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PRINCIPAL COMPONENT ANALYSIS OF GENETIC BREEDING VALUES FOR MILK AND REPRODUCTIVE TRAITS IN FRIESIAN CATTLE IN EGYPT

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ABSTRACT: The aim of this study was to assess genetic parameters and breeding values for milk traits (total milk yield, TMY and lactation period, LP) as well as reproductive traits, including days open (DO), calving interval (CI) and age at first calving (AFC) in Friesian cattle. The study also involved analyzing the relationship between genetic breeding values using principal component analysis (PC) and constructing a selection index to improve overall performance. A dataset comprising 2837 records from 1243 cows, offspring of 108 sires and 835 dams during the period from 2000 to 2015 was collected from two experimental stations, Sakha and El-Karada, managed by the Animal Production Research Institute. The estimated heritability values were 0.29, 0.23, 0.04, 0.06, and 0.07 for TMY, LP, CI, DO, and AFC, respectively. Repeatability estimates stood at 0.30 for TMY, 0.27 for LP, 0.04 for CI, and 0.12 for DO. Among four principal components, two exhibited eigenvalues greater than 1, collectively explaining 94.05% of total variance. PC1 and PC2 accounted for 67.87% and 26.18% of the variance, respectively. Genetic index equations derived from these two PCs were formulated as follows: $PCs1 = 0.361 EBV_{TMY} + 0.446 EBV_{LP} + 0.490 EBV_{AFC} + 0.475 EBV_{CI} + 0.453 EBV_{DO}$ $PCs2 = 0.643 EBV_{TMY} + 0.494 EBV_{LP} - 0.178 EBV_{AFC} - 0.421 EBV_{CI} - 0.365 EBV_{DO}$. In conclusion, PC could be utilized in genetic improvements of economic traits instead of traditional selection programs. Notably, a favorable correlation between milk production and reproductive traits was observed in the genetic index represented by PC2, suggesting its potential use in selection programs to enhance milk traits while concurrently reducing CI, DO, and AFC.

Key words: Genetic parameters, principal component analysis, milk, reproductive traits, friesian cattle.

INTRODUCTION

The productivity and reproductive efficiency of dairy cattle stand as pivotal determinants affecting the economic viability of dairy industry. Factors such as early maturity, swift postpartum conception, and heightened fertility play essential roles in augmenting calf numbers and, thus, elevating milk production over a cow's lifespan within the herd (**Laureano *et al.,* 2011; Khattab and Atil, 1999**). Estimating the genetic contribution to dairy cow fertility becomes imperative before delineating the direct effect of reproductive performance on milk production and its interplay

with fertility indices. Reproductive traits typically have low heritability, implying limited genetic advancements over time. Furthermore, it is noted that genetic enhancements aimed at bolstering milk production may inadvertently exert a negative impact on fertility traits (**Mariam *et al.,* 2013; El-Komy and Rashad, 2021**). The expansion of breeding programs to encompass multiple traits selection, facilitated by automated phenotype recording and progress in genetic evaluation methods, has introduced complexity into genetic selection decisions (**Val *et al.,* 2008**). With a greater number of traits under consideration, the adoption of complex multivariate techniques

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becomes necessary, potentially constraining the utilization and combination of various traits within a breeding scheme (**Boligon** *et al.,* **2013**).

Principal Component Analysis serves as a multivariate approach enabling researchers to condense data dimensions into new variables termed principal components (PCs) as noted by **Aschard** *et al.* **(2014)**. These PCs offer the benefit of independence owing to their orthogonal projections, along with reduced computational demands (**Pinto** *et al.,* **2006; Gaspa** *et al.,* **2013**). By utilizing Principal Component approach, researchers can delve into the relationship among estimated genetic breeding values and potentially devise more practical selection indices as opposed to purely theoretical ones (**Buzanskas** *et al.,* **2013; Agudelo-Gómez** *et al.,* **2016; Vianaa** *et al.,* **2021; Salem** *et al.,* **2021a**).

The PCA serves as a valuable tool in constructing genetic selection indexes by effectively addressing trait correlations and enabling the weighting of each trait based on its eigenvector as well as contribution to the total variance (**Kirpatrick and Meyer, 2004; Tyriseva** *et al.,* **2011**). Consequently, PC analysis facilitates the direct or indirect selection of superior genotypes within populations (**Long** *et al.,* **2011; Beheshtizadeh** *et al.,* **2013**). While an economic selection index remains the best method for genetic selection, PCA offers an objective approach to trait weighting, particularly beneficial in developing countries where detecting economic weights can be challenging for breeders due to limited economic data availability. Therefore, the aim of this study is to estimate genetic parameters and develop selection indexes that encompass milk traits (total milk yield and lactation period) and reproductive traits (days open, calving interval, and age at first calving) in Friesian cattle in Egypt using PC analysis.

