

Estimation of Genetic Parameters and Expected Response to Selection for Oviposition and Clutch Traits



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Submission: December 10, 2019; **Published:** February 03, 2020

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Abstract

Due to progressive reduction in genetic gains by traditional selection traits, a study was conducted to evaluate the genetic variability and expected genetic gains by oviposition and clutch traits. Egg number and other layer traits were recorded on 1082 pullets up to 40 weeks of age under standard conditions of management. Oviposition time, oviposition interval and clutch traits were recorded to estimate the heritability and correlation coefficients by least squares maximum likelihood method. Expected direct and indirect response was estimated for five traits by combined family index. Results show that, heritability estimates were low to moderate for oviposition and clutch traits however, much higher than traditional trait. Genetic and phenotypic correlation coefficients were favorable in magnitude and direction for majority of the traits. The expected genetic gain in 40week egg production (EN-1) was more from EN-2 (1.98 eggs) and MOT (1.76 eggs) than EN-1 (1.53 eggs). It can be concluded that mean oviposition time of laying is a potential trait, which should be given consideration in implementation of selection programmed for long term selected layer population.

Keywords: Genetic parameters; Oviposition time; Clutch; Genetic gain; Egg production

Introduction

Substantial improvement in egg production has been achieved by the application of quantitative genetics methods but further improvement in egg number is unlikely, because of losing genetic variation in the traditional selection traits [1]. Study of Oviposition time and Clutch traits as selection criterion might be useful for further improvements [2] in long term selected White Leghorn (WL) populations. Hens lay their eggs in sequences in limited part of the day. An egg per day is produced for a number of consecutive days before the hen pauses for one or more days. In a normal light programme, the maximum length of the laying period per day is restricted to 8-9 h [3]. Wide variation in the pattern of laying among pullets may be observed in the flock, as various factors affects the egg laying pattern. The less productive the hen, the more time it needs for producing an egg. The least productive hens have short sequences and many pause days and use the whole 8 to 9 h period for egg laying whereas, highly productive hens with long sequences lay most of their eggs within a period of only few hours [3]. Selection for early egg laying hens and their clutch length as selection parameter may provide an insight on the genetic variance available in the population for further improvements in egg number.

The magnitudes of genetic variation for oviposition and clutch traits have been estimated and used in selection studies [4-6] indicating a new trend for continued improvement of egg production [7]. However, reports are limited on using oviposition time and clutch traits as selection criterion [2,8,9] in a long term selected White Leghorn (WL) layer population. Because of reduced genetic gain in traditional selection trait (egg number), oviposition time of early laying hens, ovulation interval and clutch traits were considered to be analyzed as selection criterion in comparison to the traditional trait. The present study was planned to estimate the means, genetic parameters, their relationships and expected response to selection for oviposition and clutch traits by combined family index selection.

Materials and methods

Experimental stock and history

IWH strain of WL hens was used for the present experiment. This strain has been maintained as a closed flock at experimental layer farm of CARI, Izatnagar, UP since 1972. It was subjected to intense selection for part record (40 weeks) egg production up to S²² generation and 07 generation of 64week egg production,

till the present S^{29} generation. The method of selection was combined family index, in which weighing factors were derived as per [10,11]. The selected pullets were assigned at random to the selected males with only restriction that no half-sib or full sib mating were permitted. The strain has improved by about 72 % (41.69eggs) for part period egg number with average response of 0.99 to 1.25 eggs per generation [12]. The egg weight and age at sexual maturity have declined over the base population by 0.68 gm and 1.04 days per generation along with decline in 40week body weight [12]. By observing the very low heritability estimates in principal trait, it seems that, long period of selection for egg number might have exhausted the additive genetic variance for egg production and thus there is need to explore the new genetic variability in the existing stock [12].

Management practices

The chicks were obtained from hatchery on zero days, pedigreed by sire and dam, placed on floor pens under hover type brooders and were reared there until about 08 weeks of age. All chicks were vaccinated against Ranikhet disease, Merek's disease, Fowl pox, Infectious bursal disease and Egg drop syndrome-76 and viral infections as per routine vaccination schedule. Starter ration was fed from hatching to 8th week, grower ration from 9th to 16th week and layer ration thereafter. Feed and water were given ad libitum. Sexing was done at 8th week and thereafter both the sexes were kept separately in growing pens. After separation of sexes, two male chicks and six female chicks per dam were retained for further study. At 16th week of age, all the pullets were transferred to the individual laying cages arranged in a three-tier system under open sided layer house. Lighting schedule in grower house was set to 14hour light and 10hour dark cycle (photoperiod; 06.00

to 20.00h). At the beginning of 14 week the length of photoperiod was successively increased and from 16 week of age a 16 L: 8 D light programme was applied, with lights on between 06.00 and 22.00h. Light intensity at the height of bird's eye was about 30 lux. The management conditions were kept identical as far as possible for all the hatches. The study started when the hens began laying and continued until they reached an age of 40 weeks.

