966; Kaufman *et al*., 1977; Cardin and Minvielle, 1986), while it did not in an experiment with mice (Falconer and Robertson, 1956). More recently, Larzul *et al*. (2006) did not find conclusive results in selection of pigs on high or low residual variability of muscle pH, but Garreau *et al*. (2008) found significant responses in residual variance in rabbits when selecting on high or low residual variance of birth weight. The relatively substantial responses obtained by Garreau *et al*. (2008) seem to support the large responses in residual variance predicted by Mulder *et al*. (2007 and 2008) using simulation, whereas the study of Larzul *et al*. (2006) lacked power because of small numbers of sires and small numbers of progeny per sire.

One of the main problems with analysis of genetic heterogeneity of residual variance is its estimability. Rowe *et al*. (2006) used a two-step approach, in which the first stage used a model to analyze body weight with allowance for differences in residual variance among sire families, and in the second stage the variation among these estimates of the residual variance were analyzed with least squares. In some studies, log transformed squared residuals have been analyzed, also using a two-step approach (Larzul *et al*., 2006; Bolet *et al*., 2007), which gives the flexibility to account for environmental effects on the residual variance at the level of the record that is not possible in the least squares analysis of Rowe *et al*. (2006). Ideally, one would simultaneously fit a model for the mean of the trait (e.g. body weight) and for the residual variance using a structural model. Sorensen and Waagepetersen (2003), Ros *et al*. (2004) and Gutierrez *et al*. (2006) applied these structural models in a Bayesian context, implemented using Markov chain Monte Carlo sampling (MCMC). The disadvantages of those methods are that there is no standard software package available and no extension has yet been made to estimate genetic correlations between residual variances of different traits or of different sexes. Therefore, in this study, we have applied the two-step approach of Larzul *et al*. (2006) and Bolet *et al*. (2007), and extended this to bivariate analyses using standard REML-software.

The objectives of this study were to estimate genetic variance in residual variance for body weight in broilers, and to estimate the genetic correlations between the additive genetic effects for the mean and the residual variance and between female and male residual variance. It therefore provides a confirmation of the results of Rowe *et al*. (2006) and those recently presented by Wolc *et al*. (2009) using a different population of broilers and different analytical approaches.

Material and methods

Data

The data were provided by Hendrix Genetics, Boxmeer, the Netherlands, and comprised 106 818 records of body weight of birds of a maternal dam line with ongoing selection on number of eggs, breast meat, feed conversion, and average daily gain. Birds were weighed at an age between 37 and 60 days. Data were collected between 1 January 1995 and 1 June 2007. Birds were wing banded at day of hatching. Birds of both sexes were housed in two housing systems – floor housing and cage housing – and were fed *ad libitum*. From each sire family some birds were housed in cages at 3 weeks of age to measure feed conversion. The barns were fully controlled with temperature and light schemes as used in standard commercial broiler husbandry. The pedigree file comprised 123 328 animals and traced back at least four generations, so that younger animals had longer pedigrees.

Table 1 *Summary statistics of the female and male data set*

Parameter	Female offspring	Male offspring
Records (*n*)	26 972	24 407
Sires (*n*)	402	369
Dams (*n*)	3026	2814
Average dams/sire (*n*)	7.95	7.96
Hatch weeks progeny (*n*)	251	255
Hatch weeks sires (*n*)	158	150
Average body weight (g)	2048	2335
s.d. body weight (g)	217	307

First a few general edits were applied. Records of body weights over 3.5 phenotypic standard deviations from the mean were excluded (73 records $<$ mean $-$ 3.5 s.d.; 143 records $>$ mean $+$ 3.5 s.d.), considered a suitable compromise between removing severe abnormalities and minimizing the effect of data trimming on the estimated genetic variance in residual variance. Owing to very few records in some age classes, records on birds weighed outside the range 43 to 53 days were excluded (595 records), to minimize the age range. From this data set (106 007 records) two edited data sets were extracted: one for females, the other for males. For each data set, sire families were selected which had at least 50 offspring of one sex, and classes for the interaction between hatch week of the individual and the hatch week of its dam (*hwihwd*) were selected if they had at least five animals. These requirements were met by 402 sire families and 26 972 records of females, and 369 sires and 24 407 records of males. The requirements of 50 offspring per sire and five animals per *hwihwd* halved the size of the data sets. Table 1 shows some characteristics of these two data sets.

Analysis

The female and male data were analyzed separately to quantify genetic variation in residual variance using the two-stage method (Larzul *et al*., 2006; Bolet *et al*., 2007).

