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Genetic parameters for egg production traits in crosses between local and exotic chickens estimated by Bayesian inference

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Abstract

Estimates of genetic parameters for economic traits are important to enable the breeder estimate the breeding value of individuals available for selection. Thus, this study was carried out to estimate genetic parameters namely heritability and genetic correlations among egg production traits in two strain crosses using bivariate animal model in Bayesian (MCMC) method. The egg production data were obtained from four generations which comprised the base population of two commercial egg strains and the local chicken, the inbred population derived from the base population, the F_1 crossbred population obtained from the crossing of the local and exotic inbred chickens and the backcross population obtained from the backcrossing of the crossbred to their parents. A total number of 1,138 daughters of 62 sires and 620 dams were used for the study. The autocorrelations among samples in the MCMC chain were less than 0.1 for all lag values indicating that all samples of the posterior distribution were independent. The estimated heritability for age at first egg, body weight at first egg, hen day egg number, weight of first egg, egg weight at thirty week and egg weight at forty week were 0.62, 0.48, 0.47, 0.53, 0.54 and 0.56 for strain 1 crosses and 0.43, 0.48, 0.49, 0.52, 0.52 and 0.53 for strain 2 crosses. The corresponding highest posterior density interval ranged from 0.22 to 0.91 for strain 1 crosses and 0.07 to 0.83 for strain 2 crosses. The genetic correlations among egg production traits ranged from 0.06 to 1.97 in strain 1 and 0.06 to 2.59 in strain 2 crosses. The estimates were within the range reported in literature for egg production traits in chicken and imply that appreciable amount of additive genes exist in the strain crosses which could be used for the selection of superior birds. The magnitude of genetic correlations implies that selection of one trait could lead to correlated response to the other traits.

Keywords: Autocorrelations, egg production, genetic correlations, heritability, strain crosses.

Introduction

Estimates of genetic parameters for economic traits are important to enable the breeder assess the breeding value of individuals available for selection. Also estimates of genetic parameters related to crossbred and purebred populations should give some indication as to which method of selection will be most effective (Besbes and Gibson, 1998). Many methods are used in the estimation of variance components. Traditionally, ANOVA has been used to estimate variance components. The problem with ANOVA is that it requires balance data for it to work and most often it can give negative estimates of variance components (Karaman *et al*, 2014). Because data that are generated in animal breeding experiments are often unbalanced and come from different type of relationship, maximum likelihood (ML) and restricted maximum likelihood (REML) are often used to estimate variance components. The two methods are basically the same but differs by the fact that REML takes into account the loss in degree of freedom used for estimating fixed effects when estimating variance components while ML does not (Patterson and Thompson, 1971). The REML has its limitations. Some of them are discussed as follows. The use of REML in variance component estimation is based on approximation that may not work well. REML uses large sample theory to derive approximate confidence intervals that may have very poor coverage, especially for variance components. The Bayesian inference can fix the aforementioned problems by providing accurate measure of confidence interval and an easy and intuitive way of obtaining measures of confidence on derived statistics such as components of variance, correlations and predictions. Bayesian (MCMC) is also based on approximation but the accuracy of the approximation increases the longer the analysis is run for, being exact at the limit (Hadfield, 2014). The objective of this study was to estimate heritability and genetic correlations among egg production traits in crosses involving local and exotic chickens using MCMC method.

Materials and methods

The study was conducted at the Department of Animal Science, Delta State University, Asaba campus.

The Pedigree

The pedigree is made up of animal ID, sire and dam. The number of sires and dams and their progenies (daughter) per generation for the two strain crosses are shown in Table1.

