

Estimates of Genetic Parameters for Economic Traits of Holstein Friesian Dairy Cattle in Tropics: A multi-trait animal model

Destaw Worku

Department of Animal Science and Technology, Salale University P.O.Box 245, Selale, Ethiopia

Wondossen Ayalew (✉ wondessenayalew9@gmail.com)

Department of Animal Production and Technology, Wolkite University P.O.Box 07, Wolkite, Ethiopia:

<https://orcid.org/0000-0002-6673-3691>

Research Article

Keywords: Fertility traits, Genetic correlation, Genetic trend, Heritability, Production traits, Tropics

Posted Date: March 30th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-360395/v1>

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Abstract

Background: In any genetic improvement program, multi-trait estimates of genetic parameters and breeding values of economically important traits are essential to facilitate total merit index selection objectives.

Method: Data comprising 4,263 lactation records of 1,223 cows calved in the years between 1992 and 2017 were used to estimate genetic parameters and breeding values of lactation milk yield (LMY) and lactation length (LL) and fertility (age at first calving, AFC; calving interval, CI; and days open DO) traits. Preliminary analysis of fixed effects used in the mixed model analysis was tested for their significance using lm package of R software. C(o)variance components and resulting parameters were estimated by fitting single and multi-trait repeatability animal models using BLUPF90 software packages.

Results: The heritability estimates of LMY and LL were 0.21 ± 0.04 and 0.13 ± 0.02 , respectively. Heritabilities for AFC, CI, and DO were 0.53, 0.12, and 0.14 ± 0.04 , respectively. Repeatability estimates of production and fertility traits were low to moderate. The genetic correlation between LMY and LL was high (0.53) whilst, among fertility traits, the estimates were ranged from 0.09 ± 0.03 (between AFC and CI) to 0.99 ± 0.01 (between CI and DO). Genetic correlations of productive traits with fertility traits were ranged from -0.01 to 0.99. The phenotypic correlations between production and fertility traits ranged from 0.06 ± 0.02 for LL and AFC to 0.43 ± 0.02 for LL and DO. The genetic trends for LMY and LL were positive and genetically improved by $15.80 \text{ kg year}^{-1}$ and $0.92 \text{ days year}^{-1}$, respectively. Regarding fertility traits, favorable trends of -0.56 and $-0.65 \text{ days year}^{-1}$ were observed for CI and DO, respectively. However, unfavorable trends of $0.04 \text{ month year}^{-1}$ were obtained for AFC.

Conclusion: With this small herd size, the study highlighted that a high response to selection for LMY and AFC would be expected in this population. Furthermore, aggregate selection of both production and fertility traits should take into account their antagonistic genetic correlations in future improvement programs.

Introduction

In the tropics, and most developing countries, the productive and reproductive potentials of indigenous cattle are low as compared to temperate breeds. Hence several efforts are made to increase dairy production through breeding strategies and policies that encouraged the introduction and breeding of temperate breeds [1, 2]. A number of temperate breeds have long been chosen and introduced in to tropical regions and Holstein Friesian dairy cattle are among the most widely disseminated breeds for both cross breeding and as pure breed for milk production [3]. These imported exotic breeds were either maintained at research stations or institutional farms that were designed to provide comparable management to their native environment. However, the relatively high stress agro-ecosystems of the tropics often too rapidly allow animals for natural selection in terms of adaptive and/or productive traits.

It is widely accepted that, the efficiency of dairy production is highly dependent on productive and adaptive performances of the animals. Performances records of lactation milk yield (LMY), lactation length (LL) and reproductive performances like age at first calving (AFC), calving interval (CI) and days open (DO) are key breeding goal traits of traditional breeders in tropics. As a result, accurate estimation of genetic and phenotypic parameters and trends for those traits specific to the actual breed and production environment will assist better planning and implementation of efficient breeding programs in tropics [1, 4, 5].

In last decades, successful selection for milk production traits has led to a decline in female fertility in dairy cattle arising from an unfavorable correlated selection response [6, 7]. To date, multivariate analysis are generally used in animal breeding studies for aggregate selection of both productive and fertility traits, so that the effect of selection for one would be known to affect the other in anticipated direction. In addition, using such kind of analysis has a great deal of importance to provide reliable and unbiased estimates of genetic parameters as a result of the model's ability to use extra information from correlated traits [8, 9]. Joint modeling of multiple traits also helps to increase prediction accuracy, statistical power, and reduce selection bias, specifically for low-heritability traits that are genetically correlated with a high-heritability trait [10–13]. However, in tropics, performance evaluation of exotic and cross breed dairy cattle has been mostly analyzed by using univariate animal models. Such evaluation does not account the covariances among different traits and that results inaccurate estimates of breeding values, and which ultimately leads to selection bias [14–16]. In general, information on the estimates of genetic parameters of productive and fertility traits of Holstein Friesian dairy cattle particularly those with multi-trait models are scarce in tropical environments. The present study was, therefore, planned to estimate the genetic parameters and breeding values of the animals for comparative ranking for productive and fertility traits in the tropical Holstein Friesian herd. The information so generated will be useful in optimizing the future breeding programmes for genetic improvement of the Holstein Friesian population in tropical climatic conditions.