First stage: estimation of genetic variance in body weight. In all analyses, body weight data for each sex separately were first analyzed with an animal model using

ASREML (Gilmour *et al*., 2006), accounting for differences between sire families in residual variance:

$$y_{ijkln} = \mu + h_j + age_k + hwihwd_l + A_{m_i} + D_n + e_{ijkln}, \quad (1)$$

where y_{ijkln} is body weight of individual i, which has sire o and dam n, μ is the overall mean, h_j is the housing system effect j (floor and cage system), age_k is the effect for age class k (9 classes), $hwihwd_l$ is the joint effect l of the hatch week of the individual and the hatch week of its dam (1515 classes for females and 1521 for males), A_{m_i} is the random genetic animal effect for the mean for individual i (variance $\sigma^2_{A_m}$), D_n is the random maternal environmental effect of dam n (variance σ^2_D) and e_{ijkln} is the residual error with variance $\sigma^2_{e_o}$ for sire family o. The *hwihwd*-effects accounted for time effects when the dam was hatched and when the bird itself was hatched, such as seasonal effects. A model including maternal genetic effects was also tested, but did not converge for the male data set and only slightly improved likelihood for females. Therefore, maternal genetic effects were not considered in this study. In contrast to the sire and dam model used by Rowe *et al*. (2006) and Wolc *et al*. (2009), an animal model was chosen so that the residual variance was expected to be less confounded with Mendelian sampling variance and had substantially higher likelihood than a sire–dam model (females: +17; males: +29); although a formal likelihood ratio test (LR-test) can not be applied here because these models are not nested. For model comparison, the model in equation (1) was also fitted assuming a homogeneous residual variance structure.

Second stage: estimation of genetic variance in residual variance. The residuals from equation (1) were transformed by using the natural log of the squared residuals ($\ln(e^2_{ijkln})$) to reduce the dependency of e^2_{ijkln} on its variance and non-normality of the distribution of e^2_{ijkln}. Density plots showed that the log-transformation did not completely remove non-normality, but simulation showed that the transformation was adequate to estimate genetic variance.

The log-transformed squared residuals, $\ln(e^2_{ijkln})$, were analyzed as a trait. The same fixed effects were fitted as for body weight, but in this case the fixed effects (denoted * to distinguish them from those in the first stage) account for differences in $\ln(e^2_{ijkln})$ between different fixed effect levels due to environmental heterogeneity of residual variance. The model is:

$$\ln(e^2_{ijkln}) = \mu + h^*_j + age^*_k + hwihwd^*_l + A_{res_i} + e_{res_{ijkl}}, \quad (2)$$

where A_{res_i} is the additive genetic value of animal i for $\ln(e^2_{ijkln})$ (variance $\sigma^2_{A_{res}}$) and $e_{res_{ijkl}}$ is the residual effect. In equation (2), a constant residual variance (variance $\sigma^2_{e_{res}}$) was assumed for $\ln(e^2_{ijkln})$. The maternal environmental effect was excluded from the model because its variance was not significantly different from zero.

Estimation of a genetic correlation between the mean and the residual variance. To estimate the genetic correlation between the additive genetic effects for the mean and the residual variance, bivariate analyses were carried out iteratively, updating $\ln(e^2_{ijkln})$ for each of 20 iterations. Each iteration comprised an ASREML-run, which was considered converged when the REML-likelihood changed less than $0.002 \times$ iteration number (<20), and the individual variance parameter estimates changed less than 1% between successive iterations (Gilmour *et al*., 2006). The bivariate analysis can be written in matrix notation as:

$$\begin{bmatrix} \mathbf{y} \\ \ln(\mathbf{e^2}) \end{bmatrix} = \begin{bmatrix} \mathbf{X}_y & 0 \\ \mathbf{0} & \mathbf{X}_{\ln(e^2)} \end{bmatrix} \begin{bmatrix} \mathbf{b} \\ \mathbf{b}^* \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_y & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{\ln(e^2)} \end{bmatrix} \begin{bmatrix} \mathbf{a}_m \\ \mathbf{a}_{res} \end{bmatrix} + \mathbf{W}_y \mathbf{d}_y + \begin{bmatrix} \mathbf{e}_y \\ \mathbf{e}_{res} \end{bmatrix}, \quad (3)$$

