Research article

PREDICTION OF BREEDING VALUES AND SELECTION FOR EGG MASS IN A CLOSED FLOCK OF WHITE LEGHORN

R. Sh, Abou El-Ghar and A. A. Debes

Animal Production Research Institute, ARC, Ministry of Agriculture, Egypt.
E-mail: reda.abouelghar@gmail.com

ABSTRACT

A closed flock of White Leghorn was subjected to one cycle of selection for part year egg mass (at 90 and 120 d of production). Best linear unbiased prediction (BLUP) was used for predicting the breeding values and ranking then selecting hens for both egg mass and correlated traits. The correlated traits measured included egg number and egg weight at 90 and 120 d., of production. The selection differential was 11 eggs, 2.0 g and 598 g for egg number, egg weight and egg mass at 90 d of production, respectively. The corresponding values at 120 d of production were 16 eggs, 1.6 g and 829 g for the same traits. The realized genetic gain exceeded the expected genetic gain for egg mass at 90 d of production 202 vs. 83.7g and 354 vs.165.8 g for egg mass at 120 d egg production. The realized genetic gain for different correlated traits was in the same direction. It was clear that a considerable increase in egg mass was achieved as a direct response. Consequently, BLUP provides an effective methodology of ranking and selecting hens given measurements on several traits including egg mass. **Copyright © www.acascipub.com, all rights reserved.**

Key Words: Closed flocks- breeding values- responses of selection- egg mass.

INTRODUCTION

White Leghorn closed flock laying hens has been maintained mainly for experimental use in Borg El-Arab Research Station since the fifteenths. Such a random mating population of finite size, the genetic variance declines due to inbreeding. The relationship of selection to the genetic variance, to correlate responses and to plateau populations are the limits of genetic improvement for some quantitative characters under artificial selection. It is will recognized that the mean and genetic variance will change as a result of selection. Consequently selection determines both genetic gain and inbreeding rate, through decreasing genetic variations in the population. On the other hand, inbreeding reduces effectiveness of intra-line selection by increasing random drift in gene frequencies and by reducing intensity of selection through impaired reproductive fitness (Dickerson, 1973). He also conducted that selection between rather than within inbred lines is required for breeding to increase the rate of genetic improvement. Eisen *et al.* (1973) reported that the smaller effective population sizes tend to decrease selection response and realized heritability, through reducing the selection intensities per generation. Knowledge of genetic parameters such as heritability and genetic correlation are needed to predict response to selection, to choose among various breeding plans, to estimate their economic returns and to predict breeding values of candidates for selection (Sørensen and Kennedy, 1984). The validity of selection methods for genetic improvement of egg production has been investigated widely with regard to optimal breeding systems. Mass selection on annual egg records has long been regarded as ineffective, while selection based on family records and progeny testing has seemed to be the key to success (Nordskog *et al.*, 1967). Cundiff (1977) indicated that reciprocal recurrent selection was slightly more effective than intra-population selection. Genetic mating of relatives has been used to produce breeds varieties and lines. Robinson (1991) showed that the best linear unbiased prediction (BLUP) is

a technique for predicting genetic merits of animals. Jeyaruban *et al*. (1995) reported that the use of best linear unbiased prediction (BLUP) induced larger inbreeding rate compared to selection response especially for traits of low heritability. Contrarily, BLUP is an effective way of ranking and selecting animals given measurements on multiple traits of their own performance and information of their relatives, and it provides an effective alternative to the conventional selection index, which can be seen as a particular case of the BLUP estimates of random effects (Xie and Xu, 1996).

Poultry breeders are often concerned with egg mass and its component traits with regard to estimate the heritability and selection response from data undergoing early culling or selection. Selection response is a function of intensity of selection, phenotypic variance and heritability and it should decline theoretically after continuous selection over generations because additive genetic variance is exhausted (Bulmer, 1971). Responses observed in most selection experiments with egg mass as selection criterion suggested a slightly increased of direct response than correlated response. The same findings had seen in the corresponding selected sub-line of White Leghorn (Venktramaiah *et al.*, 1986). They also reported that the egg mass selected sub-line matured later and lay heavier but slightly less numerous eggs. However, egg mass is estimated to be a low heritable trait ranged from 0.05 to 0.16 (Quadeer *et al.*, 1977 and Venktramaiah *et al.*, 1986). The objective of this study is to use the best linear unbiased prediction method (BLUP) in predicting the breeding values of the studied traits and to use this information's for increasing the selection response of part records egg mass in closed flock of White Leghorn.

MATERIALS AND METHODS

The present experiment had been carried out at Borg El-Arab Research Station, Animal Production Research Institute, Agriculture Research Center, Egypt.

