Genetic and Phenotypic Trends along with Genetic Parameters of Production Traits in Murrah Buffalo

ABSTRACT (Abstract should be structured and divided into subsections like aim,study design, place of work and duration of work, methodology, results and conclusion)

This study investigates the genetic parameters and trends in production traits of Murrah buffaloes over a 24-year period (1996-2019) at a farm in Hisar, Haryana. Data on key production traits including 305 days milk yield (305DMY), peak yield (PY), lactation length (LL), dry period (DP), lactation milk yield (LMY), and wet average (WA) were collected from 614 Murrah buffaloes. Utilizing a univariate animal model, the average estimated breeding values for the production traits were computed: 2148.05 kg for 305DMY, 10.74 kg/day for PY, 319.19 days for LL, 117.88 days for DP, 2288.80 kg for LMY, and 7.12 kg/day for WA. The study revealed a minimum genetic correlation of -0.81 and a phenotypic correlation of -0.32 between LL and WA. Heritability estimates for 305DMY, PY, LL, DP, LMY, and WA ranged from 0.13 to 0.48, while repeatability estimates varied from 0.35 to 0.54. The genetic trends were positive for all production traits except LL and DP, while phenotypic trends had positive values for all traits except DP. From this study, it can be inferred that selecting based on peak yield as a benchmark would be more fit for achieving correlated improvements in other production traits.

Keywords: Murrah, univariate, genetic parameters, repeatability, genetic correlation, genetic and phenotypic trends

1.INTRODUCTION (Provide number to headings and sub-headings)

Based on the Basic Animal Husbandry Statistics (2023), India achieved a total milk production of 230.58 million tonnes in 2022-23, showing an annual growth rate of 3.83%. Despite having only one-third of the cattle population, buffaloes play a pivotal role in Indian dairying, contributing over 45% of the total milk production. Among buffalo breeds, the Murrah breed holds a prominent position due to its exceptional milk-producing abilities, primarily in its native region of Haryana and neighboring states such as Punjab, Uttar Pradesh, and Delhi. The primary determinant of buffaloes' economic value lies in their production traits. Heritability estimation, a vital genetic parameter, evaluates how closely the phenotypic value aligns with the breeding value of a trait, serving as a pivotal indicator for forecasting genetic enhancements derived from selection. Genetic correlation estimates evaluate the relationship between genes that contribute to genetic variation, whereas phenotypic correlation assesses the observed association between phenotypic traits. Genetic and phenotypic trends show improvements in overall productivity over a given period. The yearly rate of change in productive traits reflects the quantitative evaluation and annual genetic gain. By setting aside environmental trends, we can measure the change in population performance for an economic trait each year by estimating the phenotypic and genetic trends. Additionally, phenotypic trends encompass both genetic and environmental trends. Genetic trends result from the change in mean breeding value and environmental trends from the change in mean environment. Partitioning phenotypic trends into genetic and environmental components is essential for breeders to assess the effectiveness of selection and management over time. Change in mean breeding value due to selection results in the genetic and phenotypic trends (Kaur *et al.*, 2021). Monitoring genetic advancement aids in designing more effective breeding strategies to maximize genetic gains.

The aim of this study was to explore the potential for genetic enhancement of Murrah buffaloes by estimating genetic parameters related to production traits. The generated information is expected to enhance farm management practices and boost the productivity of the Murrah herd. The effectiveness of the selection can be measured by estimating the phenotypic and genetic trends of the target traits (Sahana and Sadana, 1998). The genetic and phenotypic trends of various economic traits were estimated to determine the rate of change in the population over the years, providing insights to suggest effective breeding strategies for maximizing genetic gain.

MATERIAL METHOD

Source of data

Data on production traits was gathered from history-cum-pedigree sheets maintained at the buffalo farm of the Department of Livestock Production Management (LPM) at Lala Lajpat Rai University of Veterinary and Animal Sciences (LUVAS), Hisar. Hisar has a subtropical climate and is located in a semi-arid region. Geographically, it is positioned at 29° 10' N latitude, 75° 40' E longitude, with an altitude of 215.2 meters. A comprehensive dataset encompassing 662 Murrah buffaloes was collected over ~~a span of~~ 24 years, from 1996 to 2019, focusing on production traits of the first lactation. To estimate repeatability, data from three lactations were used. The analysis included 180 sires, each with more than three progenies.

