Genetic Parameters for Egg Production with Different Animal Models in a Commercial Broiler Line

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Introduction

Egg production is an important economic trait for broiler breeders. In these populations egg production generally continues from 24 to 64 weeks of age (about 40 weeks), but selection for improving of egg production is basis of part records. However, selection based on part records has unfavorable effects, including earlier age at first egg, poorer laying persistency after peak and poor selection accuracy (Luo *et al* (2007)). For genetic evaluation of egg production traits we have to estimate heritability of part and total records and genetic correlation between them. Egg number is a longitudinal trait that depends on weeks and months of production. So it is necessary to use the suitable models for considering the relationship between different periods of production. Many genetic parameters are reported for egg production in laying hens, but there are few researches in broilers. Heritability of egg production varied strongly in various studies and depends on population, time and useful model. In experimental lines that are not selected for egg production, heritability of this trait may reach almost 0.5, whereas in commercial lines it is often less than 0.2 (Wolc *et al* (2007)). The heritability of egg number has reported from 0.01 to 0.61 in laying hens (Wolc *et al* (2007), Nurgiartiningsih *et al* (2002, 2004)**,** Unver *et al* (2004)**,** Szwaczkowski (2003)**,** Anang *et al* (2001, 2002)) and from 0.06 to 0.54 for different months in a broiler dam line (Luo *et al* (2007)). These estimations showed a range from low to high for additive genetic variance of egg production. The purpose of this study was to estimate genetic parameters of egg numbers with single-trait**,** multiple-trait and repeated records animal models in a commercial broiler line.

Materials and methods

The data were collected from a commercial broiler line. Egg production of 16830 hens from 1198 sires and 4564 dams was recorded individually in trap-nests for a period of 32 weeks, namely from 24 to 55 weeks of age. Egg productions were used to create 8 monthly records (M1 = sum of the records from 24 to 27 weeks of age to M8 = sum of the records from 52 to 55 weeks of age) by summing each 4 consecutive weekly eggs and cumulative egg number was obtained by summing all weekly egg numbers. The structure of data has shown in Table 1. An animal model using Restricted Maximum Likelihood (REML) procedures was used to estimate genetic parameters of egg production. The following linear model was used for estimating (co)variance components and genetic parameters in single-trait and multiple-trait analysis:

$$y_{ijk} = \mu + FG_i + H_j + a_k + e_{ijk}$$

Where y_{ijk}, is the monthly record or cumulative egg number of the hen, μ, is the grand mean, FG_i, is the fixed effect of flock-generation (18 levels), H_j, is the fixed effect of hatching time (4 levels), a_k, is the random additive genetic effect of the hen, and e_{ijk}, is the random residual effect.
With treating the 8 monthly records as the same traits, the following repeated-records animal model was fitted:

$$y_{ijkl} = \mu + FG_i + H_j + a_k + pe_k + e_{ijkl}$$

Where y_{ijkl}, is the repeated monthly records of each hen, μ, is the grand mean, FG_i, is the fixed effect of flock-generation (18 levels), H_j, is the fixed effect of hatching time (4 levels), a_k, is the random additive genetic effect of the hen, pe_k, is the random permanent environmental effect of the hen and e_{ijkl}, is the

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random residual effect. Variance and covariance components and their respective parameters were carried out using DFREML program (Meyer (2001)).

Table 1. Structure of data

Traits	N	Mean	SD	Minimum	Maximum	CV (%)
M1	16830	8.81	6.33	0	27	71.91
M2	16830	20.09	6.93	0	28	34.48
M3	16830	19.90	6.93	0	28	34.83
M4	16830	18.58	6.94	0	28	37.33
M5	16830	17.14	6.90	0	28	40.26
M6	16830	15.55	7.18	0	28	46.16
M7	16830	14.17	7.29	0	27	51.42
M8	16830	11.09	7.46	0	26	67.29

N=number of records, SD= standard deviation, CV= Coefficient of variance

Results and discussion

Estimates of variance components and direct heritabilities of monthly records of egg production using single-trait and multiple-trait analyses are presented in Table 2. Estimates of heritability based on single-trait analysis varied from 0.075 (M8) to 0.428 (M1). The estimates resulting multiple-trait model was similar to single-trait model and ranged from 0.076 (M8) to 0.424 (M1). Among all monthly records, M1 indicated the highest heritability. This estimate was substantially decreased in M2, and then, with a very minor fluctuation remained relatively stable for M3 to M8 records. The pattern of the heritability changes for the monthly records in the present study was similar to the results reported by Anang *et al* (2002) on White Leghorns, Nurgiartiningsih *et al* (2004) on two commercial lines of White Leghorn hens and Kranis *et al* (2007) on a large-bodied dam line turkey. In spite of the variation in the magnitude of the estimates due to the differences in population, time and statistical models (Wolc *et al* (2007)), these studies indicated that the heritability of egg production was high in the beginning of the laying period, decreasing in second period, and remained constant for the rest of the tine points. The higher estimates of heritability for the first monthly records have been attributed to the variation in age at first egg (Anang *et al* (2000)) and the variation in the rate of lay before peak (Nurgiartiningsih *et al* (2004)).

