



Estimation of heritability and genetic correlation of egg production traits using animal model in commercial layer

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ABSTRACT

Traditionally, heritability has been estimated by correlations of close kin. It is likely to be biased by determinants such as non genetic factors, inbreeding, selection and shared environment. Whereas, an animal model takes into account all relationships in a pedigree and is therefore expected to provide estimates of quantitative genetic parameters with higher precision. Therefore, the egg production data in the current study was analyzed using animal model to have more precise and accurate estimates of genetic parameters. The heritability of growth and egg weight traits was moderate to high. Whereas the heritability was lower for egg number and ASM traits. The body weights were positively correlated with egg weights and negatively correlated with egg numbers traits. The egg number produced at different age intervals was positively correlated. The genetic correlation of EP40 and EP52 with EP64 were 0.83 and 0.92, respectively. Therefore, the part period egg production of EP52 would give better selection response for egg production at 64 than EP40. Therefore, the selection of higher egg numbers can be done earlier at 52 weeks rather than waiting for EP64.

Key words: Animal Models, Egg production, IWH, REMI, White Leghorn

One of the primary objectives of livestock or any breeding plan is to predict phenotypic changes enforced through selection of parents for a particular purpose. This requires detailed knowledge of how the particular phenotypes are inherited from generation to generation. The prediction of inheritance is done through knowledge of some genetic parameters like heritability, genetic correlations, additive genetic variance, covariance of phenotypic traits etc. Therefore, the estimation of these genetic parameters form the core of the breeding plans which decides the course of the breeding success. Heritability is one of the most important considerations in determining appropriate animal evaluation methods, selection methods and mating systems. Heritability measures the relative importance of additive genetic variance which is transmitted to the next generation. More specifically, it measures that part of the total variability of the trait caused by genetic differences among the animals on which the measurements were taken. Additive genetic variances and covariance of phenotypic traits determine the response to selection and so are key determinants of the processes of adaptation in response to natural selection and of genetic improvement in response to selection (Lynch and Walsh 1998). Linear mixed model (LMM)-based inferences of genetic parameters, using the

animal model, has become common practice in animal and plant breeding (Thompson 2008, Hill and Kirkpatrick 2010). Traditionally, heritability has been estimated by correlations of close kin, e.g. parent-offspring regressions (Provine 2001). However, an animal model takes into account all relationships in a pedigree and is therefore expected to provide estimates of quantitative genetic parameters with higher precision than estimates restricted to the similarity between close kin. It is also less likely to be biased by complicating factors such as non genetic factors, inbreeding, selection and shared environment (Kruuk and Hadfield 2007). Moreover, the animal model is expected to be statistically more robust to unbalanced data sets compared to parent-offspring models. The key feature of the animal model is that it includes individual additive genetic effects, or breeding values. These additive genetic effects and, critically, their variance are estimable given relatedness data, which can be derived from pedigree data or, more recently, from genomic estimates of relatedness (Sillanpaa, 2011). Keeping in view the importance of analyzing breeding data using animal model this study was conducted with the objective of estimating the heritability, genetic correlations using animal model.

MATERIALS AND METHODS

The current study was conducted at ICAR-Directorate of Poultry Research, Hyderabad, Telangana, India. Hyderabad is located in Deccan plateau in southern part of

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India positioned between 17°23' N and 78° 28' E at height of 500 m from mean sea level. The location experiences usually hot and humid tropical climate with temperature ranging from 20°C in winter to 45°C in summer seasons. The experiment was approved by the Institutional Animal Ethics Committee.

Experimental population: The present study was done on IWH line. IWH has been derived from White Leghorn layer breed and selected for higher egg production since last four generations. The current population was generated using 200 dams and 40 sires. The selection of the sires and dams were done based on the egg production upto 64 weeks using Osborn Index. A total of 1339 day old chicks of IWH were wing banded at the time of pedigree hatch. The current population was generated in three hatches. The hatches were taken at the interval of 10 days.

Rearing and management practices: The chicks were reared in a deep litter brooder house till 16 weeks. In the brooder, the temperature was scheduled from 33°C during first week to 23°C at the end of fifth week in an open-sided house under standard management practices. The debeaking of the chicks were done on 4–5th day. The chicks were fed *ad lib.* with layer starter (2,900 kcal/kg ME and 22% CP) diet based on maize-soybean meal up to 16 weeks. Sexing was done at 6 weeks and male and females were separated. At the end of the 16 weeks period, 506 females and 200 males were transferred to individual cages in cage house. The individual data recordings of body weight, ASM and egg production and egg weights were done regularly. After 16 weeks adult females and males were given layer and males breeder ration respectively. The eight hours of day light and 7 h of artificial light was provided in the layer house. In the summer the proper ambience temperature was maintained through sprinklers on roof top. The mortality in the flock was within standard limit. The egg production was recorded daily. The birds were vaccinated against Marek's disease (1st day), Newcastle disease (ND), Lasota (7th and 30th day), infectious bursal disease (14th and 26th day), fowl pox (6th week), ND R₂B (9th week), Infectious Bronchitis (IB) and ND inactivated (18th week).