Sample size and recording of traits

Various traditional as well as non-traditional traits (Table 1) were recorded on 1082 WL hens as per standard procedure. The egg production of each pullet was recorded daily by observing the presence of an egg in individual laying cages from 06.00 hour to 17.00 hour at hourly intervals up to the age of 40 weeks. Soft shelled and abnormal eggs were not counted in the total egg production of each pullet. As the experimental strain was an elite flock with 29th generation of selection history and having nearly symmetrical distribution of oviposition time with about 90 % of eggs laid in seven hour period 06.00 hour to 13.00 hour, the mean oviposition time (MOT) for each pullet was calculated by taking the simple arithmetic mean of oviposition time [3]. Oviposition interval for each egg laid by individual pullet was calculated by subtracting the oviposition time of an egg from her subsequent egg within a sequence. A factor of 24 hour was added in every calculation to arrive at the time taken by pullet to lay an egg. Because of the preceding pause day, the oviposition interval for one egg sequences and for first egg in a sequence was not calculated. Clutch length and clutch numbers were determined as per the procedure described by [13]. Further details on recording of traits and their statistic distribution in the studied population have been reported by [14].

Table 1: Estimates of Heritability and Standard Deviation (in the Diagonal), Genetic Correlations (above Diagonal) and Phenotypic Correlations (below Diagonal) between Traits.

Traits	BW	EW	ASM	EN-1	EN-2	EN-3	MOT	MOI	ACL	TCN	MCL	TPD
BW	0.20 ±0.06	0.37	0.41	0.02	0.24	-0.24	-0.23	-0.14	0	0	0.24	-0.34
EW	0.23	0.14 ±0.06	0.75	0.01	-0.11	0.15	0.2	0.18	-0.24	0.3	0.23	-0.63
ASM	0	0.03	0.13 ±0.05	-0.7	-0.09	-0.34	-0.17	-0.13	-0.32	0.22	-0.1	0.14
EN-1	0.04	-0.05	-0.38	0.07 ±0.05	0.61	-0.04	-0.43	-0.59	0.52	-0.66	0.52	-0.85
EN-2	0.11	-0.09	-0.24	0.69	0.22 ±0.06	-0.89	-0.99	-0.6	0.72	-0.83	0.74	-0.74
EN-3	-0.11	0.06	-0.07	0.22	-0.54	0.26 ±0.06	0.97	0.31	-0.64	0.59	-0.56	0.33
MOT	-0.15	0.06	0.06	-0.2	-0.77	0.8	0.32 ±0.06	0.49	-0.71	0.73	-0.65	0.75
MOI	-0.14	0.08	0.06	-0.41	-0.49	0.17	0.4	0.20 ±0.06	-0.88	0.84	-0.83	0.9
ACL	0.08	-0.13	-0.02	0.45	0.53	-0.19	-37	-0.49	0.12 ±0.05	-0.96	0.95	-0.36
TCN	-0.09	0.12	-0.07	-0.11	-0.31	0.28	0.31	0.52	-0.7	0.09 ±0.05	-0.96	0.7

MCL	0.07	-0.11	-0.09	0.46	0.55	-0.2	-0.37	-0.52	0.76	-0.6	0.07 ±0.05	-0.57
TPD	-0.04	0.04	-0.07	-0.89	-0.63	-0.2	0.18	0.41	-0.47	0.16	-0.45	0.05 ±0.05

Statistical analysis of data

Data was corrected for significant hatch effects by fitting least squares constants from the mixed model least squares and maximum like hood (LSMLMW) computer programme [15].

Genetic parameters

Genetic parameters were estimated by mixed model least-squares and maximum likelihood (LSMLMW) computer programme [14]. Variance and covariance components for estimating heritability and genetic correlations were obtained by using model 4, which included sires, dams within sires and progeny within dams within sires as random effects and hatch as fixed effect. The general linear mathematical model that was used for parameter estimation is:

$$y_{ijk} = \mu + a_i + b_j + (ab)_{ij} + e_{ijk} \quad \text{where,}$$

y_{ijk} is the measurement of trait corrected for hatch effect on k^{th} progeny of j^{th} dam mated to i^{th} sire,

μ is the overall mean with equal subclass numbers,

a_i is the effect of i^{th} sire,

b_j is the effect of j^{th} dam mated to i^{th} sire,

$(ab)_{ij}$ is the effect of the ij^{th} sire dam subclass after the average effects of sire and dam within sire have been removed. These are the individual interaction effects, expressed as a deviation from the mean,

e_{ijk} is the uncontrolled environmental deviations (random error) attributed to the individuals and assumed to be distributed normally and with mean 0 and variance σ^2 .