Table1: Number of sires, dams and daughters with records for the two strain crosses

	Strain 1 crosses				Strain 2 crosses			
Gen	**Group**	**Sire**	**Dam**	**Daughter**	**Group**	**Sire**	**Dam**	**Daughter**
1	1	4	40	63	9	4	40	65
	2	2	20	40	10	2	20	42
2	3	8	80	130	11	6	60	120
	4	2	20	46	12	2	20	40
3	5	4	40	86	13	4	40	60
	6	4	40	87	14	4	40	70
4	7	4	40	84	15	4	40	65
	8	4	40	84	16	4	40	56

Note: Gen: Generation

Group: 1: H and N Brown Nick, 2: Local chicken replicate 1, 3: H and N Brown Nick (inbred), 4: Local chicken replicate 1 (inbred), 5: Main cross (4x3), 6: Reciprocal cross (3x4), 7:Main back cross (3x4x3), 8: Reciprocal back cross (4x3x4), 9: Black Olympia, 10: Local chicken replicate 2, 11: Black Olympia (inbred), 12: Local chicken replicate 2 (inbred), 13: Main cross (12x11), 14: Reciprocal cross (11x12), 15: Main back cross (11x12x11), 16: Reciprocal back cross (12x11x12).

In each strain cross, generation 1 which is the base population is made up of a commercial stock and the local chicken. Generation 2 is the inbred population derived from the commercial stocks and the local chicken. Generation 3 comprised F_1 crosses between the inbred progenies of the local and exotic chickens while generation 4 is the backcross population derived from the backcrossing of the local and exotic inbred chicks to their F_1 crossbred groups. Details of the crossbreeding procedures had been described (Udeh and Omeje, 2005).

Data collection

The egg production traits recorded per generation and for each strain cross were as follows: Age at first egg (AFE) in days is taken as the number of days from hatch to first egg. Bodyweight at first egg (BWFE) in kg was taken as weight of birds at when the first egg was laid. Egg number in hen day basis (HDEN) = the total number of eggs laid in a day / the average number of hens for that day. Weight of first egg (WFE) in g was the average weight of first ten eggs laid consecutively for each bird or group. Egg weight at 30 weeks (EW30) in g was determined as the average weight of samples of eggs laid on two consecutive days by each group at 30 weeks of age. Egg weight at 40 weeks (EW40) in g was taken as average weights of sample of eggs laid per genetic group on two consecutive days at 40 weeks of age.

Data analysis

Data for each egg production trait were adjusted for the effect of hatch within each generation using the method of least square. A multivariate animal model was used to analyze the data. Given that animals were ordered within traits, the multivariate model for two traits could be written as:

$$1 \qquad \begin{bmatrix} Y_1 \\ Y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

Where Yi = vector of observations for i_{th} traits (say AFE, BWFE), b = vector of fixed effects for the i_{th} trait (say GEN), u_i = vector of random animal effects for the i_{th} trait, e_i = vector of random residuals for the i_{th} trait and X_i and Z_i are incidence matrices relating records of the i_{th} trait to fixed and random animal effects respectively. The conditional distribution of the complete data, given that animals are ordered within trait is

$$1 \qquad \left\langle \begin{matrix} Y_1 \\ Y_2 \end{matrix} \right| \text{b}_1\text{, b}_2\text{, u, u}_2\text{, R} \left. \vphantom{\begin{matrix} Y_1 \\ Y_2 \end{matrix}} \right\rangle \sim \text{N} \begin{bmatrix} X_1 b_1 + Z_1 u_1 & R \otimes 1 \\ X_2 b_2 + Z_2 u_2 & \end{bmatrix}$$

It is assumed that

$$1 \qquad \left\langle \begin{matrix} u_1 \\ u_2 \end{matrix} \right| \text{G, A} \left. \vphantom{\begin{matrix} u_1 \\ u_2 \end{matrix}} \right\rangle \sim \text{N} \begin{bmatrix} 0 & G \otimes A \\ 0, & \end{bmatrix}$$

where G is the genetic covariance matrix and A is the numerator relationship matrix (Mrode, 2005). Note $\otimes$ is the symbol of Kronecker product or direct product. The multivariate animal model was implemented using MCMCglmm, an R package for fitting generalized linear mix model under Bayesian inference (R Development Core team, 2015; Hadfield, 2014). In fitting multivariate animal model under Bayesian frame work, it is necessary to consider a variance – covariance matrices of the form

