INTRODUCTION

Productive performance traits, such as milk yield and reproductive traits play an important role in the profitability of dairy cattle, because they minimize the generation interval, enhance the genetic progress, and lead to animals with better performance (Laureano et al., 2011). Moreover, the relationship that has been noticed between the direct and maternal genetic effects along with their correlation with production traits in dairy cows is essential for breeding programs and strategies (Campêlo et al., 2004). Thus, dairy cattle performance can be evaluated by milk yield...
Principle components analysis is defined as a multivariate statistical method that can be applied to minimize the number of correlated traits into a smaller number of independent variables called principle components, with minimum loss of information in the original data (Bolormaa et al., 2010). This approach produces orthogonal components that are linear combinations of the main variables, depending on the eigenvalues of the variables of interest. The eigenvalues are created in an order from the highest to the lowest one and each Principle component explains superior variability than the next PC (Meyer, 2007).

Multivariate methodologies, such as principle components analysis could be used to extract the loadings or coefficients that explain the maximum variation in the datasets, providing a tool that picks up the animals with similar characteristics. Once identified, these new components or groups could be selected for dairy breeding programs to improve both productivity and fertility (Karacaören and Kadar, 2011; Buzanskas et al., 2013; Jolliffe and Cadima, 2016; Lopes et al., 2016). Besides, multivariate statistical models might denote relationships and significant outcomes that could not be possible when using univariate approaches (Lopes et al., 2013; Moraes et al., 2015; Fraga et al., 2016). Furthermore, multivariate methods help handle pertinent decisions in animal breeding programs (Cardoso et al., 2003; Selim et al., 2018).

Several studies used principle components methodology in animal breeding. For example, PCA has been investigated for genetic assessment of beef cattle (Bignardi et al., 2014; Boligon et al., 2016; Tramonte et al., 2019) and evaluation of reproductive traits of different breeds (Savegnago et al., 2011; Buzanskas et al., 2013). Bignardi et al. (2012), Moawed and Osman (2018), and Mello et al. (2019) applied PCA for dimension reduction of dairy cow traits. A recent exploratory study was conducted by Oliveira et al. (2014) who utilized PCA to evaluate nine traits in buffalo cattle in Brazil and concluded that the first four PCs are adequate to explore the covariance structure of these traits. The previous studies concluded that PCA permits minimizing the traits dimension, simplifies the interpretation of data with few components, and visualizes the relationship between the original datasets. However, few studies considered the breeding values in the PCA and only incorporated the original phenotypic traits.

By analyzing animal breeding values, it could be possible to identify the genetic relationships among the economically important traits of dairy cows, both in magnitude and direction (Savegnago et al. 2011; Porto-Neto et al. 2013; Osorio-Avalos et al., 2015). Therefore, the present study aimed to estimate genetic parameters and breeding values for the most economic traits of Holstein dairy cows using six different animal models. Furthermore, the principle components analysis (PCA) was applied to explore the relationship between the estimated breeding values for the functional traits.

**MATERIALS AND METHODS**

**Dataset Description**

The dataset investigated in this study was provided by a commercial dairy herd belonging to Modern Agricultural Development Company (MADC) located nearly 80 km from Alexandria, Egypt. The traits analyzed in Holstein Friesian cows were milk yield (MY), 305-day milk yield (305 DMY), peak yield (PY), lactation length (LL), days open (DO), calving interval (CI), and services per conception (SC). The dataset from three stations was collected representing 18221 cows. Animals were born between 2007 and 2018. At all three stations, cows were kept under similar feeding and management systems. Animals are kept in open sheds. All year round, cows fed ad libitum using Total Mixed Ration (TMR), and the ration formulations were done by the National Research Council (NRC) program. In most herds, heifers and cows were artificially bred using frozen semen imported from U.S.A and Canada. Heifers were bred when reached 350 - 375 kg of body weight and cows were served during the first heat after the 45th day post-partum. Cows were machine milked three times daily at eight hours intervals. Cows were usually milked until two months before the expected calving date.

**Statistical Models And Genetic Parameters**

Before estimation of genetic parameters and breeding values for the studied traits, data were examined and tested to be valid for the analytical model fitting. For all traits, records with fewer than three observations, and bulls having less than three offspring were excluded from the prepared data file. Normality of the trait's residuals was verified and data with residual standard deviations greater than 3.5 and below -3.5 standard deviations were removed from the analysis (Buzanskas et al., 2013; Tramonte et al., 2019).

Six animal models were incorporated to estimate variance components, genetic parameters and subsequently breeding values for each trait. In all models, parity, age at calving, calving season (summer, autumn, winter, and spring), and year of calving (2007 and 2018) were included as fixed effects. Random effects were fitted based on the model type. Technically, the analysis was repeated several times until a minimum value of -2 Log L was detected, when -2 Log L...
In all models applied, the direct additive genetic effect of the animal was considered as a random effect along with the random effect of residuals. In model 2, the random permanent environmental effect was employed. In model 3, the maternal genetic effect of the dam was added without consideration of the direct-maternal covariance. Model 4 was similar to model 3 but the direct-maternal covariance was assumed. Model 5 and model 6 employed all random effects (animal, maternal, environmental, and residuals), but the former model assumed no direct-maternal covariance, whereas the latter one took into account such covariance. The statistical models proposed for the studied traits are summarized as follows:

