Assessment of Friesian Cattle Performance Sustainability Through the Evaluation of Phenotypic and Genetic Parameters and Trends of some Economic Traits Under Egyptian Conditions

ElSawy, M. H.; Shereen K. Genena*; A. M. Shaarawy and A. A. Mehany

Animal Production Research Institute., Agricultural Research Center, Dokki, Giza, Egypt.

ABSTRACT

Total of 3380 records from 1635 Friesian cows kept in Sakha and El Karada farms between 1988 and 2020 were utilized to measure their sustainability in performance by estimating the genetic and phenotypic parameters and trends for 305-day milk yield (MY), calving interval (CI), and age at first calving (AFC). Fixed effects are farm, year of calving – season, and animal parity. The VCE program was used to estimate variance components and genetic parameters. The MY, CI and AFC averages were 3280 kg, 15 mo and 32 mo and their heritability estimates were 0.20, 0.07 and 0.34, respectively. Genetic and phenotypic correlations among the traits ranged from 0.03 to 0.05 and from -0.04 to 0.04, respectively. The corresponding genetic (GT) and phenotypic trends for the studied traits showed deterioration in the overall rates and the ranges of breeding values were from -57 to +105 kg, -0.15 to +0.25 mo and -0.35 to +0.30 mo for MY, CI and AFC, respectively. Strong intervention in selection and management powers may alter defects by using modern reproductive techniques in breeding programs for future generations. The farm's financial aspects were disturbed by delaying AFC or extending CI. The low CI produced more profit for the farm but prolonging it even for one day caused a financial loss. Also, as AFC expanded, MY increased, but overall farm profits decreased due to the high cost of rearing and replacements after AFC of 24 months.

Keywords: Genetic aspects and trends, sustainability, economic traits, farm profits, Friesian.

INTRODUCTION

Friesian cattle are the most widespread and highly productive exotic dairy breed that was introduced to Egypt. It is ranked as the most important source of milk. Moreover, this breed adapts well at sustainable high levels of performance under various management systems and harsh conditions due to its high adaptability to local environments in Egypt (Amr, 2013). Therefore, the breed should be evaluated regularly to predict the future genetic control of its performance along with its genetic and phenotypic trends for economically important traits. On top of the list, milk production received the most apparent improvement among all production traits because historically, it acquired high attention in the selection indexes and producers were primarily paid for increased production (Guinan et al., 2023).

The estimates of genetic parameters for a given group of traits determine the method of selection to be used for predicting the direct and correlated responses, choosing the breeding system to be adopted for future improvement and the expected genetic gains (Missanjo et al., 2013; Goshu et al., 2014). Knowing the values of genetic parameters, genetic trends, and inbreeding depression is essential, as it helps to justify the decision-making process for the adopted selection procedure, management plans, and nutritional requirements necessary to improve the productive efficiency of cows (Caivio-Nasner et al., 2021).

Moreover, genetic and phenotypic correlations between traits are useful to formulate the breeding programs, since they determine the direction and magnitude of genetic improvement in other traits when selection is directed to the trait of concern (Tesfa, 2015). Keeping track of the amplitude progress of any genetic improvement program is very important for optimizing the genetic gain and, consequently farm profitability (Canaza-Cayo et al., 2016) and helps to judge the quality of the breeding programs implemented in the herd (Grosa et al., 2014; El-Awady et al., 2017).

Samarakweera et al. (2022) revealed that the genetic improvements in the set of milk yield, age at first calving, calving interval, number of services per conception, and resistance to mastitis traits have a positive impact on the profitability of dairy farms. The derived economic values of these traits are adequate enough to define the relative importance of the breeding objective for each trait and use them as economic weights in a selection index of genetic improvement programs to achieve progress in dairy cattle. Meyer et al. (2004) concluded that optimal AFC promotes the reduction of breeding costs and the extension of the herd life of dairy cows. Also, Vargas-Leitón et al. (2023) stated that the reduction in AFC contributes to a significant increase in the production and reproduction efficiency of pasture-based dairy herds.

The objectives of the current study were to assess the sustainability of Friesian cattle by estimating their genetic and phenotypic parameters and trends over time for some economic traits. Also, the impact of extended lactations on farm economy and profitability was studied.