Experimental Stock and Design: Data used in the present study were extracted from a closed flock of White Leghorn laying hens. Measurements were recorded on 400 and 600 laying hens in two successive generations (2009-2011). The laying hens were kept in battery cages, and individual egg production was recorded daily from start of lay to 4 months of production. Only hens with complete records were included in the statistical analysis. The selected dam that used to construct the next generation were kept in family pens and assigned by 10 females per each male. The description of the data set used in the analyses was presented in the following Table (1).

Item	Generation	
	G0	G1
No. of total hens	400	600
No. of selected dams	120	200
No. of control hens	100	100

Where: G0= base population and G1= selected population.

All managerial practices were similar as possible as throughout the experiment. During the production period the pullets were fed a commercial layer ration (16.5 % CP and 2750 Kcal) and received 16 hr day light. The eggs were recorded and weighed daily through the experimental period.
The traits which construct the phenotypic variance-covariance matrices are:
Early egg number: Number of eggs at 1st 90 d. of laying (EN1),
Early egg weight: Average egg weight through the 1st 90 d. of laying (EW1),
Egg mass at 90 d. of laying (EM1),
Number of eggs at 120 d. of laying (EN2),
Average egg weight at 120 d. of laying (EW2),
Egg mass at 120 d. of laying (EM2).

Statistical Analysis

The data were set up to Mixed Model Equations for the prediction of breeding values and the estimation of variance components using group observations, according to Olsen *et al*. (2006).
The model in matrix notations was: $Y = Xb + Zu + e$
Where: Y is the vector of observations, b and u are the vectors of fixed and random effects, with their respective incidence matrices X and Z, and e a vector of random environmental effects.
Under this model,
$E(Y) = Xb, E(u) = 0$ and $E(e) = 0$,

Var (**Y**) = *Var* (**u**) + *Var* (*e*), which after substitutions, becomes *Var* (**Y**) = **ZGZ'** + **R**, with *Var* (**u**) = **G** = **A**σ^2**a**, where **A** is additive genetic relationship matrix, σ^2**a** is the additive genetic variance and *Var* (*e*) = **R** = **I**σ^2**e**, where **I** is an identity matrix (i.e. assuming that there are no residual correlations between birds of the same group) and σ^2*e* random environmental variance.

The distribution of random factors is:

$$\begin{bmatrix} u \\ e \end{bmatrix} \sim N \left\{ \begin{bmatrix} 0 \\ 0 \end{bmatrix} , \begin{bmatrix} A\sigma^2u & 0 \\ 0 & I\sigma^2e \end{bmatrix} \right\}$$

The best linear unbiased prediction solutions for fixed and random effects can be obtained by solving the usual Mixed Model Equations given by (Henderson, 1975; 1984).

$$\begin{pmatrix} X'X & X'Z \\ Z'X & Z'Z+\lambda A^{-1} \end{pmatrix} \begin{pmatrix} \hat{b} \\ \hat{u} \end{pmatrix} = \begin{pmatrix} X'Y \\ Z'Y \end{pmatrix}$$

Where: λ is the ratio σ^2e/σ^2u

The (Co) variance estimates were obtained with REML individual animal model using the DEREML software (Meyer, 1989).

-The realized genetic gain (ΔRG_t) from generation 0 to t may be expressed as:

$(\Delta RG_t) = (S_t - C_t) - (S_0 - C_0)$, (Hill, 1972),

Where: S and C indicate the mean of the selected and the control lines.

-Selection differential (**S**) was calculated as the difference between the average of the selected birds as parents for a certain trait and the average of their population,

-Selection intensity (**I**) = Selection differential (**S**) / Standard deviation of the trait,

-Expected genetic gain (ΔEG) = (**S**) Selection differential x (**h**^{2}) Heritability, were estimated according the equations of (Falconer, 1982).