$$1 \qquad \begin{pmatrix} V_1 & C_{1,2} \\ C_{1,2} & V_2 \end{pmatrix}$$

where V_i is the variance (for example additive genetic) associated with trait i and $C_{1,2}$ is the covariance (for example genetic) between trait 1 and 2. Therefore, there is need to specify a kind of prior distribution relevant for the matrix. To do so, a matrix distribution known as inverse Wishart was used (de Villemereuil, 2012). A default prior specification taken from Wilson *et al* (2009) was used. The number of iterations for each run of the bivariate analysis was 65000 with a burn in of 15000 and a thin of 50. Burn in is the number of iterations to discard at the beginning of the Markov Chain sample and thin is the number of iterations stored in memory (here 1 every 50 iterations). The output of a Bayesian inference is the posterior distribution, which is a probabilistic distribution associating each value of a parameter to a degree of belief (de Villemereuil, 2012). The variance components, heritability and genetic correlations were extracted from the posterior distributions.

Results and discussion

The average inbreeding coefficients in the inbred progeny generation (Gen 2) and the backcross population (Gen 4) were 50% and 37.50% respectively. Inbreeding coefficient was zero at the base population (Gen 1) and F_1 crossbred population (Gen 2). The autocorrelations among samples in the MCMC chain for the two strain crosses is presented in Table 2.

The autocorrelation estimates the level of non independence between successive samples in the chain (HadField, 2014). In Table 2, lag 50 stands for the autocorrelation every 50 iterations while lag 2500 stands for autocorrelation every 2500 iterations (de Villemereuil, 2012). The autocorrelation for all lag values were less than 0.1 which is acceptable according to de Villimereuil (2012). Ideally, all samples of the posterior distribution should be independent and the autocorrelation for all lag values greater than zero should be near zero (Wilson *et al*, 2009). The posterior heritability and HPD intervals for egg production traits in the two strain crosses are shown in Table 3.

The heritability (h^2) was moderate to high in magnitude and ranged from 0.47 to 0.62 in strain 1 crosses and 0.43 to 0.52 in the strain 2 crosses. The corresponding HPD interval ranges were 0.22 to 0.91 for strain 1 crosses and 0.07 to 0.83 for strain 2 crosses. The HPD interval is the Bayesian equivalent of confidence interval. The h^2 of AFE was 0.62 in strain 1 crosses and 0.43 in strain 2 crosses with 95% of probability to lie between 0.30 to 0.91 for strain 1 crosses and 0.07 to 0.82 for strain 2 crosses. Tongsiri *et al* (2014) reported h^2 estimates of 0.46 and 0.43 for AFE in RIR and WPR respectively which were in agreement with h^2 estimate of 0.43 observed in strains 2 crosses. Strain 1 crosses had higher h^2 estimate than the estimates reported by Tongsiri *et al* (2014). Niknafs *et al* (2012) reported a lower estimate of 0.36 for age at sexual maturity in Mazandaran native chicken of Iran using bivariate animal model. Most studies reported medium h^2 for AFE that ranged between 0.24 and 0.55 (Guo and Wang, 2015). The h^2 estimate of 0.48 for BWFE was the same in both strain 1 crosses and strain 2 crosses. The HPD interval showed that the h^2 estimate for BWFE has 95% probability to lay between 0.25 to 0.73 (strain 1 crosses) and 0.23 to 0.74 (strain 2 crosses). The estimated h^2 for BWFE in this study was in agreement with the estimate of 0.47 reported by McClung *et al* (1976) and within the range of 0.38 to 0.57 reported by Sang *et al* (2006). Tongsiri *et al* (2015) reported a lower estimate of 0.30 to 0.40 compared to the estimate observed in this study. The h^2 estimates of HDEN were similar in strain 1 crosses (0.47) and strain 2 crosses (0.49). The HPD interval indicates with 95% probability that the h^2 estimate lies between 0.22 to 0.71 (strain 1 crosses) and 0.24 to 0.74 (strain 2 crosses). Parvaneh *et al* (2012) reported a higher h^2 estimate of 0.58 for egg number compared with what was obtained in this study. The h^2 estimates of WFE, EW30 and EW40 in strain 1 were 0.53, 0.54 and 0.56 respectively which were similar to the estimates in strain 2 (WFE=0.52, EW30=0.52 and EW40=0.53). The corresponding HPD intervals ranged from 0.25 to 0.85 for strain 1 crosses and from 0.23 to 0.83 for strain2 crosses. These estimates were within the range of 0.50 – 0.80 for h^2 of egg weight