MATERIALS AND METHODS

Data and management

A total of 3380 records from 1635 multiparous Friesian cow’s daughters of 132 sires were collected...
between 1988 and 2020. Cows were kept in Sakha and El-Karada experimental stations belonging to the Animal Production Research Institute, Agriculture Research Center, Ministry of Agriculture and Land Reclamation.

Animals were grazed on berseem (Egyptian clover: *Trifolium alexandrinum*) from December to May, and fed on a concentrate mixture and rice straw mixed with a limited amount of hay (if available) during the rest of the year. Cows producing more than 10 kg of milk per day and those in the last two months of pregnancy were supplemented with an extra concentration ration. Artificial insemination with frozen semen was routinely practiced on the two farms. Sires having fewer than five daughters were excluded from the data. Cows were machine-milked twice a day. The studied traits were: 305-day milk yield (MY), age at the first calving (AFC) and calving interval (CI). Table 1 presents a summary of the data description.

**Table 1. Description of the data set for the studied traits**

<table>
<thead>
<tr>
<th>Traits</th>
<th>No. of records</th>
<th>Mean</th>
<th>SD</th>
<th>Min.</th>
<th>Max.</th>
</tr>
</thead>
<tbody>
<tr>
<td>MY (kg)</td>
<td>3380</td>
<td>3297.5</td>
<td>1163.6</td>
<td>1053</td>
<td>7808</td>
</tr>
<tr>
<td>CI (mo)</td>
<td>3380</td>
<td>15.0</td>
<td>3.3</td>
<td>11</td>
<td>29</td>
</tr>
<tr>
<td>AFC (mo)</td>
<td>3380</td>
<td>31.6</td>
<td>3.3</td>
<td>26</td>
<td>39</td>
</tr>
</tbody>
</table>

Statistical analysis

Data were statistically analyzed using the REML procedure to estimate (co)variance components by the VCE6 program (Groeneveld et al., 2010) using the repeatability animal model. The studied fixed effects were farm, year of calving-season, and animal parity. The applied model was as follows:

\[ Y_{ijklmn} = \mu + F_i + R_j + S_k + P_l + Pe_i + a_m + e_{ijklmn} \]  

Where,  
\( Y_{ijklmn} \) = the individual observation on each of the studied traits,  
\( \mu \) = the overall mean,  
\( F_i \) = the fixed effect of the 16th farm (i = 1 or 2),  
\( R_j \) = the fixed effect of the jth year of calving season (j = 1 to 32),  
\( S_k \) = the fixed effect of the kth season of calving (k = 1 (cold) or 2 (hot)),  
\( P_l \) = the fixed effect of the lth parity (l = 1 to 9),  
\( Pe_i \) = random permanent environmental effect on the animal and  
\( a_m \) = random additive genetic effect  
\( e_{ijklmn} \) = error as a random effect.

It was assumed that the covariance between additive, permanent environmental and residual effects was zero. Multivariate estimated breeding values (EBV) were estimated by the PEST program (Groeneveld et al., 2010) by fitting an animal model and using genetic parameters obtained as described below. In matrix notation, the general model for genetic analysis can be expressed as:

\[ \mathbf{Y} = \mathbf{Xa} + \mathbf{Za} + \mathbf{Zpe} + \mathbf{e} \]  

Where:  
\( \mathbf{Y} \) is the vector of observations,  
\( \mathbf{a} \) = a vector of fixed effects  
\( \mathbf{a} \) = a vector related to animal additive genetic effects  
\( \mathbf{pe} \) = a vector of permanent environmental effects  
\( \mathbf{e} \) = a vector of residuals.

\( \mathbf{X}, \mathbf{Za} \) and \( \mathbf{Zpe} \) are incidence matrices that relate the fixed effects, animal additive genetic effects and permanent environmental effects to the vector of observations, respectively. Genetic (\( \sigma^2_a \)) and phenotypic (\( \sigma^2_e \)) correlations among the studied traits were calculated.

