

GENETIC EVALUATION AND PRINCIPAL COMPONENTS ANALYSIS FOR MILK TRAITS IN HOLSTEIN FRIESIAN CATTLE

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SUMMARY

The aim of the current study was to estimate genetic principal components analysis for milk traits of breeding value (BV) in Holstein Friesian (HF). A total number of 2067 records cow from 80 sires and 439 dams; during 10 consecutive years that included the four seasons for each year and six parities from the commercial farms nearly the Nile Delta, Egypt. Studied traits were total milk yield (TMY), lactation period (LP), calving interval (CI), number of services per conception (NSPC) and days open (DO). Data for milk traits (MT) were analyzed using a single trait animal model program used to estimate genetic parameters, in addition to using a method principal components analysis (PCA) program, which aims to increase the accuracy of estimating genetic evaluation.

The heritability (h^2_a) estimates were 0.20 ± 0.001 , 0.22 ± 0.002 , 0.02 ± 0.001 , 0.04 ± 0.001 and 0.05 ± 0.020 for TMY, LP, CI, NSPC and DO, respectively. The total variance of breeding values was 67.1, in which 46.6% and 20.5% were explained by PC_1 and PC_2 , respectively. Two principal components (1&2) were estimated by BV. Equations for PCA were: $PC_1 = 0.273 TMY + 0.342 LP + 0.371 CI + 0.318 NSPC - 0.004 DO$, and $PC_2 = 0.213 TMY - 0.069 LP - 0.146 CI + 0.045 NSPC + 0.949 DO$.

The results of genetic PCA indicate that milk traits were highly significant, also improve TMY. Improved all traits under study would be expected to use analysis PC_1 and PC_2 provides to overcome the multicollinearity problem while predicting the future TMY, thus achieving an increased economic return.

Keywords: Milk traits, genetic parameters, Principal Component Analysis, Holstein Friesian.

INTRODUCTION

Genetic improvement programs need continuous evaluation and adjustments in order to improve the economic return and increase the profitability of dairy cattle projects. The method of assessing genetic trends over a period of time is used to assess the changes occurring upon selection. (Silva *et al.*, 2001). While the genetic trend is a change in performance per unit time and this is obtained by comparing the different levels of cattle numbers for each year. Understanding the trends in genetic progression helps to determine the independent genetic trend by setting specific goals for raising the now-herd and achieving the highest economic return (profitability and sustainability of the project) (Missanjo *et al.*, 2012). Genetic evaluations used in breeding programs contain multiple traits of milk production and reproductive traits through special records of cows. Reproductive traits frequently available to cattle selection criteria are considered by breeder and genetics programmers, and the most important of these traits is the age at first calving and length of calving interval. (Boligon *et al.*, 2010).

Principal component analysis (PCA) is used to reduce a specific set of variables by eliminating redundant information while preserving the contrast structure as much as possible, it was used in animal

breeding and genetics to reduce the size of the matrix (variance-covariance structure) of these variables Boligon *et al.*, (2016) added in multiple models containing a number of production and reproductive traits and to study the relationship between the expected breeding values (Agudelo-Gómez *et al.*, 2015). Therefore, the aim of this study was to estimate the h^2_a , breeding value (BV), selection differentials and genetic trends for TMY, LP, CI, NSPC and DO in the Holstein Friesian (HF) cattle through multivariate techniques, in order to give directions in Holstein Friesian breeding programs. This leads to increased accuracy of estimating environmental and genetic parameters by starting to fix fixed effects by using the PCA.

This investigation's goal To improve the accuracy of estimating genetic evaluation by using PCA as an alternative approach to analyzing the traits study and solving the problem of multicollinearity, with the possibility of identifying a more appropriate and accurate model for predicting milk production and thus obtaining a higher economic return. Also, the objectives of the study were estimate genetic parameters and genetic trend to improve genetic merit for milk traits output and to assess the efficacy of genetic programs.