RESULTS AND DISCUTIONS

Mean performance

Within the base generation G0 means and standard deviation for the studied traits were given in Table, 2. The results showed superiority of selected line means in all the studied traits (EN1, EW1, EM1, EN2, EW2 and EM2) 48±6.0 egg, 41.1±1.9 g, 1.975±0.226 Kg, 62±8.0 egg, 41.9±1.6 g, and 2.578±0.332 kg, compared with the control 39±12.0 egg, 40.6±2.2 g, 1.580±0.474 Kg, 51±14.0 egg, 41.4±1.9 g, and 2.104±0.597 Kg, respectively. The same manner was found in the first generation G1, where the performance of the selected line was higher than the corresponding control in all traits studied (59±3.0 egg, 48.3±1.2 g, 2.832±0.163 Kg, 85±4.0 egg, 47.3±1.2 g, and 4.027±0.155 kg, vs. 48±9.0 egg, 46.3±3.2 g, 2.234±0.492 Kg, 69±14.0 egg, 45.7±2.5 g, and 3.198±0.749 Kg, respectively). It was noted that the standard deviations for the studied traits in selected line in each of two generations declined sharply than the correspondences in the control lines, because the selection leads to reduction in genetic variations in the populations. The same finding was found by Miglior *et al*. (1995). The former results showed clearly that the change in early egg number (EN1) in the selected line was higher than the corresponding change in the control lines (11 vs. 9 eggs) over the two generations. In the selected line early egg weight (EW1) improved by 7.2 g, while in the control line a positive change was observed 5.7 g. Moreover, the overall increase in egg mass at 90 d of production (EM1) was 0.654 kg, in the control line compared with 0.857 kg., in the selected line. The former result showed that there was a correlation between egg number and egg mass at 90 d. of production. The same finding was reported by Abou El-Ghar *et al*. (2010).

Regarding egg mass at 120 d of production (EM2) and its component traits EN2 and EW2 (Table 2), it can be seen that the mean of egg mass at 120 d of production (EM2) in the control line was affected mainly by the large proportion of variations in egg number at 120 d of production (EN2), since an increasing trend was observed in EM2 1.094 kg, combined with increase EN2 by 18 eggs. The same manner was found in the selected line 1.449 kg and 23 eggs, respectively. On the other hand, the changes in egg weight at 120 d., of production (EW2) were non significant (5.4 and 4.3 g in the selected and control lines, respectively).

Phenotypic and Genetic parameter

As shown in Table 3, phenotypic correlation estimates were high and positive between EN1, EM1 and EN2 and egg mass at 120 d of production (EM2) i.e. 0.9, 0.9 and 1.0, respectively. The same finding was reported by Abou El-Ghar *et al*. (2010). On the other hand, egg mass (EM2) and egg weight were low correlated 0.2 either for part period (90 d of production) or full period (120 d of production). These results were confirmed with findings of Garwood and Lowe (1978). They reported that egg mass was increased solely through change in egg weight. In despite of the low phenotypic correlation between egg weight and egg mass, and the antagonism between egg number and egg weight, it is desirable to improve both egg number and egg weight simultaneously in the commercial stocks.

Knowledge of genetic parameters such as heritability and genetic correlations are needed to predict response of selection and to estimate the economic returns of selection. The results in Table 3 indicate relatively low heritability estimates 0.01, 0.41, 0.14, 0.12, 0.43 and 0.2 for the studied traits EN1, EW1, EM1, EN2, EW2 and EM2, respectively. The interpretation of these results was reported by Eisen *et al.* (1973) who found that the smaller population sizes or closed flocks tend to decrease selection response and realized heritability. Results of heritability of egg mass are harmony with those (from 0.05 to 0.16) reported by Quadeer *et al.* (1977). Contrarily, the results of heritability estimates for egg number and egg weight were lower than those reported by (Enab *et al.,* 1992; Abdou and Enab, 1994 and El-Wardany, 1999). The results in Table 3 showed also the economic importance of negative genetic correlations between egg mass and egg production traits in closed flock of White Leghorn chicken. However, low and negative genetic correlation estimates were found among all trait relationships ranged from -1.0 for between EM2 and EN1 to - 0.3 between EM1 and EM2. Moreover, the total egg mass (EM2) and EW1, EN2 and EW2 were negatively correlated genetically -0.5, -0.4 and -0.6. The same findings were reported by (Quadeer *et al.,* 1977; and Francesch *et al*., 1997).

Phenotypic and Genetic change

Understanding of various factors influencing genetic progress what can be attained and how can be optimized is essential to utilize our most important tool in poultry breeding. In this respect, it is matters to identify how many traits we include in the breeding goal, these traits must show additive genetic variations and what proportion of genetic correlation between them. Moreover, the percentage of selected birds and how intensively that is used must be showed. From the results obtained in Table 4 it obvious that selection differential (S) estimates were 11 egg, 2.0 g, 598 g, 16 egg, 1.6 g, and 829 g, for EN1, EW1, EM1, EN2, EW2 and EM2, respectively. In addition, the selection intensities (I) for the studied traits are shown in table 4, these results reveal fairly good selection intensity for egg number and egg mass either in early period at 90 d of production (0.9 and 0.93, respectively) or in later period at 120 d. of production (0.89 and 0.87, respectively). From the results obtained it was clear that BLUP provides an effective way of ranking and selecting birds given measurements on egg mass and its component traits. The same conclusion reported by (Xie and Xu, 1996). In the case of egg weight, the selection intensity was lowered by 0.49 in the early period and by 0.52 in the later period. It can be seen from the previous results that egg mass showed a considerable improvement per generation and this was mainly due to high genetic gain in egg number. These findings agreed with those reported by Bohren (1970) who reported that the importance of negative genetic correlation between egg weight and egg production in chickens is well known and has estimated interest in egg mass.