Materials And Methods

Farm establishment and management

This study is based on the data collected from Alage Agricultural Technical and Vocational Training College dairy farm, situated at 217 km southwest of the capital in the vicinity of the Abijata and Shala lakes of the Ethiopian Rift Valley. The farm was established with 300 females and 4 males of pure Holstein Friesian recruited from locally available private dairy farms in the central highlands of Ethiopia (i.e. Stella, Holetta, and dairy farms around Addis Ababa) aiming to boost milk production in the Ethiopian rift valley. Animals are stall-fed and supplemented with concentrate feeds and mineral licks during late pregnancy and lactation. Lactating cows received concentrates before each milking at the rate of 1 kg of concentrate per 2.5 kg of milk produced. Cows are hand-milked twice a day, early in the morning (8:30 am) and late in the afternoon (4:30 pm). Calves were separated from their dams after birth then weighed, tagged and allowed to receive colostrum for the first 5 days of their age. Bucket feeding of

whole milk continued until weaning age with ad libitum roughage. Animals on the farm are routinely vaccinated against anthrax, pasteurellosis, blackleg, foot and mouth disease, lumpy skin disease, and contagious bovine pleura pneumonia. The mating system was artificial insemination using both imported and locally recruited Holstein Friesian frozen semen bringing from National Artificial Insemination Center (NAIC). Most of the cows were served at first observed heat after calving, and heifers were inseminated after maintaining 280kg of body weight.

Data and edits

The data for milk production and reproduction traits of Ethiopian Holstein were taken from Alage Agricultural Technical and Vocational Training College dairy farm. The data were compiled from records kept on each individual animal record. To avoid biases in the final estimates, data were cleaned for consistency of pedigree information, and records with inconsistencies in pedigree information and dates were discarded. Besides, lactation milk yield less than 1000 kg and lactation lengths less than 220 days and greater than 415 days were excluded [17]. The data were further edited as AFC between 18 and 53 month, calving interval between 310 and 796 days and days open between 25 and 432 days were included in the final analysis [18]. After imposing the editing criteria, data consisted of 4,263 records of 1,223 cows calved in the years between 1992 and 2017, and daughters of 165 sires were used for final analysis (Table 1). The pedigree, built using sire-dam structure and tracing back three generations with records of cows with known birth and calving dates were included. Furthermore, seasons in Ethiopian rift valley are generally classified into three groups based on rainfall patterns of the area. These included June to September as long rainy season, March to May as short rainy season and October to February as dry season [19]. Further, lactations were classified into three parities as 1, 2, and 3+. Parity three and above were all pooled together as parity three due to very few number of observations in later lactations.

Table 1
Characteristics of the data set used for genetic parameters estimation

Trait	N	Mean	SD	Minimum	Maximum
LMY	3784	3515.1	1232.4	1003	6908
LL	3164	309.64	39.98	220	415
AFC	1223	37.76	7.83	18	53
CI	2935	423.18	86.37	310	796
DO	2972	130.19	73.39	25	432

N, number of observations; SD, standard deviation; 305-d MY, 305 days milk yield; LMY, lactation milk yield; LL, lactation length; AFC, age at first calving; CI, calving interval; DO, days open.

Statistical analysis

(co)variance components were estimated using the software that comprises a family of program in Fortran 90/95 for mixed model computations in animal breeding (BLUPF90) using average information restricted maximum likelihood algorithm (AIREMLF90) [20]. Single and multi-trait repeatability animal models were implemented for the estimation of variance components and resulting genetic parameters. The estimates from single trait repeatability model were used for both valuations of production and fertility traits, as well as used as a starting value for subsequent multi-trait models. The fixed effects fitted in the mixed model analysis were performed by lm package of R program V.3.6.1 [21]. In general, the effects included in these models were season of calving, year of calving/birth and parity as fixed effects, whilst permanent environmental effect, animal genetic effect and random residuals as random effects. It was assumed that the covariances between additive, permanent environmental and residual effects were zero and that levels of each were independently distributed with variance σ_a^2 for animals, σ_{pe}^2 for permanent environmental effects, and σ_e^2 for residuals. After running several preliminary analyses, four different models were selected and fitted to the data in the mixed model analysis. Model 1 was used for the univariate analysis of AFC whilst in models 2, permanent environmental effect due to the repeated records per animals taken into account as additional random effect for univariate analysis of LL, LMY, CI and DO. The general descriptions of the models in matrix form are given below:

$$Y = Xb + Zu + \epsilon \quad (1)$$

$$Y = Xb + Zu + Zp + \epsilon \quad (2)$$

Where Y is vector of observation for the traits includes in this study (AFC, CI, DO, LMY and LL), X is incidence matrix of the fixed effects, b is vector of fixed effect; Z_c is incidence matrix of the permanent environmental (random) effect, P is vector of the permanent environmental (random) effect, Z is incidence matrix of the animal (random) effect, a is vector of the animal (random) effect and ϵ is vector of random residual effect.

Multiple trait models

To estimate covariances and correlations, a full multiple trait (5x5) animal model was initially tried but it was not computationally feasible. However, by reducing the number of traits one at a time, both bi-variate and tri-variate models resulted logical estimates with acceptable memory requirements and convergence time. Then, several runs of bi- and tri-variate models were used to estimate covariances and correlations between the 5 traits. The following multiple-trait animal models were used for the five traits.

Mode 2 for bi-varate analysis of five traits

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} x_1 & 0 \\ 0 & x_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} z_{c1} & 0 \\ 0 & z_{c2} \end{bmatrix} \begin{bmatrix} p_1 \\ p_2 \end{bmatrix} + \begin{bmatrix} z_1 & 0 \\ 0 & z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \end{bmatrix} \quad (3)$$

Model 3 were used for tri-variate analysis of five traits

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix} +$$

$$\begin{bmatrix} z_{c1} & 0 & 0 \\ 0 & z_{c2} & 0 \\ 0 & 0 & z_{c3} \end{bmatrix} \begin{bmatrix} p_1 \\ p_2 \\ p_3 \end{bmatrix} + \begin{bmatrix} z_1 & 0 & 0 \\ 0 & z_2 & 0 \\ 0 & 0 & z_3 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \epsilon_3 \end{bmatrix} \quad (4)$$

Where Y is vector of observation for the traits includes in this study (AFC, CI, DO, LMY and LL), X is incidence matrix of the fixed effects, b is vector of fixed effect; Zc is incidence matrix of the permanent environmental (random) effect, P is vector of the permanent environmental (random) effect, Z is incidence matrix of the animal (random) effect, a is vector of the animal (random) effect and ε is vector of random residual effect.