MATERIALS AND METHODS

Management and feeding:

The feed provided included Egyptian clover during winter while clover straw hayrice in addition to wheat and rice straw during summer. Heifers were served when they reach the appropriate size and weight by artificial insemination; pregnancy was diagnosed rectally. As for the milking process, it takes place in the places designated for milk, where the supplies and hygiene are available, as the cows are milked twice a day, once in the morning and again in the evening. The drying process of cows was performed two months before calving. Medical supervision and vaccinations are done by veterinarians.

Structure of data:

The data used in this study from Holstein Friesian cattle records, These studied traits included: TMY, LP, CI, NSPC and DO. A total number of records 2067 cow from 80 sire and 439 dam; during ten consecutive years that included the four seasons for each year and six parity from the commercial farm near the Nile Delta, Egypt.

Statistical analysis:

The data for milk traits (TMY, LP, CI, NSPC and DO) were analyzed using the single trait animal model by the STDFRAML program (Boldman *et al.*, 1995). The matrix representation of the model was:

$$Y = Xb + ZaUa + Zpe Upe + e;$$

Where Y = the vector of observations traits on the evaluated animal; b = the vector of fixed effects (i.e. year, season and Parity); Ua = the vector of random animal effects; Upe = the vector of random permanent environmental; e = vector of random residual and Xb, Za and Zpe are incidence matrix relating records to fixed, animal and permanent environmental effects, respectively.

Principal Components Analysis:

Principal component analysis using the breeding values predicted (EBV) for milk traits breeding values of total milk yield (EBV_{TMY}), breeding values of lactation period (EBV_{LP}); breeding values of calving interval (EBV_{CI}), breeding values of the number of services per conception (EBV_{NSPC}) and breeding values of days open (EBV_{DO}).

Table1. Variance components (σ^2_a , σ^2_{pe} , σ^2_e and σ^2_p), heritability (h^2_a), maternal permanent environmental effect (P_e^2) and error (e^2) for studied traits in Holstein Friesian herd

Parameter	TMY	LP	CI	NSPC	DO
σ^2_a	641187.6	1167.8	119.8	0.13	429.0
σ^2_{pe}	4167.7	144.0	17.8	0.17	110.0
σ^2_e	2564750.8	3884.4	5368.3	2.92	7542.0
σ^2_p	3205938.5	5196.2	5505.9	3.22	8081.0
h^2_a	0.20±0.001	0.22±0.002	0.02±0.001	0.04±0.001	0.05±0.020
P_e^2	0.0013±0.001	0.028±0.001	0.003±0.001	0.051±0.001	0.014±0.039
e^2	0.80±0.0001	0.75±0.02	0.98±0.001	0.91±0.01	0.93±0.038

TMY = Total milk yield; LP = Lactation period; CI= calving interval; NSPC = number of services per conception, and DO= days open.

The Principal Component Analysis (PCA) was using the program of SPSS 16; 2007, statistical analysis of PCA is used to summarize the original variables into a smaller set of new variables called the main components (PC) while retaining the necessary information and discovering the relationship between (EBVs) using the method single trait analysis for adjectives (EBV) TMY, EBV LP, EBV CI, EBV NSC and EBV DO. To show and explain the structure of the data (Buzanskas *et al.* 2013). The values of (PC) for the study traits were standardized by using the standard normal distribution to determine PC that showed the highest variance ratio for the traits that contain greater than one eigen values, in accordance with Kaiser's criteria the standardized score coefficients of each (EBV) in each PC were obtained by the formula:

$$SCC_{ir} = \frac{igenvector_{is}}{\sqrt{eigenvalue_s}}$$

Where SSC_{ir} = SSC for (EBV)s of i^{th} trait in the j^{th} principal component.

The principal component scores were estimated by:

$$PCS_{ri} = \sum m_i = 1SSC_{ir} EBV_i$$

Where PCS_{r1} is the PC score for the 1^{th} animal in the j^{th} PC, SSC_{ir} is the SSC for (EBVs) of i^{th} trait in the j^{th} (PC) and (EBV)_{ii} is the standardized estimated BV of the i^{th} trait for the 1^{th} cow.

The genetic trend (GT) was estimated of breeding value (EBV) of cows on the year of calving for all traits (SAS, 2003).

