Estimation of Genetic and Phenotypic Parameters for Growth Traits of Friesian Cattle Raised in Egypt.
Safa'a, S. Sanad and M. G. Gharib
Animal production research Institute (APRI) – Research center – Egypt.

ABSTRACT

Growth traits (GT) of 1691 Friesian calves by 74 sires and 789 dams over a 20 years (1997 to 2016) in Alkarda Farm, Egypt. Traits studied were weight at birth weight (BW), weaning weight (WW) and daily gain (DG). Records were analyzed Multiple Trait Likelihood (MTDFREML) to estimate covariance components and Heritability ($h^2$), genetic correlations ($r_g$), maternal correlations ($r_m$) and phenotypic correlations ($r_p$), breeding values (BV), and Epigenetic trend (EGT) for growth traits (GT) of Friesian cattle raised in Egypt. Actual mean for BW, WW and DG were 28.6kg, 92.6kg and 0.60 gm, respectively. Direct heritability ($h^2_{direct}$) estimates for BW, WW and DG were 0.32±0.06, 0.22±0.06 and 0.34±0.85, respectively; on the same time low maternal heritability ($h^2_{maternal}$) were 0.12±0.35, 0.08±0.49 and 0.18±0.71, respectively. The permanent environment ($P^2$) was 0.021±0.70, 0.030±0.77 and 0.058±0.72 for BW, WW and DG, respectively. Phenotypic correlation ($r_p$) were 0.99 while, direct genetic correlation ($r_g$) are ranged from 0.56 to 0.96. While, maternal correlations ($r_m$) ranged from 0.48 to 0.93. Range of breeding value (BV) estimated of calves for BW, WW and DG were 51.5kg, 10.1kg and 31.2 kg, the BV of sire for the same traits 17.7 kg, 101.0kg and 12.0g. While the range of dams BV were 11.4kg, 17.8kg and 17.7gm respectively.

Keywords: Friesian, Growth traits (GT), Animal model, Genetic parameters, Epigenetics TREND (EGT), Calves.

INTRODUCTION

Genetic improvement is necessary factor for economically of dairy cattle, also it's important to improve milk traits Sarakul et al. (2011).

Apart from the genotype effects; sex, year of birth and parity were the main non genetic factors that influenced growth and daily weight gain traits until one year of age (Abera et al., 2012). Therefore, the actual performance of animals could be adjusted by removing non-genetic sources of variation from the performance data to get accurate estimates of genetic parameters and breeding values.

A genetic trend is defined as a change in performance per unit of time due to change in mean breeding value and it is derived by comparing the average levels in the cow populations for each year. The understanding of trends in genetic progress will help future genetic direction to be established by definition of specific goals for breeding a profitable.

Therefore in any genetic improvement program, there is the need of tracking the results to evaluate their progress, to make adjustments aiming to optimize genetic gain, and to increase farm profitability in the future. One of the ways to perform such monitoring is through the assessment of genetic trends over time, which evaluates the changes brought by the selection process (Silva et al., 2001).

This study aims to estimate the genetic effects of the traits) BW, WW, DG). Moreover, the study attempted to estimates of BV for all traits, by using analysis MTDFREML, estimate Epigenetics trend (EGT) and environmental trend by determine the effects of various environmental factors on the traits study of Friesian calves raised under Egyptian farm condition.

MATERIALS AND METHODS

Population.
The study was conducted on the calves of Alkarda farm, Kafr El-Sheikh, Egypt. Calves were were allowed to suckle their dam’s colostrum’s (the first three days) after birth. Each calf was given 500 kg of milk during the feeding period. Plus availability alphalpa fresh hay, nutrition plan was according to the system of (APRI).

Data collection and traits.
The data used in this study were taken from the collected records of APRI during the period of 1997-2016. Data were extracted from various growth records (BW and WW) of Friesian cattle raised in Egypt. Table (1): show structure of data.

<table>
<thead>
<tr>
<th>Items</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sire</td>
<td>74</td>
</tr>
<tr>
<td>Dam</td>
<td>789</td>
</tr>
<tr>
<td>Animals weaned</td>
<td>1691</td>
</tr>
<tr>
<td>Total number of animals in the pedigree record</td>
<td>2543</td>
</tr>
</tbody>
</table>

Data analysis.
Data were analyzed using multi-trait animal model for three traits (birth weight, weaning weight and daily gain). Heritability, genetic correlations, phenotypic correlations and BV of studied traits were estimated with...
derivative-free restricted maximum likelihood (REML) procedures using the MTDFREML (Boldman et al., 1995). Also (SAS, 2003).