To pick the heritability and repeatability estimates of the studied traits in the bi-variate and tri-variate analysis, the objective of the farm and different literature were used as basic criteria for selecting major traits. It is known that in most tropical countries the primary objectives of importations of improved dairy breeds was to boost milk production. Accordingly, Alage dairy farm has been set milk production performance of cows as major breeding goal trait and implemented long term milk production performance based selection practices. Besides, multiple-trait models including milk production trait(s) have better stability and predictive ability than single-trait models for genetic evaluation of fertility traits [6, 22]. As a result, in the bi-variate analysis, the heritability and repeatability estimates of LL and fertility traits were taken estimates from their combined analysis with LMY whilst, for tri-variate analysis the combined runs of other traits with LMY and AFC were used. Here we used AFC as a second breeding goal trait based on its genetic variability and economic value as suggested by Emanu [23].

Estimation of breeding value and trends

Breeding values of animals for milk production and fertility traits were computed from the Best Linear Unbiased Predictions (BLUP) solutions obtained from BLUPF90 [20]. Least square means for annual breeding values was calculated by the General Linear Model procedure of the R statistical package and deviations from the mean of the base year were considered as estimates of annual breeding value. Similarly, genetic trends of production and fertility traits were calculated through linear regression of the EBV as a function of birth year of the animals.

Results

Genetic parameter estimates

Heritabilities and repeatabilities of milk production and fertility traits for univariate, bi-variate and tri-variate animal models are presented in Table 2. From univariate, bi-variate and tri-variate models, lactation milk yield showed a moderate heritability (0.21 ± 0.04) and repeatability (0.38 ± 0.02) estimates. These moderate genetic parameter estimates of LMY indicate presence of modest genetic variability of tropical Holstein Friesian. Again, both the heritability and repeatability estimates of LL revealed lower estimates in univariate, bi and tri-variate models.

Table 2

Estimates of permanent environmental (σ^2_{pe}), additive genetic (σ^2_a), and residual variances (σ^2_e), heritability (h^2) and repeatability (r) of production and reproduction traits using univariate, bi-variate and tri-variate animal models

Models	Traits	σ^2_{pe}	σ^2_a	σ^2_e	$h^2 \pm SE$	$r \pm SE$
Univariate model	LMY	230630	275290	816440	0.21 ± 0.04	0.38 ± 0.02
	LL	59.4	311.47	2026.2	0.13 ± 0.02	0.15 ± 0.02
	AFC	-	28.649	23.302	0.55 ± 0.059	-
	CI	1286.9	1739.9	10990	0.12 ± 0.04	0.22 ± 0.23
	DO	613.91	1626.3	9064.9	0.14 ± 0.04	0.20 ± 0.02
Bivariate model	LMY	229820	278120	816280	0.21 ± 0.04	0.38 ± 0.02
	LL	125.84	302.61	2176.8	0.12 ± 0.02	0.16 ± 0.02
	AFC	-	27.998	22.463	0.55 ± 0.05	-
	CI	1030.7	1818.8	11205.	0.14 ± 0.04	0.20 ± 0.02
	DO	466.09	1632.4	9233.2	0.14 ± 0.04	0.19 ± 0.02
Tri-variate model	LMY	239360	264690	816460	0.20 ± 0.04	0.38 ± 0.02
	LL	123.67	303.00	2179.2	0.12 ± 0.02	0.16 ± 0.02
	AFC	-	27.643	23.63	0.53 ± 0.06	-
	CI	1018	1912.2	11191	0.14 ± 0.03	0.20 ± 0.02
	DO	320.81	1635.6	9548.5	0.14 ± 0.02	0.19 ± 0.02
SE, standard error; LMY, lactation milk yield; LL, lactation length; AFC, age at first calving; CI, calving interval; DO, days open						

Heritability estimates for AFC were 0.55, 0.54, and 0.53 from univariate, bivariate and trivariate models, respectively (Table 2). These relatively high heritability estimates of AFC confirmed the presence of

genetic variability in the small herd. The heritabilities of CI from univariate, bivariate and trivariate models were 0.12 ± 0.04 , 0.14 ± 0.04 and 0.14 ± 0.03 , respectively. The multi-trait (bivariate and trivariate) models contributed to the slight improvement in the heritability estimates of CI whilst, the heritability values of DO were similar in all three animal models (0.14). Over all repeatability values for both CI interval and DO from three animal models were 0.20 ± 0.02 .

Genetic and phenotypic correlations

Table 3 presented the genetic and phenotypic correlations between milk production and fertility traits of Ethiopian Holsteins. Genetic correlations between LMY and LL were moderate (0.53 ± 0.02). While, the genetic correlations between fertility traits were ranges from low to high correlations with estimates of -0.15 to 0.99. Furthermore, the genetic correlations between milk production and fertility traits were directionally favorable, with estimates ranging from -0.01 to -0.37. Concerning the phenotypic correlation between LL and LMY was low whilst, lowest to highest phenotypic correlations between fertility traits were observed, with values ranging from 0.05 ± 0.03 to 0.98 ± 0.01 . Also, the phenotypic association between milk production and fertility traits were ranged from -0.07 ± 0.02 to 0.43 ± 0.02 (Table 3). Estimated SE values were high in some traits, perhaps owing to less data available for these traits and the results needs to be interpreted with caution.

