

Effective Factors on Genetic Parameters of Day-Old Chicken's Body Weight in a Commercial Broiler Line

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Introduction

Considering the maternal effects in biometrical models cause to obtain better estimations of (co)variance components and genetic parameters for production and reproduction traits in poultry and ignoring this effect in statistical models tend to overestimate direct additive genetic variance and heritability (Seraj *et al.* (2007), Shafaat *et al.* (2008)). Also, genetic correlation between direct and maternal additive genetic effects (r_{am}) was reported negative. This negative correlation has been observed for different traits in other domestic species (Konstantinov and Brien (2003), Lee and Pollak (1997), Robinson (1996)). Those researchers showed that when the data, containing sire by year interactions effect (SY) and were analysed by ignoring SY, the direct and maternal variances were inflated and a negative (co)variance was observed between them. But ignoring SY for the data without significant interaction effect has no changed on genetic parameters. In a study on body weight at 6 weeks in a commercial broiler line, a reduction in direct and maternal heritability has been occurred when fitting SY effect in the analysis model (Shafaat *et al.* (2008)). In the present study, the data from a commercial broiler line were used to explore consequences of including random effects, such as maternal and generation-hatch-sire interaction (GHS) effects on the estimates of genetic parameters for day-old chicken's body weight.

Material and Methods

The data included day-old chicken's body weights information from a commercial broiler line. The structure of the data is summarized in Table 1.

Table 1: Structure of data

Information	Record
Number of Generations	15
Number of Pedigree records	67365
Number of animals with records	34430
Trait Mean \pm SD (gr)	46.28 \pm 4.37
CV (%)	9.44
Minimum value (gr)	30
Maximum value (gr)	62

For investigating maternal effects on day-old chickens' body weight (BWT1) and influence of generation-hatch-sire interaction (GHS) effect on maternal models, 10 different animal models were fitted. The animal models in matrix notations are presented in table 2. In these models, \mathbf{y} is a vector of observations, \mathbf{b} is a vector of fixed effects (Generation-Hatch, Sex and Dam age), \mathbf{a} is an unknown random vector of direct additive genetic effect, \mathbf{m} is an unknown random vector of maternal additive genetic effect, \mathbf{c} is an unknown random vector of maternal environmental effect, \mathbf{s} is an unknown random vector of GHS effect, and \mathbf{e} is an unknown random vector of residuals. \mathbf{X} , \mathbf{Z}_1 , \mathbf{Z}_2 , \mathbf{W} and \mathbf{S} are known incidence matrices relating observations to \mathbf{b} , \mathbf{a} , \mathbf{m} , \mathbf{c} and \mathbf{s} , respectively. Also, cov_{am} is the covariance between direct and maternal additive genetic effects. Estimates of genetic parameters and (co)variance components were obtained by restricted maximum likelihood (REML) method, using the ASREML software. Determination of superiority of one model over another was made by Likelihood ratio test (Dobson (1991)).

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Table 2: Matrix forms of studied models

Models Num.	Models Matrix Notations	
1	$y = \mathbf{Xb} + \mathbf{Z}_1\mathbf{a} + \mathbf{e}$	
2	$y = \mathbf{Xb} + \mathbf{Z}_1\mathbf{a} + \mathbf{Wc} + \mathbf{e}$	
3	$y = \mathbf{Xb} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{e}$	$\text{cov}_{am} = 0$
4	$y = \mathbf{Xb} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{e}$	$\text{cov}_{am} \neq 0$
5	$y = \mathbf{Xb} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{Wc} + \mathbf{e}$	$\text{cov}_{am} = 0$
6	$y = \mathbf{Xb} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{Wc} + \mathbf{e}$	$\text{cov}_{am} \neq 0$
7	$y = \mathbf{Xb} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{Ss} + \mathbf{e}$	$\text{cov}_{am} = 0$
8	$y = \mathbf{Xb} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{Ss} + \mathbf{e}$	$\text{cov}_{am} \neq 0$
9	$y = \mathbf{Xb} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{Wc} + \mathbf{Ss} + \mathbf{e}$	$\text{cov}_{am} = 0$
10	$y = \mathbf{Xb} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{Wc} + \mathbf{Ss} + \mathbf{e}$	$\text{cov}_{am} \neq 0$

Results and discussion

Estimates of (co)variance components and genetic parameters for day-old chickens' body weight (BWT1) with logarithm of likelihood ratio from each animal model are shown in tables 3. Based on model 1, direct additive genetic variance and direct heritability for BWT1 were estimated 11.21 and 0.770, respectively. Adding maternal environmental (model 2) and maternal additive genetic (model 3) effects in model 1 caused to significant reduction in additive genetic variance and its heritability ($p < 0.01$). Direct heritability (h^2_a) using models 2 and 3 were 0.217 and 0.069, respectively. Base on these models, maternal environmental variance as a proportion of the phenotypic variance (c^2) and maternal heritability (h^2_m) were estimated 0.398 and 0.485, respectively. Comparison between these three models indicated that ignoring maternal effects in the analysis tended to overestimate direct additive genetic variance and heritability.

As can be seen from table 3, introducing the covariance between direct and maternal additive genetic effects (model 4), increased direct and maternal additive genetic variances in approximately 30% and 11% in comparison to model 3, respectively ($p < 0.01$). This increasing is because of negative covariance (-0.96) between direct and maternal additive genetic effects. Estimations of 0.091 and 0.542 were obtained for h^2_a and h^2_m , respectively, by using model 4. Comparing model 5 with model 3 showed that omitting maternal environmental effect in the analysis of BWT1 tended to overestimate the maternal additive genetic variance (σ^2_m) and heritability (h^2_m). Maternal heritability (h^2_m) was estimated 0.371 with model 5 compare to 0.485 in model 3. When we put covariance between direct and maternal additive genetic effects in model 5 (model 6), a significant increase ($p < 0.01$) was observed in logarithm of likelihood ratio. By using model 6, h^2_a , h^2_m and c^2 were estimated 0.092, 0.433 and 0.085, respectively. Comparing models 1 and 6 showed clearly that maternal additive genetic variance has most affective effect on day-old chickens' body weight.