Table 2. Variance components and heritability of egg production using single-trait and multiple-trait analysis

Trait	σ_a^2		σ_e^2		σ_p^2		$h^2 \pm$ SE	
	single	Multiple	single	Multiple	single	Multiple	single	Multiple
M1	15.95	15.79	21.33	21.43	37.28	37.22	0.428 ± 0.019	0.424 ± 0.018
M2	7.03	6.42	39.89	40.33	46.92	46.75	0.150 ± 0.016	0.137 ± 0.013
M3	4.30	4.18	42.60	42.70	46.90	46.88	0.092 ± 0.012	0.89 ± 0.012
M4	4.36	4.06	43.04	43.26	47.39	47.32	0.092 ± 0.014	0.086 ± 0.012
M5	3.77	3.69	43.24	43.31	47.01	46.99	0.080 ± 0.013	0.078 ± 0.011
M6	4.52	4.40	45.04	45.14	49.56	49.54	0.091 ± 0.014	0.089 ± 0.012
M7	4.09	4.16	46.00	45.96	50.09	50.12	0.082 ± 0.012	0.083 ± 0.011
M8	3.07	3.11	37.78	37.76	40.85	40.88	0.075 ± 0.011	0.076 ± 0.011

σ_a^2 = additive genetic variance, σ_e^2 = residual variance; σ_p^2 = phenotypic variance; h^2 =heritability; SE= standard error.

Heritability and proportion of permanent environmental variance to phenotypic variance for eight monthly records were estimated 0.067 and 0.312, respectively, using repeated records model. In other research in laying hens, heritability and the ratio of permanent environmental variance to phenotypic variance for months 1 to 11 were 0.06 and 0.01, respectively. These estimations for months 1 to 5 were zero (Anang *et al* (2001)). In a study on Turkeys and using repeated records model, proportion of permanent environmental variance to phenotypic variance for months 1 to 5 was reported higher (0.45) (Kranis *et al* (2007)). Whereas Wolc *et al* (2007) in similar research on laying hens used repeated records model to estimate variance components of nine monthly egg productions and reported Heritability and repeatability in studied lines from 0.02 to 0.03 and from 0.04 to 0.38, respectively.

Covariance components and correlations between different months using multiple-trait model are presented in Table 3. Genetic correlations between monthly egg productions varied from 0.358 (between M1 and M7) to 0.986 (between M4 and M5). First month had a low genetic correlation with middle and final months (from 0.358 to 0.384). Genetic correlation between middle and final months of production was high (from 0.792 to 0.979). Phenotypic correlations of various months ranged from 0.183 to 0.859 and decreased as the interval between periods increased. These results were in agreement with report from Wolc *et al*, (2007). They found that genetic correlation between the first two periods and the other months were low and even negative between the first month and more distant periods. Genetic correlations between middle and final periods were reported moderate to high (from 0.44 to 0.99). Kranis *et al*, (2007) investigated genetic parameters of egg production for different months using multiple model in Turkey. Months 1 and 4 had lowest genetic correlations (0.05). The highest genetic correlation was between months 4 and 5 (0.88). These estimations between first and other months were low (from 0.05 to 0.17). In other study, genetic parameters of monthly egg production and the influence of Box–Cox transformation on the parameters from a population of White Leghorns were reported. The differences between the estimates from untransformed and transformed data were small. Genetic correlations between consecutive months were high and it decreased with increasing the distance between months. According to other studies, genetic correlation between first and second months of production was high (0.76), but it was low between first and upper 3 months (from 0.05 to 0.22).