Table 3
Genetic (above diagonal) and phenotypic correlations (below diagonal) with standard errors

Traits	LMY	LL	AFC	CI	DO
LMY	-	0.53 ± 0.18	-0.37 ± 0.08	0.26 ± 0.17	0.26 ± 0.17
LL	0.3 ± 0.02	-	-0.01 ± 0.09	0.87 ± 0.12	0.85 ± 0.11
AFC	-0.19 ± 0.03	0.07 ± 0.03	-	0.09 ± 0.03	-0.15 ± 0.13
CI	0.06 ± 0.02	0.4 ± 0.02	0.09 ± 0.03	-	0.99 ± 0.01
DO	0.07 ± 0.02	0.43 ± 0.02	0.05 ± 0.03	0.98 ± 0.01	-
LMY, lactation milk yield; LL, lactation length; AFC, age at first calving; CI, calving interval; DO, days open.					

Genetic trend

The genetic trends for LMY and LL over birth years increased genetically by $15.80 \text{ kg year}^{-1}$ and $0.92 \text{ days year}^{-1}$, respectively (Figs. 1 and 2). Over the study periods, a small and positive genetic trend of $0.04 \text{ month year}^{-1}$ for AFC (Fig. 3) and decreasing trends by -0.56 and $-0.65 \text{ days year}^{-1}$ were observed for CI and DO, respectively (Fig. 4).

Discussion

Estimation of variance components and associated breeding values of economically important traits in dairy cows are an important strategic step for implementing efficient breeding programs. The present study investigated genetic variability of Holstein Friesian dairy cattle using single and multi-trait models combining information of milk production and fertility traits. Heritability estimates for LMY from single and multi-traits models were moderate which corresponds with most of the literature estimates for the same breed in different production environments [5, 16, 24, 25]. The moderate heritability obtained for LMY elucidates availability of reasonable genetic variability for genetic selection to improve milk production efficiency in this population. However, it was lower than values of 0.43 ± 0.24 obtained in a Thai multi-breed dairy population [26] and 0.30 for Karan Fries dairy cattle population [27]. Although the heritability of LL was low, there was exploitable genetic variance in this trait as compared with the estimated values for Ethiopian Holstein and multi-breed dairy cattle population [16, 28]. Differences between the estimates of heritability obtained in this study and estimates from other countries are most likely caused by breed, management and climate differences affecting genetic and environmental variances. Genetic parameters are specific to a population, i.e., estimates from one population in a breed may not be appropriate when applied to other herd of the same breed or a different breeds [29]. Furthermore, different estimates of the same character on the same breed show wide range of variation, some of which may reflect real differences between populations and/or the conditions under which they are studied and difference in estimation methods [30] and may change over time due to selection and management decisions [31, 32].

The estimated repeatability for LL and LMY were small to moderate estimates, respectively (Table 2). The results presented generally within the range of previous estimates [16, 27, 33]. The moderate repeatability estimates for LMY imply that information from the first parity could be used for early prediction of EBV and cow selection. This would also improve overall performance of the herd since only good producers would be retained. Low repeatability estimates of LL, however, suggested that it is more influenced by variation in management and feeding in the given environment of a particular lactation rather than of factors associated genetic makeup of the cow [33].

Accurate stages of AFC have a significant role for low replacement costs, longer fertility lifespans, and eventually boost life time dairy production efficiency [34]. The estimated heritability for the AFC was generally high from three different models (ranges 0.53 to 0.55). These relatively high heritability estimates of AFC confirmed the presence of genetic variability in the small herd thereby proper feeding and breeding management on the farm. These results correspond with the results presented by many other authors [25, 35] who reported that AFC has a relatively high heritability value than other fertility traits. Thus, higher efficiency of genetic improvement can be achieved by genetic selection. However, the estimate from the current study was higher than that of 0.031 by BrzÁková et al. [36] for Czech Holstein, 0.28 by Montaldo et al. [37] for Mexican Holstein and 0.38 for Kenyan Holstein cattle [33]. The same trait is measured in a slightly different way in some other group of animals; the estimate of heritability can be expected to be different [38]. Accordingly, Pirlo et al. [39] have pointed out that estimates of heritability of

AFC are in a wide range (0.05–0.75) and that inconsistencies in estimates may be caused by confounding of sire and management effects.

Heritability and repeatability estimates of CI and DO found to be low however, the heritability of CI revealed slight improvement from univariate to multi-traits models (0.12 to 0.14, Table 2). The heritability estimates for CI mostly in the range of 0.034 to 0.17 for Friesian cattle in different production environments [6, 16, 33, 36, 40], although some have reported estimates as large as 0.35 for Karan-Fries [27]. The heritability estimate obtained in this study for DO was greater than has previously been reported for Holstein Friesians in both temperate and tropical environment [16, 24, 34, 36]. VanRaden et al. [41], in a review of estimates used for genetic evaluations of fertility traits worldwide, concluded that fertility traits in dairy cattle populations have heritability of 0.04 or less. The relatively low heritability estimates for CI and DO could be explained by large environmental variance and herd management policies. However, in this study, multi-trait analysis with milk production trait indicates slight improvement in the estimates of heritability of CI. Using such kind of analysis has a great deal of importance to provide reliable and unbiased estimates of genetic parameters as a result of the model's ability to use extra information from correlated traits [8, 9]. Thus, evaluation of fertility with milk production traits helps to increase prediction accuracy, statistical power, and reduce selection bias made by single trait analysis [10–13]. The repeatability estimates of single versus multi-trait analysis of CI and DO were small. This is as expected because genetic and permanent environmental variances of fertility traits themselves are not expected to be different, regardless of adding milk yield in a joint analysis [6]. This implies selection of animals with early lactation record would tend to be wrong decisions.