Model 1:  
$$Y = Xb + Z_a u_a + e$$

Model 2:  
$$Y = Xb + Z_a u_a + Z_{pe} u_{pe} + e$$

Model 3:  
$$Y = Xb + Z_a u_a + Z_m u_m + e$$  \[\sigma_{AM} = 0\]

Model 4:  
$$Y = Xb + Z_a u_a + Z_m u_m + e$$  \[\sigma_{AM} \neq 0\]

Model 5:  
$$Y = Xb + Z_a u_a + Z_m u_m + Z_{pe} u_{pe} + e$$  \[\sigma_{AM} = 0\]

Model 6:  
$$Y = Xb + Z_a u_a + Z_m u_m + Z_{pe} u_{pe} + e$$  \[\sigma_{AM} \neq 0\]

In which $Y$ is $n \times 1$ vector of observations for the traits; $b$ is $p \times 1$ vector of fixed effects, $p$ = number of levels for fixed effects; $u_a$ is $q \times 1$ vector of random animal effects, $q$ = number of levels for random effects; $u_{pe}$ is the vector of random permanent maternal environmental effects; $u_m$ is the vector of $N \times N_m$ maternal additive genetic effects; $X$ is the design matrix of order $n \times p$, which relates records to fixed effects; $Z_a$ is the design matrix of order $n \times q$, which relates records to random animal effects; $Z_m$ is the incidence matrix of permanent maternal environmental effects; $Z_{pe}$ is the incidence matrix of maternal genetic effects, and $e$ is $n \times 1$ vector of random residual effects.

The estimated heritabilities for both direct additive genetic effect and maternal genetic effects are given by the following equations (Willham, 1980):

$$h^2_a = \frac{\sigma^2_a}{\sigma^2_p} \quad \text{and} \quad h^2_m = \frac{\sigma^2_m}{\sigma^2_p}$$

Where, $h^2_a$ is the direct heritability; $h^2_m$ = maternal heritability; $\sigma^2_a$, $\sigma^2_m$ and $\sigma^2_p$ are the direct additive genetic variance, maternal additive genetic variances, and phenotypic variance, respectively. Variance components estimation, genetic parameters, and estimated breeding values (EBVs) for all traits were performed using VCE version 6.0.2 software according to permission from Groeneveld et al. (2008), based on the restricted maximum likelihood procedures of the general linear models.

**Principle Component Analysis**

Principle component analysis (PCA) is a multivariate dimensionality reduction statistical method and aimed to summarize the information involved in the original EBVs of studied traits into a smaller number of newly generated variables called principle components, without loss of vital information. Moreover, the analysis endeavored to find out the relationships between the EBVs (Hair et al., 2009). The EBVs of all traits were standardized through the standard normal distribution.

The Kaiser- Meyer-Olkin (KMO) and Bartlett’s tests were inserted for checking the sampling sufficiency of PCA (Cerny and Kaiser, 1977; Snedecor and William, 1989). The Kaiser criterion was also applied to choose the number of principle components that explain the maximum genetic variation in the data. Such criterion deemed only the principle components with eigenvalues greater than one. The eigenvalue of the principle component is connected with the variability of all EBVs of traits involved in the principle component, which intern constitutes an eigenvector (Rencher, 2002). These eigenvectors explain the correlation of each trait’s variance with the principle component. The KMO was calculated according to the following equation:

$$\text{KMO} = 1 - \frac{\sum_{i\neq j} R_{ij}^2}{\sum_{i\neq j} R_{ij}^2 + \sum_{i\neq j} C_{ij}^2}$$

Where $R_{ij}$ is the correlation matrix and $C_{ij}$ is the partial covariance matrix.

Bartlett’s test of sphericity was utilized to detect the appropriateness of the data to be analyzed using PC analysis. This test compares the correlation matrix of EBVs of traits with the corresponding zero matrices, or identity matrix, to check the overall correlations among EBVs. This test is distributed as chi-square with $[p (p-1) / 2]$ as the degree of freedom, and is given as follows:

$$\chi^2 = (1 + \frac{2p+5}{6} - n) \log |R|$$

The expected values and variance components are presented as follows:

$$E(y) = Xb; \quad E(e) = 0, \quad \text{therefore,} \quad \text{var} (e) = I \sigma^2_e = R; \quad \text{var} (a) = A \sigma^2_a = G, \quad \text{var} (pe) = \sigma^2_{pe} \quad \text{and} \quad \text{var} (m) = \sigma^2_m$$

Where $A$ is the numerator relationship matrix and $I$ is identity matrix.

The Kaiser criterion was also applied to choose the number of principle components that explain the maximum genetic variation in the data. Such criterion deemed only the principle components with eigenvalues greater than one. The eigenvalue of the principle component is connected with the variability of all EBVs of traits involved in the principle component, which intern constitutes an eigenvector (Rencher, 2002). These eigenvectors explain the correlation of each trait’s variance with the principle component. The KMO was calculated according to the following equation:

$$\text{KMO} = 1 - \frac{\sum_{i\neq j} R_{ij}^2}{\sum_{i\neq j} R_{ij}^2 + \sum_{i\neq j} C_{ij}^2}$$

Where $R_{ij}$ is the correlation matrix and $C_{ij}$ is the partial covariance matrix.
In which $p$ is the number of traits, $n$ is the overall sample size, and $|R|$ is the determinant of correlation matrix $R$. The null hypothesis for Bartlett’s test of sphericity states that the correlation matrix is not diverged from the identity matrix ($H_0$: traits are orthogonal). If $H_0$ is rejected, PCA will do the reduction process for EBVs of traits without loss of information.