Effective population size and rate of inbreeding

Effective population size (N_e) in the present generation was calculated by

$$N_e = (4N_m N_f) / (N_m + N_f) \quad [16], \text{ where}$$

N_e is the effective population size or effective number

N_m is the number of male parents

N_f is the number of female parents

Only those male and female parents were counted whose progeny survived till 40 weeks of age.

The expected increase in coefficient of inbreeding (ΔF) in present generation due to finite population size was estimated by

$$\Delta F = (1 / 8 N_m) + (1 / 8 N_f) \quad [16] \text{ where,}$$

N_m and N_f are the number of male and female parents which had progeny surviving till 40 weeks of age.

Combined family selection indices

EN-1, EN-2, MOT, MOI and ACL were used as primary trait to construct five separate single trait selection indices. The method of selection was combined family index in which individual's own performance, dam and sire family averages were used for selection of pullets, while, dam and sire family averages were used for selection of cockerels with appropriate weight attached to each of the components. The weighting factors were derived as per [11,12].

The indices that were used are as follows

$$I_F = (P - P) + W_2 (F_D - P) + W_3 (F_S - P)$$

$$I_M = W_2 (F_D - P) + W_3 (F_S - P)$$

Where,

P is the individual's own performance,

P is the flock average,

F_D is the dam family performance average,

F_S is the sire family performance average,

W_2 and W_3 are the weightage given to dam and sire family averages respectively.

$$W_2 = 2n(1 - h^2) / 4 + (n - 2)h^2,$$

$$W_3 = 4n^{-1}d(1 - h^2)(2 - h^2) / [4 + (n^{-1} - 2)h^2] [4 + \{n^{-1}(1 + d) - 2\}h^2],$$

Where,

n^{-1} is the average number of pullets per dam,

d is the number of dams mated to a sire,

h^2 is the heritability of the trait under selection.

Pullets were arranged in descending order based on their index values for all the five traits. Top ranking 200 pullets (about 20 %) were selected from their own index value, while top 50 (10 %) cockerels were selected from the index value obtained for each sire family.

Expected selection differential

The expected selection differentials for all the five traits were calculated as the difference between the mean of selected individuals to be used as parents and the mean of population from which they were selected. Expected selection differentials

for the female parents (S_f) were calculated from the pullets own mean performance while, expected selection differential for male parents (S_m) were derived from the sire family averages. Average expected selection differential (S_A) were calculated by taking the mean of expected selection differentials obtained for male and female parents.

Intensity of selection

The intensities of selection in different traits were calculated by dividing the expected selection differentials with the respective phenotypic standard deviations (σ_p). Average intensity of selection (I_A) in respective trait was calculated by taking the mean of selection intensities in male (I_m) and female parents (I_f).

Expected direct response

The expected direct response from five different Osborne selection indices were calculated as per [9,16] using following formulae

$$\Delta G = \{(i_{\sigma} + i_{\phi}) / 2\} h \sigma_p \{[i_{\phi} / (i_{\sigma} + i_{\phi})] R_{G\phi P\sigma} + \{(i_{\sigma} / (i_{\sigma} + i_{\phi})) R_{G\sigma P\phi}\}$$

$$R_{G\phi P\sigma} = h \{[(n-1) / \{2n(2-h^2)\} + (d-1)(n+2)^2 / 4nd\} \{4 + (n-2)h^2\}$$

$$+ (s-1)\{n(1+d)+2\}^2 / 4snd\} \{4 + \{n(1+d)-2\}h^2\}^{1/2}$$

$$R_{G\sigma P\phi} = h / 2 \{n/d\} \{(d-1) / \{4 + (n-2)h^2\} + \{(s-1)(d+1)\}^2 / s\} \{4 + \{n(d+1)-2\}h^2\}^{1/2}$$

where,

ΔG is the expected response from combined selection,

i is the standardized selection differential,

h is the square root of heritability

σ_p is the phenotypic standard deviation of the trait

$R_{G\phi P\sigma}$ is the multiple correlation coefficients between pullet's index and the genotype of the trait measured,

$R_{G\sigma P\phi}$ is the multiple correlation coefficients between cockerel's index and the genotype of the trait measured,

n is the average number of progenies per dam = 3.82,

d is the average number of dams per sire = 5.66,

s is the number of sires.