Estimates of genetic and phenotypic correlations are considered as decisive tools for multiple traits genetic improvement programmes as different traits may be influenced by the same genes, implying that expression of one trait depends on the other. The genetic correlation between LMY and LL reported in this study implies that genes that positively influence LMY would result in longer LL; thus cows that milked for longer periods will be produce more LMY. The results are consistent with those reported in same breed in Ethiopian Holstein [16, 25] and Ethiopian multi-breed dairy cattle population [28].

The magnitude of genetic and phenotypic correlations between fertility traits ranged from low to high, where the highest positive correlations were observed between CI and DO. This high genetic correlation is explained by the fact that they represent almost the same overlapping traits which result in the genetic correlation close to 1 and this is an evidence for common genetic and physiological mechanism controlling these traits [29]. Similar findings have been reported for the Holstein-Friesian [16, 36]. Corroborating the present study, this high association revealed that the improvement of CI has a positive impact on DO in the anticipated direction. Again, CI and DO is strongly influenced by breeder's decisions based on the milk-production level and management protocol [36]. In high-yielding cows, early pregnancy can negatively influence milk yield, so farmers in tropics postpone first service after calving to sustain their temporary livelihoods. To a certain extent these systematic effects of management contribute to high phenotypic correlations besides their genetic connections. Given this high genetic correlation between the two traits, selection based on CI alone could be practiced in production systems constrained

by poor recording, as is the case in developing countries (16). Furthermore, milk production traits showed positive genetic and phenotypic correlations with CI and DO. This antagonistic relationship between production and fertility was, therefore, due to both genetic and environmental factors. Several authors have supported the statement that animals with higher production have the poorest reproduction [16, 24, 33]. Interestingly, in this study, the negative correlation between AFC and LMY suggests that selection for milk production contributed to early calving of heifers. A high heritability estimate (0.54) and favorable genetic and phenotypic correlations of AFC with milk production traits indicates that there is potential for improvement of this trait in tropical environments through selection. A similar correlation was reported for the same breed in the tropics (16). On the other hand, a high and positive correlation was reported for Kenyan Holsteins [33].

In fact, the efficiency of selection procedures could be visualized by the determination of genetic trend and it gives us an indication of the amount of the genetic changes of the traits since the start of the genetic improvement program. The overall genetic trend of production traits with various ups and downs during different years depicted a positive trend. Similar to this, a positive genetic trend was reported for Kenyan Holsteins [33] and Ethiopian multi-breed dairy cattle population [28]. In Ethiopia, the breeding sires imported from different sources aiming to boost milk production (16). As a result, across the study years, the selection program implemented in this population was able to identify sires with the best combination of genes for milk production (15.80 kg year⁻¹ milk gains). However, the overall genetic trend for AFC was unfavorable in the studied herd. This might be due to poor breeding management and long-term phenotypic performance based culling practice of heifers. Conversely, higher negative genetic trends of -0.34 month year⁻¹ and -0.21 month year⁻¹ were reported for the US Holstein [42] and Colombian multi-breed dairy cattle's [43]. In line with this study, favorable EBV for CI and DO were reported for the same breed and production system [33]. This can be interpreted as improvement in milk production was accompanied by a reduction in calving interval, showing that higher yields per animal were due to factors other than an increase in the lactation length. In short, the performance traits in the said herd would need further improvement. It is therefore, imperative to emphasize improvement in management and breeding evaluation techniques to make corrections on the possible mistakes made by wrong phenotypic appraisals.

Conclusions

The design of dairy breeding programs for the tropics requires knowledge of genetic parameters and breeding values for economically important traits under tropical conditions. Heritability estimates of LMY and AFC showed reasonable genetic variation; indicating that response to selection would be expected for these traits. Although, the low heritability estimates of LL, CI and DO were obtained for the studied population, improvement of feeding and breeding management of the herd would be an ideal option for genetic progress in fertility traits. The genetic correlation between yield and fertility (CI and DO) was shown to be undesirable; hence, merely the use of production measures in bull indices may be questionable. Therefore, future selection of herds needs relative economic values of each trait for local markets and total merit index selection practices are recommended.

Declarations

Conflict of interest

The authors declare that they have no conflict of interest.

Funding sources

This research did not receive any specific funding.

Acknowledgments

We are greatly indebted to Alage Agricultural TVTE College for allowing us to use their farm records.

Data availability statement

The data set is fully available with the corresponding author.

Authors' contributions

Conceptualization: Wondossn A, Destaw W.; Data curation: Wondossn A, Destaw W; Formal analysis: Wondossn A, Destaw W.; Software: Wondossn A, Destaw W.; Writing - original draft: Wondossn A, Destaw W. and Validation: Wondossn A, Destaw W.

Ethics approval and consent to participate

This manuscript does not require IRB/IACUC approval because there are no human and animal participants.