The model was:

\[ y = Xb + Z_1a + Z_2m + Z_3p + e, \]

\[ \text{Cov (a,m)} = A \sigma_{am}, \]

where,

- \( y \): a vector of observations,
- \( b \): a vector of fixed effect,
- \( a, m, p \) are the vectors of direct additive genetic effect, maternal genetic effect, and the residual effect, respectively,
- \( X, Z_1, Z_2, Z_3 \) are incidence matrix relating individual records to \( b, a, m \) and \( p \), respectively.

**Epigenetic Trend (EGT):**

Genetic improvement of cattle for economically important traits, particularly growth traits, is an important component of an overall strategy to improve milk traits of cows. Factors that influence genetic improvement may vary across environmental situations. Differences among such as (season, parity and year) (Hassan et al. 2010 and 2013). The cumulative effects of such genes, coupled with environmental effects produce continuous variation in the phenotypic values of individual. The differences among classes of distinctive environmental situations may affect growth traits genetic improvement within cattle populations, and will help identify common factors that influence genetic improvement across populations in Friesian cattle raised in Egypt.

EGT was estimated using the method procedures Legates and Myers (1988). Environmental using (SAS, 2003). The resultant output was then plotted in graphs to represent the general trend of the behavior of the fixed effect under consideration (parity, year and season).

**Environmental Trend (ENV):**

ENV are estimated as the result of subtracting BV of growth traits (GT) values of an animal from its observed phenotypic values of the GT, all as deviations from the means, the resultant values are regressed matching their respective parity, season, and year effects as done with EGT. They evaluated by the same way done with EGT.

**RESULTS AND DISCUSSION**

(Table 2) Means for BW, WW and DG were 28.6, 92.6 and 0.60 kg., respectively. Mean of BW lower than those reported by Hullya Atil et al., (2005) (31.8 kg) and higher than Hwang et al. (2008) (24.4 kg). While Mean of WW higher than While, Hwang et al., (2008) (91.77 kg) and lower than Hulya Atil et al., (2005) (97.4 kg).

**Table 2. Actual Means(X) , standard deviation (S.D) and coefficients of variation (CV%) for GT in Alkarda farm.**

<table>
<thead>
<tr>
<th>Traits</th>
<th>X</th>
<th>S.D</th>
<th>CV%</th>
</tr>
</thead>
<tbody>
<tr>
<td>BW,kg</td>
<td>28.6</td>
<td>3.2</td>
<td>11.1</td>
</tr>
<tr>
<td>WW,kg</td>
<td>92.6</td>
<td>11.2</td>
<td>12.1</td>
</tr>
<tr>
<td>DG, gm.</td>
<td>0.60</td>
<td>0.10</td>
<td>17.5</td>
</tr>
</tbody>
</table>

The coefficient of variation for BW, WW and DG were 11.1, 12.1 and 17.5 % respectively. Hullya Atil et al (2005) estimates for BW and WW were 14.4 and 10.5 Hwang et al., (2008) found that BW and WW were 15.3 and 22.0. Differences between the results of this study and the results of previous research may be due to differences in the methods of statistical analysis or the number of records used or due to different management and ways of care.

**Genetic parameters**

**Heritability estimates.**

Estimation of heritability (direct \( h^2a \) and maternal \( h^2m \)) of BW, WW and DG are presented in Table 3. Estimates of \( h^2a \) were Moderate and were 0.52, 0.22 and 0.34, respectively. While, \( h^2m \) were 0.12, 0.08 and 0.18 respectively. in Table 3.

**Table 3 .Heritability estimates \( (h^2a \pm SE) \) and \( (h^2m \pm SE) \), \( (P^2 \pm SE) \), and error (e²) for GT.**

<table>
<thead>
<tr>
<th>Traits</th>
<th>( h^2a \pm SE )</th>
<th>( h^2m \pm SE )</th>
<th>( P^2 \pm SE )</th>
<th>e²</th>
</tr>
</thead>
<tbody>
<tr>
<td>BW</td>
<td>0.32±0.06</td>
<td>0.12±0.05</td>
<td>0.021±0.70</td>
<td>0.46</td>
</tr>
<tr>
<td>WW</td>
<td>0.22±0.06</td>
<td>0.08±0.49</td>
<td>0.030±0.77</td>
<td>0.57</td>
</tr>
<tr>
<td>DG</td>
<td>0.34±0.85</td>
<td>0.18±0.71</td>
<td>0.058±0.72</td>
<td>0.30</td>
</tr>
</tbody>
</table>

\( h^2a \): additive heritability, \( h^2m \): maternal heritability, \( P^2 \): permanent environmental variance, \( e² \): residual variance, \( (BW) \): weight at birth, \( (WW) \): weight at weaning and \( (DG) \): daily gain.

