

SELECTION FOR SOME PRODUCTIVE TRAITS IN NORFA LAYING HENS

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ABSTRACT: *The present experiment has been carried out at the Poultry Experimental Farm, Faculty of Agriculture, Menoufia University, Shebin El-Kom, Egypt, during the period from 2013 to 2017 on Norfa chickens. Total number of 475 dams were used in the present experiment in the base population, first and second generations. Independent culling levels (ICL) method of selection has been applied on the selected flock ($\bar{X}+0.5sd$). The criterion of ICL method of selection was to select hens having at least average $EN_{90d} + 0.5 sd$ on condition that egg size and body weight should be around the average flock.*

Results obtained and conclusions can be summarized as follows:

The heritability estimates (h^2) showed that Age_{SM} had low h^2 estimates, both of BW_{SM} and BW_M showed moderate h^2 estimates, EW_{SM} showed moderate to high h^2 estimates while EW_M had moderate h^2 estimates and the heritability estimates for EN_{90d} and EN_{42WK} were moderate to high. The expected genetic changes for Age_{SM} , BW_{SM} , BW_M , EW_{SM} , EW_M , EN_{90d} and EN_{42WK} in the base population were -1.12 d, 41.82 g, 22.28 g, 1.19 g, 0.46g, 3.57egg and 1.70 eggs respectively. While the actual genetic gains were 7.79, 17.9, -0.093, -1.60, -1.60, 5.18 egg and 8 eggs respectively. The expected genetic changes for Age_{SM} , BW_{SM} , BW_M , EW_{SM} , EW_M , EN_{90d} and EN_{42WK} in the first generation of Norfa chicken were 1.69 d, 22.43 g, 31.01 g, .89 g, .32g, 1.8 egg and 1.27 eggs respectively. While the actual genetic gains were -13, -29.9, -38, -1, -1.180, 5.8 egg and 5.24eggs, in the same order. The expected genetic changes for Age_{SM} , BW_{SM} , BW_M , EW_{SM} , EW_M , EN_{90d} and EN_{42WK} in the first generation of Norfa chicken were 1.31 d., 26.14 g, .27, .73 g, 0.87 g, .026 g, 2.95 egg and 2.91 eggs respectively. While the actual genetic gains were -10, -30, -22, -1.4, 1, 14.05 egg and 19.72 eggs respectively.

The actual genetic gains for EN_{90d} and EN_{42WK} were high than the expected genetic changes through the base population, first and second generations by applied the Independent culling levels. The selected line was better than the control line for productive traits in Norfa laying hens.

Key words: Selection, productive traits, Norfa.

INTRODUCTION

In Egypt, a lot of efforts have been done to improve indigenous chickens. The Egyptian indigenous breeds of chickens have many advantageous such as their high adaptability to local environment and genetic resistance to some serious diseases such as Marek's beside the highly acceptable taste and favorable flavor for its meat and egg products. Abdou *et al.* (2017) summarized

the history of Norfa breed from 1980 to 2017. A base population of Norfa chickens was formed through crossing two indigenous breeds of chickens (Fayoumi and W-Baladi) with two strains of W. Leghorn imported from Norway in 1980 (L2 which was developed for high egg number and L7 which was developed for heavy egg weight). Generally, as layers Norfa chickens have low body weight (less than 1500g) which means

low maintenance requirements and early sexual maturity Zanaty *et al.* (2001). Since 1980 till 2007 many researchers worked on Norfa strain. Enab (1982) evaluated the performance of parental purebreds (L2, L7 and Fayoumi). Abdou and Kolstad (1984) evaluated the performance of two-way crosses of the parental purebreds. Enab (1991) applied different selection indices (i.e. general, reduced, restricted and two – stage indices) in Norfa strain. Shebl *et al.* (1991) studied the genotype-environment interaction for growth and reproductive traits in Norfa chickens. Abou El-Ghar (1994) developed two divergent selected lines from Norfa strain on body weight by using tandem selection. Harfoush (1997) studied the effect of different management and environmental conditions (i.e. lighting, temperature and dietary protein level) on the performance of Norfa layers. El-Sakka (1999) studied the effect of selection on some egg quality traits on Norfa strain. Abou El-Ghar and Abdou (2004) evaluated the hybrid vigor in egg production traits in the diallel crosses of different four lines of Norfa strain.