where $\mathbf{y}$ is the vector of y_{ijkln}; $\ln(\mathbf{e^2})$ is the vector of $\ln(e^2_{ijkln})$; $\mathbf{X}_y$ and $\mathbf{X}_{\ln(e^2)}$ are the incidence matrices for the fixed effects for body weight and $\ln(e^2_{ijkln})$, respectively; $\mathbf{b}$ and $\mathbf{b}^*$ are the solution vectors for the fixed effects; $\mathbf{Z}_y$ and $\mathbf{Z}_{\ln(e^2)}$ are the incidence matrices for the additive genetic effects A_{m_i} and A_{res_i}; $\mathbf{a}_m$ and $\mathbf{a}_{res}$ are the solution vectors with estimates of A_{m_i} and A_{res_i}; $\mathbf{W}_y$ is the incidence matrix for maternal environmental effects that are modeled only for body weight; $\mathbf{d}_y$ is the solution vector for the random maternal environmental effect D_n; and $\mathbf{e}_y$ and $\mathbf{e}_{res}$ are the vectors with residuals for body weight ($=e_{ijkln}$ in equation (1)) and $\ln(e^2_{ijkln})$ ($=e_{res_{ijkl}}$ in equation (2)). The vector $\ln(\mathbf{e^2})$ was updated in each iteration using $\mathbf{e}_y$ of the previous iteration. The additive genetic effects A_m and A_{res} are assumed bivariate normally distributed as $\begin{bmatrix} \mathbf{a}_m \\ \mathbf{a}_{res} \end{bmatrix} \sim MVN(\mathbf{0}, \mathbf{A} \otimes \mathbf{G}_{mv})$, $\mathbf{A}$ is the additive genetic relationship matrix, $\mathbf{G}_{mv} = \begin{bmatrix} \sigma^2_{A_m} & r_{A_m,\,A_{res}}\sigma_{A_m}\sigma_{A_{res}} \\ r_{A_m,\,A_{res}}\sigma_{A_m}\sigma_{A_{res}} & \sigma^2_{A_{res}} \end{bmatrix}$ and $r_{A_m,\,A_{res}}$ is the genetic correlation between A_m and A_{res}. The residuals $\mathbf{e}_y$ and $\mathbf{e}_{res}$ are assumed bivariate normally distributed as $\begin{bmatrix} \mathbf{e}_y \\ \mathbf{e}_{res} \end{bmatrix} \sim MVN(\mathbf{0}, \mathbf{I} \otimes \mathbf{R})$, where $\mathbf{I}$ is the identity matrix and $\mathbf{R} = \begin{bmatrix} \sigma^2_{e_o} & 0 \\ 0 & \sigma^2_{e_{res}} \end{bmatrix}$, including heterogeneous residual variances per sire family o for body weight and homogeneous residual variance for $\mathbf{e}_{res}$. The residuals e_{ijkln} and $e_{res_{ijkl}}$ are assumed uncorrelated, because $\mathrm{cov}(e, e^2) = 0$ when e is normally distributed. Parameter estimates oscillated somewhat (the standard deviation of parameter estimates was less than 5% of the average parameter estimate) between two very similar sets of parameters after the first five to ten iterations; therefore, results are presented as the average of the last ten iterations. Oscillations can be explained by the interplay between A_{m_i} and A_{res_i}, the residual e_{ijkln} and the other effects in the model. When A_{m_i} increases, the residual e_{ijkln} decreases and therefore A_{res_i} decreases; and when A_{m_i} and A_{res_i} are genetically correlated, one will also affect the other directly. Both mechanisms explain the oscillations.

Estimation of a genetic correlation between female and male residual variance. To calculate the genetic correlation between the additive genetic effects for the residual variance in females and males, the data sets were combined using $\ln(e^2_{ijkln})$ of iteration 20 of equation (3). The bivariate analysis in matrix notation can be written as:

$$\begin{bmatrix} \ln(\mathbf{e}^2_F) \\ \ln(\mathbf{e}^2_M) \end{bmatrix} = \begin{bmatrix} \mathbf{X}_F & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_M \end{bmatrix} \begin{bmatrix} \mathbf{b}^*_F \\ \mathbf{b}^*_M \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_F & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_M \end{bmatrix} \begin{bmatrix} \mathbf{a}_{res_F} \\ \mathbf{a}_{res_M} \end{bmatrix} + \begin{bmatrix} \mathbf{e}_{res_F} \\ \mathbf{e}_{res_M} \end{bmatrix}, \quad (4)$$

where the effects are the same as in equation (3), but now with subscripts *F* and *M* to indicate whether it is for females and males, A_{res_F} and A_{res_M} are assumed to be bivariate normally distributed as $\begin{bmatrix} \mathbf{a}_{res_F} \\ \mathbf{a}_{res_M} \end{bmatrix} \sim MVN(\mathbf{0}, \mathbf{A} \otimes \mathbf{G}_{FM})$, where $\mathbf{G}_{FM} = \begin{bmatrix} \sigma^2_{A_{res_F}} & r_{A_{res_F}, A_{res_M}} \sigma_{A_{res_F}} \sigma_{A_{res_M}} \\ r_{A_{res_F}, A_{res_M}} \sigma_{A_{res_F}} \sigma_{A_{res_M}} & \sigma^2_{A_{res_M}} \end{bmatrix}$, where $r_{A_{res_F}, A_{res_M}}$ is the genetic correlation between A_{res_F} and A_{res_M}. The residuals $\mathbf{e}_{res_F}$ and $\mathbf{e}_{res_M}$ are assumed to be bivariate normally distributed as $\begin{bmatrix} \mathbf{e}_{res_F} \\ \mathbf{e}_{res_M} \end{bmatrix} \sim MVN(\mathbf{0}, \mathbf{I} \otimes \mathbf{R})$, where $\mathbf{R} = diag(\sigma^2_{e_{res_F}}, \sigma^2_{e_{res_M}})$.

