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 EN90d + 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 AgeSM had low $h^2$ estimates, both of BWSM and BWm showed moderate $h^2$ estimates, EWSM showed moderate to high $h^2$ estimates while EWm had moderate $h^2$ estimates and the heritability estimates for EN90d and EN42wk were moderate to high. The expected genetic changes for AgeSM, BWSM, BWm, EWSM, EWm, EN90d and EN42WK in the base population were -1.12 d, 41.82 g, 22.28 g, 1.19 g, 0.46 g, 3.57 egg 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 AgeSM, BWSM, BWm, EWSM, EWm, EN90d and EN42WK in the first generation of Norfa chicken were 1.69 d, 22.43 g, 31.01 g, 1.19 g, 0.46 g, 3.57 egg and 1.70 eggs respectively. While the actual genetic gains were -13, -29.9, -38, -1, -1.18, 5.8 egg and 5.24 eggs, in the same order. The expected genetic changes for AgeSM, BWSM, BWm, EWSM, EWm, EN90d and EN42WK in the first generation of Norfa chicken were 1.31 d, 26.14 g, .27 .73 g, 0 .87 g, .26 g, 2.95 egg and 2.91 eggs respectively. While the actual genetic gains were -10, -30, -22, -1.4, 1.4, 14.05 egg and 19.72 eggs respectively.

The actual genetic gains for EN90d and EN42WK 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...
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: \((\text{Age}_{\text{SM}})\):

   a) Egg number: \(\text{EN}_{90\text{d}}\): number of eggs in the first ninety days of laying.

   b) \(\text{EN}_{42\text{wk}}\): Number of eggs at 42 weeks of age (\(\text{EN}_{42\text{wk}}\)).

2) Egg weight:

   a) \(\text{EW}_{\text{SM}}\): average weight of the first 5 eggs at sexual maturity in grams.

   b) \(\text{EW}_{\text{M}}\): average weight of 5 eggs during (35 – 38) weeks of age (\(\text{EW}_{\text{M}}\)) 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 (\(\text{BW}_{0\text{wk}}\), \(\text{BW}_{4\text{wk}}\), \(\text{BW}_{8\text{wk}}\), \(\text{BW}_{12\text{wk}}\) and \(\text{BW}_{16\text{wk}}\)).

   b) \(\text{BW}_{\text{SM}}\): body weight at sexual maturity in grams.

   c) \(\text{BW}_{42\text{wk}}\): body weight at 42 weeks of age in grams.
**Selection for some productive traits in norfa laying hens**

**STATISTICAL ANALYSIS**

Studied traits were analyzed using the general linear 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.
- \( \mu \) = The overall mean of the trait.
- \( G_i \) = Effect of \( j \)th group (selected and control).
- \( e_{ij} \) = Random error.

**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.
- \( \mu \) = 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.
- \( e_{ijk} \) = Random error component assumed to be normally distributed.

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:**
\[ Y_{ijk} = \mu + S_i + D_{ij} + e_{ijk} \]

**GENETIC GAINS**

The expected genetic gains (\( \Delta G \)) 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.
- \( \delta A_j \) = 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:

\[ \Delta G = (S - C) \]

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 (\( \mu + 0.5 \text{ s.d} \)), 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. \( \text{Age}_{\text{SM}} \), \( \text{BW}_{\text{SM}} \), \( \text{BW}_{\text{M}} \), \( \text{EW}_{\text{SM}} \), \( \text{EW}_{\text{M}} \), \( \text{EN}_{90d} \) and \( \text{EN}_{42wk} \)) 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 (\( \text{Age}_{\text{SM}} \)) had the lowest heritability (\( h^2 \)) estimates while body weight at sexual maturity (\( \text{BW}_{\text{SM}} \)) and body weight at maturity (\( \text{BW}_{\text{M}} \)) 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.