The principle components are independent variables representing a linear combination of variables (estimated breeding values). The first extracted and rotated principle component elucidates the highest percent of the total genetic variation in EBVs, followed by the second and third components. With a dataset consisted of $p$ variables, the given variations in EBVs, followed by the second and third components elucidates the highest percent of the total genetic variation values). The first extracted and rotated principle component representing a linear combination of variables (estimated breeding values). The principle components are independent variables representing a linear combination of variables (estimated breeding values). The first extracted and rotated principle component elucidates the highest percent of the total genetic variation in EBVs, followed by the second and third components. With a dataset consisted of $p$ variables, the given variations in EBVs, followed by the second and third components elucidates the highest percent of the total genetic variation values).

The principle components could be used as an index to assess animals for different traits. The standardized coefficients were estimated as follows:

$$PC_i = a_{i1}X_1 + a_{i2}X_2 + a_{i3}X_3 + \ldots + a_{ip}X_p$$

Where, $i = 1,2,3,\ldots,p$ and $j = 1,2,3,\ldots,p = j^{th}$ standardized coefficient of the $j^{th}$ EBV of the $i^{th}$ principle component. $X_j$ is the value of the original EBV.

By using the standardized EBVs of traits, the principle components score can be outputted. These scores resulted from the sum of standardized BVs for each trait weighted by the corresponding standardized score coefficient. The principle components could be used as an index to assess animals for different traits. The standardized coefficients were estimated as follows:

$$a_{ij} = \frac{\text{eigenvector}_{ij}}{\text{eigenvalue}_{ij}}$$

Where, $a_{ij}$ is the standardized coefficient for EBVs of the $j^{th}$ productive or reproductive trait in the $i^{th}$ principal component. Data mining and analyses were conducted by SPSS software (SPSS, version 25) and the PRINCOMP procedure statement of SAS (SAS 9.4, USA).

**RESULTS AND DISCUSSION**

The descriptive statistics for the productive and fertility traits obtained in this study are presented in Table 1. The means of milk yield, peak yield, lactation length, days open, calving interval, and services per conception were 5397.1 kg, 38.98 kg, 198.7 days, 159.7 days, 439.3 days, and 3.98, respectively. The values of the coefficient of variations were high and ranged from 20.96 % to 84.17 %. The heritability estimates and their standard errors for the investigated traits obtained from the six models are presented in Table 2. The direct heritability estimates for productive traits ranged from 0.21 to 0.35, from 0.02 to 0.30, and from 0.15 to 0.33, for MY, PY, and LL, respectively. The estimated direct heritabilities for fertility traits varied from 0.04 to 0.18, from 0.05 to 0.18, and from 0.05 to 0.15, for DO, CI, and SC, respectively. It was noticed that the standard errors of heritability estimates were all low.

Table 2 showed the values of maternal heritability for all traits as estimated by models 3, 4, 5, and 6. The values of maternal heritability of MY, PY, and LL ranged from 0.21 to 0.32, from 0.01 to 0.17, and from 0.03 to 0.07, respectively. Fertility traits presented maternal heritability estimates ranged from 0.04 to 0.21 for DO, from 0.04 to 0.14 for CI, and from 0.02 to 0.11 for SC. It was apparent that the model used in the estimation process considerably affected the values of direct and maternal heritability. In general, the estimates of maternal heritability for productive traits were lower than the direct heritabilities in the four mentioned models. While as, models 4 and 6 informed maternal heritability estimates higher than direct heritability values of reproductive traits.

According to models, the current results revealed that the inclusion of maternal effects (permanent environmental and additive genetic) in some models along with the existence of covariance between the direct effect of animals and maternal effects lead to varied heritability estimates and intern their variance components. Overall, an increase was observed in the values of direct heritability for productive traits (Table 2) following the insertion of maternal effects. Model 4 informed moderate to high direct heritability values (≥ 0.30) for MY, PY, and LL, accompanied by an increase in maternal heritabilities. Model 6 behaved like model 4, but with lower estimates. On the other hand, although, the direct heritability estimates for fertility traits were low, models 4 and 6 informed higher maternal heritabilities compared to other models. In terms of the chosen model, the results of the likelihood ratio test are presented in Table 3. Model 4 showed the lowest -2 Log-likelihood value (13882.24).