Moderate heritability for body weight and gains obtained in the present study were similar Dodenhoff et al. (1999) ranged from 0.17 to 0.33.

In this results higher than Keeton et al. (1996), found that estimates \( h^2a \) WW and \( h^2m \) WW were 0.25 and 0.19, respectively. Hulya Atil et al (2005) found that the estimates of \( h^2a \) BW and WW were (0.28) and 13 respectively ,while, \( h^2m \) of WW were 0.06, but, lower than results of Maarof et al. (1988) (0.43) ; Goyache et al. (2003) found \( h^2m \) of WW was 0.67. The estimates of WW is similar Lengyl et. al. (2001).

Koch et al., (1994), Waldron et al.,(1993) and Lee and pollak,(1997) reported maternal heritability estimate of WW were 0.17, 0.14 and 0.15, respectively, in beef cattle which are not also far from what has been reported from our study. However the present estimateson maternal heritability coincide with others reported in literature (Berweger Baschmagel et al., (1999) (0.04) ; Lee and pollak,(1997) (0.09).

As shown from Table.3 WW (0.22) rather than BW (32), however, higher estimate of \( h^2m \) for BW (0.12) than WW (0.08) indicating that \( h^2m \) genetic effects for BW Similar to results obtained by (Lengyl et al. 2001) low of \( h^2m \) for WW may be dam effect. (Maternal effect) Heritability estimates observed for BW indicated that in Friesian faster genetic improvement through selection is possible for BW and WW.

The estimates of \( h^2a \) and \( h^2m \) for WW were 0.22 and 0.08 (Table.3) were highest estimate obtained Lee et al. (2000) found that estimates for WW were \( h^2a \) (0.13) and \( h^2m \) (0.07) ; Assan and Masache (2012) observed that, the \( h^2a \) 0.25 when the maternal genetic effects were included in the model, while \( h^2a \) estimates were 0.21 . The maternal heritability \( h^2m \) was lower (0.04) than \( h^2a \) (0.09) when only maternal genetic effects were included in the model, and were 0.13 and 0.17 when the permanent environmental effects of the dam was fitted. The permanent environmental effects of the
predicted breeding value for birth, weaning and one
generation in the next generation for both sires and
dams, Hossen et al. (2012) found that range of
duced breeding values (PBV) ranged from (4.4 to 8.3
tral permanent were 0.021, 0.030 and 0.058 for BW, WW and DG, respectively (Table 3). Hulya Atil et al. (2005) found that the estimates \( P_e^2 \) were 0.47 and 0.018 for BW and WW, respectively. Hwang et al., (2008) observed that, \( P_e^2 \) were 0.02 and 0.06 were 0.47 and 0.018 for BW and WW, respectively by DF-REML method. Gutierrez et al (1997) using 7 models found that, \( P_e^2 \) were 0.00, 0.00 and 0.00 (model 4) and 0.06 and 0.06 (model 7) for BW, WW and DG, respectively.

Significantly estimates of genetic \( (r_g) \), maternal \( (r_m) \) and phenotypic \( (r_p) \) correlations among previous traits were highly positive. (Table 4). \( (r_g) \) were 0.58, 0.56 and 0.96, while, \( (r_m) \) were 0.48, 0.40 and 0.93. but \( (r_p) \) were 0.99, 0.99 and 0.99 among previous traits. Similar to estimate reported by Koster et al (2000) found that genetic correlation were moderate 0.33. 0.50 and 0.93. While, highly maternal correlations were 0.72, 0.51 and 0.96. Phenotypic correlations \( (r_p) \) were 0.82, 0.86 and 0.96 between BW, WW and DG. Steinhardt and Thielischer (2000) and Cantet et al. (2003) found that high \( (r_g) \) BW and WW also Lengyel et al (2001) found that \( (r_g) \) and \( (r_p) \) for BW and WW were 0.90 and 0.89 ; Hulya Atil et al (2005) found that genetic correlations \( (r_g) \) were positive between BW, WW \( (r_g) = 0.80 \) and Phenotypic correlations \( (r_p) \) were positive between BW, WW \( (r_p) = 0.89 \). El-Awady (2003) reported that there were positive genetic and \( (r_g) \) between BW and WW. Also, observed that genetic and \( (r_p) \) between BW and WW were 0.49 and 0.56, respectively. WW was significantly and positively correlated with all traits under study could be increased as a result of selection for the heavier WW