MATERIAL AND METHODS

Dataset Description and Herd Management

The data analyzed in this study originated from two Friesian cattle experimental herds, namely El-Karada and Sakha, associated with the Animal Production Research Institute, Agriculture Research Center, Ministry of Agriculture and Land Reclamation, Egypt. The study focused on various milk traits, including total milk yield (TMY) and lactation period (LP) as well as reproductive traits, including days open (DO), calving interval (CI), and age at first calving (AFC). The dataset consisted of 2837 records from 1243 cows, offspring of 108 sires and 835 dams during the period from 2000 to 2015.

Both experimental herds were raised under similar management and feeding practices. The cows were housed in open sheds and provided with Total Mixed Ration (TMR) throughout the year. Rations were formulated using the National Research Council (NRC). Heifers were inseminated once they reached an appropriate size and weight range (350-375 kg), while cows were inseminated during the first post-partum heat cycle after the 45th day; pregnancy was detected through rectal examination. Cows were machine milked twice daily, in the morning and evening, until two months before their expected calving date. Veterinary supervision ensured vaccinations and medical care for the animals.

Variance Components and Genetic parameters

Prior to estimating genetic parameters and breeding values of the examined traits, the dataset underwent rigorous validation to ensure suitability for the analytical model fitting. Records with fewer than three observations and bulls with fewer than three offspring were removed from the dataset. Moreover, data points exhibiting residual standard deviations greater than 3.5 or below -3.5 standard deviations were excluded from the analysis, according to the methodology outlined by **Buzanskas** *et al.* **(2013) and Tramonte** *et al.* **(2019)**. The data pertaining to all traits under study were subjected to analysis using the single-trait animal model through the DFRAML program (**Boldman** *et al.,* **1995**). Two statistical models were employed to assess genetic parameters and breeding values of studied traits, incorporating fixed effects such as parity order (seven parities) for all traits except AFC, herd (2 herds), kidding season (4 seasons), kidding year (16 years), and the interaction between year and season.

For the analysis of AFC, the first model utilized was:

$$y = Xb + Z_1a + e$$

For all available records across parities, the second model was utilized to estimate heritability, repeatability, and breeding values for all traits except AFC, as follows:

$$y = Xb + Z_1a + Z_2c + e$$

Where, y represents the vector containing phenotypic data; b signifies the vector of fixed effects mentioned before; a denotes the vector of random additive animal effects; c represents the permanent environmental effect; and e stands for the vector of residual effects associated with the studied trait. The matrices X, Z_1 and Z_2 correspond to the incidence matrices for fixed effects, additive genetic and permanent environmental effects, respectively.

Direct heritability (h^2d) and repeatability (r) were computed using the following formulas

$$h^2d = \frac{\sigma^2 d}{\sigma^2 p} \quad r = \frac{\sigma^2 d + \sigma^2 pe}{\sigma^2 p}$$

Here, $\sigma^2 d$, $\sigma^2 pe$, and $\sigma^2 p$ are the variances for additive genetic effects, permanent environmental effects, and phenotypic variance, respectively.

Principal Components Analysis

The breeding values estimated for all traits under investigation in this study were standardized to have a unit variance and a mean of zero. This standardization process was performed to avoid the influence of varying magnitudes and scales across the traits, following the method outlined by **Boligon et al. (2016)**. The standardization formula used was incorporated as following:

$$Z_i = (X_i - \bar{x})/S_i$$

Here, Z_i represents the standardized value of x_i trait, $\bar{x}$ is the mean of the ith trait, and S_i is the corresponding standard deviation.