Abou Elewa (2004) studied the direct selection for general immune response and its relation to some economic traits in Norfa chickens. Ben-Naser (2007) developed two different specialized lines in body weight (i.e. light and heavy body weight lines) by using different selection indices (i.e. general, sub-indices, reduced and restricted indices) during two consequently generations of Norfa strain. El-Weshahy (2010) used independent culling levels method in three generations in three lines (EN, BW and control) for improving Norfa hens during three generations and crossing to get hybrid vigor for some egg production traits. Abou-Elewa *et al.* (2016) studied determination age at sexual maturity of cocks depending on the first response of semen collection and to characterize the

semen parameters in Norfa chickens. Abdou *et al.* (2017) explained improving indigenous chickens in developing countries and showed the outlet of the Norwegian-Egyptian Project "NORFA" in Egypt (1980-2017).

The main aim of the present study is trying to improve some egg production traits of Norfa chickens by using independent culling levels method during the three generations.

MATERIALS AND METHODS

The present experiment has been carried out at the Poultry Experimental Farm, Faculty of Agriculture, Menoufia University, Shebin El-Kom, Egypt, during the period from 2013 to 2017 on Norfa chickens. Total of 475 dams were used in the present experiment in the base population, first and second generations.

The studied traits

- 1) Age at sexual maturity: (Age_{SM}): number of days at the first egg laid.
 - a) Egg number: EN_{90d} : number of eggs in the first ninety days of laying.
 - b) $EN_{42weeks}$: Number of eggs at 42 weeks of age (EN_{42WK}).
- 2) Egg weight:
 - a) EW_{SM} : average weight of the first 5 eggs at sexual maturity in grams.
 - b) EW_M : average weight of 5 eggs during (35 – 38) weeks of age (EW_M) in grams
- 3) Body weights (BW):
 - a) Body weight at different ages. Body weight during the base population, first and second generation were taken at 0, 4, 8, 12 and 16 weeks of age (BW_0 , BW_{4wk} , BW_{8wk} , BW_{12wk} and BW_{16wk}).
 - b) BW_{SM} : body weight at sexual maturity in grams.
 - c) BW_{42wk} : body weight at 42 weeks of age in grams.

STATISTICAL ANALYSIS

Studied traits were analyzed using general linier model (GLM), SAS computer program SAS (2002) as following two models:

Model I:

$Y_{ij} = \mu + G_i + e_{ij}$ Where:

Y_{ij} = Observation on the i^{th} chick.

μ = The overall mean of the trait.

G_i = Effect of j^{th} group (selected and control).

e_{ij} = Random error.

The Least Squares Program SAS (2002) was also used to calculate the analysis of variance and least square means of all effects in the model. Standard deviation of the parameters was estimated and tests of the significances were applied. Furthermore, the least squares program SAS (2002) was used to estimate the analysis of variance overall two lines (selected and control lines) as well as to calculate least square means of all effects in the following mixed model which was used for overall lines:

Model II:

$Y_{ijk} = \mu + S_i + D_{ij} + e_{ijk}$ Where

Y_{ijk} = The value of a trait of k^{th} progeny from the j^{th} dam mated to the i^{th} sire.

μ = The overall mean of the trait.

S_i = Random effect of the i^{th} sire.

D_{ij} = Random effect of the j^{th} dam mated to i^{th} sire.

e_{ijkl} = Random error component assumed to be normally distributed.

The program calculates the values of Heritability, genetic and least square means for all effects in the model. Standard errors of these parameters and testing of significance were also given.

GENETIC GAINS

The expected genetic gains (ΔG) were calculated according to the formula given by (Prichener's, 1979) as follow.

$$\Delta G = i \cdot h_j \cdot \delta A_j$$

Where:

i = Selection intensity.

h_j = Square root of heritability for the j^{th} trait.

δA_j = Additive genetic standard deviation of the j^{th} trait.

Actual genetic gain was calculated as deviation from the control line performance by equation given by Hill (1972) as follows:

$$\Delta G = (S - C_t)$$

Where:

S and C are the means of selected and control lines in generation number (t).

SELECTION PROCEDURES

Independent culling levels method was applied in the three generations. All individuals that failed to come up with a certain standard for each trait and regardless of their record in any other trait, have been discarded.