Expected correlated response

Expected correlated response were also estimated for EW, ASM and five index traits by selecting one trait at a time as primary trait and rest four as secondary trait.

The expected genetic response in correlated traits were calculated from following formulae

$$CR_y = i_x h_x h_y r_{Gxy} \sigma_{py} [16].$$

where,

CR_y is the expected correlated response in trait y,

h_x is the square root of heritability of trait x (primary trait),

h_y is the square root of heritability of trait y (secondary trait),

r_{Gxy} is the genetic correlation between trait x and y,

i_x is the intensity of selection for trait x,

σ_{py} is the phenotypic standard deviation of trait y,

Results and Discussion

Present study was planned to evaluate the genetic variability in existing population of WL hens selected over 29 generations for egg number as principal trait and body weight, egg weight at 40 weeks of age and age at sexual maturity as secondary trait. Time of oviposition was recorded on individual pullet from her first egg to 40 weeks of age, to compare the genetic variability in oviposition time and clutch traits with the traditional traits (Table 1). Expected direct and indirect response was also calculated to compare the genetic gains expected from each trait.

Genetic parameter estimates

Estimates of heritability, genetic and phenotypic correlations from sire plus dam component of variance between studied traits have been presented in table 1. Heritability estimates from sire component of variance was low in comparison to dam component for most of the traits. Data was not transformed to follow normal distribution, which may be one of the reasons for low heritability estimates from sire component [8], apart from the gradual decline of additive genetic variance due to longer generations of selection.

The lowest heritability estimates were observed in EN-1 in comparison to other egg number traits. In general, maternal and / or non-additive gene effect was evident in all egg number traits. The heritability estimates for EN-2 was moderate but higher than EN-1 [2]. Higher heritability estimates for oviposition traits in comparison to egg production traits have been reported in literature [3,5,7]. Among clutch traits, heritability estimates were not consistent from different component of variance. Heritability estimates of clutch traits showed maternal and / or non-additive gene effects of lesser magnitude than heritability estimates of egg number and oviposition traits. Heritability estimates in general were low among clutch traits. Heritability estimates for clutch traits were lower than the findings of [18,8,7]. Asymmetry of trait's distribution might be the reason for lower heritability of clutch traits. However, the results confirm the presence of lesser additive genetic variability in traditional trait (EN-1) in comparison to any of the proposed traits.

Genetic and phenotypic correlation estimates between various studied traits were found to be following the general trend of association in magnitude and direction as per the reported literature [2]. EN-1 was positively correlated with oviposition and clutch traits, except TCN. The results for genetic correlation between EN-1 and clutch traits were similar to the

reports of [18,8]. The overall correlation estimates of EN-1 with traits shown in Table 1 suggested dominance of non-additive and / or maternal and / or environmental effects than additive gene effects. Genetic correlations of EN-2 with majority of the traits were high which suggest that selection for improvement in EN-2 would lead to desirable improvement in oviposition traits and clutch traits. Similar observation was reported by [2] from the correlation of EN-2 with egg production traits. High and positive genetic association of EN-3 with other traits were observed, however, it is not desirable to use EN-3 as selection traits because of the hypothesis that early layers are better hens than late layers. Oviposition time, oviposition interval and other clutch traits were showing higher estimates of genetic correlation than EN-1, among themselves and with other traits, which makes them potential trait to be included in selection index either as principal trait or as secondary trait. Literature also supports this finding with similar results.

Effective population size and rate of inbreeding

The number of pullets, number of sires, number of dams and effective population size of the study were 1082, 50, 283 and 169.78 respectively. The observed rate of inbreeding was 0.0029. Effective population size was calculated by the number of sires and dams, which survived up to 40 weeks of age.

Selection differential and intensity of selection

Female (200) and male (50) parents were selected based on their rank for [10,11] index values and the expected selection differentials (SD) were calculated for EN-1, EN-2, MOT, MOI and ACL. The standardized selection differentials, or, intensities of selection were obtained from the selection differentials in male (I_M) and female (I_F) parents for traits shown in Table 2. Expected selection differential for EN-1 was comparable to the results of [18] while intensity was comparable with the results of [20,21]. For other traits, reports from literature on selection differentials were not available for comparison. There was no scope to calculate effective selection differential and effect of natural selection, with present data.

Table 2: Expected Selection Differential (SD) and Intensity in Male (IM) and Female (IF).