Subsequently, these standardized breeding values were utilized in Principal Component Analysis (PC) with a covariance matrix using GraphPad Prism 9.0. In this study, principal components (PC) with eigenvalues greater than 1, indicating those that explain the highest

percentages of variance, were selected based on Kaiser's criteria. Each PC, utilizing the standardized breeding values, could generate a new value called a Principal Component Score (PCS). The PCS is computed as the sum of standardized breeding values for each trait weighted by their respective Standardized Score Coefficient (SSC), as outlined by **Buzanskas et al. (2013)**. Consequently, PCs could be employed to assess animals across multiple traits. The SSC for each standardized breeding values in each PC is determined using the following formula:

$$SCC_{ij} = \frac{\text{Eigenvector}_{ij}}{\sqrt{\text{Eigenvector}_j}}$$

Where SSC_{ij} is the SSC of Standardized Estimated Breeding Values (SEBVs) of the ith trait in the jth PC

The Principal Component Scores (PCS) are calculated as follows:

$$PCS_{j1} = \sum_{I=1}^{m} SCC_{ij} \times SEBV_{il}$$

Where PCS_{jl} represents the principal component score for the lth animal in the jth PC, SSC_{ij} signifies the SSC of SEBVs of the ith trait in the jth PC, and $SEBV_{il}$ stands for the standardized estimated breeding value of the ith trait for the lth animal.

RESULTS AND DISCUSSION

Table 1 presents the descriptive statistics for the productive and reproductive traits in this study. The mean total milk yield (TMY) was 3781.13 kg. Contrasting this, previous literature reported varying milk yield averages for Holstein Friesian cows in Egypt: 3597 kg (**Ghazy et al., 2024**) 5397.1 kg (**Moawed et al., 2021**), 9038 kg (**Salem et al., 2006**), 8455.4 kg (**Hammoud, 2013**), and 6384.95 kg (**Faid-Allah, 2015**). The lactation period (LP) was determined to be 326.15 days, aligning with the range of 286 to 407 days reported by **El-Arian et al. (2003), Salem et al. (2006), Hammoud (2013) and Osman et al. (2013)** in Friesian cattle in Egypt. The overall mean calving interval (CI) and days open (DO) were 415.23 and 112.8 days, respectively. These values were

Table 1. Descriptive statistics for the milk and reproductive traits in Friesian dairy cattle

Items	TMY, kg	LP, days	CI, days	DO, days	AFC, days
Mean	3781.13	326.15	415.23	112.80	892.12
S.D	1350.07	96.02	104.39	45.66	180.40
CV (%)	35.70	29.44	25.14	40.48	20.22
No. of records			2837		
No. of animals			1243		
No. of sires			108		
No. of dams			835		

SD, standard deviation; CV, coefficient of variation; CL, calving interval; DO, days open; AFC, age at first calving; LP, lactation period; TMY, total milk yield

lower than those found in an earlier study by **Moawed et al. (2021)** at 439.3 days for CI and 159.7 days for DO. The average age at first calving (AFC) was 892.12 days, a figure close to **Faid-Allah's (2015)** estimate of 30.51 months for Friesian dairy cattle in Egypt. A low AFC in a specific dairy cattle herd typically indicates effective herd management tactics. Effective management practices can ensure heifers reach the suitable breeding weight earlier, leading to a reduced AFC. Discrepancies in the means of milk and reproductive traits between this study and former ones may stem from various factors highlighted by **Atil (2006)**, including the origin of animals (imported vs. locally bred), differences in managerial and climatic conditions, and genetic and phenotypic variations between herds.

Table 2 illustrates the variances component and genetic parameters for milk and reproductive traits. In this study, moderate heritability (0.29 for TMY and 0.23 for LP) and repeatability estimates (0.30 for TMY and 0.27 for LP) were observed for milk traits, suggesting that genetic improvement for these traits through selection could be effective. These results align with the findings of **Moawed et al. (2021)**, which reported heritability estimates ranging from 0.21 to 0.35 for TMY and 0.15 to 0.33 for LP. Similarly, Sanad and Gharib (2021) detected moderate heritability estimates in Holstein Friesian Cattle. Conversely, lower heritability estimates for TMY (0.16) and LP (0.112) were reported by **Salem et al. (2021b) and Faid-Allah (2015)**, respectively. The variations in

heritability estimates in this study compared to previous literature for the same traits may be attributed to changes in herd size (number of records utilized), statistical model used, herd management practices (such as husbandry and nutritional factors), herd performance, and temporary environmental influences.

With regard to fertility traits, low heritabilities (0.04 for CI, 0.06 for DO, and 0.07 for AFC) and repeatabilities (0.04 for CI and 0.12 for DO) were obtained in this study, aligning with the results of **Zahed et al. (2020) and Moawed et al. (2021)** they noted lower heritability estimates for reproductive traits. The low heritability and repeatability estimates for all fertility traits in this study suggest that these traits could be enhanced with improved managerial and environmental conditions. Additionally, relying solely on first parity records to predict future animal reproduction may not be dependable.