Consent for publication

Not applicable

References

1. Aynalem H. Genetic and Economic Analysis of Ethiopian Boran Cattle and their Crosses with Holstein Friesian in Central Ethiopia. A Ph.D. Thesis division of dairy cattle breeding National dairy research institute, Karnal-132001 (Haryana), India. 2006; pp.65–146.
2. Habtamu L, Kelay B, and Desie S. Study on the fertility performance of Jersey cows at Wolaita Sodo dairy farm, Southern Ethiopia. *Ethiop. Vet. J.* 2010; 14:53–70.
3. Ruegg PL. Health and production management in dairy herds, In: O. M. Radostits (ed), *Herd Health: Food Animal Production*, 3rd Edn., (Saunders, London), 2001; 211–254.
4. Choudhar, V, Kothekar MD, Raheja KL, Kasturiwale NN, Khire DW, and Kumar P. Genetic evaluation of first lactation traits in Sahiwal cattle using restricted maximum likelihood technique. *Asian-*

- Australian J. Anim. Sci. 2003; 16:639–643.
5. Wasana N, Cho G, Park S, Kim S, Choi J, Park B, Park C, and Do C. Genetic relationship of productive life, production and type traits of Korean Holsteins at early lactations. *Asian-Australasian J of Anim Sci.* 2015; 28:1259–1265. <https://doi.org/10.5713/ajas.15.0034>.
 6. Kadarmideen HN, Thompson R, Coffey MP, Kossaibati MA. Genetic parameters and evaluations from single and multiple trait analysis of dairy cow fertility and milk production. *Livest Prod Sci.* 2003; 81:183–95.
 7. Liu Z, Jaitner J, Pasma E, Rensing S, Reinhardt F, and Reents R. Genetic evaluation of fertility traits of dairy cattle using a multiple-trait model. *Inter bull Bull,* 2007; 37:134–139.
 8. Strabel T, Misztal I and Bertrand JK. Approximation of reliabilities of multiple trait models with maternal effects. *J. Anim. Sci.* 2001; 79: 833–839.
 9. Unalan A, and Cebeci Z. Estimation of genetic parameters and correlations for the first three lactation milk yields in Holstein Friesian cattle by the REML method. *Turk. J. Vet. Anim. Sci.* 2004; 28:1043–1049.
 10. Pollak, E.J., van der Werf, J., & Quaas, R.L. (1984). Selection bias and multiple trait evaluation. *J Dairy Sci,* 67, 1590–1595.
 11. Schaeffer LR. Sire and cow evaluation under multiple trait models. *J Dairy Sci.* 1984; 67:1567–1580.
 12. Henderson CR, and Quaas RL. Multiple trait evaluation using relatives' records. *Journal of Animal Science,* 1976; 43:1188–1197. <https://doi.org/10.2527/jas1976.4361188x>.
 13. Jiang J, Zhang Q, Ma L, Li J, Wang Z, Liu JF. Joint prediction of multiple quantitative traits using a Bayesian multivariate ante-dependence model. *Heredity (Edinb).* 2015; 115:29–36.
 14. Henderson CR. A simple method for computing the inverse of a numerator relationship matrix used in prediction of breeding values. *Biometrics* 1976; 32: 69–93
 15. Mrode RA. *Linear models for the prediction of animal breeding values.* CAB Int., Wallingford, UK. 2005.
 16. Ayalew W, Aliy M, and Negussie E. Estimation of genetic parameters of the productive and fertility traits in Ethiopian Holstein using multi-trait models. *Asian Australasian J Anim. Sci.* 2017; 30: 1550–1556. <https://doi.org/10.5713/ajas.17.0198>.
 17. Ayied YA, Jadoa JA, and Abdulrada JA. Heritabilities and breeding values of production and reproduction traits of Holstein cattle in Iraq. *J. Basrah Res. Sci.* 2011; 37: 66–70.
 18. Ajili N, Rekik A, Gara B, and Bouraoui R. Relationships among milk production, fertility traits, and herd life for Tunisian Holstein Friesian cows. *African J Agric Res.* 2007; 2: 047–051.
 19. Fekadu A, Kassa T, and Belehu K. Study on fertility performance of Holstein-Friesian dairy cows at Alage Dairy Farm, Rift Valley of Ethiopia. *Trop Anim Health Prod.* 2011; 43: 581–586. <https://doi.org/10.1007/s11250-010-9734-8>
 20. Misztal I, Tsuruta S, Lourenco D, Aguilar I, Legarra A, Vitezica Z. *Manual for BLUPF90 Family of Programs;* University of Georgia: Athens, GA, USA. 2014