The genetic trend (GT) was estimated as the linear regression of the yearly means of EBV on years of birth for all traits. The phenotypic trend (PT) was estimated by regressing the yearly means of phenotypic values on years of birth using the SAS program (SAS, 2011). The expectations and variances of the model are presented in equation 2.

\[( a_i - \mu ) \sim N(0, V) \text{ where, } V = \text{Var}(a_i) = \begin{pmatrix} \sigma^2_g & \rho \sigma_g \sigma_e \\ \rho \sigma_g \sigma_e & \sigma^2_e \end{pmatrix} \]

\[( e_i - \mu ) \sim N(0, V) \text{ where, } V = \text{Var}(e_i) = \begin{pmatrix} \sigma^2_e \\ \rho \sigma_g \sigma_e & \sigma^2_e \end{pmatrix} \]

The General Linear Model (GLM) procedure (SAS program) was used to estimate least squares means for the 305-day milk yield under many classes of AFC and CI traits. Relationships between MY and each of AFC or CI traits as classes were estimated by the model:

\[ Y = \mu + F_i + P_j + S_k + AFC_j + CI_m + e_{ijklmn} \]  

Where,  
\( Y_{ijklmn} \) = the individual observation of the 305-day milk yield trait (kg),  
\( \mu \) = the overall mean of MY,  
\( F_i \) = the fixed effect of ith farm (i = 1 or 2),  
\( P_j \) = the fixed effect of parity (j = 1 to 9),  
\( S_k \) = the fixed effect of the kth season of calving (k = 1 (cold) or 2 (hot)),  
\( AFC_j \) = the fixed effect of the jth age at the first calving classes (j = 1 to 15),  
\( CI_m \) = the fixed effect of the mth calving interval classes (m = 1 to 27),  
\( e_{ijklmn} \) = error as a random effect.

**RESULTS AND DISCUSSION**

Means and standard deviations

Table 1 shows that, the least square mean (LSM) of MY (3297.5 kg ± 1163.6 kg) was higher than those of 2632, 3103 and 2939 kg reported by El–Awady et al. (2017), Abdelrahim and Genena (2017) and Sanad et al. (2020), respectively, but lower than 7387.70 and 4646 kg estimated by Kamal El-Den et al. (2020) and Abou saque et al. (2021), respectively. The differences among the averages of milk production in different studies may be attributed to the diverted genetic potentiality and/or management practices in different herds, in addition to the subtle variability of environmental conditions.

The LSM of CI (15 ± 3.3 months) was within the range of 12-15 months stated by El–Awady et al. (2017), Hermiz and Hadad (2020), Farrag et al. (2020), Sanad et al. (2020), Habib et al. (2020) and Refaey et al. (2022), but shorter than 15.7 month interval obtained by Farrag et al. (2017).

Regarding AFC, the current LSM (31.6 ± 3.3 mo) was higher than that of 27 mo reported by Hermiz and Hadad (2020) and Farrag et al. (2020), but was close to 30.6 mo interval as obtained by Faid–Allah (2015).

**Heritability estimates**

Table 2 displays the estimates of genetic variance (\( \sigma^2_g \)), permanent environmental variance (\( \sigma^2_pe \)), phenotypic variance (\( \sigma^2_p \)), residual variance (\( \sigma^2_e \)) and heritability estimates (\( h^2 \)) for the studied traits.
Table 2. Variance components, heritability estimates ±SE for the studied traits

<table>
<thead>
<tr>
<th>Traits</th>
<th>σ²a</th>
<th>σ²pe</th>
<th>σ²r</th>
<th>h²(SE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MY</td>
<td>270774.7</td>
<td>1338087.9</td>
<td>0.20 (0.0002)</td>
<td></td>
</tr>
<tr>
<td>CI</td>
<td>1.3</td>
<td>15.85</td>
<td>0.07 (0.0001)</td>
<td></td>
</tr>
<tr>
<td>AFC</td>
<td>4.1</td>
<td>7.9</td>
<td>0.34 (0.0002)</td>
<td></td>
</tr>
</tbody>
</table>

MY = 305-day milk yield; CI = calving interval; AFC = age at first calving; σ²a = additive genetic variance; σ²pe = permanent environmental effect; σ²r = residual variance; h² = phenotype variance; ±SE = standard error.

The h² estimate of MY (0.20 ± 0.002) was similar to that of 0.19 obtained by Arango and Echeverri (2014), lower than the range of 0.24 to 0.33 found by Rashad (2013), El-Awady et al. (2017), Öztürk et al. (2021) and Shalan et al. (2022), and higher than the range of 0.14 - 0.18 stated by Faid Allah (2015), Vasquez et al. (2021) and Pangmiao et al. (2022). The current low h² estimate of MY relative to some of those reported above may indicate a small additive genetic variance and/or high residual variance, which suggests that this trait was highly affected by some environmental factors such as farm, feed, management and climatic changes. Moreover, the size and structure of different data sets and the analytical model utilized may influence the estimates.