Table 3 displays the genetic breeding value estimates for the traits under investigation. The cow breeding value ranges for milk traits were (1388.28 kg for TMY and 88.11 days for LP), In terms of reproductive traits, the breeding value ranges were 15.70, 17.98 and 55.92 days for CI, DO, and AFC, respectively. The present results are consistent with the findings of **Sanad and Gharib (2021)**, who also observed wide ranges in cow breeding values of milk traits, being 3188.28 kg, 109.7 days for TMY and LP, respectively. Meanwhile, they were 12.1 days, and 40.7 days for CI and DO, respectively. **Ghazy et al. (2024)** presented breeding values:

Table 2. The estimates of variance component and genetic parameters of milk and reproductive traits in Friesian dairy cattle

Items[*]	$\sigma^2 a$	$\sigma^2 pe$	$\sigma^2 e$	$\sigma^2 p$	h^2	r
TMY, kg	528579.81	9113.45	1284988	1822681	0.29±0.06	0.30
LP, days	2119.551	368.74	6727.15	9215.44	0.23±0.03	0.27
CI, days	435.89	10.90	10448.38	10895.17	0.04±0.02	0.04
DO, days	125.09	116.75	1842.93	2084.77	0.06±0.04	0.12
AFC, days	2358.09	----	30263.81	32621.90	0.07±0.02	----

*, See abbreviations in Table 1; $\sigma^2 a$, additive genetic variance; $\sigma^2 pe$, permanent environmental variance; $\sigma^2 e$, residual variance; $\sigma^2 p$, phenotypic variance; h^2, heritability; r, repeatability.

Table 3. Minimum, maximum, accuracy, and range of predicted breeding values for milk and reproductive traits in Friesian dairy Cattle

Traits[*]	Minimum	Accuracy	Maximum	Accuracy	Range
TMY, kg	-411.43	0.73	976.85	0.83	1388.28
LP, days	-36.33	0.85	51.78	0.70	88.11
CI, days	-6.69	0.43	9.01	0.41	15.70
DO, days	-7.27	0.46	10.71	0.49	17.98
AFC, days	-19.75	0.55	36.17	0.53	55.92

*, See abbreviations in Table 1

1397 kg, 31.91, 13.84, and 16.57 days for TMY, LP, CI, and DO, respectively. The broad range in breeding values for milk traits indicates substantial genetic variation, offering opportunities for trait improvement through selection based on the superior breeding values of individual animals.

Recently, principal components analysis (PC) has been used to explore the variability in estimated breeding values (EBV) for economically important livestock traits. In this study, the PC was carried out on the EBV for milk and reproductive traits in Friesian cattle in Egypt. Among the four PC, two PC exhibited eigenvalues greater than 1, collectively responsible for 94.05% of the total variance. PC1 and PC2 elucidated 67.87% and 26.18% of total variance, respectively (Table 4). As a result, these initial two PC effectively captured a significant portion of the variance in EBV related to milk and reproductive traits. The EBV for DO, CI, LP, and AFC displayed strong correlations with

PC1, ranging from 0.575 to 0.902. Conversely, TMY exhibited a notable correlation with PC2 at 0.735 (Table 5 and Fig. 1).

The current results align closely with the findings of Sanad and Gharib (2021), who noted a strong correlation between milk and reproductive traits in Friesian cattle with PC1 and PC2, explaining 46.6% and 20.5% of total variance, respectively. Similarly, **Salem _et al._ (2021b)** showed that PC1 was associated with the overall average performance of reproductive traits, while PC2 correlated with the overall average performance of milk traits in Egyptian buffaloes. In this study, the principal component score (PCS) for each animal in the first two PCS was derived by dividing the eigenvector by the square root of the eigenvalue of EBV traits, resulting in the following two equations:

$PCS1 = 0.361EBV_{TMY} + 0.446EBV_{LP} + 0.490EBV_{AFC} + 0.475EBV_{CI} + 0.453EBV_{DO}$

$PCS2 = 0.643EBV_{TMY} + 0.494EBV_{LP} - 0.178EBV_{AFC} - 0.421EBV_{CI} - 0.365EBV_{DO}$

Table 4. Eigenvalue and variance proportion for the Principal Component on standardized genetic breeding values

Principal Component (PCs)	Eigenvalue	Variance	Cumulative variance
PC1	3.39	67.87	67.87
PC2	1.31	26.18	94.05
PC3	0.286	5.72	99.78
PC4	0.011	0.22	100