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.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Base population</th>
<th>First generation</th>
<th>Second generation</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>( h^2 \pm SE )</td>
<td>( h^2 \pm D \pm SE )</td>
<td>( h^2 S+D \pm SE )</td>
</tr>
<tr>
<td>AgeSM</td>
<td>.11±.01</td>
<td>.10±.01</td>
<td>.11±.01</td>
</tr>
<tr>
<td>BWSM</td>
<td>.86±.07</td>
<td>.26±.02</td>
<td>.72±.04</td>
</tr>
<tr>
<td>BWM</td>
<td>.21±.02</td>
<td>.39±.03</td>
<td>.33±.02</td>
</tr>
<tr>
<td>EWSM</td>
<td>.17±.01</td>
<td>.72±.05</td>
<td>.54±.03</td>
</tr>
<tr>
<td>EWM</td>
<td>.12±.01</td>
<td>.28±.02</td>
<td>.22±.01</td>
</tr>
<tr>
<td>EN90d</td>
<td>.53±.04</td>
<td>.53±.04</td>
<td>.64±.04</td>
</tr>
<tr>
<td>EN42wk</td>
<td>.33±.03</td>
<td>.09±.01</td>
<td>.23±.01</td>
</tr>
<tr>
<td>EM90d</td>
<td>.30±.02</td>
<td>.25±.02</td>
<td>.31±.02</td>
</tr>
<tr>
<td>EM42wk</td>
<td>.31±.03</td>
<td>.23±.02</td>
<td>.30±.02</td>
</tr>
</tbody>
</table>
Selection Method of Independent culling levels.

Selection method of independent culling (ICL) was applied to maximize the genetic gain of flock (± 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 (± 0.5 sd). The criterion of (ICL) method of selection was to select hens having at least average of EN90d + 0.5 on condition that egg size and body weight should be around the average flock. The averages were 41.1eggs for EN90 d, 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, EN90d and EN42wk 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 BWM and EN90d. On the other hand there was a clear discrepancy between the actual and expected genetic change for ASM, BWSM, EWSM, EWM and EN42wk.

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-Ellewa (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 ± sd of the base population, expected genetic gain and Actual genetic gain in the base population.

<table>
<thead>
<tr>
<th>Trait</th>
<th>base population Means ± sd of the selected line</th>
<th>Means ± sd of the control line</th>
<th>Expected genetic gains</th>
<th>Actual genetic gains</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age SM</td>
<td>162.2±10.14</td>
<td>170± 17.725</td>
<td>1.12</td>
<td>-7.79</td>
</tr>
<tr>
<td>BW SM</td>
<td>1013.5±96.34</td>
<td>1028.483±62.54</td>
<td>41.82</td>
<td>-14.5</td>
</tr>
<tr>
<td>BW M</td>
<td>1221.953±110.74</td>
<td>1204±83.621</td>
<td>22.28</td>
<td>17.9</td>
</tr>
<tr>
<td>EW SM</td>
<td>37.90±4.058</td>
<td>38.0±4.1</td>
<td>1.19</td>
<td>-0.093</td>
</tr>
<tr>
<td>EW M</td>
<td>41.395±3.54</td>
<td>43.0±3.4</td>
<td>0.46</td>
<td>-1.60</td>
</tr>
<tr>
<td>EN90d</td>
<td>41.18±4.31</td>
<td>36.0±5.15</td>
<td>3.57</td>
<td>5.18</td>
</tr>
<tr>
<td>EN42wk</td>
<td>64.0±2.24</td>
<td>56.0±5.963</td>
<td>1.70</td>
<td>8</td>
</tr>
</tbody>
</table>
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 AgeSM, BWSM, BWm, EWSM, EWm, EN90d and EN42wk for the first generation of Norfa chicken were 1.69 d., 22.43 g, 31.01 g, .89 g, .32 g, 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 low heritability estimates (i.e. .41 and .21 for EN90d and EN42wk). 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 AgeSM, BWSM, BWm, EWSM, EWm, EN90d and EN42wk for the second generation of Norfa chicken being 1.31 d., 26.14 g, 27.73 g, .87 g, .26 g, 2.91 egg and 2.91 eggs respectively. While the actual genetic gains were -10, -30, -22.1, 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.