Traits under study

The production traits examined in this study encompassed 305 days of milk yield (305DMY), peak yield (PY), lactation length (LL), dry period (DP), lactation milk yield (LMY), and wet average (WA). The wet average is determined by dividing the total lactation milk yield by the total number of days the animal was in milk during that lactation period. To ensure data integrity and accuracy, animals with lactation periods shorter than 150 days and those flagged as suspected outliers due to abnormal records such as abortion, mastitis, or long-term illness were removed from the analysis.

Statistical analysis

Animal model and (Co) variance component estimation

Covariance components were calculated using the restricted maximum likelihood (REML) method, using the average information (AI) algorithm of WOMBAT described by Meyer (2007). The linear model used to represent the animal model for individual records was formulated as:

$$\mathbf{y = Xb + Za + e}$$

Covariance component estimation for studied traits was derived by using univariate animal models exclusively for first lactation performance traits. This was accomplished through an AIREML algorithm implemented using WOMBAT, following the methodology described by Meyer (2007).

Assumptions of the model are:

$$V(a) = A\sigma^2_a\ ,\ V(m) = A\sigma^2_m\ ,\ V(c) = I\sigma^2_c\ ,\ \text{and } V(e) = I\sigma^2_e$$

Where, I = Identity matrix; σ^2_a = Direct additive genetic variance; σ^2_p = Phenotypic variance

Estimated (co) variance components were used to obtain heritability,

$(h^2=\sigma^2_a/\sigma^2_p)$ = Direct heritability

Genetic and phenotypic correlations were estimated by using Bivariate analysis.

Repeatability animal model

Apart from the univariate animal model, a repeatability model was applied using WOMBAT to conduct genetic evaluations for production parameters across up to three lactation orders. When multiple records exist for a trait within an animal, the repeatability model facilitates genetic evaluation and prediction of breeding values. The repeatability model extends beyond solely estimating the breeding value of an animal; it also accounts for permanent environmental effects. This model is expressed as $y = Xb + Za + Wpe + e$,
where pe represents the vector of permanent environmental effects and non-genetic factors, and W is the incidence matrix linking records to permanent environmental effects. Under this model, permanent environmental effects and residual effects are assumed to be normally and independently distributed, with means zero and variances σ^2pe and σ^2e, respectively. This comprehensive model enables the evaluation of genetic and environmental influences on production traits across multiple lactation orders in Murrah buffaloes.

Estimation of genetic and phenotypic trends:

Estimation of genetic trends

To estimate the genetic trends of various production traits, a regression analysis was conducted by regressing the weighted average of the sire's estimated breeding value (WAEBV) for each year on the corresponding year. The WAEBV for the kth year was estimated using the formula:

$$\sum \mathbf{n_{ik} S_i / n_{.k}}$$

Where, n_{ik} = number of daughters of sire i (i =1,2,3.4………………. n) in year k; S_i = estimated breeding value of sire i; $n_{.k}$ = total no. of daughters of n sires in year k.

This calculation involves summing the products of the number of daughters of each sire in a given year and their respective estimated breeding values, and then dividing by the total number of daughters of all sires in that year. This weighted average provides a representative measure of the genetic potential for a specific trait in a given year. By regressing these WAEBV values against the corresponding years, genetic trends for the performance traits can be estimated.

Estimation of phenotypic trends

To estimate phenotypic trends for each trait, a linear regression analysis was conducted by regressing the performance of the population in the corresponding year. The standard error for linear regression, necessary for estimating phenotypic and genetic trends, was calculated using the formula provided by Falconer (1991). S.E. (b) = $\sqrt{[\{1 / (N-2)\}\ \{(\sigma^2_x / \sigma^2_y) - b^2\}]}$ Where, N = number of period observations of x and y, σ^2_y = variance of y, σ^2_x = variance of x and b = regression coefficient of y on x.