During three generations of selection the independent culling levels procedure was applied in the base population to divide it into two lines (selected and control). The egg number line (EN) was determined by using the overall mean for egg number at 90 days of the base population plus 0.5 standard deviation ($\mu + 0.5$ s.d), while body and egg weight should be around the average flock. The same selection method was applied in each of the following generation. Also, the cocks of the base population were divided into these three lines upon this procedure. The birds of the control line were chosen randomly before applying the independent culling levels. Norfa layers of the base flock had been faced some unfavorable conditions (ration shortage). Therefore selection under feed stress had applied on Norfa layers and this may be affected some low means of some performance.

RESULTS AND DISCUSSION

Heritability

The estimates of heritability of all

studied traits (i.e. Age_{SM}, BW_{SM}, BW_M, EW_{SM}, EW_M, EN_{90d} and EN_{42WK}) based on sire, dams and sire + dam variance components during the base population, first and second generation are presented in Table (1). Heritability estimates of age at sexual maturity (Age_{SM}) had the lowest heritability (h²) estimates while body weight at sexual maturity (BW_{SM}) and body weight at maturity (BW_M) had the highest estimates.

Generally, Table (1) shows that the estimate of heritability for age at sexual maturity was low. On the other hand, the heritability estimates of the body weight at sexual maturity or at maturity were moderate. Also, the heritability estimates of egg weight at sexual maturity, at maturity, egg mass of 90 day and egg mass of 42 weeks were lowest.

Furthermore, egg number during the first 90 d or till 42 week had moderate heritability estimates.

Most of the estimates were in a good agreement with those found on Norfa strain by Enab (1991), Sherif (1991), Enab *et al.* (1992), El-Wardany and Abdou (1993), Abou El-Ghar (1994), Enab (1996), Abou Sada (2007), Ben-Naser (2007), El-Weshahy (2010), Abou-Elewa (2010), Enab *et al.* (2015), Abou-Elewa *et al.* (2016) and Abdou *et al.* (2017).

Moreover, some of heritability estimates were beyond of the biological limits (more than one or less than zero) and these illogical values may be found when the selection emphasized highly on some traits and / or due to sampling errors Enab (1991).

Table (1): Heritability estimates of the studied traits in base population, first and second generations in Norfa chickens.

Trait	Base population			First generation			Second generation		
	h ² s± SE	h ² D ± SE	h ² S+D ± SE	h ² s± SE	h ² D ± SE	h ² S+D ± SE	h ² s± SE	h ² D ± SE	h ² S+D ± SE
Age _{SM}	.11±.01	.10±.01	.11±.01	.26±.02	.13±.009	.21±.013	.22±.17	.05±.004	.14±.009
BW _{SM}	.86±.07	.26±.02	.72±.04	0.43±.03	41±.02	.49±.03	0.4±.032	.44±.031	.50±.030
BW _M	.21±.02	.39±.03	.33±.02	.80±.06	.15±.01	.6±.031	.42±.033	.37±.026	.46±.028
EW _{SM}	.17±.01	.72±.05	.54±.03	.33±.027	.56±.039	.52±.031	.44±.036	.38±.027	.43±.026
EW _M	.12±.01	.28±.02	.22±.01	.02±.002	.33±.023	.19±.011	.12±.010	.13±.009	.13±.008
EN _{90d}	.53±.04	.53±.04	.64±.04	.4±.03	.33±.023	.41±.025	.41±.032	.56±.039	.56±.035
EN _{42wk}	.33±.03	.09±.01	.23±.01	.37±.03	.02±.002	.21±.013	.41±.033	.33±.02	.43±.026
EM _{90d}	0.30±.02	.25±.02	0.31±.02	.37±.02	.29±.02	.37±.02	.16±.013	.38±.027	.31±.018
EM _{42wk}	0.31±.03	.23±.02	0.30±.02	.53±.042	.03±.002	.32±.019	.34±.028	.31±.002	.37±.022

Selection Method of Independent culling levels.

Selection method of independent culling (ICL) was applied to maximize the genetic gain of flock ($\bar{X} \pm 0.5$ sd). The main of selection of laying flock of the hen is to increase egg number. Increasing egg number should be done on condition that egg size is not affected due to the fact that increasing egg number is associated with decreasing body and egg weights. Therefore, selection program applied on laying flock always focused on increasing egg number on condition that egg and body weights should be around the main flock. Independent culling levels (ICL) method of selection has been applied on the selected flock ($\bar{X} + 0.5$ sd). The criterion of (ICL) method of selection was to select hens having at least average of $EN_{90d} + 0.5$ on condition that egg size and body weight should be around the average flock. The averages were 41.1eggs for EN_{90d} , 38 g for EW_{SM} and 1013.5 g for BW_{SM} . The differences among these means were significant (.05).