The h² estimate of CI was low (0.07 ± 0.001) close to estimates of 0.04 as obtained by Sigurdsson and Jonmundsson (2011), Abdel-Hamid et al. (2017), Zahed et al. (2019), Lopez et al. (2019), Óparinsdóttir et al. (2021) and Refaey et al. (2022), and lower than the range of 0.11 - 0.29 as stated by Hammoud et al. (2014), Ayalew et al. (2017), El-Awady et al. (2017), Öztürk et al. (2021) and Shalan et al. (2022).

The h² estimate of AFC (0.344±0.002) was higher than the range from 0.11 to 0.27 reported by Buaban et al. (2015), Zahed et al. (2020) and Stefani et al. (2021), and lower than a range from 0.36 to 0.47 as obtained by Ayied et al. (2011), Abdel-Hamid et al. (2017) and Ayalew et al. (2017).

Genetic correlations (rs):

The rs estimate between MY and CI (0.05) was close to an estimate of 0.01 (Table 3) as reported by Shalan et al. (2022), and lower than 0.28 and 0.17 (El-Awady et al. 2017 and Sagwa et al. 2019, respectively) and a range from 0.35 to 0.75 as revealed by Eaglen et al. (2013). Hammoud et al. (2014), Abdel-Hamid et al. (2017) and Habib et al. (2020).

Table 3. Genetic (SE) (above diagonal) and phenotypic (below the diagonal) correlations among the studied traits .

<table>
<thead>
<tr>
<th>Traits</th>
<th>MY</th>
<th>CI</th>
<th>AFC</th>
</tr>
</thead>
<tbody>
<tr>
<td>MY</td>
<td>0.05 (0.007)</td>
<td>0.04 (0.004)</td>
<td></td>
</tr>
<tr>
<td>CI</td>
<td>-0.04</td>
<td>0.03 (0.004)</td>
<td></td>
</tr>
<tr>
<td>AFC</td>
<td>0.04</td>
<td>0.01</td>
<td></td>
</tr>
</tbody>
</table>

MY: 305-day milk yield; CI: calving interval; AFC: age at first calving

Also, the rs of AFC with MY estimated 0.04 being lower than 0.20 as recorded by Sagwa et al. (2019), but was close to a range from 0.01 to -0.18 obtained by Faid-Allah (2015), Brito et al. (2020) and Stefani et al. (2021). Concurrent results were confirmed with those of Shalan et al. (2022), who revealed that increasing MY is not associated with deteriorated CI or AFC, and the selection for it seems to have no merit for genetically improving reproductive performance.

The present RG estimate between AFC and CI (0.03) was within a range from -0.06 to 0.08 reported by Do et al. (2013) for the first and second CI with AFC, but lower than 0.11 obtained by Abu El Naser et al. (2019). However, Kelleher et al. (2016) and Ibrahim (2018) revealed negative RG estimates of -0.12 and -0.40, respectively, between CI and AFC.

Phenotypic correlations (rp):

As presented in Table 3, the rp between MY and CI (-0.04) was similar to the values of -0.04 and -0.01 reported by Rashad et al. (2019) and Shalan et al. (2022), respectively, but lower than a range from 0.06 to 0.29 as obtained by Hammoud et al. (2014), El-Awady et al. (2017), Sagwa et al. (2019) and Habib et al. (2020).

The rp estimate between MY and AFC was 0.04 compared to 0.16 and -0.21 obtained by Salem and Hammoud (2016a) and Sagwa et al. (2019), respectively, and within a range of -0.05 to 0.08 as estimated by Brito et al. (2020) and Stefani et al. (2021).

Also, CI showed a low rp estimate with AFC (0.01) which was in accordance with the results of 0.09 and 0.04 as reported by Abu El Naser et al. (2019) and Farrag et al. (2020), and close to -0.02 as revealed by Kelleher et al. (2016).

Genetic (GT) and phenotypic (PT) trends for the studied traits

Figures 1-6 present GT and PT for each studied trait over the years of study (1988-2020). The GT was estimated by regressing the yearly average of EBV for each trait over the same period, while the PT was estimated by regressing the yearly phenotypic averages of each trait over the same years.