Traits measured: The data used in this study was collected during the year 2015–17 and the recording of traits was done for 72 weeks. The primary traits of selection in IWH line was egg production up to 64 weeks and based on

the performance of egg production up to 64 weeks birds were selected for pedigree hatching using Osborn Index. Therefore, after 64 weeks birds were rearranged for pedigree hatching hence analysis of data was done only for 64 weeks. Growth traits such as body weights on day of hatch (BW1), 16 (BW16), 20 (BW20) and 40 (BW40) weeks; production parameters like age at sexual maturity (ASM), egg weights at 28 (EW28), 40 (EW40), 52 (EW52) and 64 (EW64) weeks and Egg productions up to 28 (EP28), 40 (EP40), 52 (EP52) and 64 (EP64) weeks were recorded and analyzed. The female birds were housed in individual cages at 16 weeks and the egg production data of individual birds were recorded every day.

Statistical analysis: Genetic parameter estimates for all the traits under study were calculated by animal model with animal as the only random effect. The linear model for data analyses was:

$$y = X\beta + Z_a a + \varepsilon$$

where, y , vector of records; β , a and ε vectors of fixed, additive animal genetic and residual effects, respectively; with association matrices X and Z_a . Fixed effects in the model included the date of hatch. The significance of fixed effects on the production traits were analysed by SPSS (2005). Estimates of genetic parameters for different traits were obtained by restricted maximum likelihood (REML) WOMBAT (Meyer 2007) using an average information (AI) algorithm. Convergence was assumed when change of value of the natural logarithm of the restricted likelihood function in 2 consecutive iterations was lower than 5×10^{-4} . Bivariate animal model were run to know the genetic correlation between the traits.

RESULTS AND DISCUSSION

Body weight: The body weights of IWH at different age intervals were analyzed using general linear model taking hatch (three levels) as fixed effect. The Least Square Means (LSM) of body weight of IWH at different ages was similar to the earlier report (Laxmi *et al.* 2009) (Table 1). However, the body weights of different indigenous birds were lesser than the present reports (Dana *et al.* 2011). The BW1 of H1 was significantly higher than that of H2 and H3. Similarly the BW1 of H3 was higher than H2. BW16 of H3 was higher than H1 and H2. However, in case of BW20, H1 was higher

Table1. Least Square Means of body weight, egg production and egg weight in IWH line.

	BW1	BW16	BW20	BW40	ASM	EP28	EP40	EP52	EP64	EW28	EW40	EW52	EW64
Sample size (n)	1339	706	279	467	506	437	4437	437	437	467	451	327	421
Mean	32.57	949.38	1120.51	1421.07	139.27	42.62	118.02	189.75	254.31	44.86	50.76	54.21	56.07
H1	30.11 ^c	886.43 ^b	-	1436.57 ^a	138.20 ^b	49.67 ^a	125.71 ^a	197.83 ^a	264.00 ^a	45.22 ^a	51.13 ^a	54.12 ^a	56.49 ^a
H2	34.86 ^a	880.60 ^b	1135.72 ^a	1423.65 ^a	139.94 ^b	48.34 ^a	123.46 ^a	194.96 ^a	259.63 ^a	43.76 ^b	51.24 ^a	54.31 ^a	55.95 ^a
H3	33.39 ^b	1022.25 ^a	1100.35 ^b	1392.80 ^b	140.12 ^a	23.96 ^b	98.71 ^b	170.14 ^b	232.03 ^b	45.80 ^a	49.48 ^b	-	55.56 ^a
SD	4.76	160.51	135.39	165.58	8.63	14.53	17.73	21.76	29.00	3.37	3.95	4.15	4.49
CV	14.61	16.91	12.08	11.65	6.19	34.09	15.02	11.47	11.40	7.51	7.78	7.66	8.01

Same superscripts between rows show nonsignificant difference and different superscript shows significant difference ($P \leq 0.05$).