RESULTS AND DISCUSSION

Genetic parameters

Estimates of variance (σ^2), heritability (h^2_a), relatively permanent and environmental variance P_e^2 and error e^2 for TMY, kg, LP, CI, NSPC and DO are presented in Table1. Heritability estimate h^2_a for TMY, kg, LP, CI, NSPC, and DO were 0.20±0.001, 0.22±0.002, 0.02±0.001, 0.04±0.001, and 0.05±0.020, respectively (Table1). They are higher than those recorded by Zahed *et al* (2020) who found that h^2 estimates were 0.20, 0.11, 0.010, and 0.044 for 305-dMY, LP, NSPC, and DO, respectively.

Estimate of heritability (h^2_a) for LP trait was 0.22 ± 0.002 , being higher than that found by Hussein *et al.*, 2016 (0.39). Estimate of h^2_a for NSPC was 0.04 ± 0.001 which was similar to that found by Kadarmideen *et al.*, 2003; (0.016 ± 0.005); (De Haas *et al.*, 2007; 0.01) and Zahed *et al.*, 2020; (0.01). Heritability estimates for DO in the present study (0.05 ± 0.020) were greater than the ranger of (0.044 to 0.03) reported by Kadarmideen *et al.*, (2003); Almaz (2012) and Zahed *et al.* (2020).

The differences in the estimated h^2_a in the present study for the same traits compared by the different studies may due to management of herd (nutritional factors in herds), change in herd size (number of records used), and temporary environmental factors. The permanent environment (P^2_e) was 0.0013 ± 0.001 ,

0.028 ± 0.001 , 0.003 ± 0.001 , 0.051 ± 0.001 , and 0.014 ± 0.039 . It was higher than that found by Kamal El-den *et al.* (2020) found that P^2_e for TMY and LP were 0.0071 ± 0.089 and 0.00024 ± 0.10 .

Minimum, maximum, standard errors, accuracy, and range of cow breeding values (CBV) for milk production and reproductive traits are presented in table 2. The ranges of CBV were 3414.3kg 109.7 days; 12.1 days ,0.95 and 40.7days for TMY, kg, LP, CI, NSPC and DO respectively. The wide range for CBV refers to the wide genetic variation which gives the chance for improving traits through selection according to the superiority of the CBV. The same was obtained by Safaa Sanad and Gharib (2017); Tamer *et al.* (2017) and Safaa Sanad (2019).

Table 2. Minimum, maximum, range and accuracy of predicted breeding values for milk traits in Holstein Friesian cows

Traits	Minimum	Standard error	Accuracy	Maximum	Standard error	Accuracy	Range
TMY	-1618.9	533.9	0.75	1795.41	567.25	0.71	3414.3
LP	-49.14	18.6	0.84	60.59	21.08	0.79	109.7
CI	-01.40	9.95	0.42	10.73	10.90	0.39	12.1
NSPC	-0.41	0.32	0.46	0.54	0.33	0.42	0.95
DO	-19.65	13.31	0.49	21.04	14.04	0.40	40.7

+ Traits as defined in Table 1.

Principal component analysis (PCA):

The Principal Component Analysis (PCA) was applied to five breeding values of milk traits. Estimates breeding values(EBV) of TMY, LP, CI, NSPC, and DO in Holstein cattle cows and the general mean value of Kaiser-Meyer Olkin (KMO) measures of sampling adequacy was obtained as 0.674, Chi-Square was 590.086, this indicated that the suitability of the data for PCA. The same model was reported by several authors Eydurán *et al.* (2013) and Sinha *et al.* (2021) with different cattle and observed that KMO measure of sampling adequacy were 0.867; 0.692 and 0.669, respectively.

Five principal components PC, as shown in Table 3, indicate that the total variation of breeding values was 67.05, which obtained by the first component (PC_1)46.6 % and the second component (PC_2) 20.5%, of the results, are the total variance, where the results

showed that the differences in the first two main components of all the traits of the study were found, while it was found that more than 67% of the total differences were through them. The same model was used by Eydurán *et al.* (2009), Eydurán *et al.* (2010); and Eydurán *et al.*, (2013) and Tramonte *et al.* (2019) for the discard of variables. Buzanskas *et al.* (2013) on Can him cattle found two principal components of breeding values was expounded at 73.4 % of the total variance (additive) and was considered that PC is a genetic indicator of reproductive traits. While Tramonte *et al.* (2019) observed that, the first component was 55.15%, and the second was 13.07%, of the total variation of breeding values, whereas more than 68% of the total variation.