RESULTS AND DISCUSSION

The average values along with the standard error, of the production traits under investigation, namely 305 days milk yield (305DMY), peak yield (PY), lactation length (LL), dry period (DP), lactation milk yield (LMY), and wet average (WA) were 2257.36±25.24 kg, 11.68±0.09 kg/day, 303.07±2.75 days, 147.16±3.12 days, 2358.66±30.42 kg and 7.88±0.07 kg/day, respectively. Feathers of data structure of production traits including mean, standard deviation, maximum values, minimum values and coefficient of variation are depicted in Table 1. The mean estimated breeding values (EBVs) by employing the univariate animal model in WOMBAT software for production traits including 305DMY, PY, LL, DP, LMY, and WA were obtained as 2152.15 kg, 10.74 kg/day, 316.21 days, 118.27 days, 2334.28 kg and 7.55 kg/day, respectively as shown in Table 1. The breeding values of production traits viz. 305DMY, PY, LL, DP, LMY and WA ~~were~~ ranged from -336.526 to 172.65 days, -0.46 to 0.48 kg/day, -42.12 to 30.14 days, -16.41 to 63.87 days, -381.15 to 361.12 kgs, -0.19 to 0.20 kg/day, respectively. The mean values of estimated production traits were close to the findings of Jamuna (2015b), Jakhar et al. (2016), Patil et al. (2018), Jamal et al. (2018) and Kaur et al. (2020) in Murrah buffaloes and the estimated breeding values were in alliance with the findings of Gaur (2003) in Friesian breed and Jadoa et al. (2011) in Holstein cattle.

3.1 Heritability and repeatability of production traits using univariate animal model

The heritability measures of production traits of the first lactation *viz.* 305DMY, PY, LL, DP, LMY and WA were 0.37±0.05, 0.45±0.10, 0.15±0.07, 0.18±0.05, 0.25±0.03 and 0.35±0.07, respectively and the repeatability measures upto third lactations were 0.40±0.05 for 305DMY, 0.36±0.03 for PY, 0.34±0.03 for LL, 0.42±0.05 for DP, 0.40±0.04 for LMY and 0.36±0.02 for WA (Figure 1). Notably, the repeatability of certain traits was observed to be lower than their heritability, particularly in the cases of PY and WA. This discrepancy might be attributed to several factors, including: (i) variations in the genetic composition of the measured traits, (ii) the influence of permanent maternal effects counteracting direct additive genetic effects, (iii) negative correlations between the temporary environmental conditions affecting each trait, (iv) the presence of significant genotype-environment interactions, and

(v) the impact of maternal effects on trait expression. The variance of the permanent effect for traits with repeatability was 10-20 times higher than the mean value valuing as 18154.60, 12.47, 24352.80, 40986.90, 18216.50 and 10.10 for 305DMY, PY, LL, DP, LMY and WA, respectively. Conversely, for traits influenced by maternal effects such as PY and WA, the variance equalled the average value, specifically measured as 12.47 and 10.11, respectively. Moderate heritability estimates (0.37±0.05) for 305DMY were consistent and accompanied the findings of Chakraborty et al. (2010a), Dev et al. (2015), Singh & Barwal (2012) and Patil et al. (2018). Lower heritability measures were documented by Jamuna et al. (2015b) and Pareek & Narang (2014), while Jakhar et al. (2016) reported a higher value. For PY, a high heritability (0.45±0.10) was observed, surpassing the values of Patil et al. (2018). LL exhibited low heritability (0.15±0.07) in the present study, near to values reported by Koçak et al. (2019) and Thiruvenkadan et al. (2010), whereas Jakhar et al. (2016) reported a moderate value (0.36±0.09). The heritability estimate for DP was lower (0.18±0.05) compared to that reported by Jakhar et al. (2016) but similar (0.19±0.13) to Thiruvenkadan et al. (2010). LMY was moderately heritable (0.25±0.03), consistent with Pareek & Narang (2014) and Patil et al. (2018), although Thiruvenkadan et al. (2010) reported lower values and Jakhar et al. (2016) and Koçak et al. (2019) reported higher ones. WA exhibited a moderate heritability (0.35±0.07) in our study, aligning with Singh & Barwal (2012), Dev et al. (2015), and Patil et al. (2018), while Jamuna et al. (2015b) reported lower values. Lower repeatability estimates for production traits were noted by Jamuna et al. (2015a) and Kumar et al. (2022).

The disparities in heritability estimates across different research studies, along with their standard errors, could stem from differences in data collection and methods of standardization for various non-genetic factors, as well as the methodologies or models used to estimate heritability for the traits. Moreover, factors such as herd size, feeding practices on different farms, and climatic conditions or study locations may also contribute to these variations. The estimates for the production traits with moderate heritability indicated that improvement could be possible through selective breeding.