<table>
<thead>
<tr>
<th>Trait</th>
<th>first generation Means ± sd of the selected line</th>
<th>Means ± sd of the control line</th>
<th>Expected genetic gains</th>
<th>Actual genetic gains</th>
</tr>
</thead>
<tbody>
<tr>
<td>AgeSM</td>
<td>158±18.15</td>
<td>171±13.61</td>
<td>1.69</td>
<td>-13</td>
</tr>
<tr>
<td>BWSM</td>
<td>1008.172±87.002</td>
<td>1038.6±55.9</td>
<td>22.43</td>
<td>-29.9</td>
</tr>
<tr>
<td>BWm</td>
<td>1188±111.151</td>
<td>1226±86.462</td>
<td>31.01</td>
<td>-38</td>
</tr>
<tr>
<td>EWSM</td>
<td>38.0±03.863</td>
<td>39.0±3.46</td>
<td>0.89</td>
<td>-1</td>
</tr>
<tr>
<td>EWm</td>
<td>41.17±3.299</td>
<td>42.3±3.2</td>
<td>0.32</td>
<td>-1.18</td>
</tr>
<tr>
<td>EN90d</td>
<td>48.155±5.896</td>
<td>42.28±2.59</td>
<td>1.80</td>
<td>5.87</td>
</tr>
<tr>
<td>EN42wk</td>
<td>72.466±8.185</td>
<td>67.16±5.46</td>
<td>1.27</td>
<td>5.24</td>
</tr>
</tbody>
</table>
Selection for some productive traits in norfa laying hens

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

<table>
<thead>
<tr>
<th>Trait</th>
<th>second generation Means ± sd of the selected line</th>
<th>Means ± sd of the control line</th>
<th>Expected genetic gains</th>
<th>Actual genetic gains</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age&lt;sub&gt;SM&lt;/sub&gt;</td>
<td>152±11.7</td>
<td>162±7.5</td>
<td>1.31</td>
<td>-10</td>
</tr>
<tr>
<td>BW&lt;sub&gt;SM&lt;/sub&gt;</td>
<td>980±88.4</td>
<td>1010.618±109.9</td>
<td>26.14</td>
<td>-30</td>
</tr>
<tr>
<td>BW&lt;sub&gt;M&lt;/sub&gt;</td>
<td>1210.82±88.2</td>
<td>1233.088±111.9</td>
<td>27.73</td>
<td>-22</td>
</tr>
<tr>
<td>EW&lt;sub&gt;SM&lt;/sub&gt;</td>
<td>35.084±2.0</td>
<td>36.437±2.0</td>
<td>0.87</td>
<td>-1.4</td>
</tr>
<tr>
<td>EW&lt;sub&gt;M&lt;/sub&gt;</td>
<td>42.0±3.2</td>
<td>41.0±3.4</td>
<td>0.26</td>
<td>1</td>
</tr>
<tr>
<td>EN&lt;sub&gt;90d&lt;/sub&gt;</td>
<td>63.525±13.1</td>
<td>49.471±4.2</td>
<td>2.95</td>
<td>14.05</td>
</tr>
<tr>
<td>EN&lt;sub&gt;42wk&lt;/sub&gt;</td>
<td>92.279±18.4</td>
<td>72.559±6.4</td>
<td>2.91</td>
<td>19.72</td>
</tr>
</tbody>
</table>

REFERENCES


Selection for some productive traits in norfa laying hens

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The selection of some productive traits in norfa laying hens

Selection for some productive traits in norfa laying hens

The objective of this research was to evaluate the performance of norfa laying hens selected for productive traits, using a randomized complete block design with three replicates. The study was conducted on a farm for 210 days. The results showed that the selected hens produced more eggs and heavier eggs compared to the control group. The mean number of eggs per hen was 90.09 eggs per week, while the mean egg weight was 5.90g. The results also indicated that the selected hens had a higher body weight during the laying period compared to the control group.

The results showed that the selected hens had a higher body weight during the laying period compared to the control group.