Table 3. Eigen values for the principal components of the breeding values

PC	Eigen values	VP	CVP
1	2.330	46.6	46.59
2	1.023	20.5	67.05
3	0.692	13.8	80.89
4	0.647	12.9	93.82
5	0.309	06.2	100.00

VP=Variance proportion; CVP=Cumulative variance proportions

The indices weights (IW) were standardized score coefficients for all estimates of breeding values (EBV) in Table 4, as it was reported that the increase of the absolute value of the standardized score

coefficients, the greater the relative significance of the EBV in the principal components (PC). The two PC (1&2) allowing being associated with key information in the expected breeding value of the

traits. In this research, the importance of the linear correlation between the traits of the main component can be explained in Table 4, with the highest values of the vector eigenvectors within each major component. Also, Principal Component (PC₁) can be considered a genetic indicator of the reproductive as it can access animals that are genetically superior to EBV (TMY, LP, and DO). It is necessary to take into account that the positive breeding values for the TMY trait because the goal is to increase TMY, which is required for improvement negative EBV (CI) for reproductive traits will be more important so PC₂ can be considered a genetic index for

reproduction because it shows and detects EBV (TMY) genetically superior animals. It is necessary to bear in mind that positive breeding values for TMY traits are required for improvement and negative EBV (CI) for reproductive traits will be more important. While the reduce CI. Buzanskas *et al.* (2013) reported that PC₁ can be mind to be a genetic index for reproduction that promotes animals that are genetically superior to EBV (CI). Therefore it was important to bear in mind that negative EBV for reproductive traits.

Table 4. Correlation coefficients between EBV of the milk traits with (PC₁) and (PC₂)

Traits	PC ₁	PC ₂
EBV _{TMY}	0.647 ^{***}	0.245 ^{***}
EBV _{LP}	0.791 ^{***}	-0.034 ^{ns}
EBV _{CI}	0.854 ^{***}	-0.113 ^{**}
EBV _{NSPC}	0.743 ^{***}	0.077 [*]
EBV _{DO}	0.042 ^{ns}	0.979 ^{***}

*=significant(P<0.05), **=significant(P<0.01),***=significant (P<0.001); ns= non-significant; EBV_{TMY}= breeding values of Total milk yield, EBV_{LP} = breeding values of Lactation period; EBV_{CI}= breeding values of calving interval ; EBV_{NSPC}= breeding values of number of services per conception and EBV_{DO}= breeding values of days open.

According to Table 5, the principal components (PC) showed that breeding value for traits TMY, LP, CI, and NSPC were reported to have a highly significant (P<0.001) correlation with the first PC₁ and ranged from moderates (0.64) to high (0.85). Thus, trait DO was found to be non-significant while the second PC₂ ranged from low (0.07) to high (0.98). While the CI trait (-0.1) was reported a negative correlation with PC₂. These results are similar to those of similar by Karaca and Kadarmideen, (2008) and Tramonte *et al.*, (2019).

The genetic variation of recombinant traits is PC₁ or PC₂, and thus this can be tested by numerical scores resulting from PC₁ or PC₂ to further improve TMY. This is what was found by Mello *et al.*, (2020), where females can be selected through the numerical scores resulting from PC₁ and PC₂ to improve the traits of CI, TMY, and LP.

The principal components scores (index values) for each animal in each PC can be estimated as follows:

$$PC_1 = 0.273 \text{ TMY} + 0.342 \text{ LP} + 0.371 \text{ CI} + 0.318 \text{ NSPC} - 0.004 \text{ DO.}$$

$$PC_2 = 0.213 \text{ TMY} - 0.069 \text{ LP} - 0.146 \text{ CI} + 0.045 \text{ NSPC} + 0.949 \text{ DO.}$$

Table 5, shows the extent of the contribution of principal component analysis (PC₁ or PC₂) in the variance of the traits under this study; indicating that PC₁ contributes a greater amount of the variance of CI traits reached on 0.371. While it does not contribute badly to the contrast of LP and NSPC traits, In addition to PC₁ contributes a moderate amount to the total milk yield = 0.273, also., the PC₂ for TMY=0.213, while DO = -0.004 for PC₁ and PC₂ = 0.949, this study agrees by Eyduran *et al.*, (2013), Rebeka *et al.* (2020) and Sinha *et al.* (2021).