Table 5. Correlation coefficients between standardized breeding values of the studied traits with the first 2 principal components

Traits*	PC1	PC2
TMY, kg	0.575	0.735
LP, days	0.622	0.566
DO, days	0.835	-0.418
CI, days	0.874	-0.482
AFC, days	0.902	-0.203

*, See abbreviations in Table 1
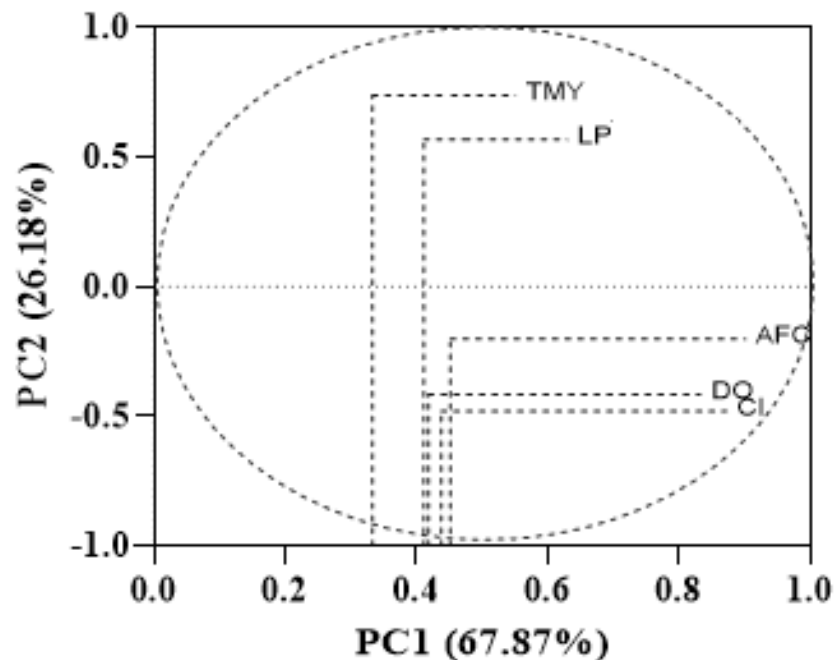
Fig. 1. Distribution of the estimated genetic breeding values for milk and reproductive traits in each of the first two principal components, PC1 (Dim 1) *vs*. PC2 (Dim 2). See key Table 1 for abbreviations

The scores derived from the first two PCs in this study effectively captured the essential information regarding EBVs for reproduction and milk traits in Friesian Cattle. These PCs could be used as genetic indices instead of the traditional selection index method (**Buzanskas et al., 2013; Boligon et al., 2016**). Unlike traditional approaches that necessitate economic weights for each trait, the use of these PCs proves advantageous, especially in situations where assigning economic values to economic traits poses challenges, such as in the context of fluctuating Egyptian markets. Utilizing principal component analysis enables the selection of animals based on just the results produced by PC1 and PC2, rather than relying on five distinct breeding values. This streamlined method allows for an effective and balanced selection of animals as soon as the results from each component become available. This assertion is supported by the former studies indicated that the utilization of numerical scores derived from PC1 and PC2 facilitated the selection of animals to improve the economic traits such as CI, DO, AFC TMY, and LP (**Mello et al., 2020; Amaya et al., 2021**)

In this study, PC1, which showed stronger loading for reproductive traits (DO, CI, and AFC), not only captured a significant portion of total variance but also highlighted an unfavorable genetic correlation between milk and reproduction traits, as indicated by the positive correlation coefficients. Conversely, PC2 illustrated a favorable correlation between milk production and reproduction traits. This was evidenced by positive correlations for milk traits and negative signs for reproductive traits. The preceding correlation coefficients between the various traits within the principal components underscored the intricate relationships among these traits and the genetic complexity of quantitative traits, affected by multiple genes that contribute differentially to each trait (**Boligon et al., 2016; Salem et al., 2021b**). Consequently, incorporating scores from PC2 in the selection process for improving TMY and LP could potentially lead to improvements in reproduction traits. So that, opting for animals with superior PC2 corresponds with the breeding objectives of dairy farmers and proves more advantageous for Friesian Cattle selection programs. The present results

corresponded with **Amaya et al. (2021)** who reported PCS2 could also be leveraged to improve milk production in Simmental cattle. Specifically, calving interval emerged as the most significant trait within PC2, attributable to the negative correlation observed as well as its eigenvector.