The trend in realized genetic gain (ΔRG) estimates demonstrates a considerable genetic improvement not only in selected line but also it is very clear in the control line. However, when the mean of selected line was adjusted by subtracting the mean of the appropriate control within generation, the realized genetic gain in the studied traits were 2 egg, 1.5 g, 202 g, 5 egg, 1.1 g and 354 g for EN1, EW1, EM1, EN2, EW2 and EM2, respectively. Moreover, the expected genetic gain (ΔEG) was 0.1 eggs, 0.82 g, 83.7 g, 1.9 eggs, 0.7 g and 165.8 g for EN1, EW1, EM1, EN2, EW2 and EM2, respectively. In fact the disagreement between expected and realized genetic gain is probably because of a reduction in additive genetic variance and consequently low estimates of heritability. Other factors such as small population size, inbreeding, drift change in fitness and/or approach to genetic/physiological limits might also influence the rate of response. The same conclusion was reported by (Quinton *et al*., 1992; Quinton and Smith, 1995 and Sharma *et al*., 1998). It was clear that EM2 showed a considerable improvement per generation in spite of egg weight, this was probably due to a high response in egg number. The same finding was found by (Verma *et al*., 1984) who reported that direct selection for any trait resulted in maximum response in that particular trait. Contrarily, such results indicated that the direction of the genetic correlation between partial and full egg record could change in the course of selection. The same conclusion was found by (Bohren *et al*., 1966 and Bohren, 1970).

In conclusion, a considerable increase in egg mass was achieved by using best linear unbiased prediction methodology (BLUP). Consequently, it provides an effective method of ranking and selecting hens given measurements on several traits including egg mass.

Table 2: Means and standard deviation of some egg production traits for two successive generations

Genotypes		Traits					
		EN 1	EW 1	EM 1	EN 2	EW 2	EM 2
G0	Selected	48±6.0	41.1±1.9	1.975±0.226	62±8.0	41.9±1.6	2.578±0.332
	Control	39±12.0	40.6±2.2	1.580±0.474	51±14.0	41.4±1.9	2.104±0.597
G1	Selected	59±3.0	48.3±1.2	2.832±0.163	85±4.0	47.3±1.2	4.027±0.155
	Control	48±9.0	46.3±3.2	2.234±0.492	69±14.0	45.7±2.5	3.198±0.749

G0= Base generation, G1= Selected population, EN1= Egg number at the first 90 d., of laying, EW1 = early egg weight (g.) at the first 90 d., of laying, EM1= egg mass (Kg.) at the first 90 d., of laying, EN2 = egg number at 120 d., of laying, EW2 = average egg weight (g.) at 120 d., of laying, EM2 = egg mass (Kg.) at 120 d., of laying.

Table 3: Heritability h^2, phenotypic r_p and genetic r_G correlations between egg mass at 120 d of production and other studied traits

Traits	h^2	r_p	r_G
EN 1	0.01	0.9	-1.0
EW 1	0.41	0.2	-0.5
EM 1	0.14	0.9	-0.3
EN 2	0.12	1.0	-0.4
EW 2	0.43	0.2	-0.6
EM 2	0.2	-	-

EN1= Egg number at the first 90 d., of laying, EW1 = early egg weight at the first 90 d., of laying, EM1= egg mass at the first 90 d., of laying, EN2 = egg number at 120 d., of laying, EW2 = average egg weight at 120 d., of laying, EM2 = egg mass at 120 d., of laying.

Table 4: Selection differential S, Selection Intensities I, the realized genetic gains ΔRG, expected genetic gains ΔEG of the studied traits

Traits	S	I	ΔRG	ΔEG
EN 1	11	0.9	2	0.1
EW 1	2	0.49	1.5	0.82
EM 1	598	0.93	202	83.7
EN 2	16	0.89	5	1.9
EW 2	1.6	0.52	1.1	0.7
EM 2	829	0.87	354	165.8

EN1= Egg number at the first 90 d., of laying, EW1 = early egg weight at the first 90 d., of laying, EM1= egg mass at the first 90 d., of laying, EN2 = egg number at 120 d., of laying, EW2 = average egg weight at 120 d., of laying, EM2 = egg mass at 120 d., of laying.

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