The expected and actual genetic changes by applying independent

culling levels for the base population

Table (2) illustrated expected and actual genetic gains for all traits of selected flock. Table (33) shows that the expected genetic changes of Age_{SM} , BW_{SM} , BW_M , EW_{SM} , EW_M , EN_{90d} and EN_{42WK} for the base population were -1.12 d., 41.82 g, 22.28 g , 1.19 g , .46g , 3.57egg and 1.70 eggs respectively. While the actual genetic gains were -7.79, 17.9, -0.093, -1.60, -1.60, 5.18 egg and 8 eggs. The results in Table (2) show that there was a good agreement between the actual and expected genetic change for BW_M and EN_{90d} . On the other hand there was a clear discrepancy between the actual and expected genetic change for A_{SM} , BW_{SM} , EW_{SM} , EW_M and EN_{42wk} .

Most of the estimates were in a good agreement with those found on Norfa strain by Abdou *et al.* (1998), El-Sakka (1999), Abou El-Ghar (2003), Ben Nasr (2007), Abou-Elewa (2010) and, El-Weshahy, (2010).

These discrepancies between the actual and expected genetic changes might be due to missing progeny of some selected dams and sampling errors.

Table (2): Means \pm sd of the base population, expected genetic gain and Actual genetic gain in the base population.

Trait	base population Means \pm sd of the selected line	Means \pm sd of the control line	Expected genetic gains	Actual genetic gains
Age_{SM}	162.2 \pm 10.14	170 \pm 17.725	1.12	-7.79
BW_{SM}	1013.5 \pm 96.34	1028.483 \pm 62.54	41.82	-14.5
BW_M	1221.953 \pm 110.74	1204 \pm 83.621	22.28	17.9
EW_{SM}	37.90 \pm 4.058	38.0 \pm 4.1	1.19	-0.093
EW_M	41.395 \pm 3.54	43.0 \pm 3.4	0.46	-1.60
EN_{90d}	41.18 \pm 4.31	36.0 \pm 5.15	3.57	5.18
EN_{42wk}	64.0 \pm 2.24	56.0 \pm 5.963	1.70	8

4.5. The expected and actual genetic changes by applying independent culling levels for the first generation

Table (3) shows that the expected genetic changes of Age_{SM}, BW_{SM}, BW_M, EW_{SM}, EW_M, EN_{90d} and EN_{42WK} for the first generation of Norfa chicken were 1.69 d., 22.43 g, 31.01 g , .89 g , .32g , 1.8 egg and 1.27 eggs respectively. While the actual genetic gains were -13, -29.9, -38, -1, -1.180, 5.8 egg and 5.24 eggs respectively. This low expected genetic gains for egg number were mainly due to mainly to low heritability estimates (i.e. .41 and .21 for EN_{90d} and EN_{42WK}). On the other hand there was a clear discrepancy between the actual and expected genetic change for all traits.

Most of the estimates were in a good agreement with those found on Norfa strain by Abdou *et al.* (1998), El -Sakka (1999), Abou El-Ghar (2003), Ben Nasr

(2007), Abou-Elewa (2010) and El-Weshahy, (2010).

4.6. The expected and actual genetic changes by applying independent culling levels for the second generation.

Table (4) illustrates, expected genetic changes of A_{SM}, BW_{SM}, BW_M, EW_{SM}, EW_M, EN_{90d} and EN_{42WK} for the second generation of Norfa chicken being 1.31 d., 26.14 g, 27.73 g , .87 g , .26g , 2.95 egg and 2.91 eggs respectively. While the actual genetic gains were -10, -30, -22-1.4, 1, 14.05 egg and 19.72 eggs in the same order. On the other hand there was a clear discrepancy between the actual and expected genetic change for all traits.

Most of the estimates were in a good agreement with those found on Norfa strain by Abdou *et al.* (1998), El-Sakka (1999), Kosba *et al.* (2002), Abou El-Ghar (2003), Ben Nasr (2007), Abou-Elewa (2010), El-Weshahy, (2010).

Table (3): Means ± sd of the first generation, Expected genetic gain and Actual genetic gain in the first generation.