21. R Core Team. A language and environment for statistical computing. R foundation for statistical computing, Vienna. 2013.
22. Sun C, P Madsen, MS Lund, Y Zhang, US Nielsen and G Su. Improvement in genetic evaluation of female fertility in dairy cattle using multiple-trait models including milk production traits. *J. Anim. Sci.* 2010; 88:871–878. doi:10.2527/jas.2009-1912
23. Emana G. Economic index weight age for dairy traits preference in central highlands of Ethiopia [master's thesis]. Jimma, Ethiopia: Jimma University; 2015.
24. Zink V, J Lassen and Stipkova M. Genetic parameters for female fertility and milk production in first-parity Czech Holstein cows. *Czech. J. Anim. Sci.* 2012; 57: 108.
25. Goshu G, Singh H, Petersson K, and Lundeheim N. Heritability and correlation among first lactation traits in Holstein cows at Holeta Bull Dam Station, Ethiopia. *Int. J. Livest. Prod.* 2014; 5: 47.
26. Seangjun A, Koonawootrittriron S, Elzo MA. Characterization of lactation patterns and milk yield in a multibreed dairy cattle population in the central Thailand. *Kasetsart J Nat Sci.* 2009; 43:74–82.
27. Saha S, Joshi BK, Singh A. Generation-wise genetic evaluation of various first lactation traits and herd life in Karan Fries cattle. *Ind. J. Ani. Sci.* 2010; 80:451–456.
28. Gebreyohannes G, Koonawootrittriron S, Elzo MA, and Suwanasopee T. Variance components and genetic parameters for milk production and lactation pattern in an Ethiopian multibreed dairy cattle population. *Asian-Australasian journal of animal sciences*, 2013; 26: 1237–1246. <https://doi.org/10.5713/ajas.2013.13040>.
29. Falconer DS. Introduction to quantitative genetics (3rd ed.). Longman Press, Essex, England; 1989.
30. Changunda MG. Genetic evaluation of the performance of Holstein Friesian cattle on large scale dairy farm in Malawi. *Livest. Prod. Sci.* 2000; 11: 305–310.
31. Koots KR, JP Gibson and JW Wilton. Analysis of published genetic parameters estimates for beef production traits. 1. Heritability. *Anim. Breed. Abstr.* 1994; 62:309–388.
32. Lobo RNB, FE Madalena, and AR Vieira. Average estimates of genetic parameters for beef and dairy cattle in tropical regions. *Anim. Breed. Abst.* 2000; 68:433–462.
33. Ojango JM and Pollott GE. Genetics of milk yield and fertility traits in Holstein Friesian cattle on large scale Kenyan farms. *J Anim Sci.* 2001; 79:1742–50.
34. González-Recio O, and Alenda R. Genetic parameters for female fertility traits and a fertility index in Spanish dairy cattle. *J. Dairy Sci.* 2005; 88:3282–3289.
35. Divya P. Single versus multi-trait models for genetic evaluation of fertility traits in Karan Fries cattle. MSc. Thesis, NDRI (Deemed University), Karnal, India, 2012.
36. Brzakova M, Zavadilova L, Pribyl J, Pesek P, Kasna E, and Kranjcevicova A. Estimation of genetic parameters for female fertility traits in the Czech Holstein population. *Czech J. Anim. Sci.* 2019; 64:199–206.
37. Montaldo HH, Castillo-Juárez H, Valencia-Posadas M, Cienfuegos-Rivas EG, Ruiz- López FJ. Genetic and environmental parameters for milk production, udder health, and fertility traits in Mexican

Holstein cows. J. Dairy Sci. 2010; 93:2168–75.

38. Bennet C. Using Heritability for Genetic Improvement. Issued in furtherance of Cooperative Extension work, Virginia Polytechnic Institute and State University, Virginia State University, and the U.S. Department of Agriculture cooperating. 2009. <https://pubs.ext.vt.edu/404/404-084/404-084.html>.
39. Pirlo G, F Miglior, and M Speroni. Effect of age at first calving on production traits and on difference between milk yield returns and rearing costs in Italian Holsteins. J. Dairy Sci. 2000; 83:603–608.
40. Hermiz HN, Juma KH, Saadi SK, and Aldoori TS. Genetic parameters of production, reproduction and growth traits of Holstein cows. Dirasat Agric Sci. 2005; 32:157–62.
41. Van Raden PM, AH Sanders, ME Tooker, RH Miller, HD Norman, MT Kuhn and GR Wiggans. Development of a national genetic evaluation for cow fertility. J. Dairy Sci. 2004; 87:2285–2292.
42. Hare E, Norman HD, Wright JR. Trends in calving ages and calving intervals for dairy cattle breeds in the United States. J. Dairy Sci. 2006; 89:365–370.
43. Vergara OD, Elzo MA, Cer on-Munoz MF. Genetic parameters and genetic trends for age at first calving and calving interval in an Angus-Blanco Orejinegro-Zebu multi-breed cattle population in Colombia. Livest. Sci. 2009; 126:318–322.

Figures

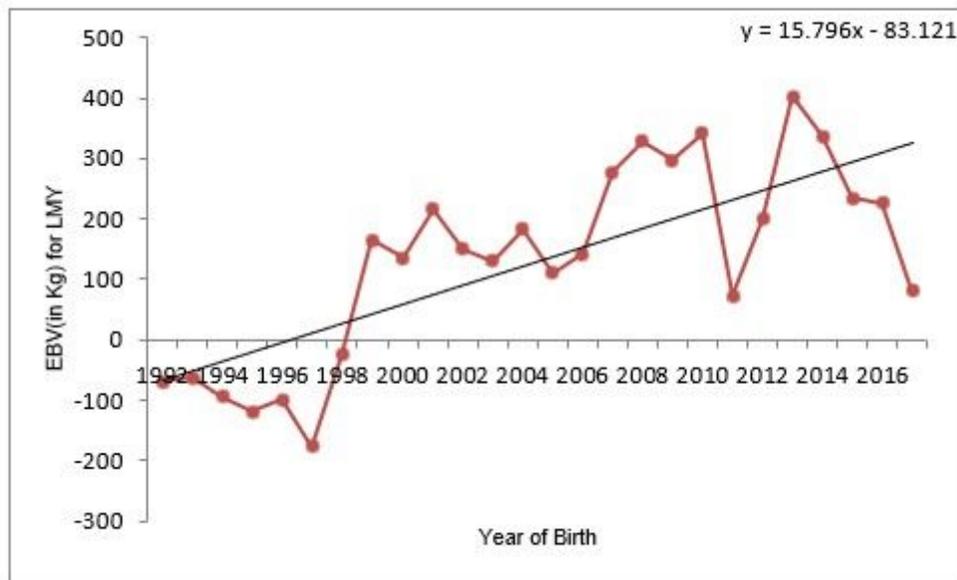


Figure 1

Trends of breeding values (EBVs) by year of birth for LMY of tropical Holstein Friesian