PCA was conducted using the EBVs of MY, PY, LL, DO, CI, and SC. The measures of sampling adequacy and the validity index of PCA are presented in Table 4. Kaiser-Meyer-Olkin (KMO) measures of sampling adequacy were 0.669, 0.735, 0.745, 0.592, 0.742, and 0.542 for models 1, 2, 3, 4, 5, and 6, respectively. Also, Bartlett’s test of Sphericity denoted significant chi-square statistics ($P \leq 0.0001$) for all studied models. The number of extracted PC, eigenvalues, percentage of additive genetic variance explained by each component along with the cumulative proportion of genetic variance of EBVs of traits are presented in Table 5. Based on the best-fitted model (Table 3), model 4 retained only two components (eigenvalues > 1.0). From the six original traits (EBVs$_{MY}$, EBVs$_{PY}$, EBVs$_{LL}$, EBVs$_{DO}$, EBVs$_{CI}$, and EBVs$_{SC}$), 75.04 % of the total
Table 1: Descriptive statistics for the productive and reproductive traits studied in Holstein dairy cattle

| Trait investigated       | Mean   | Standard deviation | Coefficient of variation |
|--------------------------|--------|--------------------|--------------------------|
| Milk yield, kg           | 5397.1 | 3821.8             | 70.81                    |
| Peak yield, kg           | 38.98  | 8.18               | 20.96                    |
| Lactation length, days   | 198.7  | 150.2              | 75.56                    |
| Days open                | 159.7  | 124.9              | 78.26                    |
| Calving interval, days   | 439.3  | 125.3              | 28.52                    |
| Services per conception  | 3.98   | 3.35               | 84.17                    |

Table 2: Direct ($h^2_d$) and maternal ($h^2_m$) heritability estimates ± standard errors observed in the final data from the six animal models for investigated traits in Holstein dairy cattle

| Model   | Heritability | MY     | PY     | LL     | DO     | CI     | SC     |
|---------|--------------|--------|--------|--------|--------|--------|--------|
| Model 1 | Direct       | 0.23 ± 0.04 | 0.02 ± 0.03 | 0.18 ± 0.03 | 0.14 ± 0.03 | 0.14 ± 0.03 | 0.07 ± 0.02 |
|         | Maternal     |        |        |        |        |        |        |
| Model 2 | Direct       | 0.26 ± 0.09 | 0.08 ± 0.11 | 0.22 ± 0.07 | 0.18 ± 0.05 | 0.18 ± 0.06 | 0.10 ± 0.03 |
|         | Maternal     |        |        |        |        |        |        |
| Model 3 | Direct       | 0.21 ± 0.01 | 0.02 ± 0.01 | 0.15 ± 0.02 | 0.09 ± 0.01 | 0.09 ± 0.01 | 0.05 ± 0.01 |
|         | Maternal     |        |        |        |        |        |        |
| Model 4 | Direct       | 0.35 ± 0.03 | 0.30 ± 0.02 | 0.33 ± 0.02 | 0.06 ± 0.01 | 0.09 ± 0.01 | 0.09 ± 0.01 |
|         | Maternal     |        |        |        |        |        |        |
| Model 5 | Direct       | 0.32 ± 0.02 | 0.12 ± 0.01 | 0.05 ± 0.01 | 0.25 ± 0.02 | 0.13 ± 0.01 | 0.21 ± 0.02 |
|         | Maternal     |        |        |        |        |        |        |
| Model 6 | Direct       | 0.27 ± 0.01 | 0.04 ± 0.01 | 0.19 ± 0.01 | 0.13 ± 0.01 | 0.13 ± 0.01 | 0.09 ± 0.01 |
|         | Maternal     | 0.02 ± 0.01 | 0.01 ± 0.01 | 0.03 ± 0.01 | 0.05 ± 0.01 | 0.05 ± 0.01 | 0.02 ± 0.01 |

The overall description of the traits in this study (Table 1) were consistent with the findings of (Salem et al., 2006; Sahin et al., 2017; Mello et al., 2019), who conducted similar studies and estimated genetic parameters using the same six animal models. The high percentages of the coefficient of variations for all traits indicated the presence of high phenotypic variations among individual animals and hence, suggesting the possibility of selection and improvement of the current herd. Among the studied traits, the highest CV % was recorded for MY, LL, DO, and SC, which means that these traits could have a superior chance of being included in the selection index.

Overall, the direct heritability estimates for MY were moderate, and the highest values were informed by model 4. These values were in accordance with the findings reported by (Tilki et al., 2008; Karabulut et al., 2012; Agudelo-Gomez et al., 2015), who estimates direct heritability estimates for milk yield from 0.15 to 0.37. The direct heritabilities for PY were low in magnitude and the only improvement was observed in model 4, where the maternal genetic effect was added to the model, assuming the
### Table 4: Measures of sampling adequacy and validity index of principle components analysis for the standardized breeding values of traits, estimated by the six animal models

| Model   | Kaiser-Meyer-Olkin (KMO) test | Bartlett's test of sphericity |
|---------|-------------------------------|------------------------------|
|         |                               | Chi-square | df | P value |
| Model 1 | 0.669                         | 45848.025  | 21 | 0.0001  |
| Model 2 | 0.735                         | 58994.413  | 21 | 0.0001  |
| Model 3 | 0.745                         | 58274.774  | 21 | 0.0001  |
| Model 4 | 0.592                         | 38314.448  | 21 | 0.0001  |
| Model 5 | 0.742                         | 57139.315  | 21 | 0.0001  |
| Model 6 | 0.542                         | 37349.861  | 21 | 0.0001  |