Table 5. Contribution of principal component analysis (PC₁& PC₂) in the variance of the traits under this study for prediction TMY

Trait	Principal Component Analysis		
	PC ₁	PC ₂	Communality
EBV _{TMY}	0.273	0.213	0.469
EBV _{LP}	0.342	-0.069	0.630
EBV _{CI}	0.371	-0.146	0.749
EBV _{NSPC}	0.318	0.045	0.555
EBV _{DO}	-0.004	0.949	0.950

+ Traits as defined in Table 4.

In this study, the factor (PC) was conducted using the estimated genetic values (EBV) for all study traits to aims; increasing TMY would be expected to increase with increasing PC₁&PC₂; in addition to can be solved the multicollinearity problem, also prediction of total milk yield (TMY); this study agrees Sanad *et al.* (2021) may be helpful in the early selection of cattle based on initial lactation records.

With Principal Component Analysis (PCA), it is possible to select animals based on only two results generated by PC₁ and PC₂ rather than five breeding selection values. When using this method, animals can be chosen in a balanced way that is effective as soon as the results of each appear. The main component is linear combinations of all EBVs traits evaluated breeding programs. Tramonte *et al.* (2019).

Genetic trends (GT):

Genetic trends of some milk production and reproduction traits are given in Figures 1 to 5, which indicated that the genetic trend of TMY was positive during the interval from 1990-1996, after that, it was reduced from 1999-2004 and rose again from 2007 to 2011 and reduced again from 2012 -2014, (estimated

to be 0.04 kg/year, Figure1). The positive values of the regression coefficient suggest genetic improvement in the farm for TMY and the right selection procedures. On the other hand, a declined trend in TMY was observed throughout the period from 1998-2002. Similar results were found by Nehara (2012) and Khorshidie *et al.* (2012).

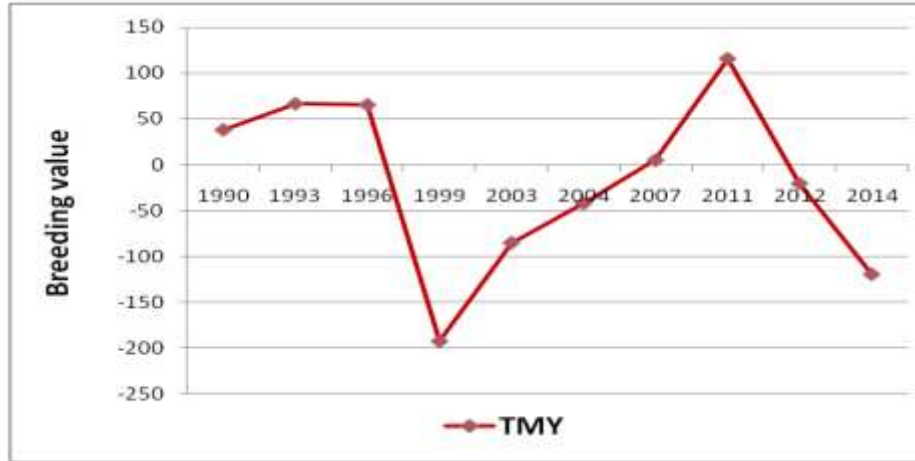


Figure 1. Genetic trend of TMY trait in Holstein Friesian cattle.