### Table 4. Estimates of breeding values (BV) for study traits in Karada herds.

<table>
<thead>
<tr>
<th>Traits</th>
<th>BV</th>
<th>Maximum ± SE</th>
<th>Accuracy %</th>
<th>Minimum ± SE</th>
<th>Accuracy %</th>
<th>Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Calves (CBV)</td>
<td>BW</td>
<td>28.47(10.5)</td>
<td>79</td>
<td>32.05(10.14)</td>
<td>80</td>
<td>51.5</td>
</tr>
<tr>
<td>WW</td>
<td>9.99 (9.5)</td>
<td>74</td>
<td>-0.10(10.42)</td>
<td>68</td>
<td>10.1</td>
<td></td>
</tr>
<tr>
<td>DG</td>
<td>16.65 (7.5)</td>
<td>78</td>
<td>-14.55(10.1)</td>
<td>80</td>
<td>31.2</td>
<td></td>
</tr>
<tr>
<td>Sires (SBV)</td>
<td>BW</td>
<td>10.23(11.43)</td>
<td>74</td>
<td>-7.91(10.72)</td>
<td>78</td>
<td>17.7</td>
</tr>
<tr>
<td>WW</td>
<td>5.01(13.2)</td>
<td>36</td>
<td>-9.6(8.7)</td>
<td>79</td>
<td>101.0</td>
<td></td>
</tr>
<tr>
<td>DG</td>
<td>6.87(11.6)</td>
<td>42</td>
<td>-5.16(8.0)</td>
<td>78</td>
<td>12.0</td>
<td></td>
</tr>
<tr>
<td>Dams (DBV)</td>
<td>BW</td>
<td>5.94(12.4)</td>
<td>68</td>
<td>-5.43(10.8)</td>
<td>77</td>
<td>11.4</td>
</tr>
<tr>
<td>WW</td>
<td>7.91(12.2)</td>
<td>51</td>
<td>-9.9(13.3)</td>
<td>51</td>
<td>17.8</td>
<td></td>
</tr>
<tr>
<td>DG</td>
<td>11.08(11.1)</td>
<td>49</td>
<td>-6.6(11.1)</td>
<td>49</td>
<td>17.7</td>
<td></td>
</tr>
</tbody>
</table>

### Table 5. Estimates of breeding values (BV) for study traits in Karada herds.

<table>
<thead>
<tr>
<th>BV</th>
<th>Traits</th>
<th>Maximum ± SE</th>
<th>Accuracy %</th>
<th>Minimum ± SE</th>
<th>Accuracy %</th>
<th>Range</th>
</tr>
</thead>
<tbody>
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<td></td>
</tr>
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<tr>
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<td>74</td>
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<td>78</td>
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</tr>
<tr>
<td>WW</td>
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<td>36</td>
<td>-9.6(8.7)</td>
<td>79</td>
<td>101.0</td>
<td></td>
</tr>
<tr>
<td>DG</td>
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<td>42</td>
<td>-5.16(8.0)</td>
<td>78</td>
<td>12.0</td>
<td></td>
</tr>
<tr>
<td>Dams (DBV)</td>
<td>BW</td>
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<td>68</td>
<td>-5.43(10.8)</td>
<td>77</td>
<td>11.4</td>
</tr>
<tr>
<td>WW</td>
<td>7.91(12.2)</td>
<td>51</td>
<td>-9.9(13.3)</td>
<td>51</td>
<td>17.8</td>
<td></td>
</tr>
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<td>49</td>
<td>17.7</td>
<td></td>
</tr>
</tbody>
</table>

Abra (2017) found that, the overall mean predicted breeding value for birth, weaning and one year weight were 0.11±0.06kg, 0.13± 0.09kg and 1.1±1.4kg, respectively.

These results indicate that higher genetic improvement. The present results found that CBV positive value for WW 1676 (65.9%) Table 5. These results indicate that selection of calves on the basis of higher breeding value for BW, will increase WW production in the next generation for both sires and dams, Hossen et al. (2012) found that range of predicted breeding values (PBV) ranged from (4.4 to 8.3 kg) indicates a degree of additive genetic variation, which exists in a population. Enough variation for a trait in the population is needed so that the level for the trait can be changed along with the breeding objectives.

### Environmental trend (ENV)

The figures (1- 3) are shown EGT for (BW), (WW) and DG affected by season, parity and year.

As regard to GT environmental changing by season, negative (-) ENV during the first season (autumn , summer and spring) , While the positive (+) in the winter, meaning that effects of environment was favorable versus animals during winter figure (1), the effects of environment was favorable versus animals during winter.