### Table 5: Eigenvalues for the retained principle components, the percentage and cumulative percentage of total additive genetic variance extracted in each animal model

| Animal model | Principle component | Eigenvalue | Percentage of total additive genetic variance (%) | Cumulative percentage of total additive genetic variance (%) |
|--------------|---------------------|------------|---------------------------------------------------|-------------------------------------------------------------|
| Model 1      | PC1                 | 4.458      | 63.68 %                                           | 63.68 %                                                     |
|              | PC2                 | 1.577      | 22.53 %                                           | 86.22 %                                                     |
| Model 2      | PC1                 | 5.056      | 72.23 %                                           |                                                            |
|              | PC2                 | 1.336      | 19.09 %                                           |                                                            |
| Model 3      | PC1                 | 5.006      | 71.52 %                                           |                                                            |
| Model 4      | PC1                 | 4.042      | 57.74 %                                           |                                                            |
|              | PC2                 | 1.211      | 17.29 %                                           |                                                            |
| Model 5      | PC1                 | 5.336      | 76.23 %                                           |                                                            |
| Model 6      | PC1                 | 3.121      | 44.59 %                                           |                                                            |
|              | PC2                 | 1.898      | 27.11 %                                           |                                                            |
|              | PC3                 | 1.183      | 16.89 %                                           |                                                            |
|              |                     |            |                                                   |                                                            |

### Table 6: Linear correlations between the standardized estimated breeding values (genetic values) of the traits and the principle components

| Model   | Principle component | Estimated Breeding Values (EBVs) of traits |
|---------|---------------------|--------------------------------------------|
|         |                     | EBVs\textsubscript{MY} | EBVs\textsubscript{PY} | EBVs\textsubscript{LL} | EBVs\textsubscript{DO} | EBVs\textsubscript{SC} | EBVs\textsubscript{CI} |
| Model 1 | PC1                 | 0.862 | 0.585 | 0.965 | 0.940 | 0.667 | 0.882 |
|         | PC2                 | 0.176 | 0.746 | -0.150 | -0.281 | -0.434 | -0.368 |
| Model 2 | PC1                 | 0.848 | 0.620 | 0.968 | 0.960 | 0.866 | 0.941 |
|         | PC2                 | 0.059 | 0.747 | -0.205 | -0.240 | -0.338 | -0.279 |
| Model 3 | PC1                 | 0.846 | 0.747 | 0.988 | 0.954 | 0.555 | 0.851 |
| Model 4 | PC1                 | 0.733 | 0.336 | 0.852 | 0.875 | 0.922 | 0.777 |
|         | PC2                 | -0.475 | 0.756 | -0.363 | 0.428 | 0.103 | 0.574 |
existence of direct-maternal covariance. The estimates for LL behaved as recorded in MY, but the estimates for LL were quite lower as compared to MY. The direct heritability estimates for PY and LL were lower than previously reported values (Rosati and Van Vleck, 2002; Bolivar-Vergara et al., 2012), but higher than that reported by (Boligón et al., 2010; Seno et al., 2010; Buzanskas et al., 2013). It was obvious that the direct heritability estimates for all fertility traits were low (< 0.20) in all models, which agrees with the results of Sahin et al. (2017) who applied similar six animal models, reporting the same findings. In terms of accuracy and validity of the current estimates, the standard errors of heritability estimates were low for all traits and models, indicating that the current estimates are reliable and unbiased (Buzanskas et al., 2013). The present estimates of direct heritability revealed that selection based on productive traits, particularly MY and LL may be more effective and would lead to genetic progress compared with selection based on fertility traits because they denoted the highest estimates compared with other traits. Although, the direct heritability of fertility traits was low, suggesting that these traits could be influenced by the environmental conditions, however, the inclusion of these traits in the selection index is important to improve the cow's performance (Buzanskas et al., 2013; Shalaby et al., 2015).

The present study showed lower estimates of maternal heritability (Table 2) as compared with the corresponding direct heritabilities for productive traits, indicating that the maternal additive genetic variances were lower than the direct additive genetic variance of the animals. These findings were in agreement with those reported by (Tilki et al., 2008; Abera et al., 2011; Sahin et al., 2012) who determined higher direct heritability estimates for Brown Swiss Cattle. Contrary, Karabulut et al. (2012) estimated higher maternal heritability estimates for the same studied traits. The estimated maternal heritability for fertility traits agrees with values denoted by (Albuquerque and Meyer, 2001; Malhado et al., 2007; Bolivar-Vergara et al., 2012) who reported values between 0.02 and 0.18.

In this research, the maternal effects were separated into two units, maternal environmental and maternal genetic effects. The current results revealed that model 4 with maternal additive genetic effects along with the direct-maternal covariance informed the highest improvement in heritability values, particularly for MY trait. These results came in accordance with those in the study of (Agudelo-Gomez et al., 2015; Shalaby et al., 2015) who estimated genetic parameters in Holstein-Friesian cows and fitted a similar model as best for genetic evaluation of dairy cattle. Although, model 6 informed similar results to model 4, however, the latter denoted superior improvement, both indirect and maternal heritabilities. This suggested that the insertion of permanent maternal environmental effect in the analytical model was insignificant. This conclusion is in contradiction with the results of Tilki et al. (2008) who mentioned that model 6 was the best. Based on the present heritability estimates and the best-fitted model (lowest LRT), where the direct-maternal genetic covariance has existed, it was concluded that the inclusion of maternal genetic effect in the model allows for a better estimation of heritability for productive traits. Besides, the reproductive efficiency of cows is affected by their dams. Accordingly, the improvement of health status, reproductive performance of dams would have an impact on cows in the future.