According to the table 3, generation-hatch-sire interaction (GHS) effect was accounted for 5% of the phenotypic variance. Introducing the GHS effect reduced direct heritability in all corresponding models by approximately 64 to 78%. Fitting GHS effect in full model ($a + m + c + \text{cov}_{am}$) resulted to obtain the lowest negative estimates of direct-maternal correlation in all corresponding models (table 3). Whereas set of the GHS effect without fitting maternal environmental effect (model 8 = $a + m + s + \text{cov}_{am}$) did not decreased in negative direct-maternal genetic correlation in comparison to model 4 ($a + m + \text{cov}_{am}$). A comparison between models 6 and 10 showed that although GHS had a minor proportion of phenotypic variance, but ignoring it from the model made up 70% of negative covariance between direct and maternal genetic effects.

Many studies demonstrated the importance of maternal effect on production and reproduction traits in poultry. Hartmann *et al.* (2003) reported an intermediate (0.5) maternal heritability (h^2_m) for chick weight, whereas the direct heritability was close to zero. This result is in line with the finding of Koerhuis *et al.* (1977) who found substantial variation in chick weight due to the dam. Prado-Gonzalez *et al.* (2003) showed that direct heritability (h^2_a) was low for body weight of Mexican Creole chickens during rearing. They also showed that maternal additive and environmental were not important source of variation after 4 weeks of age in Creole chickens. But seraj *et al.* (2006) in a study on Iranian native fowl reported that maternal additive genetic and environmental effects with the covariance between direct and maternal additive genetic effects were important for body weight of 8 weeks. In these studies, the estimation of direct-maternal genetic correlation (r_{am}) was negative.

Different reasons such as adaptation of a species to a trait optimum emerging as a result of natural selection (Hartmann *et al.* (2002)), decrease of egg shell quality and inattention to the maternal effect during previous generations (Robinson *et al.* (1993)), linkage disequilibrium and pleiotropic effects of the same gene (Grindstaff *et al.* (2003)) are suggested for this negative correlation. This negative correlation between direct and maternal additive genetic effects has been observed in other domestic species. The results of Lee and Pollak (1997) indicated that if sire by year (SY) interactions are detected, then they are true effects, not spurious results due to incorrect direct and maternal covariance. According to these authors, the SY effect is either a true interaction, perhaps caused by different environmental factors associated with different years, or indication of confounding of sire effects with other unidentified sources of covariance between progeny records in the same year.

Conclusion

The results of this study indicated that ignoring maternal effects in the analysis of BWT1 tended to overestimate direct additive genetic variance and heritability. With considering the cov_{am} in models, higher estimations of direct and maternal genetic variances were obtained that could be because of negative covariance between these effects. The investigations showed that negative estimates of cov_{am} are not only because of genetic antagonism, but also because of the influence of GHS interaction effects. Comparison between different models of this study indicated that although GHS had a small part of phenotypic variance (5%), but 70% of negative covariance between direct and maternal genetic effect resulted in ignoring this effect from analysis model.

Table 3: Estimates of (co)variance components and genetic parameters for day-old chicken body weight (BWT1)

Model	σ_a^2	σ_c^2	σ_s^2	σ_m^2	σ_{am}	σ_e^2	σ_p^2	h_a^2	c^2	s^2	h_m^2	r_{am}	LogL
1	11.21	-	-	-	-	3.35	14.55	0.770	-	-	-	-	-56442/02
2	2.94	5.39	-	-	-	5.22	13.55	0.217	0.398	-	-	-	-54988/71
3	0.97	-	-	6.79	-	6.25	14.01	0.069	-	-	0.485	-	-54756/69
4	1.27	-	-	7.58	-0.96	6.09	13.98	0.091	-	-	0.542	-0.31	-54749/39
5	0.963	1.42	-	5.06	-	6.20	13.64	0.071	0.104	-	0.371	-	-54732/18
6	1.27	1.16	-	5.93	-0.70	6.04	13.71	0.092	0.085	-	0.433	-0.26	-54728/70
7	0.32	-	0.68	6.82	-	6.06	13.89	0.023	-	0.049	0.492	-	-54400/30
8	0.45	-	0.68	7.32	-0.57	5.99	13.88	0.033	-	0.049	0.528	-0.31	-54397/33
9	0.25	1.46	0.67	5.57	-	6.08	14.02	0.018	0.104	0.048	0.397	-	-54376/56
10	0.27	1.50	0.65	5.76	-0.21	6.06	14.03	0.020	0.107	0.046	0.411	-0.17	-54375/46

σ_a^2 Direct Additive Genetic Variance, σ_c^2 Maternal Environmental Variance, σ_s^2 Generation-Hatch-Sire Interaction Effect, σ_m^2 Maternal Additive Genetic Variance, σ_{am} Covariance between Direct and Maternal Additive Genetic Effects, σ_e^2 Residual Variance, σ_p^2 Phenotypic Variance, h_a^2 Direct Heritability, c^2 Maternal Environmental Variance as a Proportion of the Phenotypic Variance, s^2 Generation-Hatch-Sire Interaction as a Proportion of the Phenotypic Variance, h_m^2 Maternal Heritability, r_{am} Correlation between Direct and Maternal Additive Genetic Effects, **LogL** Logarithm of Likelihood Ratio

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