More generally, the results of this study indicate that breeding value for birth, weaning and one year weight were highly positive. These results also indicate that selection of calves on the basis of higher breeding value for BW, will increase WW production in the next generation for both sires and dams.
Interaction, data of ENV presented in figures (2). Revealed that the effects of environmental was negative for BW in the 1st and 2nd parity otherwise. This positive ENV seems to concentrate in the 1st and 2nd parity, the positive (BW) 4th, 5th, 6th and 7th, it started to have a positive trends especially in the 1st and 2nd ones. While the effects of environmental was negative for WW in the 1st, 2nd, 6th and 7th parity otherwise and positive 3rd, 4th and 5th. Abdel-Ghil and Elbanna (2001) found that birth weight of the calf increased with advance of parity and reached its peak in the fourth one.

Study traits environmental regressed against by year, showed that (BW), (WW) and DG traits have a negative ENV during The 1st, 2nd, 3rd, 5th, 12th, 13th and 14th years of (BW), (WW) and DG. While the remainder year gave positive (+) trends (6th to 11th) figures (3). Similar results were obtained by Faid-Allah(2010).

Epigenetic trend (EGT): figures (4, 5 and 6). EGT for study traits as affected by season, parity and year. Effect of season positive trend in autumn and summer while winter and spring negative trends in figures (4). The positive (high) EGT for (GT) during winter and spring due to environmental conditions and alfalfa is available during this period.

Study traits estimated genetic trends, as a deviation from the overall-BV mean, in Fig. 1. Shows that study traits of the Friesian herd have positive genetic trend in summer and autumn. The maxi value for the evaluated study traits were generally in winter. The high genetic trend during the winter because of the availability of green fodder.

As regard to weights genetic trends, Fig. 2 shows that weight traits of the Friesian have negative genetic trend in winter and spring but positive in summer and autumn.

Figure (5). revealed that the 4th and 5th parity of BW, WW and DG gave negative(-) trends while the remainder parities gave positive(+) trends6th and 7th parity in Friesian cattle parities. The high milk traits EGT parity is apparently due to peak production (persistency) as observed in this study (Figure 3.). The same trend Usman
et al. (2012) on GT may be due to the physiological state and environmental conditions between parties.

Fig. 4. EGT of study traits changed versus season

Positive genetic trend seems to concentrate in second parity with sporadic sharing from the third parity. The high genetic trend at the 6 and 7 parities is clearly due to that the animals reach their premium physiological reproductive maturity and development. However, the lowering trends following these premium parities became lowest at the later ones. Results in figure 6. The (2006 to 2008), (2012 to 2014) years of BW and 1999, 2003, 2010, 2016 years of WW traits gave negative (-) trends while, 2009, 2010 and 2015 years of BW gave positive (+) trends also (2005 to 2008) and (2010 to 2013) years of WW traits positive trends. In general, year of calving is considered the most important source of variation in body weight and this may be attributed to changes in management and feeding systems from year to other, Holloway et al. (2002) reported that year effects were important (P ≤ 0.05) for performance traits. Abera (2017) found that, breeding value trends have been improving and there was about 0.016 kg, 0.031 kg, 0.14 kg genetic gain in BW, WW and YW per year. The same trend Hossen et al. (2012), also positive genetic and ENV are indicators of favorable selection methods and good management (Plasse et al. 2002).

Fig. 5. EGT of study traits changed versus parity

Fig. 6. EGT of study traits changed versus year

CONCLUSION

In Egypt, seems to be a productive local Friesian breed. It was ignored for many times without selection. It needs to be genetically ameliorated to produce more meat and cover the consumers demand. An attention of modern husbandry could be paid to realize this objective. Fortunately, the obtained estimates of heritability and most of the genetic correlation coefficients were high; they will be used in a breeding plan that will be effective to improve rapidly this breed. Daily gain effect is very important for post-weaning traits; we can conclude that the daily gain effect should be included in the genetic evaluation of breeding programs.

In the present study calving of season, calving of year and parity were important factors affecting birth weight. In the next studies, the effects of environmental factors should be eliminated for the effective selection program based on birth weight.

High and positive genetic and phenotypic correlation between BW and WW. Phenotypic correlation indicating that the growth rate from birth to weaning may be an appropriate selection criterion for improving growth. The selection based on the CBV of calves increases the WW of sires and dams in the next generation.

Figures of Epigenetic trend (EGT) showed that the effect of year of calving is considered the most important
source of variation in body weight and this may be attributed to changes in management and feeding systems from year to other. Also study trends of the Friesian herd have positive genetic trend in summer and autumn. The main value for the evaluated study traits were generally in winter. The high genetic trend during the winter may be due to availability green fodders.

REFERENCES