PCA was conducted using breeding values estimated by the six models for all traits. The high KMO values (Table 4) in the present study imply that the correlation between EBVs of traits was not unique, which is not related to the remaining EBVs outside each sample correlation. The values of KMO in this study are in agreement with the measures evaluated by Verma et al. (2015), who reported KMO measure of sampling adequacy to be 0.75, and Egena et al. (2014), who reported that KMO was equal to 0.80. The significance of correlation matrices tested with Bartlett’s test of Sphericity (Table 4) gives support for the authenticity of PCA analysis for the data set. The results of PCA (Table 5) are consistent with the previous reports (Buzanskas et al., 2013; Agudelo-Gomez et al., 2015; Moawed and Osman, 2018; Tramonte et al., 2019), indicating the usefulness of PCA to reduce data dimensions. According to Val and Ferraudo (2008), the first two components explained 71 % of the total variation in the original traits of dairy cattle. Oliveira et al. (2014) evaluated seven productive and reproductive traits in Brazil and concluded that the first three PCs are sufficient to explain more than 80 % of the total variance of EBVs of traits. The positive correlations of PCs with EBVs of traits (Table 6, model 4) suggested that the selection of animals could be made

| Model 5 | PC1  | 0.865 | 0.759 | 0.977 | 0.959 | 0.738 | 0.898 |
|--------|------|-------|-------|-------|-------|-------|-------|
| Model 6 | PC1  | 0.678 | -0.545| 0.906 | 0.746 | 0.006 | 0.525 |
|        | PC2  | -0.225| -0.017| -0.343| 0.533 | 0.800 | 0.789 |
|        | PC3  | -0.395| 0.672 | 0.084 | 0.393 | -0.553| 0.303 |
CONCLUSIONS

According to the estimated heritability in this study, MY and LL would be the most representative traits to the selection schemes, while fertility traits could respond slowly to selection due to their low heritabilities. Moreover, considering the maternal effects of the dam in breeding programs may increase the rate of genetic improvement. PCA facilitates and ameliorates the selection process in dairy cattle by using correlations between traits EBVs and principle components, subsequently, reduce the domain of the analysis. Because the extracted components are independent, it can be concluded that EBVs of the studied traits can be analyzed and evaluated separately based on the first two PCs, allowing better planning for the selection process and thus genetic gains.

CONFLICT OF INTEREST

The authors declared no conflict of interest.

ACKNOWLEDGEMENT

Nothing to declare.

AUTHORS CONTRIBUTION

SAM, KME, and AFF designed the study. SAM and AFF collected the datasets and handled the data. SAM, EAR, and KME shared in the statistical analysis of the data. SAM and AFF edited the manuscript. All authors shared in the interpretation of results. The final copy of the manuscript was read and carefully approved by all authors.