Table 2: Autocorrelations among samples in the MCMC chain for the strain crosses

	Strain 1 crosses				**Strain 2 crosses**			
	Animal		**Units**		**Animal**		**Units**	
	Animal	**Units**	**Animal**	**Units**	**Animal**	**Units**	**Animal**	**Units**
	AFE							
Lag 0	1.000	-0.160	-0.16	1.000	1.000	-0.047	-0.047	1.000
Lag 50	-0.015	-0.069	-0.03	0.005	0.059	-0.017	-0.009	0.044
Lag 250	0.018	-0.005	-0.023	0.008	-0.058	0.031	0.011	-0.012
Lag 500	0.043	-0.002	-0.008	-0.042	-0.009	-0.035	0.006	-0.001
Lag2500	0.050	-0.041	0.043	0.034	-0.033	0.004	-0.040	-0.004
	BWFE							
Lag0	1.000	0.312	0.312	1.000	1.000	0.268	0.268	1.000
Lag50	0.018	0.035	0.003	-0.007	0.012	0.044	0.026	-0.01
Lag250	-0.016	-0.053	0.044	0.058	-0.011	-0.035	-0.028	-0.001
Lag500	-0.013	-0.036	0.008	0.029	-0.042	-0.024	0.008	0.014
Lag2500	0.013	-0.025	0.051	0.037	-0.013	0.001	-0.044	-0.051
	HDEN							
Lag0	1.000	0.213	0.213	1.000	1.000	0.257	0.257	1.000
Lag50	0.001	-0.012	0.018	0.021	-0.013	0.026	-0.017	0.019
Lag250	-0.009	0.030	-0.023	-0.040	-0.063	-0.038	0.038	0.035
Lag500	-0.044	-0.012	-0.002	-0.009	0.017	-0.011	0.022	-0.024
Lag2500	0.012	0.006	0.029	-0.019	0.025	-0.005	-0.001	-0.006
	WFE							
Lag0	1.000	0.114	0.114	1.000	1.000	0.122	0.122	1.000
Lag50	-0.026	-0.024	-0.053	-0.048	-0.011	-0.029	0.028	0.002
Lag250	-0.039	0.041	-0.060	0.022	-0.031	-0.023	0.014	-0.003
Lag500	-0.030	-0.009	-0.009	0.003	-0.002	0.005	0.002	-0.027
Lag2500	0.025	-0.011	0.029	-0.050	0.049	-0.005	0.020	-0.023
	EW30							
Lag0	1.000	0.045	0.045	1.000	1.000	1.000	0.056	1.000
Lag50	0.005	-0.018	-0.025	-0.031	-0.054	-0.065	-0.054	-0.065
Lag250	0.004	-0.001	-0.048	0.005	-0.018	0.031	-0.018	0.031
Lag500	0.066	0.057	0.023	-0.023	-0.009	-0.009	-0.009	-0.009
Lag2500	0.005	0.007	0.018	0.045	0.064	-0.028	0.064	-0.028
	EW40							
Lag0	1.000	0.114	0.114	1.000	1.000	0.041	0.041	1.000
Lag50	0.022	-0.029	-0.002	-0.051	-0.005	-0.034	-0.039	-0.029
Lag250	0.008	0.066	-0.012	0.011	0.012	-0.075	-0.012	-0.086
Lag500	0.024	-0.045	0.083	0.006	-0.009	-0.027	0.031	0.059
Lag2500	0.016	-0.021	0.040	0.033	-0.081	-0.003	-0.008	0.022