Collectively, prior to implementing selection processes, breeders should determine the desired level of genetic improvement for each trait and establish the breeding goals for their animals. This information is crucial for identifying which animals within the PCS could be utilized effectively in the selection programs (**Salem et al., 2021b**). In our study, incorporating animals with higher scores in PC1 into genetic index may lead to undesired increases in CI, DO, and AFC. On the other hand, animals with elevated scores in PC2 could be targeted in selection programs aimed at enhancing milk traits (TMY and LP) while concurrently reducing reproductive traits (CI, DO, and AFC). Nonetheless, dairy farmers typically prioritize raising cattle that yield higher milk production without compromising reproductive traits, as emphasized by **Abdel-Salam (2019)**.

Conclusion

The results revealed moderate heritability and repeatability values for milk traits (TMY and LP) and lower values for reproductive traits (DO, CI, and AFC). Through principal component analysis (PCs), breeders can develop genetic indexes that concurrently enhance milk traits and reproductive traits in Friesian cattle. Furthermore, the two principal components accounted for 94.05% of the total variance, indicating their effectiveness in capturing the breeding value variation of the traits under the performance level of these herds. Finally, animals with higher scores in PC2 align with the breeding goals of milk-producing farmers and offer greater benefits for selection programs of Friesian cattle by improving milk traits while simultaneously reducing CI, DO, and AFC.

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تحليل المكــون الرئيسـي للقيــم التربــوية لصفــات اللبــن والتناسل فى أبقار الفريزيان فى مصر

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تهدف هذه الدراسة إلى تقييم المعايير الوراثية والقيم التربوية لصفات اللبن (انتاج اللبن الكلى وطول موسم الحليب) وصفات التناسل (الفترة من الولادة حتى التلقيحة المخصبة و الفترة بين ولادتين و العمر عند أول ولادة) كما تضمنت الدراسة أيضا تحليل العلاقات بين القيم التربوية باستخدام تحليل المكون الرئيسي وتصميم أدلة انتخابية لتحسين الآداء العام. تم تجميع 2837 سجل حليب لعدد 1243 بقرة نتاج ل 108 ذكر و 835 أنثي خلال الفترة من عام 2000 حتى عام 2015 من قطيعين لأبقار الفريزيان بمحطتى بحوث سخا والقرضة التابعين لمعهد بحوث الإنتاج الحيواني. كانت قيم المكافئ الوراثي 0.29 و 0.23 و 0.04 و 0.06 و 0.07 لإنتاج اللبن الكلى وطول موسم الحليب والفترة بين ولادتين والفترة من الولادة حتى التلقيحة المخصبة والعمر عند أول ولادة على التوالي. بينما كانت قيم المعامل التكراري 0.30 لإنتاج اللبن الكلى و 0.27 لطول موسم الحليب و 0.04 للفترة بين ولادتين و 0.12 للفترة من الولادة حتى التلقيحة المخصبة.من بين أربعة مكونات رئيسية كان للمكونان الرئيسيين الأول والثانى قيم ذاتية (eigenvalues) أعلى من الواحد الصحيح ويمثلان 94.05% من التباين الكلى (67.87 و26.18% للمكون الرئيسي الأول والثانى على التوالى) .وجاءت الأدلة الإنتخابية المشتقة منهم على النحو التالي:

$$PCs1=0.361EBV_{TMY}+0.446EBV_{LP} +0.490EBV_{AFC}+0.475EBV_{CI}+0.453EBV_{DO}$$

$$PCs2=0.643EBV_{TMY}+0.494EBV_{LP} -0.178EBV_{AFC}-0.421EBV_{CI}-0.365EBV_{DO}$$

فى الخاتمة، يمكن استخدام تحليل المكون الرئيسي فى التحسين الوراثي للصفات الإقتصادية بدلاً من طرق الإنتخاب التقليدية.جدير بالذكر أن المكون الرئيسي الثانى أظهر ارتباط مرغوب فيه بين صفات اللبن وصفات التناسل مما يقترح امكانية استخدامه فى تحسين إنتاج اللبن بالتزامن مع تقليل الفترة بين ولادتين والفترة من الولادة حتى التلقيحة المخصبة والعمر عند أول ولادة.

الكلمات الإسترشادية: المعايير الوراثية ، تحليل المكون الرئيسي، صفات اللبن والتناسل، ابقار الفريزيان.