![Genetic trend of milk yield](image1)

**Fig.1. Genetic changes in 305-day milk yield (MY) in years (1990-2020)**

![Phenotypic trend of milk yield](image2)

**Fig. 2. Phenotypic changes in 305-day milk yield in years (1990-2020).**
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Genetic trend of milk yield

Estimates of GT of MY increased positively throughout the periods 1992-1994, 1996-2000 and showed a gradual increase up to 2012, then showed irregular and fluctuated decreased up to 2020. This trend indicated that the applied selection criterion wasn’t satisfactory for improving the trait overtime.

The current range of EBVs for MY (-57 to 105 kg) was shorter than the ranges -1698.0 to 1337.8 kg/year in Frisian and -2598 to 1709 kg/year in Holstein cows as reported by Salem and Hammoud (2016b) and Abdel-Hamid et al. (2017), respectively.

The present GT for MY in the years of study, being -1.39 kg/year was close to - 2.46 kg/year (Şahin et al., 2012; Vasquez et al., 2021) and is in agreement with the results of Effa et al. (2011) and Shalan et al. (2022), who revealed that a negative GT of milk production traits occurred under the tropical conditions. However, Hossein-Zadeh (2011), Chegini et al. (2013), Haiduck et al. (2019) and Abou Saq and Ben Naser (2021) reported significant (p<0.0001) positive estimates of GT, ranging from +4.15 to +21 kg/year for MY which probably as a result of selecting bulls with high genetic value.

According to Araújo et al. (2003), an explanation for the variation in GT estimates is the disorganized flow of genetic stimuli, that is, each breeder adopts his own selection objectives independent from the others. Similarly, the selection objectives in the current study have varied through the years due to the utilization of frozen semen from different sources and years. However, Pangmao et al. (2022) claimed that some factors might impact the expected genetic gain to accelerate or slow down improvement in milk production such as financial support, inconsistent management and feeding practices. Moreover, the restrictions of selection, semen used with an ineffective breeding plan and involuntary culling due to health problems in high producing cows may impact the genetic progress. Thus, investigating the previous issues under research farm management conditions and developing a long-term breeding strategy can enhance the performance status of these herds.

Phenotypic trend of milk yield

The PT of MY was -67.2 kg/year ($R^2 = 0.11$) throughout the period of study. The highest MY was obtained in the first two years of the study, but descended rapidly thereafter, showing irregular fluctuations, and increased slightly from 2012 until the end of the experiment. Similarly, Abou-Bakr (2009) reported a significant (P<0.02) negative PT for MY (-91.6 ± 35.16 kg/ year) in Holstein cattle.

The relatively high MY in the first 2 years was associated with general conditions more convenient to good productivity in the herd, including breeding plans and good environments. However, in general, the diminished MY could be attributed to the involuntary culling of high-milking cows, a lack of long-term improvement plans, bad management systems and nutrition, and an unfavourable climate. The negative PT was in accordance with the results of Katok and Yanar (2012), who revealed that the decrease in MY was due to adverse environmental factors, the presence of diseases, insufficient feeding, and harsh climatic situations.
On the other hand, Abou Saq and Ben Naser (2021) obtained a large positive (p<0.0001) PT of +65.71 kg/year presenting phenotypic values between 915 and 13845.6 kg/year in Friesian cattle. Also, Dash et al. (2016), Konkruua et al. (2017) and Vasquez et al. (2021) obtained positive trends of +18.71, 21.3 and 294.3 kg/year, respectively, for the milk of Holstein cows and suggested that yield improvement is a result of the applied selection policy emphasizing exclusively the production trait and improvements in management. According to M’hamdi et al. (2012), changes in herd size, age of cows, and management practices introduced from one year to another could be responsible for variation in milk production.

Genetic trend of calving interval

The GT for CI in the current study (Fig.3) ranged between -0.15 and +0.25 month/year, but showed considerable positive and negative irregular fluctuations throughout the experimental period. These trend revealed an increase in CI by advancing time, ascending from 1994-1996; 2001-2005 and 2011-2017 with a slope towards the end of the studied years which indicated a deteriorated genetic change in CI overall the years of the current study.