Table 3: Posterior heritability and highest posterior density (HPD) intervals of two strains of crossbred chickens

	Strain 1 crosses			Strain 2 Crosses		
		HPD Interval			HPD Interval	
Traits	**h^2**	**Lower**	**Higher**	**h^2**	**Lower**	**Higher**
AFE	0.62	0.30	0.91	0.43	0.07	0.82
BWFE	0.48	0.25	0.73	0.48	0.23	0.74
HDEN	0.47	0.22	0.71	0.49	0.24	0.76
WFE	0.53	0.26	0.81	0.52	0.24	0.81
EW30	0.54	0.25	0.81	0.52	0.26	0.83
EW40	0.56	0.25	0.85	0.53	0.23	0.80

HPD Probability: 0.95

Table 4: Genetic correlations among egg production traits in strain 1 crosses (lower matrix) and strain 2 crosses (upper matrix)

	AFE	BWFE	HDEN	WFE	EW30	EW40
AFE	1	0.19	0.06	1.04	0.43	2.59
BWFE	0.06	1	0.26	0.22	0.29	0.33
HDEN	0.07	0.14	1	0.68	0.80	0.78
WFE	1.97	0.54	0.63	1	0.79	1.03
EW30	1.33	0.34	0.90	0.94	1	0.85
EW40	1.21	0.46	0.92	0.85	0.96	1

reported by Besbes and Gibson (1998). The implication of these h^2 estimates is that appreciable amount of additive genetic variance exists in the crossbred populations of chicken waiting to be exploited for the improvement of egg production traits. The genetic correlations among egg production traits in the two strain crosses are shown in Table 4.

All the correlations were positive. AFE was lowly correlated with BWFE and HDEN in both strains 1 and 2. However, the genetic correlations among AFE and WFE, EW30 and EW40 were high in both strain crosses. Tongsiri *et al* (2014) reported high genetic correlation between AFE and WFE in RIR (0.38) and WPR (0.58). Similarly, Sang *et al* (2006) reported high genetic correlation of 0.48 and 0.66 between AFE and WFE in Korean native chicken. Wolc *et al* (2012) reported medium genetic correlation of 0.24 between AFE and EW in chicken while Firozjah *et al* (2015) reported genetic correlation of 0.32 between AFE and EW28-32. This implies that hens with longer AFE would produce heavier eggs. The genetic correlations between BWFE and HDEN were low in strain 1 (0.14) and moderate in strain 2 (0.26) while the genetic correlation among BWFE and WFE, EW30 and EW40 were moderate to high in strain 1 and strain 2 crosses. Tongsiri *et al* (2014) reported moderate genetic correlations among BWFE and WFE (0.40) and EWT (0.48) for RIR and BWFE and WFE (0.33) and EWT (0.46) in WPR. The genetic correlation among WFE, EW30 and EW40 were very high in strain 1 crosses (range: 1.21 – 1.97) and moderate to high in strain 2 crosses (range: 0.43 – 2.59). Similar results were reported by Tongsiri *et al* (2014). The genetic correlation among HDEN and WFE, EW30 and EW40 ranged from 0.68 – 0.80 (strain 1) and 0.63 – 0.92 (strain 2) implying that the number of eggs produced did not affect the size of eggs laid contrary to the reports of Niknafs *et al* (2012) and Firozjah *et al* (2015) who reported negative genetic correlation between EN and EW in the domestic chickens.

Conclusion

The estimates of heritability of egg production traits in the two strain crosses were moderate to high and range from 0.48 to 0.62 (strain 1 crosses) and 0.42 to 0.53 (strain 2 crosses).

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