REFERENCES

• Abarca H, Abegaz S, Mekeasha Y (2011). Genetic parameter estimates of preweaning weight of Horro (Zebu) and their crosses with Holstein Friesian and Jersey cattle breeds in Ethiopia. Int. J. Livest. Prod. 2: 84–91.
• Agudelo-Gómez D, Pineda-Sierra S, Cerón-Muñoz MF (2015). Genetic Evaluation of Dual-Purpose Buffaloes (Bubalus bubalis) in Colombia Using Principal Component Analysis. PLoS ONE. 10: 1–9. https://doi.org/10.1371/journal.pone.0138316
• Albuquerque LG, Meyer K (2001). Estimates of direct and maternal genetic effects for weights from birth to 600 days of age in Nelore cattle. J. Anim. Breed. Genet. 118: 83–92. https://doi.org/10.1046/j.1439-0388.2001.00279.x
• Bignardi AB, El Faro L, Rosa GJM, Cardoso VL, Machado PF, Albuquerque LG (2012). Principal components and factor analytic models for test-day milk yield in Brazilian Holstein cattle. J. Dairy Sci. 95: 2157–64. https://doi.org/10.3168/jds.2011-4494
• Bignardi AB, Santana ML, Eler JP, Ferraz JBS (2014). Models for genetic evaluation of growth of Brazilian Bonsmara cattle. Livest. Sci. 162: 50–58. https://doi.org/10.1016/j.livsci.2014.01.031
• Boligon AA, Albuquerque LG, Mercadante MEZ, Lo´bo RB (2010). Study of relations among age at first calving, average weight gains and weights from weaning to maturity in Nellore cattle. Rev. Brasil. Zoot. 39: 746–751. https://doi.org/10.1590/S1516-35982010000400007
• Boligon AA, Vicente IS, Vaz RZ, Campos GS, Souza FRB, Carvalheiro R, Albuquerque LG (2016). Principal component analysis of breeding values for growth and reproductive traits and genetic association with adult size in beef cattle. J. Anim. Sci. 94: 5014–5022. https://doi.org/10.2527/jas.2016-0737
• Bolivar-Vergara DM, Cerón-muñoz MF, Ramírez J, Agudelo-Gómez DA, Cifuentes T (2012). Genetic parameters for growth traits of buffaloes (Bubalus bubalis) in Colombia. Revista Colombiana de Ciencias Pecuarias. 25: 202–209.
• Bolormaa S, Pryce JE, Hayes BJ, Goddard ME (2010). Multivariate analysis of a genome-wide association study in dairy cattle. J. Dairy Sci. 93: 3818–3833. https://doi.org/10.3168/jds.2009-2980
• Buzanskas ME, Savegnago RP, Grossi DA, Venturini GC, Queiroz SA, Silva LOC, Torres (2013). Genetic parameter estimates and principal component analysis of breeding values of reproduction and growth traits in female Canchim cattle. Reprod. Fertil. Develop. 25(5): 775–781. https://doi.org/10.1071/RD12132
• Campelo JEG, Lopes PS, Torres RA, Silva LOC, Euclydes RF, Araújo CV, Pereira CS (2004). Maternal effects on the genetic evaluation of Tabapuã beef cattle. Genet. Moléc. Biol. 27: 517–521. https://doi.org/10.1590/S1415-4757200400000009
• Cardoso V, Roso VM, Severo JLP, Queiroz SA, Fries LA (2003). Formando lotes uniformes de reprodutores múltiplos e usando-os em acasalamentos dirigidos, em populações Nelore. Rev. Brasíl. Zoot. 32: 834–842. https://doi.org/10.1590/S1516-35982003000400008
• Cerny CA., Kaiser HF (1977). A study of a measure of sampling adequacy for factor-analytic correlation matrices. Multiv. Behav. Res. 12: 43–47. https://doi.org/10.1207/s15327906mbr1201_3
• Egena S, Ijaiya A, Ogah D, Aya V (2014). Principal component analysis of body measurements in a population of indigenous Nigerian chickens raised under extensive management system. Slovak J. Anim. Sci. 47: 77–82.
• Fraga AB, De Lima Silva F, Hongyu K, Da Silva Santos D, Murphy TW, Lopes FB (2016). Multivariate analysis to evaluate genetic groups and production traits of crossbred Holstein × Zebu cows. Trop. Anim. Health Prod. 48: 533–538. https://doi.org/10.1007/s11250-015-0985-2
• Groeneveld E, Kovac M, Mielenz N (2008). VCE 6, Users Guide and Reference Manual, Version 6.0.
• Hair JF, Black WC, Babin BJ, Anderson RE (2009). ‘Multivariate data analysis.’ (Prentice Hall: Upper Saddle River, NJ.)
• Jolliffe IT, Cadima J (2016). Principal component analysis: a review and recent developments. Philosophical Transactions of the Royal Society A Mathematical, Phys. Eng. Sci. 374:
• Junior RAA, Munari DP, Alencar MM (2013). Genetic parameter estimates and principal component analysis of breeding values of reproduction and growth traits in female Canchim cattle. Reprod. Fertil. Develop. 25: 775–781. https://doi.org/10.1071/RD12132
• Karabulut O, Mundan D, Sehar Ö (2012). Variance components and breeding values of birth weight in Holstein calves. Harran University J. Faculty Vet. Med. 1: 28–34.
• Karacao˘ren B, Kadamideen HN (2008). Principal component and clustering analysis of functional traits in Swiss dairy cattle. Türk. J. Vet. Anim. Sci. 3: 163–171.
• Laureano MMM, Boligon AA, Costa RB, Forni S, Severo JLP, Albuquerque LG (2011). Estimativas de herdaibilidade e tendências genéticas para características de crescimento e reprodutivas em bovinos da raça Nelore. Arquivo Brasil. Med. Vet. Zoot. 63: 143–152. https://doi.org/10.1590/S0102-09352011000100022
• Lee S, Taper ML (2002). A composite likelihood approach to (co)variance component estimation. J. Statist. Plann. Inf. 103: 117–135. https://doi.org/10.1016/S0378-3758(01)00215-4
• Lopes FB, Magnabosco CU, Mamede MM, Da Silva MC, Miyagi ES, Paulini F, Lôbo RB (2013). Multivariate analysis for young bull selection from a performance test using multiple traits of economic importance. Trop. Anim. Health. Prod. 45: 1375–1381. https://doi.org/10.1007/s11250-013-0373-8
• Lopes FB, Silva MC, Magnabosco CU, Narciso MG, Sainz RD (2016). Selection indices and multivariate analysis show similar results in the evaluation of growth and carcass traits in beef cattle. PLoS One. 11: 147–180. https://doi.org/10.1371/journal.pone.0147180