Calculation of quantitative genetic parameters

To facilitate interpretation and implications for breeding, two standardized parameters were calculated: the heritability of residual variance h^2_v and the genetic coefficient of variation GCV_E. Both h^2_v and GCV_E are possible measures to choose: the former largely determines the accuracy of estimated breeding value (EBV) for residual variance and the latter, the size of the possible selection response relative to the current residual variance. These were calculated as $h^2_v = \sigma^2_{A_v}/(2\sigma^4_P + 3\sigma^2_{A_v})$ and $GCV_E = \sigma_{A_v}/(\overline{\sigma^2_e})$, where $\sigma^2_P = \sigma^2_{A_m} + \sigma^2_D + \overline{\sigma^2_e}$ and $\overline{\sigma^2_e}$ is the average residual variance (Mulder *et al.*, 2007). Therefore, the genetic variance in $\ln(e^2_{ijkln})$ needs to be converted to $\sigma^2_{A_v}$, which is the genetic variance of the additive genetic effect for residual variance (A_v) in the quantitative genetic model for genetic heterogeneity of residual variance (Hill and Zhang, 2004; Mulder *et al.*, 2007). The genetic variance $\sigma^2_{A_v}$ can be calculated as $\sigma^2_{A_v} = h^2_{res} 2(\overline{\sigma^2_e})^2$, where $h^2_{res} = \frac{\sigma^2_{A_{res}}}{\sigma^2_{A_{res}} + \sigma^2_{e_{res}}}$ is the heritability of $\ln(e^2_{ijkln})$.

The heritability of the mean was calculated as $h^2_m = \sigma^2_{A_m}/\sigma^2_P$ and the maternal environment variance ratio as $c^2 = \sigma^2_D/\sigma^2_P$. Approximate standard errors were calculated for estimated variance components and variance ratios using ASREML (Gilmour *et al.*, 2006). For h^2_v, the standard error was crudely approximated as $h^2_v * se(h^2_{res})/h^2_{res}$. For GCV_E and $\sigma^2_{A_v}$, no simple approximations were available to calculate the standard error.

Comparison of models with and without heterogeneity of sire-family residual variance

The model variants in equation (1), with and without heterogeneity of residual variance, were compared using a LR-test, assuming χ^2 with $n_s - 1$ degrees of freedom for the increase from fitting estimated variance components (one for each of n_s sires) in the full model compared to the reduced model of homogeneity (Wilks, 1938). REML likelihoods were obtained from ASREML. Models were also compared using Akaike's information content (AIC) (Akaike, 1973) and the Bayesian or Schwarz information criterion (BIC) (Schwarz, 1978) to penalize those with a large number of parameters. BIC produces a more drastic penalty than AIC, which increases with sample size.

Relationships between sire EBV and residual variance of offspring

Plots were used to visualize the relationship between sire EBV for residual variance (equation (3)) and the observed log-transformed residual variance of its offspring (i.e. the phenotypic variance corrected for fixed effects, genetic effects for the mean and maternal environmental effects), which would be of relevance when improving uniformity by selection. EBVs ($\hat{A}_{res}$) of iteration 20 of the bivariate analyses (equation (3)) were used. To quantify the strength of the relationship, correlations were calculated between these EBVs and the observed log-transformed residual variance of its offspring.

Results

Comparison of models with homogeneous or heterogeneous residual variance among sire families

Table 2 shows estimated variance components, estimates of variance ratios and likelihood-based parameters for females and males for models (equation (1)) with homogeneous and heterogeneous residual variances among sire families. For both sexes, fitting heterogeneous residual variance for each sire family increased the estimates of genetic variance in mean body weight ($\sigma^2_{A_m}$) and decreased those for maternal environmental variance (σ^2_D). Estimated variance components, especially the average residual variance $\overline{\sigma^2_e}$, were larger for males than for females, resulting in a larger h^2_m ($\sigma^2_{A_m}/\sigma^2_P$) for females. A model with heterogeneous residual variances among sire families fitted significantly better than one with a homogeneous residual variance (LR-test: $P < 0.001$). Taking into account the number of parameters estimated, it is not obvious which model is better because the AIC is lower (i.e. better fit), but the BIC is higher (i.e. poorer fit) for the model with heterogeneous residual variance among sire families.