than H2. Similarly, BW40 of H3 was higher than that of H2 and H1. Hatch had a significant effect on body weight. It may be due to non genetic factors like variation in temperature of environment, the density of chicks at brooding and grower stages (Table1). The genetic parameters like heritability, genetic and phenotypic correlations were estimated using animal model. The heritability of body weights at different age was moderate to high (Table 2). This. However, the heritability of BW1 was very high in contrast to other body weights (Table 2). Similar findings were reported by earlier workers too (Chaudhary *et al.* (2009); Chandan *et al.* 2019). In the current study the heritability was analyzed by additive genetic model which has lower error variance and a higher additive variance than sire-dam model (Wei and vander Werf,1993). Animal models consider animal relationships among all animals which are ignored in case of sire-dam models. Therefore animal model yielded higher heritability than reported in literature (Fairfull and Gowe,1990). But in the current study the additive genetic variance was not partitioned into maternal genetic and maternal permanent variance which might have resulted into over estimation of heritability (Aslam *et al.* 2011). When maternal and common environmental variance was taken into consideration the heritability of BW1 ranged from 0.14 to 0.15 in chicken (Ghorbaani *et al.* 2013). If maternal variance is not included in the model it resulted into higher heritability for body weight (Dana *et al.* 2011 and Abbasi *et al.* 2012). Similar trend of higher heritability of BW1 may be attributed to maternal variance which was not portioned in the current study leading to estimation of heritability on higher side. The heritability of BW16, BW20 and BW40 was low to moderate. As the chicks grew older, the maternal effect which is non additive factor reduced, thereby resulting into reduced heritability.

The genetic correlations among body weights were high except that of BW1. The genetic correlation between BD1 and BW16 were moderate. It means birds can be selected for body weight at day1 body weight and 16 weeks which were very high to moderate. As the birds became older the non additive effects had more influence on body weights. It means the more body weights can be achieved with better management and environment. Body weight is negatively correlated with egg production but positively correlated with egg weight.

ASM: The age at sexual maturity is defined as the number of days after hatching when the first egg is laid (Dunnington and Siegel, 1984). The average Age at Sexual Maturity (ASM, the age at which first egg is laid) was 139.35 days (Table1). The ASM was influenced by the body weights of the birds. The ASM was negatively correlated with BW16 and BW20. It was positively correlated with BW1 and BW40. The heritability estimate of ASM was moderate (0.33) which is similar to a report by Chandan *et al.* (2019). However, Ananta *et al.* (2016) reported lower heritability of ASM. This difference in the results may be due to the method used in estimating the heritability of the traits. Some

Table 2. Heritability, genetic and phenotypic correlation of body weight, egg production and egg weight in IWH line

Trait	BW1	BW16	BW20	BW40	ASM	EP28	EP40	EP52	EP64	EW28	EW40	EW52	EW64
BW1	0.835±0.079	0.506±0.141	0.401±0.175	0.356±0.151	0.070±0.184	-0.555±0.341	-0.497±0.251	-0.561±0.211	-0.485±0.198	0.677±0.131	0.606±0.116	0.312±0.163	0.312±0.139
BW16	0.196±0.044	0.245±0.077	1.00±0.115	0.801±0.132	-0.126±0.259	-0.460±0.476	-0.496±0.325	-0.555±0.270	-0.488±0.266	0.534±0.0211	0.524±0.202	0.696±0.222	0.606±0.190
BW20	0.401±0.175	0.701±0.031	0.443±0.143	0.646±0.037	-0.184±0.247	-0.216±0.27	-0.253±0.245	-0.127±0.242	-0.004±0.243	0.667±0.180	0.670±0.154	0.747±0.162	0.879±0.114
BW40	0.356±0.151	0.553±0.036	0.068±0.099	0.470 ±0.107	0.195±0.227	-0.43.0±0.223	-0.165±0.21	-0.213±0.212	-0.160±0.212	0.482±0.174	0.551±0.144	0.694±0.150	0.687±0.121
ASM	-0.084±0.055	-0.422±0.042	-0.207±0.06	-0.03±0.052	0.333±0.104	-1.000±0.273	-1.000±0.342	-0.726±0.253	-0.582±0.260	0.549±0.213	0.281±0.205	0.333±0.234	0.175±0.199
EP28	-0.191±0.048	0.051±0.058	0.277±0.068	-0.045±0.053	-0.548±0.035	0.069±0.077	0.958±0.065	0.896±0.136	0.610±0.302	-0.694±0.420	-0.433±0.441	-0.679±0.466	-0.627±0.343
EP40	-0.204±0.049	0.055±0.058	0.153±0.071	-0.026±0.054	-0.451±0.040	0.910±0.009	0.147±0.098	0.976±0.036	0.833±0.129	-0.657±0.275	-0.377±0.298	-0.375±0.321	-0.432±0.276
EP52	-0.216±0.049	0.032±0.058	0.081±0.073	-0.045±0.055	-0.379±0.044	0.786±0.019	0.922±0.008	0.210±0.109	0.926±0.050	-0.490±0.245	-0.414±0.243	-0.266±0.283	-0.348±0.296
EP64	-0.214±0.049	0.002±0.058	0.061±0.072	-0.071±0.056	0.275±0.040	0.630±0.030	0.779±0.020	0.918±0.008	0.237±0.116	-0.355±0.205	-0.402±0.171	-0.119±0.226	0.319±0.319
EW28	0.112±0.051	0.273±0.050	0.257±0.063	0.345±0.047	0.128±0.050	-0.300±0.047	-0.296±0.049	-0.288±0.050	-0.186±0.056	0.366±0.102	1.000±0.060	1.000±0.084	0.999±0.063
EW40	0.222±0.051	0.233±0.052	0.326±0.061	0.405±0.045	0.095±0.053	-0.025±0.051	-0.057±0.053	-0.105±0.053	-0.228±0.054	0.641±0.031	0.581±0.111	0.982±0.031	0.937±0.038
EW52	0.194±0.057	0.225±0.061	0.429±0.069	0.349±0.054	0.108±0.058	-0.229±0.060	-0.263±0.059	-0.303±0.057	-0.276±0.060	0.580±0.039	0.787±0.023	0.522±0.138	0.988±0.032
EW64	0.151±0.055	0.349±0.048	0.474±0.055	0.444±0.044	0.044±0.055	-0.171±0.056	-0.190±0.051	-0.235±0.050	-0.308±0.049	0.610±0.034	0.782±0.022	0.784±0.023	0.683±0.117