• Malhado CHM, Ramos AA, Carneiro PLS, de Souza JC, Lamberson WR (2007). Genetic and phenotypic trends for growth traits of buffaloes in Brazil. Italian J. Anim. Sci. 6: 325–327. https://doi.org/10.4081/ijas.2007.s2.325
• Mello C, Sinedino LD, Ferreira JE, Sousa SLG, Mello MRB (2020). Principal component and cluster analyses of production and fertility traits in Red Sindhi dairy cattle breed in Brazil Raquel Rodrigues. Trop. Anim. Health Prod. 52: 273–281. https://doi.org/10.1007/s11250-019-02009-7
• Meyer K (2007). WOMBAT: a tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). J. Zhejiang University Sci. B. 8: 815–821. https://doi.org/10.1631/jzus.2007.B0815
• Moawed SA, Osman MM (2018). Dimension reduction of phenotypic yield and fertility traits of Holstein-Friesian dairy cattle using principle component analysis. Int. J. Vet. Sci. 7: 75–81. https://www.cabdirect.org/cabdirect/abstract/20183291045
• Moraes LE, Kebreab E, Strathe AB, Dijkstra J, France J, Casper DP, Fadel JG (2015). Multivariate and univariate analysis of energy balance data from lactating dairy cows. J. Dairy Sci. 98: 4012–4029. https://doi.org/10.3168/jds.2014-9895
• Oliveira DB, Barros CC, Neto FRA, Lourenco DAL, Hurtado-Lugo NA, Tonhati H (2014), Principal Components for Reproductive Traits in Buffaloes from Brazil. Livest. Prod. 10: 3–5.
• Osorio-Avalos J, Menéndez-Buxadera A, Serradilla JM, Molina A (2015). Use of descriptors to define clusters of herds under similar environmental conditions to improve the level of connection among contemporary groups of mutton type Merino sheep under an extensive production system. Livest. Sci. 176: 54–60. https://doi.org/10.1016/j.livsci.2015.03.029
• Porto-Neto LR, Sonstegard TS, Liu GE, Bickhart DM, Da Silva MV, Machado MA, Utsunomiya YT, Garcia JF, Gondro C, Van Tassell CP (2013). Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. BMC Genom. 14: 876–882. https://doi.org/10.1186/1471-2164-14-876
• Rencher AC (2002). ‘Methods of multivariate analysis.’ (Wiley-Interscience: New York.) https://doi.org/10.1002/0471271357
• Rosati A, Van Vleck LD (2002). Estimation of genetic parameters for milk, fat, protein and mozzarella cheese production for the Italian River buffalo Bubalus bubalis population. Livest. Prod. Sci. 74: 185–190. https://doi.org/10.1016/S0301-6226(01)00293-7
• Sahin A, Ulutas Z, Yilmaz AA (2012). Estimates of phenotypic and genetic parameters for birth weight of Brown Swiss calves in Turkey using an animal model. Trop. Anim. Health Prod. 44: 1027–1034. https://doi.org/10.1007/s11250-011-0036-6
• Şahin A, Ulutaç Z, Ügürluetepe E (2017). The application of six different models to estimate the genetic parameters, variance components and breeding values for birth weight of Holstein calves. J. Appl. Anim. Res. 45: 598–602. https://doi.org/10.22475/jaar.2016.1239581
• Salem M, Esmoil H, Sadek R, Nigm A (2006). Phenotypic and genetic parameters of milk production and reproductive performance of Holstein cattle under the extensive production system in Egypt. Egyptian J. Anim. Prod. 43: 1–10. https://doi.org/10.21608/ejap.2006.93085
• Savengnago RP, Caetano SL, Ramos SB, Nascimento GB, Schmidt GS, Ledur MC, Munari DP (2011). Estimates of genetic parameters, and cluster and principal components analyses of breeding values related to egg production traits in a White Leghorn population. Poult. Sci. 90: 2174–2188 https://doi.org/10.3382/ps.2011-01474
• Selim AM, Elhaig MM, Moawed SA, El-Nahas E (2018). Modeling the potential risk factors of bovine viral diarrhea prevalence in Egypt using univariable and multivariable logistic regression analyses. Vet. World. 11: 259–267. https://doi.org/10.14202/vetworld.2018.259-267
• Seno LO, Cardoso VL, El-Faro I, Sesana RC, Aspilcueta-Borquis RR, De Camargo GMF (2010). Genetic parameters for milk yield, age at first calving and interval between first and second calving. Livest. Res. Rural Develop. 22: 123–131.
• Shalaby N, Moawed S, El-Bayomi K (2015). A comparison of linear models for estimating covariance components and genetic parameters in Holstein dairy cattle. J. Anim. Poult. Fish Prod. 4: 7–15. https://doi.org/10.21608/japfp.2015.7424
• Snedecor G, William G (1989). Statistical Methods/George W. Snedecor And William G. Cochran.
• Tölli M, Saatc M, Colak M (2008). Genetic parameters for direct and maternal effects and estimation of breeding values for birth weight in Brown Swiss Cattle. Turkish J. Vet. Anim. Sci. 32: 287–292.
• Tramonte NC, Grupioni NV, Stafuzza NB, Guidolin DGF, Savegnago RP, Bezerra LAF, Lôbo RB, Munari DP (2019). Genetic parameters, genetic trends, and principal component analysis for productive and reproductive traits of Guzera beef cattle. Rev. Brasil. Zoot. 48:1–11. https://doi.org/10.1590/rbz4820180034
• Val JE, Ferraudo AS (2008). Alternativas para seleção de touros da raça Nelore considerando características múltiplas de importância econômica. Arquivo Brasil. Med. Vet. Zoot. 60: 705–712. https://doi.org/10.1590/S0102-09352008000300027

• Verma D, Sankhyan V, Katoch S, Thakur Y (2015). Principal component analysis of biometric traits to reveal body confirmation in local hill cattle of Himalayan state of Himachal Pradesh, India. Vet. World. 8: 1453-1462. https://doi.org/10.14202/vetworld.2015.1453-1457

• Willham R (1980). Problems in estimating maternal effects. Livest. Sci. 7: 405-418. https://doi.org/10.1016/0301-6226(80)90080-9