Table 3. Covariance components and correlations between egg production traits using multivariate model

Trait 1	Trait 2	σ_{a12}	σ_{e12}	σ_{p12}	$r_{a12} \pm SE$	$r_{e12} \pm SE$	$r_{p12} \pm SE$
M1	M2	7.30	12.46	19.77	0.725 ± 0.033	0.424 ± 0.011	0.474
	M3	3.30	7.61	10.90	0.406 ± 0.057	0.252 ± 0.013	0.261
	M4	3.00	6.71	9.71	0.375 ± 0.059	0.220 ± 0.013	0.231
	M5	2.92	6.16	9.08	0.384 ± 0.061	0.202 ± 0.013	0.217
	M6	3.03	5.59	8.62	0.363 ± 0.059	0.180 ± 0.013	0.201
	M7	2.90	5.53	8.43	0.358 ± 0.060	0.176 ± 0.013	0.195
	M8	2.60	4.53	7.13	0.370 ± 0.062	0.159 ± 0.013	0.183
M2	M3	4.19	29.02	33.21	0.809 ± 0.033	0.699 ± 0.005	O.709
	M4	3.55	25.25	28.80	0.695 ± 0.047	0.605 ± 0.007	0.612
	M5	3.19	23.07	26.26	0.657 ± 0.053	0.552 ± 0.007	0.560
	M6	3.46	20.77	24.23	0.652 ± 0.053	0.487 ± 0.008	0.504
	M7	3.17	18.92	22.09	0.614 ± 0.058	0.439 ± 0.008	0.456
	M8	2.77	14.23	17.00	0.621 ± 0.061	0.365 ± 0.009	0.389
M3	M4	3.92	35.02	38.93	0.950 ± 0.015	0.815 ± 0.003	0.827
	M5	3.57	31.15	34.72	0.911 ± 0.025	0.724 ± 0.005	0.740
	M6	3.80	27.59	31.39	0.885 ± 0.031	0.629 ± 0.006	0.651
	M7	3.47	25.14	28.62	0.833 ± 0.041	0.568 ± 0.007	0.590
	M8	2.86	18.97	21.83	0.792 ± 0.050	0.473 ± 0.008	0.499
M4	M5	3.81	36.38	40.19	0.986 ± 0.009	0.840 ± 0.003	0.852
	M6	4.05	31.75	35.79	0.957 ± 0.018	0.718 ± 0.005	0.739
	M7	3.69	28.67	32.36	0.899 ± 0.031	0.643 ± 0.006	0.665
	M8	3.03	21.71	24.74	0.853 ± 0.043	0.537 ± 0.007	0.563
M5	M6	3.94	36.31	40.24	0.979 ± 0.012	0.821 ± 0.003	0.834
	M7	3.86	32.37	36.05	0.941 ± 0.022	0.725 ± 0.005	0.743
	M8	2.95	24.68	27.64	0.873 ± 0.038	0.610 ± 0.006	0.631
M6	M7	4.19	38.61	42.80	0.979 ± 0.009	0.848 ± 0.003	0.859
	M8	3.47	29.42	32.89	0.938 ± 0.022	0.713 ± 0.005	0.731
M7	M8	3.45	33.77	37.22	0.958 ± 0.016	0.811 ± 0.003	0.822

σ_{a12}, σ_{e12} and σ_{p12} = direct additive genetic, residual and phenotypic covariance components, respectively; r_{a12}, r_{e12} and r_{p12} = direct additive genetic, residual and phenotypic correlations, respectively and SE= standard

Based on the heritability estimates from the single-trait, multiple-trait and repeated models, a heritability profile was plotted by joining the estimates for each month point and thus covering the whole months (Figure 1). Estimates resulting single-trait and multiple-trait models were similar. Heritability of repeated records model remained constant for the whole production periods. The multiple-trait model had an advantage over two other models, because it allowed the modeling of the genetic and phenotypic correlations between periods. Repeated records model assumes a constant value for genetic variance during egg production period. Also a value of 1 is supposed for genetic correlations between periods in this model. Whereas genetic correlation between various months varied from 0.358 to 0.986 using multiple-trait analysis that indicates the assumption of repeated records model is not true. Genetic correlation between continuous periods was high, but it decreased when the interval of periods increased. First two months of production had the lowest genetic correlation with other months that indicates these part records might be unsuitable to use for selection.

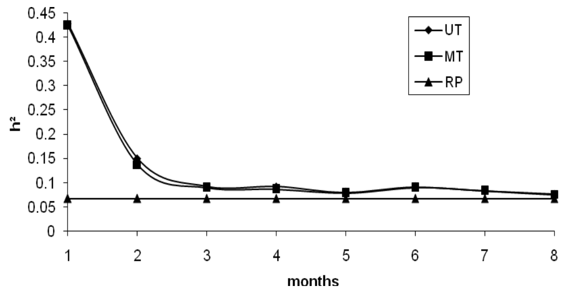

Figure 1. Heritability profile for all models (single-trait = line and squares, and multiple-trait = line and diamonds, repeated records = line and triangles)

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