The genetic trend of LP was positive during the interval from 1990-1999, after that, it was reduced from 2003 to 2007 and rose again till 2011 and was reduced again from 2012 to 2014, (estimated to be 0.03day/year, Figure 2). Similar results were reported by Herintstad and Larsgaid, (2010) and Sanad and Gharib (2017). While, the genetic trend of CI was positive during the interval from 1990 to 1993, after that, it was reduced till 2014, (estimated to be -0.23day/year Figure 3). The present result was comparable with that obtained by Abdelharith (2008), who reported estimates of genetic trends -0.09 ± 0.17 d per year, for CI. Atil and Khattab (2005) found that the genetic trend (GT) for CI was -0.95 day/year. While Ibrahim *et al.* (2009) reported that GT for CI was significantly positive 0.06 ± 0.02 day/year, $P < 0.01$, indicating a genetic increase in CI. On the other hand, the genetic trends of DO and NSPC were negative during most of the studied intervals of years, and estimated as -0.031 day/year and -1.06% year for (DO and NSPC, respectively (Figures 4 and 5). The present results are in accordance with the findings reported by Deljoolsaloo *et al.* (2012); Solemani-Baghshah *et al.*, (2014); Sanad and Gharib, (2017) and Sanad and Gharib (2020).

Canaza-Cayo *et al.* (2016) reported that the genetic program has a positive role in milk yield. This is due to the different genotypes that are affected by different environmental factors and accordingly, management in addition to providing appropriate environmental conditions are needed.

In selection programs, the decrease in the genetic progression of reproduction traits can be explained by two factors. The greater focus was on the performance traits compared to the reproductive traits. The reason may be due to the low genetic susceptibility to these traits, which follows the slow genetic progression. (Solemani-Baghshah *et al.*, 2014).

Sanad and Gharib (2020) observed that a clear trend in the 3rd and 10th, while 305 was lower in the rest of the years, Also Safaa Sanad and Gharib, (2020) found that, the importance of good care by improving the environmental conditions surrounding the animals. Where figures of additive variance components revealed the strong and the importance of the environmental component linked with the genetic differences affecting productive traits and management practices. Improving environmental conditions and improved genetic potential of dairy animals in the farms would be effective approaches for high milk productivity (Sanad, 2016).

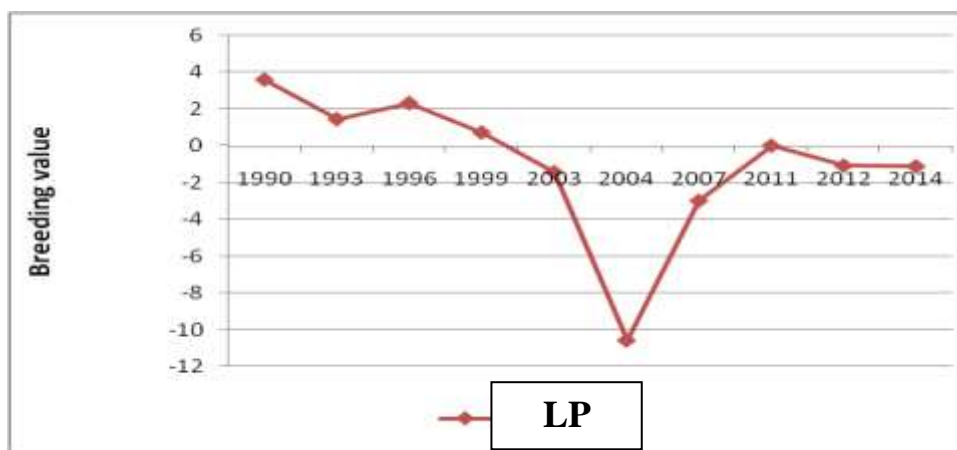


Figure 2. Genetic trend of LP trait in Holstein Friesian cattle.