Genetic variation in residual variance

Table 3 shows estimates of genetic variance in residual variance using a univariate (equation (2)) and a bivariate analysis (equation (3)) to analyze data for females and males. Estimates of $\sigma^2_{A_{res}}$ deviated significantly from zero ($P < 0.001$). With the bivariate analysis estimates of $\sigma^2_{A_{res}}$, h^2_v and GCV_E increased substantially in comparison to the univariate analysis. Table 4 shows that $\sigma^2_{A_m}$ and h^2_m also

Table 2 *Variance component estimates, estimates of variance ratios and likelihood-based parameters for body weight (g) of females and males using models (equation (1)) with homogeneous or heterogeneous residual variance structure (approximate s.e. within brackets)*

	Female offspring		Male offspring	
Parameter[a]	Homogeneous	Heterogeneous	Homogeneous	Heterogeneous
$\sigma^2_{A_m}$	9379 (856)	10 118 (868)	10 791 (1282)	11 734 (1333)
σ^2_D	1092 (180)	870 (168)	1761 (314)	1229 (291)
σ^2_e or $\overline{\sigma^2_e}$	18 512 (435)	18 187 (447)	34 459 (687)	34 321 (735)
σ^2_P	28 984 (438)	29 175 (456)	47 012 (655)	47 284 (701)
h^2_m	0.324 (0.026)	0.347 (0.026)	0.230 (0.025)	0.248 (0.026)
c^2	0.038 (0.006)	0.030 (0.006)	0.037 (0.007)	0.026 (0.006)
L	−3456	−2675	−5257	−4549
AIC	6918	6158	10 519	9839
BIC	6925	7140	10 526	10 725

[a]$\sigma^2_{A_m}$ is the estimated genetic variance in the additive genetic effect for the mean A_m; σ^2_D is the estimated variance of the maternal environmental effect; σ^2_e or $\overline{\sigma^2_e}$ is the (average) estimated residual variance with homogeneous (heterogeneous) residual variance per sire family; σ^2_P is the estimated phenotypic variance ($= \sigma^2_{A_m} + \sigma^2_D + \sigma^2_e$); $h^2_m = \sigma^2_{A_m}/\sigma^2_P$; $c^2 = \sigma^2_D/\sigma^2_P$, L is log-likelihood; AIC is Akaike's information criterion and BIC is the Bayesian information criterion.

Table 3 *Comparison of estimated genetic variance in residual variance of body weight (g) (approximate s.e. within brackets for $\sigma^2_{A_{res}}$ and h^2_v) using univariate or bivariate analysis[a] for male and female broilers*

	Female offspring		Male offspring	
Parameter[b]	Univariate	Bivariate	Univariate	Bivariate
$\sigma^2_{A_{res}}$	0.506 (0.050)	0.832 (0.071)	0.308 (0.050)	0.607 (0.066)
$\sigma^2_{A_v}$	6.43E + 07	9.81E + 07	1.43E + 08	2.55E + 08
h^2_v	0.034 (0.003)	0.047 (0.004)	0.029 (0.003)	0.046 (0.005)
GCV_E	0.441	0.573	0.349	0.493

[a]In the univariate analysis only log-transformed squared residuals (equation (2)) are analyzed; in the bivariate analysis body weight and its log-transformed squared residuals (equation (3)) are analyzed with iterative updating of the residuals.
[b]$\sigma^2_{A_{res}}$ is the estimated genetic variance of the additive genetic effect A_{res} for $\ln(e^2)$ (equation (2)); $\sigma^2_{A_v}$ is the estimated genetic variance for A_v in the quantitative genetic model for genetic heterogeneity of residual variance (Hill and Zhang, 2004; Mulder *et al.*, 2007); $h^2_v = \sigma^2_{A_v}/2\sigma^2_P + 3\sigma^2_{A_v}$ and $GCV_E = \sigma_{A_v}/\overline{\sigma^2_e}$.

Table 4 *Comparison of estimates of variance components and variance ratios obtained by univariate (equation (1)) and bivariate analysis (equation (3)) of body weight (g) and the log-transformed squared residuals of female and male broilers (approximate s.e. within brackets)*

	Female offspring		Male offspring	
Parameter[a]	Univariate	Bivariate	Univariate	Bivariate
$\sigma^2_{A_m}$	10 118 (868)	11 964 (886)	11 734 (1333)	15 630 (1519)
σ^2_D	870 (168)	697 (162)	1229 (291)	835 (296)
σ^2_e	18 187 (447)	17 271 (452)	34 321 (735)	32 360 (804)
σ^2_P	29 175 (456)	29 932 (470)	47 284 (701)	48 825 (777)
h^2_m	0.347 (0.026)	0.400 (0.024)	0.248 (0.026)	0.320 (0.027)
c^2	0.030 (0.006)	0.023 (0.006)	0.026 (0.006)	0.017 (0.006)

[a]See Table 2.

increased, while the maternal environment variance and c^2 decreased with the bivariate analysis. It can be concluded that substantial genetic variance in residual variance exists for body weight of broilers. Accounting for genetic heterogeneity of residual variance also affects conventional genetic parameters, such as the usual heritability of the mean h^2_m.