The current range of BVs for CI was shorter than the ranges from -8.14 to 11.91, -5.72 to 10.60 and -5.92 to 10.6 days obtained by Ayied et al. (2011), El-Awady et al. (2017) and Abdel-Hamid et al. (2017), respectively. However, the slight positive improvement in GT was close to the values of 0.03, 0.06, 1.34 and 0.82 d/yr, as reported by Abdelharith (2008), Ibrahim et al. (2009), Ramatsoma et al. (2014) and Zahed et al. (2019), respectively.

Conversely, Atil and Khattab (2005), Rahbar et al. (2016) and Ghiasi and Honarvar (2016) estimated a favourable negative GT between -0.01 and -0.95 d/yr for CI. Such unfavorable positive GT could be attributed to inaccurate culling procedures, increasing selection pressure or a possible increase in the percentage of inbreeding. Haile-Mariam et al. (2014) stated that a 1% increase in inbreeding in the herd was associated with a prolongation of +0.22 ± 0.17 days in CI, suggesting that applying inbreeding control programs to Friesian cattle was essential for keeping their genetic resources.

Since the h² estimate of this trait is low, it could be more preferable to issue strict management instructions to perform the right technical operations in the herd instead of applying insufficient selection programs to reduce CI (Öztürk et al., 2021). However, genomic selection could help in practicing improvement in low- h² traits like fertility and reproduction (Berry et al., 2014).

Phenotypic trend of calving interval

As presented in Fig. 4, the PT of CI ranged from 12 to 18 months during the period of this study, showed slight positive fluctuations due to selection pressure for reproductive efficiency and variations in PT among years probably revealing management alterations and feed accessibility (M’hamdi et al., 2012) and extensive use of supported technologies during the latest years.

The current positive PT for CI (0.03 mo/yr) was confirmed with the value of 0.82 d/yr reported by Zahed et al. (2019), while, Abdelharith (2008), Ibrahim et al. (2009) and Rahbar et al. (2016) obtained negative PTs of -0.48, -0.09 and -2.54 d/yr, respectively. Moreover, El-Awady et al. (2017) reported PT for CI between -22.47 and 43.44 d/yr.

Genetic trend of age at first calving

As presented in Fig. 5, the GT of AFC ranged from -0.35 to +0.30 mo/yr and was shorter than the ranges of -2.10 to 2.3 and -5.75 to 5.09 mo/yr reported by Ayied et al. (2011) and Abdel-Hamid et al. (2017), respectively. However, the regression coefficient of AFC average BVs per year on years of study was close to zero (0.0024 mo/yr), indicating a lack of trend, and close to the values of 0.020 and -0.002 mo/yr, as stated by Abdel-Hamid et al. (2017) and Zahed et al. (2020), respectively.

The PT of AFC (Fig. 6) ranged between 24 and 40 months, showing gradually a fluctuated decrease with a slight descending slope throughout the years of study. A desirable decrease of -0.17 mo/yr in AFC was obtained. This might be due to favourable farm environmental conditions and to making the right decisions to breed heifers as soon as being ready for first mating. The descending PT reveals early maturity of calves by time due to enhanced rearing and feeding conditions, offering enough feed requirements with high quality to the growing heifers, preceded by good suckling systems that accelerate the attainment of puberty and consequently reduce AFC (Shortle, 2014).

The moderately high h² estimate of AFC suggested that it could be advisable to practice genetic improvement by selection. However, being associated with reproductive efficiency traits, reducing AFC might inversely affect MY because of the negative correlation between MY and fertility (Kgari et al. 2023). Yet, the regression of the yearly mean of AFC on years of study was generally small (-0.17 mo/yr), but higher than the regression of 0.02 mo/yr, as obtained by Zahed et al. (2020).

The impact of extended AFC on the herd milk production

Fig. 7 showed that the highest MY (3808 kg) was obtained from cows calving for the first time at the age of 32 months, while those calving at 24 mo produced the lowest MY (3244kg). Moreover, the early first calving below 24 mo of age may cause the heifers to suffer from a frequent incidence of dystocia. However, the rearing costs for each extra month heifer calving above 24 mo of age were about 2484 LE. In addition, the costs of producing one kg of milk increased by increasing AFC (Table 4). Low production costs per kg of milk were obtained from heifers having an AFC of < 25 mo/yr, but those costs increased sharply from heifers calving for the first time at older ages.