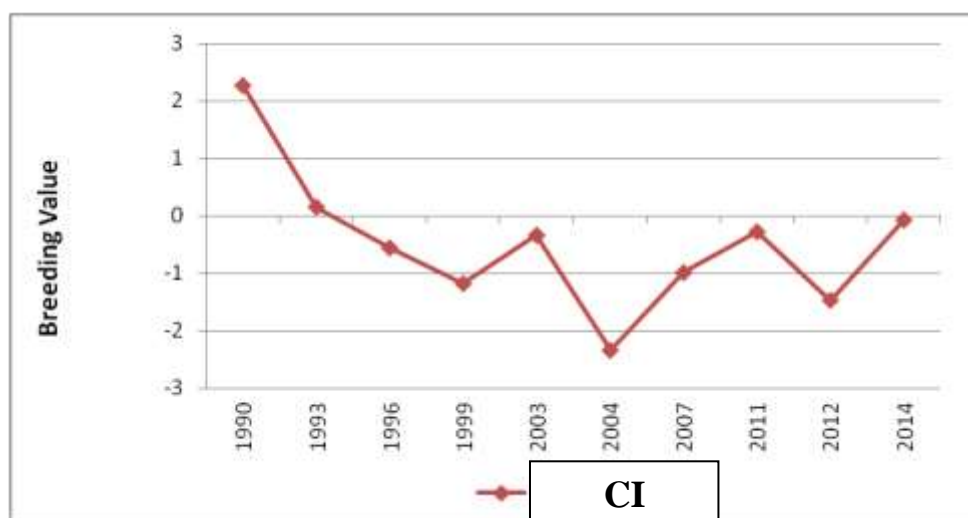


Figure 3. Genetic trend of CI trait in Holstein Friesian cattle.

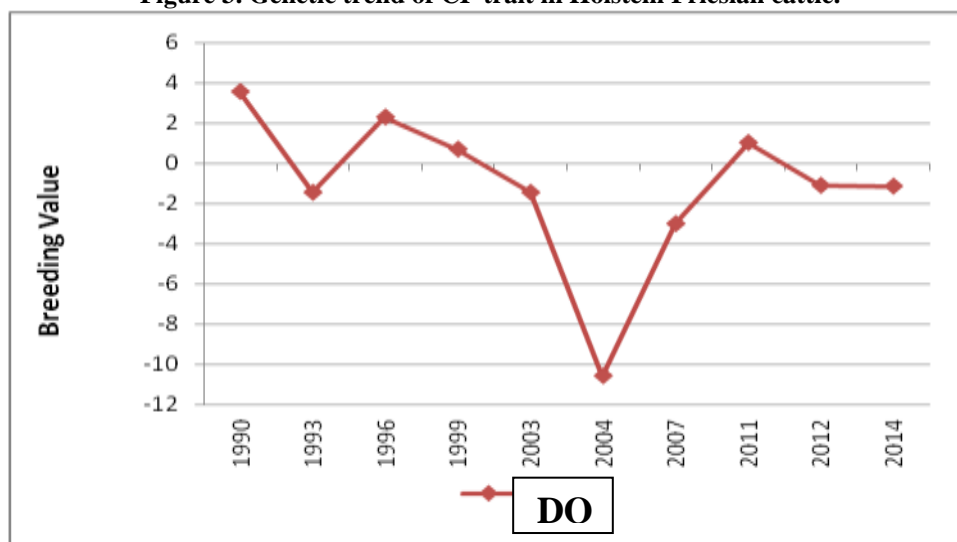


Figure 4. Genetic trend of DO trait in Holstein Friesian cattle.

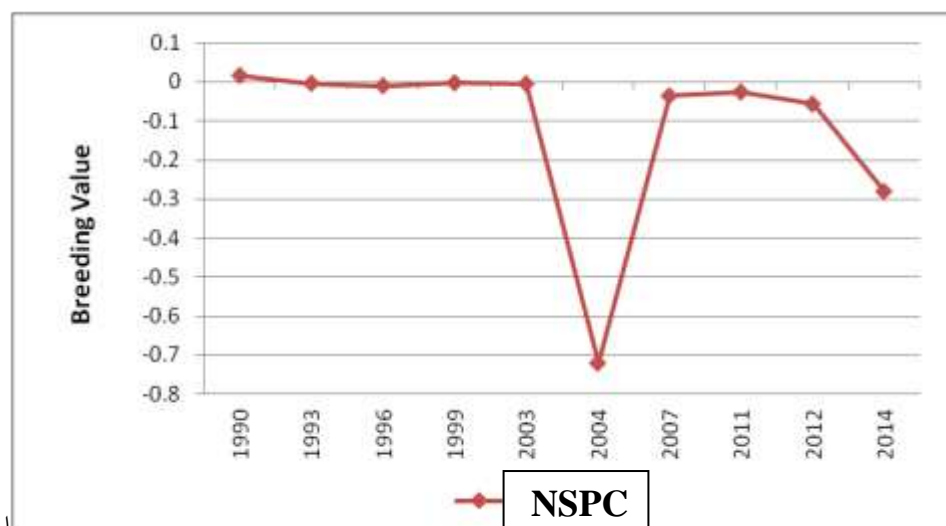


Figure 5. Genetic trend of NSPC trait in Holstein Friesian cattle.