Genetic correlation between mean and residual variance and between female and male residual variance

The estimates from the bivariate analysis of body weight and log-transformed squared residuals (equation (3)) of the genetic correlations between A_m and A_{res} ($r_{A_m, A_{res}}$) were −0.41 (s.e. = 0.032) and −0.45 (s.e. = 0.040) in females and males, respectively. The estimate of $r_{A_{res_F}, A_{res_M}}$, the

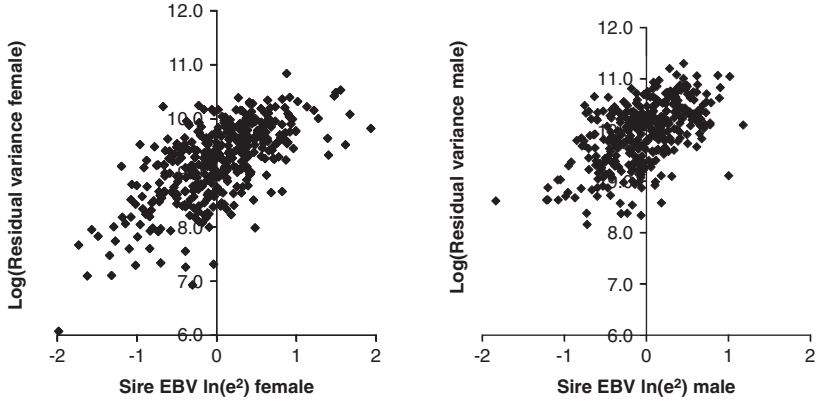

Figure 1 Scatter plots of residual variance of female and male offspring as a function of the sire's estimated breeding value (EBV) based on log-transformed squared residuals (ln(e^2)) ($\hat{A}_{res_F}$ and $\hat{A}_{res_M}$).

genetic correlation between female and male residual variance (equation (4)), was very small: 0.11 (s.e. = 0.089).

Relationships between sire EBV for residual variance and the observed residual variance of offspring

The scatter plots of log-transformed residual variance of female and male offspring as a function of $\hat{A}_{res,f}$ and $\hat{A}_{res,m}$ in Figure 1 show that there was substantial variability in residual variance between sires. There was a positive trend between the EBVs for residual variance and the observed log-transformed residual variance, but there was also substantial noise, especially for male offspring. The correlation between $\hat{A}_{res,f}$ and log-transformed residual variance of female offspring was 0.65, and the equivalent for male offspring was 0.54.

Discussion

In this study, it was shown that there is substantial genetic variation in residual variation, the so-called genetic heterogeneity of residual variance, for body weight in broilers. A REML-analysis on log-transformed squared residuals was used (e.g. Larzul *et al*., 2006; Bolet *et al*., 2007) and extended to multivariate approaches to estimate genetic correlations between the additive genetic effects for mean and residual variance, and between additive genetic effects for residual variance in males and females. The iterative bivariate analysis with body weight itself and log-transformed squared residuals of body weight was closest to a structural model, as suggested by SanCristobal-Gaudy *et al*. (1998) and Sorensen and Waagepetersen (2003). It had a side effect in that the estimate of h^2_m increased by 15% in females and 29% in males, thereby increasing the accuracy of $\hat{A}_m$, unless the genetic variance in mean ($\sigma^2_{A_m}$) is biased upwards and the residual variance (σ^2_e) is biased downward. A similar trend was also observed by Sorensen and Waagepetersen (2003), who observed an increase of 15% in h^2_m when extending a model with homogeneous residual variance to a model with genetically structured residual variances. Ibanez-Escriche *et al*. (2008a) reported increases in additive genetic variance of the mean between 28% and 200%.

The method used, incorporates both genetic and environmental effects on the residual variance, but heterogeneous residual variance and effects on the mean are not estimated simultaneously at the level of individual records. Although in principle less appealing, the current method is flexible and can be applied in standard REML-software. This enables the study of genetic relationships between residual variances of different traits, environments, and so on, and can be applied to breeding value estimation using standard BLUP-software (e.g. Lidauer and Stranden, 1999), in contrast to a structural model in a Bayesian context implemented using MCMC sampling. The same two-step method was used in selection experiments to change the residual variance (Larzul *et al*., 2006; Bolet *et al*., 2007; Garreau *et al*., 2008). The method presented here was tested using simulations with one generation of parents and offspring, and results showed that it is able to estimate genetic variance in residual variance. Wolc *et al*. (2009) used a similar REML approach as in this study and also a Bayesian approach, and the two methods yielded similar results. In this study, the BIC favored the model with homogeneous residual variance, although both the LR-test and AIC favored the model with heterogeneous residual variance per sire family. This probably indicates that the residual variances were estimated with low accuracy in each sire family rather than the absence of heterogeneity of residual variance. Future research may focus on evaluating different modeling approaches.