On the contrary, Almasri et al. (2020), Ilhan et al. (2022) and Vargas-Leiton et al. (2023) claimed that the optimum AFC to achieve the maximum lifetime milk yield, productive life, and lactation number was below 26 months relative to those calving above this age. According to Atashi et al. (2021), decreasing AFC below 27 months had no effect on subsequent CI, but maximizing or diminishing it induced a multiplied risk of dystocia, which showed TG values of 0.30 with AFC (Stefani et al., 2021). Also, calves birth weights increased curvilinearly with increasing AFC (Kamal et al., 2014).
combined with boosted herd income. Culling non-pregnant cows was balanced by the costs of producing each kg of milk and a consequent decrease in the dairy farm’s net income from the sale of milk (Fig. 8, Table 5). In contrary, Samaraweera et al. (2022) revealed that prolonging the CI of lactating cows permits lactations to extend, but the low daily milk yield diminishes the annual income for MY, and therefore, selection for short CIs benefits dairy farms. Moreover, Zahed et al. (2019) reported that reducing CI is more profitable for the farms, but expanding it even for one extra day will cause financial loss, while reducing it between 7 and 23 days will increase the annual gross margin per cow (Bekara et al., 2017).

The impact of length of CI on milk yield

The average daily milk yield decreased with the prolongation of CI, causing an obvious increase in the costs of milk per kg. The total cost of milk per kg was lower when shortening CI, which was associated with a smaller number of calves per lifetime without a voluntary waiting period for insemination for 50 days or 6 months CI was generally considered optimal for dairy cows. However, Sha et al. (2022) stated that extended CI through expanding the voluntary waiting period for insemination, which extends the CI, was more profitable than shortening it. Even for one extra day will cause financial loss, while reducing it between 7 and 23 days will increase the annual gross margin per cow (Bekara et al., 2017).

Also, Dono et al. (2013) reported that the highest profitability was achieved when reducing CI, which presented the best performance model and economic feeding efficiency. The longest CI, however, was associated with 8.58% calves loss (P<0.05) and the economic advantage of reducing CI by culling non-pregnant cows was balanced by the costs combined with boosted herd income. Kvapilík et al. (2015) and Néměcková et al. (2015) reported that a long CI above the optimal length of 400 d decreased the average daily milk yield and led to a smaller number of calves per lifetime without a positive economic impact on the herd. Also, Krpálková et al. (2017) reported that herds with a low CI below 389 d caused low cow depreciation costs and high total costs per kg of milk. However, Shalloo et al. (2014) claimed that the expansion of CI was more profitable than shortening it.

On the other hand, most investigators revealed that 12-months CI was generally considered optimal for dairy cows from an economic point of view (Steeneveld and Hogeveen, 2012; Kok et al., 2019; Burgers et al., 2022). Although, recently, some dairy farmers have been deliberately extending the voluntary waiting period for insemination, which extends the CI (Lehmann et al., 2017; Burgers et al., 2021). Burgers et al. (2022) stated that extended CI through expanding the voluntary waiting period for insemination for 50 days or 6 weeks was more strongly associated with a greater maximum yearly yield of cows, which means higher yearly revenues, costs, and net partial cash flow.
CONCLUSION

Estimating the genetic and phenotypic trends for MY, CI and AFC demonstrated very short ranges for the breeding values, which reflected low genetic diversity among cows for the studied traits and indicated deterioration in the overall rate of genetic progress. There is an urgent need for improving breeding strategies and applying selection based on reliable measures of breeding value for the studied traits. Also, ensuring the absence of inbreeding and accurate future performance recording can offer a great opportunity to maximize productivity. Moreover, the declining phenotypic values of the studied traits over time require strict management decisions to be taken at an early age to ensure optimal performance in order to achieve more profit per year.

Strong intervention of selection and management powers can alter defects and shorten generation intervals using modern reproductive technologies in breeding programs in a connection between the fields of animal research authorities. Such coordination achieves high potential for the sustainably continuous genetic development of this breed under the local conditions for future generations. At that time, the dairy industry will then benefit from the new developments to enlarge the herds' profits. However, the ambiguity of the overlap between MY and CI and/or AFC suggests further cost-benefit analysis to increase the economic efficiency of dairy farms.

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