Traits*	SD		I M	I F
	Female	Male		
EN-1	13.51	13.8	0.565	0.577
EN-2	24.51	31.31	0.892	1.139
MOT	-0.7	-0.95	0.925	1.253
MOI	-0.2	-0.23	0.587	0.69
ACL	5.4	6.84	0.822	1.041

Expected direct response from Osborne selection indices

Expected direct response were estimated for EN-1, EN-2, MOT, MOI and ACL from expected selection intensity in each trait

by combined selection index procedure of [10,11]. The response from combined selection index in each trait has been shown in Table 3. The expected response in EN-1 was higher than the results of [21] (1.30 and 1.34 eggs per generation in two strains) but little lower (1.73 eggs per generation in IWH strain) than the results of [22]. The expected genetic gain in EN-2 was much higher than the reports of [2]. [2] reported 03 % realized genetic gain in 06-11.00-hour rate of lay after 06 generation of multiple trait selection. The differences might be due to differences in basis of selection and measurement of trait. The expected gain of 8.49 eggs in EN-2 indicates that a greater number of eggs would be laid in 06-11.00h in comparison to full day (6.00 to 17.00 h).

Table 3: Expected Direct Response (above Diagonal) and Correlated Response (below Diagonal) from Selection on Primary and Secondary Traits.

Secondary traits	Primary traits				
	EN-1	EN-2	MOT	MOI	ACL
EW	0.002	-0.053	0.121	0.052	-0.076
ASM	-0.447	-0.174	0.415	0.151	-0.409
EN-1	X	1.977	1.761	1.149	1.116
EN-2	1.285	X	8.112	2.296	3.035
MOT	-0.03	-0.208	X	-0.061	-0.098
MOI	-0.015	-0.045	-0.047	X	-0.044
ACL	0.188	0.787	0.989	0.579	X

The direct responses in MOT, MOI and ACL indicates that, one generation of direct selection for these traits was expected to decrease the mean oviposition time by 0.34 hour, mean oviposition interval by 0.06 hour and increase the average clutch length by 1.02 eggs. Literature supports the finding that direct selection for MOT and ACL would decrease the oviposition interval and increase the clutch length [4,23]. However, [4] reported decrease of -11.72 minutes in MOT per generation, which is higher than the present results. The expected genetic gain in ACL was higher than the results (0.65 days per generation) of [4].

Expected correlated response from Osborne selection indices

Selection based on EN-1 is expected to result marginal but positive response in EW (0.002 g), whereas, EN-2 is expected to give marginal but negative response (-0.053 g). EN-2 revealed greater correlated response in EN-1 (1.977 eggs) than the direct response observed in EN-1 (1.53 eggs). Selection based on EN-2 is expected to give 1.29 times more genetic gain in EN-1 as a correlated response than by direct selection on EN-1. [2] have reported similar results by comparing 06-11.00 h rate of lay and part period rate of lay for improvement in long period egg production as a correlated response. Based on the expected genetic response observed in EN-1, the primary traits may be arranged in descending order as: EN-2 (1.977eggs) > MOT (1.761eggs) > EN-1 (1.53eggs) > MOI (1.149eggs) > ACL (1.116eggs). For EW, the

observed order was as follows: MOT (0.121g) > MOI (0.052g) > EN-1 (0.002g) > EN-2 (-0.053g) > ACL (-0.076g).

Since, MOT and EN-2 are closely related traits; selection based on any of the two is expected to improve each other as a correlated response. Some reports in literature have indicated significant improvement in egg production by selection on oviposition interval and clutch length (Sheldon et al., 1979; Gow et al., 1985 and Chen and Tixier-Biochard, 2003), however, the magnitude of correlated response in egg number has not been discussed in detail. Chen and Tixier-Biochard (2003) have reported higher genetic gains than the present results in total egg number (3.076eggs), BW42 (-0.11.07g), EW36 (0.017g) and ASM (-0.59days) as a correlated response obtained from selection on average clutch length from the normalized data in dwarf brown egg layers. Among 05 Osborne (combined) indices, EN-2 followed by MOT was observed to be more efficient than EN-1 for expected genetic response in part period egg production (EN-1) with little decrease expected in EW from EN-2, which might be overcome by fixing mild culling level for EW in selected parents. From the present study, it may be inferred that, mean oviposition time of egg laying, oviposition interval and clutch traits are the potential traits, which can be used alone or, in combination with traditional selection trait in multi-trait selection index to augment the genetic gain in egg number. However, the population must be studied for more generations, before actual inclusion of these traits into selection index.

Conflict of Interest

The authors declare that there being no conflict of interest.

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DOI: [10.19080/AAPS.2020.01.555564](https://doi.org/10.19080/AAPS.2020.01.555564)

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