In general, estimates of h^2_v obtained here are higher than those of Rowe *et al*. (2006), who used a different method and data set. When the least-squares method of Rowe *et al*. (2006) was applied to the current data set, however, estimates of h^2_v were higher: 0.088 in females and 0.087 in males. The large difference found using the same method is probably due to more severe confounding of genetic and environmental heterogeneity of residual variance, because the data in this study spanned a longer time period than for

Rowe *et al*. (2006) and because the ages at which birds were weighed ranged more widely, between 43 and 53 days of age, possibly introducing an extra source of heterogeneity. Wolc *et al*. (2009) used data that partly overlapped those in the study of Rowe *et al*. (2006) and estimates of h_v^2 were very similar to those of our univariate analysis. Estimates of h_v^2 from studies in other species (e.g. SanCristobal-Gaudy *et al*., 2001; Sorensen and Waagepetersen, 2003; Ros *et al*., 2004) are in the same range as those obtained here (see review in Mulder *et al*. (2007)). The estimate of the genetic correlation between the additive effects for the mean and the residual variance ($r_{A_m,A_{res}}$) was more negative in this study than obtained by Rowe *et al*. (2006). Variation in estimates of this genetic correlation between studies is large, although generally negative for body weight traits. Estimates obtained were −0.07 for slaughter weight in pigs (Ibanez-Escriche *et al*., 2008b), −0.31 and −0.38 for body weight at two ages in mice (Ibanez-Escriche *et al*., 2008a) but, exceptionally, a highly positive genetic correlation of 0.81 for adult body weight in snails (Ros *et al*., 2004).

In this study, body weights of females and males were analyzed separately because they differ greatly in the variance of observations. A large difference in estimated variance components and estimated variance ratios (Tables 3 and 4) was found between them; rather more extreme than in the studies of Rowe *et al*. (2006) and Wolc *et al*. (2009). The large difference in h_m^2 indicates that it might be advantageous in breeding value estimation to use different variance ratios for female and male offspring. The genetic correlation between female and male residual variance was close to zero, rather surprisingly indicating that these traits have different genetic bases. Whilst Rowe *et al*. (2006) also found a low correlation for $\ln(s^2)$ between sexes, Wolc *et al*. (2009) obtained an estimate of the genetic correlation of 0.36 using an improved method. It would be useful to understand the basis of these low correlations; but, assuming they are real, it is recommended that the body weight and (log-transformed) squared residuals of females and males be analyzed as four different traits.

Genetic heterogeneity of residual variance may have biological meaning in terms of environmental sensitivity, disease resistance, biological limits and mean–variance relationships. Genotypes that are very sensitive to changes in micro-environment (e.g. feed changes, weather changes and so on) would have a larger residual variance than those insensitive to such changes. The moderate negative genetic correlation between the additive genetic effects for the mean and the residual variance may indicate that animals with a higher mean are also less sensitive; but another explanation is that animals with a lower mean are more sensitive to diseases and have higher residual variance because of higher disease incidence. Therefore, mixture models for diseased and non-diseased animals (e.g. Odegard *et al*., 2005) and models for genetic heterogeneity of residual variance might capture part of the same genetic information. If there is a biological limit caused by an environmental constraint (e.g. restricted feeding) it may also create a negative genetic correlation between the mean and the residual variance, because the variability would be reduced on one side of the distribution. A positive mean–variance relationship (scale effect), however, would create a positive genetic correlation between the mean and the residual variance, in contrast to the negative genetic correlation found here.

This study shows that there is substantial genetic variation in residual variance (high genetic coefficient of variation, GCV_E). Although the underlying model is slightly different, we use the methodology of Mulder *et al*. (2008) to show what could be achieved in a breeding program based on sib-testing with 50 half-sibs. Based on the estimates obtained, h_v^2 between 2.9% and 4.7% and GCV_E between 0.35 and 0.57, it would be possible to decrease the residual variance by 20% to 30% when selecting solely on it for one generation. The phenotypic standard deviation would then be substantially reduced, for example, from 173 g to 145–155 g in females. Furthermore, the genetic correlation between the mean and the residual variance is negative, which is favorable when the breeding goal is to increase the mean and to decrease the residual variance. In addition, the negative genetic correlation would counterbalance the increase in residual variance, because of intense selection mainly on ones' own performance (Hill and Zhang, 2004; Mulder *et al*., 2007). Results seem to be promising for selection for increased uniformity, but it should be noted that the accuracy of EBV for residual variance is not high (Figure 1). Another complication is that the additive genetic effects for female and male residual variances are correlated to a very less extent and, therefore, phenotypic information on one sex adds little to the accuracy of the EBV of residual variance in the other sex.

Acknowledgements

Hendrix Genetics B.V. is acknowledged for providing the broiler data. Mario Calus and John Hickey are acknowledged for helping with ASREML. HAM and RFV were partially financed by the RobustMilk project that is financially supported by the European Commission under the Seventh Research Framework Programme, Grant Agreement 211708. The content of this paper is the sole responsibility of the publishers, and it does not necessarily represent the views of the Commission or its services.

References

Akaike H 1973. Information theory and an extension of the maximum likelihood principle. In Proceedings of the 2nd International Symposium on Information Theory (ed. BN Petrov and F Csaki), pp. 267–281. Akademiai Kiado, Budapest, Hungary.