Diagonal, h^2 ; above diagonal, genetic correlation; below diagonal, phenotypic correlation.

differences between these methods is anticipated as the regression of half sib average on individual is equivalent to the analysis of variance of half sibs, whereas REML considers all genetic relationships and offspring-parental and collateral information, which is likely to yield a higher pooled estimates of the heritability (Hill, 1978). ASM was negatively correlated with BW16 and BW20 whereas it was poorly positively correlated with BW1 and BW40. It means better the body weight at maturity (BW16 and BW20) early the hen will start laying eggs (Table 2).

Egg production: The LSM of egg productions at EP28, EP40, EP52 and EP64 were 42.62, 118.02, 189.75 and 254.31 respectively (Table 1). Egg productions of H1 and H2 were significantly higher than that of H3 at EP28, EP40, EP52 and EP64. However, the egg productions of H1 and H2 were similar across all age intervals (Table 1). The heritability of egg productions was low to moderate which is similar to the earlier reports (Ananta *et al.* 2016; Chandan *et al.* 2019). In the current population intensive selection for the egg production up to 64 weeks was applied therefore, resulting into lower heritability of egg production traits at different age intervals. The heritability of egg production reported in literatures often varies in a wide range depending on the population, time and model of analysis. Under intensive selection heritability may be even less than 0.2 (Preisinger and Savas, 1997). Wolc *et al.* (2013) observed that heritability estimates increased with age up to mid production stage and decreased afterwards. The egg production was inversely correlated with egg weight, body weight and ASM (Table 2). Subsequent egg production traits were perfectly correlated as the gap increases the correlation decreases.

Egg weight: The egg weights of H2 were higher than that of H1 and H2 in case of EW28 but the H1 and H2 did not vary significantly. In case of EW40, the egg weights of H1 and H2 were higher than H3. While egg weight did not vary significantly among hatches at EW52 and EW64 (Table 1). Similar egg weights of IWH were reported by previous workers (Laxmi *et al.* 2009).

The heritability of egg weight was moderate to high in the current study which was in accordance with values reported by Veronica *et al.* (2004). Egg weights are highly correlated traits with egg weights at different age intervals. Egg weights were inversely correlated with egg production and positively correlated with the body weight (Table 2).

The moderate to higher heritability estimates were obtained for growth and egg weight traits. It was lower for egg number and ASM traits. The body weights were positively correlated with egg weights and negatively correlated with egg numbers. The egg numbers were positively correlated at different time intervals. The perfect correlation was observed between EP52 and EP64. Therefore, the selection of higher egg numbers can be done earlier at 52 weeks rather than waiting for EP64. The current study estimates genetic parameters for different traits obtained by restricted maximum likelihood (REML) using animal models which considered all possible relationships

among pedigreed individuals. Therefore, it is assumed that the estimates are better than the simple parent offspring regression method.

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