3.2 Genetic and phenotypic correlation of production traits using a bi-variate animal model

The genetic correlations (below diagonal) and phenotypic correlations (above diagonal) of production traits are presented in Table 2 using a bi-variate animal model. The least genetic correlation was found between LL and WA, valued at -0.81±0.21, while the lowest phenotypic correlation was between the same traits, resulting in -0.32±0.04. Conversely, the highest genetic correlation was observed between 305DMY and LMY, with a value of 0.89±0.11, while the highest phenotypic correlation was also between these traits, at

0.96±0.12. 305DMY and PY had moderate to high genetic correlation with mentioned production traits except WA whereas DP had negative genetic correlation with studied traits ranging from -0.06±0.05 (LMY) to -0.79±0.12 (LL) except with 305DMY (0.16±0.02) and PY (0.17±0.06). WA had a negative genetic correlation from -0.08±0.07 (DP) to -0.81±0.21 (LL) except with LMY (0.86±0.25). 305DMY and LMY had significant ($p<0.01$) and positive phenotypic correlation traits except between 305DMY and WA. The genetic correlations between 305DMY and LMY as well as LL were notably positive and high, contrasting with the lower genetic correlation observed with PY and DP. Moreover, a negative genetic correlation was found between 305DMY and WA (-0.62). Consistently, previous studies by Singh et al. (2011), Chakraborty et al. (2010b), Chaudhari (2015), and Patil et al. (2018) also reported significant and positive genetic correlations among production traits (305DMY, LMY, LL, and PY) in Murrah buffalo. Moderate to high positive phenotypic correlation was reported between most of the production traits. It indicated that selection for production traits goes hand-in-hand. WA had a significant phenotypic association with all other production traits which was positive with PY (0.82±0.05) and LMY (0.71±0.02) whereas it had a negative correlation with 305DMY (-0.29±0.03), LL (-0.32±0.04) and DP (-0.09±0.05). PY exhibited a notably strong positive genetic correlation with LMY~~,~~ while displaying a highly negative genetic correlation with WA (-0.88). However, contrasting findings were reported by Patil et al. (2018), revealing negative genetic and phenotypic correlations between PY and LMY. PY also showed significantly positive phenotypic correlations with all studied traits except LL. Consistent with the current study, Singh & Barwal (2012), Chakraborty (2010b) and Dev et al. (2015) discovered highly positive genetic and phenotypic correlations between LMY and PY. The presence of moderate to high genetic and phenotypic correlations among most production traits suggests a syncretistic approach in the selection process for economic traits in the buffalo herd. However, the positive correlation with the dry period raises concerns, as an increase in economically idle days could potentially impact the productivity of the herd.

Upon critical examination of heritability and genetic and phenotypic correlations among production traits, it can be concluded that selecting on the basis of peak yield would likely be more effective. This is because this trait's production potential manifests early in lactation and demonstrates relatively high (0.45) heritability estimates, along with genetic and phenotypic correlations with other production traits in desirable directions.

3.3 Genetic and Phenotypic trends of production traits

The regression genetic trend values for production traits, namely 305DMY, PY, LL, DP, LMY, and WA, were observed as follows: 1.510±0.96 days, 0.011±0.005 kg/day, -

0.220±0.114 days, -0.290±0.130 days, 0.759±0.778 kg, and 0.011±0.007 kg/day, respectively. Among these, the genetic trend value of DP was found to be significant ($p<0.05$), as indicated in Table 3. Notably, most traits displayed positive genetic trends, except LL and DP. Correspondingly, the phenotypic regression trends for these traits were determined as 60.110±7.611 days, 0.199±0.028 kg/day, 1.412±0.610 days, -2.310±0.502 days, 64.132±8.106 kg, and 0.192±0.020 kg/day, respectively, and were highly significant ($p<0.01$). Here, major traits exhibited positive trends except DP, which was favourable as a reduction in DP reflected a beneficial outcome of selective breeding and management practices across the years. The genetic coefficient of determination values (R^2_G) ranged from 4.6% (LMY) to 18.4% (DP), while the phenotypic coefficient of determination (R^2_P) varied from 19.2% (LL) to 81.4% (WA).