Bolet G, Garreau H, Joly T, Theau-Clement M, Falieres J, Hurtaud J and Bodin L 2007. Genetic homogenisation of birth weight in rabbits: indirect selection response for uterine horn characteristics. Livestock Science 111, 28–32.

Cardin S and Minvielle F 1986. Selection on phenotypic variation of pupa weight in *Tribolium castaneum*. Canadian Journal of Genetics and Cytology 28, 856–861.

Falconer DS and Robertson A 1956. Selection for environmental variability of body size in mice. Zeitschrift fur Inductive Abstammungs- und Vererbungslehre 87, 385–391.

Garreau H, Bolet G, Larzul C, Robert-Granie C, Saleil G, SanCristobal M and Bodin L 2008. Results of four generations of a canalizing selection for rabbit birth weight. Livestock Science 119, 55–62.

Gilmour AR, Gogel BJ, Cullis BR and Thompson R 2006. ASREML User Guide Release 2.0. VSN International Ltd, Hemel Hempstead, UK.

Gutierrez JP, Nieto B, Piqueras P, Ibanez N and Salgado C 2006. Genetic parameters for canalisation analysis of litter size and litter weight traits at birth in mice. Genetics Selection Evolution 38, 445–462.

Hill WG and Zhang X-S 2004. Effects of phenotypic variability of directional selection arising through genetic differences in residual variability. Genetical Research, Cambridge 83, 121–132.

Hohenboken WD 1985. The manipulation of variation in quantitative traits: a review of possible genetic strategies. Journal of Animal Science 60, 101–110.

Ibanez-Escriche N, Moreno A, Nieto B, Piqueras P, Salgado C and Gutierrez JP 2008a. Genetic parameters related to environmental variability of weight traits in a selection experiment for weight gain in mice; signs of correlated canalised response. Genetics Selection Evolution 40, 279–293.

Ibanez-Escriche N, Varona L, Sorensen D and Noguera JL 2008b. A study of heterogeneity of environmental variance for slaughter weight in pigs. Animal 2, 19–26.

Kaufman PK, Enfield FD and Comstock RE 1977. Stabilizing selection for pupa weight in *Tribolium castaneum*. Genetics 87, 327–341.

Larzul C, Le Roy P, Tribout T, Gogue J and SanCristobal M 2006. Canalizing selection on ultimate pH in pigs: consequences on meat quality. In Proceedings of the 8th World Congress on Genetics Applied to Livestock Production, Communication 13-09, Belo Horizonte, Brazil.

Lidauer M and Stranden I 1999. Fast and flexible program for genetic evaluation in dairy cattle. Interbull Bulletin 20, 20–25.

Mackay TFC and Lyman RF 2005. Drosophila bristles and the nature of quantitative genetic variation. Philosophical Transactions of the Royal Society B: Biological Sciences 360, 1513–1527.

Mulder HA, Bijma P and Hill WG 2007. Prediction of breeding values and selection responses with genetic heterogeneity of environmental variance. Genetics 175, 1895–1910.

Mulder HA, Bijma P and Hill WG 2008. Selection for uniformity in livestock by exploiting genetic heterogeneity of residual variance. Genetics Selection Evolution 40, 37–59.

Odegard J, Madsen P, Gianola D, Klemetsdal G, Jensen J, Heringstad B and Korsgaard IR 2005. A Bayesian threshold-normal mixture model for analysis of a continuous mastitis-related trait. Journal of Dairy Science 88, 2652–2659.

Rendel JM, Sheldon BL and Finlay DE 1966. Selection for canalization of the scute phenotype. II. American Naturalist 100, 13–31.

Ros M, Sorensen D, Waagepetersen R, Dupont-Nivet M, SanCristobal M, Bonnett JC and Mallard J 2004. Evidence for genetic control of adult weight plasticity in the snail *Helix aspersa*. Genetics 168, 2089–2097.

Rowe SJ, White IMS, Avendano S and Hill WG 2006. Genetic heterogeneity of residual variance in broiler chickens. Genetics Selection Evolution 38, 617–635.

SanCristobal-Gaudy M, Bodin L, Elsen JM and Chevalet C 2001. Genetic components of litter size variability in sheep. Genetics Selection Evolution 33, 249–271.

SanCristobal-Gaudy M, Elsen JM, Bodin L and Chevalet C 1998. Prediction of the response to a selection for canalisation of a continuous trait in animal breeding. Genetics Selection Evolution 30, 423–451.

Sorensen D and Waagepetersen R 2003. Normal linear models with genetically structured residual variance heterogeneity: a case study. Genetical Research, Cambridge 82, 207–222.

Schwarz G 1978. Estimating the dimension of a model. Annals of Statistics 6, 461–464.

Wilks SS 1938. The large-sample distribution of the likelihood ratio for testing composite hypotheses. Annals of Mathematical Statistics 9, 60–62.

Wolc A, White IMS, Avendano S and Hill WG 2009. Genetic variability in residual variation of body weight and conformation scores in broiler chickens. Poultry Science 88, 1156–1161.