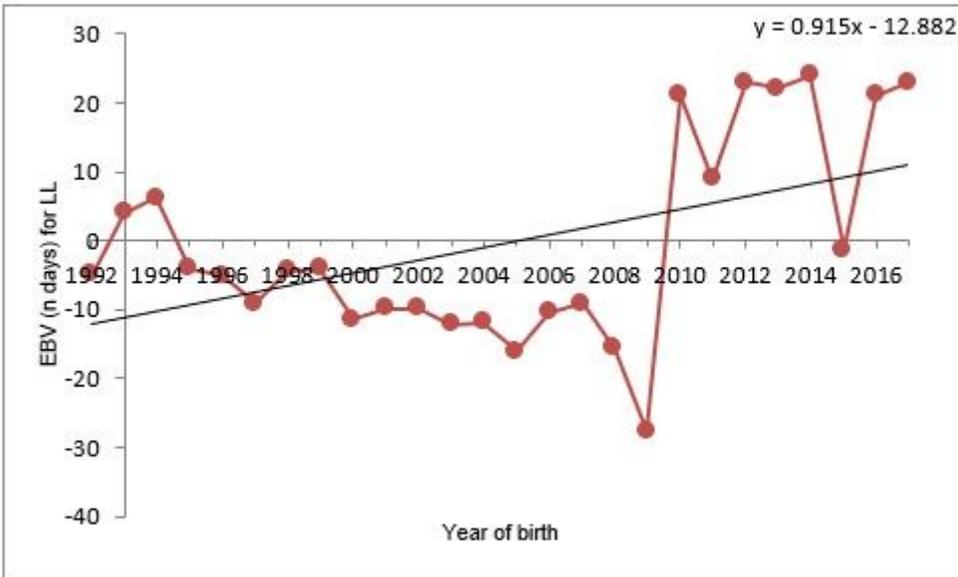


Figure 2

Trends of breeding values (EBVs) by year of birth for LL of tropical Holstein Friesian

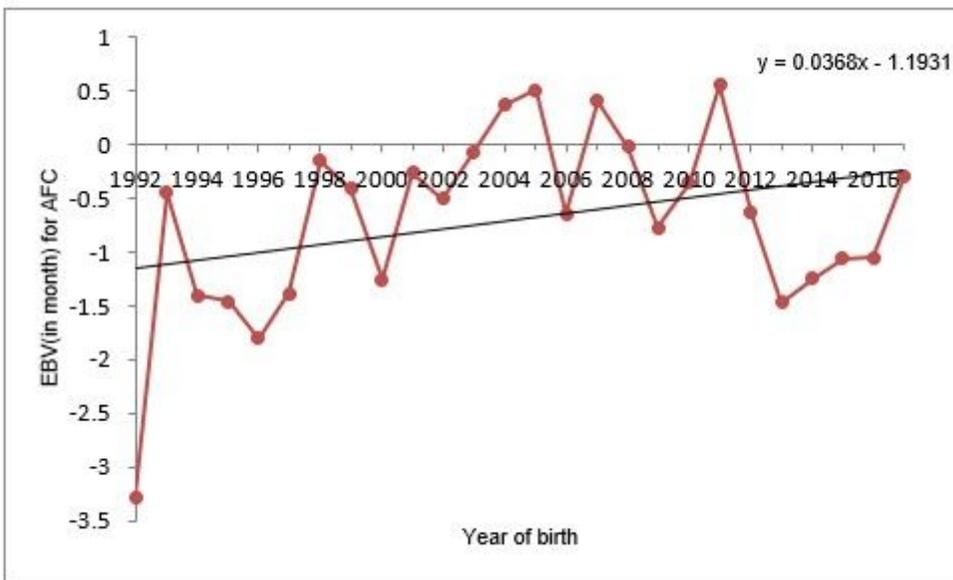


Figure 3

Trends of breeding values (EBVs) by year of birth for AFC of tropical Holstein Friesian

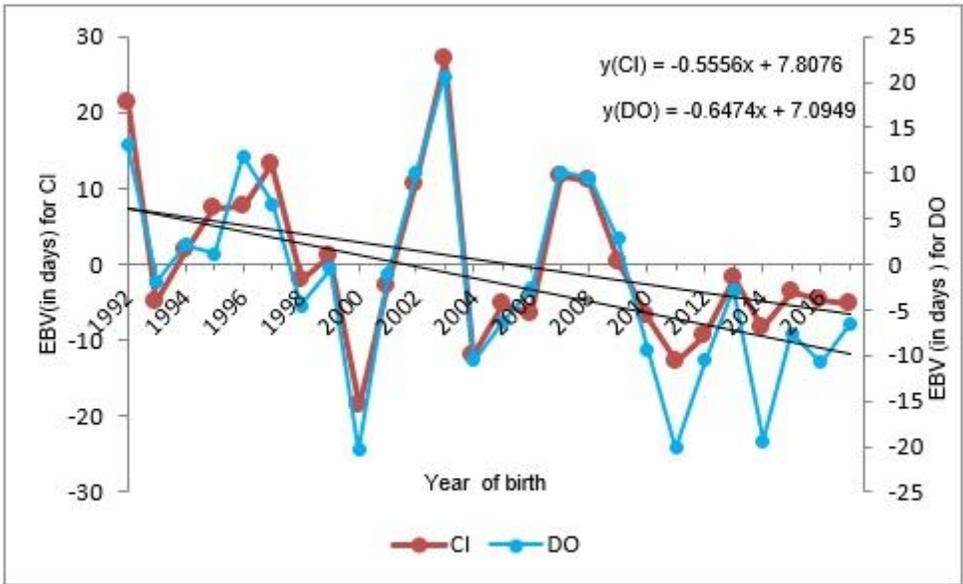


Figure 4

Trends of breeding values (EBVs) by year of birth for CI and DO of tropical Holstein Friesian