Trait	first generation Means ± sd of the selected line	Means ± sd of the control line	Expected genetic gains	Actual genetic gains
Age _{SM}	158±18.15	171±13.61	1.69	-13
BW _{SM}	1008.172±87.002	1038.6±55.9	22.43	-29.9
BW _M	1188±111.151	1226±86.462	31.01	-38
EW _{SM}	38.0±03.863	39.0±3.46	0.89	-1
EW _M	41.17±3.299	42.3±3.2	0.32	-1.18
EN _{90d}	48.155±5.896	42.28±2.59	1.80	5.87
EN _{42wk}	72.466±8.185	67.16±5.46	1.27	5.24

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Table (4): Means \pm sd of the second generation, Expected genetic gain and Actual genetic gain the second generation.

Trait	second generation Means \pm sd of the selected line	Means \pm sd of the control line	Expected genetic gains	Actual genetic gains
Age _{SM}	152 \pm 11.7	162 \pm 7.5	1.31	-10
BW _{SM}	980 \pm 88.4	1010.618 \pm 109.9	26.14	-30
BW _M	1210.82 \pm 88.2	1233.088 \pm 111.9	27.73	-22
EW _{SM}	35.084 \pm 2.0	36.437 \pm 2.0	0.87	-1.4
EW _M	42.0 \pm 3.2	41.0 \pm 3.4	0.26	1
EN _{90d}	63.525 \pm 13.1	49.471 \pm 4.2	2.95	14.05
EN _{42wk}	92.279 \pm 18.4	72.559 \pm 6.4	2.91	19.72

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الإنتخاب لبعض الصفات الإنتاجية في دجاج النورفا البياض

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الملخص العربي

أجريت هذه الدراسة في مزرعة الدواجن - كلية الزراعة - جامعة المنوفية بشبين الكوم جمهورية مصر العربية كجزء من المشروع المصري النرويجي لتحسين أداء سلالة النورفا خلال الفترة من (٢٠١٣ - ٢٠١٧) ، محاولة لتحسين أداء سلالة النورفا في القطيع الأساس والجيل الأول والجيل الثاني - تم تلقيح كل ديك مع ٣ دجاجات اصطناعيا . عدد الامهات الكليه المستخدمه في التجريه ٤٧٥ أنثى خلال القطيع الأساسي والجيل الأول والجيل الثاني. الهدف الأساسي من هذه التجربة هو لتحسين أداء سلالة النورفا باستخدام طريقة إنتخاب مستويات الإستبعاد المستقلة خلال ثلاث أجيال من الانتخاب . الإنتخاب بالمستوي الإستبعاد المستقل يطبق بإنتخاب قطع $\bar{X} + 0.5sd$ متوسط عدد القطيع خلال ٩٠ يوم $+ 0.5sd$ وحجم البيضه ووزن الجسم عند النضج الجنسي حول المتوسط القطيع.

ويمكن تلخيص النتائج المتحصل عليها كآآي:

بصفة عامة كانت قيمة المكافئ الوراثي للعمر عند النضج الجنسي منخفضة في حين كانت قيمة المكافئ الوراثي لكل من وزن الجسم عند النضج الجنسي والناضج كانت متوسطة ،بالنسبة لوزن البيض فان قيمة المكافئ الوراثي لوزن البيض عند النضج الجنسي ووزن البيض الناضج كانت متوسطة، وفيما يتعلق بقيم المكافئ الوراثي لصفتي عدد البيض حتي ٩٠ يوم الاولي وحتى ٤٢ اسبوع فقد كانت مابين المتوسطه الى المرتفعه.

كان من الواضح أن الأستجابه المحققه لصفه عدد البيض خلال ٩٠ يوم وعدد البيض خلال ٤٢ إسبوع كانت أعلى من الإستجابه المتوقعه خلال قطع الأساس والجيل الأول والثاني بواسطه تطبيق الإنتخاب بالمستويات الاستبعادية المستقلة.

أوضحت النتائج في هذه الدراسة تفوق الخط المنتخب عن خط الكنترول في الصفات الإنتاجيه في دجاج النورفا البياض . عموما دجاجات النورفا حققت تقدما في النضج الجنسي وبشكل عام تمتاز دجاجات النورفا بإنتاج بيض متوسط الحجم وهذا يرجع الى أن متوسط وزن الجسم لهذه السلالة .

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