CONCLUSION

Improving the performance of the herd depends on focusing on the total milk yield and lactation period traits qualities and an increase in focus on reproductive traits, in addition, that the milk production can be improved independently as well as the traits of the period between calving's. While the number of services per conception and days opens traits respond to selection slowly due to the decrease in their genetic competence, their rate of improvement can be increased if selected for them; thus indicators are baseline ingredients to use. For improving all traits understudy would be expected to use of first component (PC_1) and the second component (PC_2) provides to overcome the multicollinearity problem while predicting the future total milk yield, thus achieving an increased economic return.

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التقييم الوراثي وتحليل المكونات الأساسية لصفات اللبن في أبقار الهولستين-فريزيان

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كانت أهداف الدراسة هي التقييم الوراثي عن طريق تحليل المكونات الرئيسية لصفات اللبن ذات القيمة التربوية (BV) في ابقار الهولشتين فريزيان (HF). كانت الصفات المدروسة هي إنتاج اللبن الكلي (TMY كجم) ، طول فترة الحلب (LP) ، الفترة بين الولادتين (CI) ، عدد مرات التلقيح اللازمة للإخصاب (NSPC) والأيام المفتوحة (DO) . عدد السجلات المستخدمة 2067 سجل بنات 80 طلوقة و439 أم خلال عشر سنوات متتالية اشتملت على أربعة مواسم لكل عام و 6 مواسم حلب، تم تحليل بيانات صفات اللبن باستخدام برنامج نموذج الحيوان لتقدير المعالم الوراثية، بالإضافة إلى استخدام برنامج تحليل المكونات الرئيسية (PCA) ويهدف إلى زيادة دقة تقدير التحليل الوراثي.

النتائج: تقديرات العمق الوراثي (h^2) كانت 0.001 ± 0.20 ، 0.002 ± 0.22 ، 0.001 ± 0.02 ، 0.001 ± 0.04 و 0.05 ± 0.020 لصفات إنتاج اللبن الكلي، طول فترة الحلب ، الفترة بين ولادتين ، عدد مرات التلقيح اللازمة للإخصاب والأيام المفتوحة ، على الترتيب.

وجد أنه بالنسبة لجميع صفات الدراسة ان المكونات الأساسية الأول PC_1 والثاني PC_2 كان يمثلان أكثر من 67.1 من التباين الكلي ، حيث تم شرح 46.6% و 20.5% بواسطة PC_1 و PC_2 على الترتيب. تم تقدير المكونين الرئيسيين (1 و 2) بواسطة القيم التربوية BV . وكانت المعادلات التي تم الحصول عليها لتحليل المكونات الرئيسية (PCA) هي كالتالي:

$$PC_1 = 0.273 TMY + 0.342 LP + 0.371 CI + 0.318 NSPC - 0.004 DO$$

$$PC_2 = 0.213 TMY - 0.069 LP - 0.146 CI + 0.045 NSPC + 0.949 DO$$

تشير نتائج تحليل المكونات الرئيسية المقدر وراثيا إلى أن صفات اللبن كانت عالية المعنوية ، وانها تتحسن أيضاً. وانه من المتوقع أن يؤدي ذلك الي تحسين جميع الصفات قيد الدراسة عن طريق استخدام برنامج تحليل المكونات الرئيسية (PCA) لاستخدام PC_1 و PC_2 بهدف التغلب على مشكلة الأزواج الخطية الخطية وزيادة دقة تقدير التحليل الجيني وراثياً ، للتنبؤ بإنتاج اللبن الكلي (TMY) وبالتالي تحقيق عائد إقتصادي متزايد.