The genetic and phenotypic trends for 305DMY showed an increase at an annual rate of 1.510±0.960 kg and 60.110±7.611 kg, respectively, with the phenotypic trends being highly significant ($p<0.01$). Similar positive trends were noted by Chaudhari (2015) in Murrah buffaloes, with yearly genetic and phenotypic trends of 0.36±0.11 kg and 25.89±5.29 kg, respectively and Dash et al. (2023) in Sahiwal cattle. However, contrasting results were observed by Tirupude et al. (1995) for Sahiwal cattle, reporting negative phenotypic and genetic trends for the same trait. Peak yield displayed positive genetic trends and highly significant ($p<0.01$) phenotypic trends across the years (0.011±0.005 kg/day and 0.199±0.028 kg/day, respectively). In contrast, Chakraborty & Dhaka (2012) reported negative and low genetic and phenotypic trends (-0.004 kg/day and -0.02 kg/day) for FPY. Furthermore, Chaudhari (2015) found negative genetic and positive phenotypic trends for PY (-0.16±0.19 kg/day and 0.10±0.02 kg/day) in Murrah buffaloes. Nevertheless, positive genetic trends were reported by Yadav et al. (1983) and Sahana & Sadana (1998) for PY in Murrah buffaloes. Despite non-significant and negative annual genetic trends for LL (-0.220±0.114 days), the phenotypic trends were highly significant ($p<0.01$) and positive (1.412±0.610 days) which was aligned with the results of Choudhary et al (2018) in Tharparkar cattle. This suggests a decrease in variability of this trait due to long-term selection and improved management practices. Contrasting findings were reported by Kuralkar & Raheja (1997), Singh et al. (2011), and Chaudhari (2015) in Murrah buffaloes, where annual genetic and phenotypic trends for LL were positive and negative genetic trends for LL was reported by Dash et al. (2023) in Sahiwal cattle. Annual genetic trends of DP were negative and significant ($p<0.05$), indicating a decrease in DP and thus an increase in the productive time of the animals. Similar negative phenotypic trends were observed by Singh & Nagarcenkar

(2000) for Sahiwal cattle and Kaur et al. (2021) for Murrah buffaloes and the negative genetic trend was observed by Dash et al. (2023) in Sahiwal cattle. Conversely, positive phenotypic trends were noted by Chaudhari et al. (2014) in crossbred cattle, Ambhore et al. (2017) in Phule Triveni synthetic cows and Choudhary et al (2018) in Tharparkar cattle.

In the present study, LMY exhibited positive genetic and highly significant ($p<0.01$) phenotypic trends (0.759±0.778 kg and 64.132±8.106 kg, respectively). However, Chakraborty & Dhaka (2012) reported contrary results, with negative genetic (-1.11±0.44 kg) and phenotypic (-3.00±1.76 kg) trends for first lactation milk yield. Similarly, Chaudhari (2015) found annual negative genetic (-0.006±0.005 kg) and positive phenotypic (27.21±5.35 kg) trends for FLY in Murrah buffaloes. The positive phenotypic trends align with the results of Nehara et al. (2013) in Karan Fries cattle, Chaudhary et al. (2018) in Tharparkar cattle, Singh et al. (2011) in Nili-Ravi buffalo, as well as Chander (2002), Ramos et al. (2006), and Kour et al. (2021) in Murrah buffaloes. However, Kuralkar and Raheja (1997) and Chakraborty (2008) reported negative phenotypic trends in Murrah buffaloes. WA showed positive genetic and highly significant ($p<0.01$) phenotypic trends annually (0.011±0.007 kg/day and 0.192±0.020 kg/day, respectively), indicating concurrent improvements in selection and management practices to enhance production performance traits. Conversely, Chakraborty and Dhaka (2012) reported negative genetic and phenotypic trends for WA. Overall, genetic trends were positive for all production traits except LL and DP, while phenotypic trends were positive for all production traits except DP. These positive trends suggest improvements in production traits over time, reflecting enhanced selection strategies, nutritional approaches, and management practices. Additionally, a decrease in the dry period signifies positive selection aimed at reducing unproductive periods. From these findings, one may infer that opting for peak yield as the selection criterion would be better suited for enhancing other production traits in a favorable direction through correlated responses.

AVAILABILITY OF DATA AND MATERIAL

The data will be made available upon request.

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TABLES AND FIGURES

Table 1. Features of the data structure for production traits (Table outline should be as per the authors guidelines)

Attributes	305DMY	PY	LL	DP	LMY	WA
Count of Animal IDs in the Data File	662	662	662	662	662	662
Total Sires	180	180	180	180	180	180
Sires with Records and Progeny Count in Data	172	172	172	172	172	172
Dam count with progeny in data	128	128	128	128	128	128
EBV	2152.15	10.74	316.21	118.27	2334.28	7.55
Mean	2257.36	11.68	303.07	147.16	2358.66	7.88
Standard Deviation	618.31	2.54	66.56	11.48	731.16	1.58
Minimum	595.3	4.20	110	105	582.36	1.50
Maximum	3919.72	19.16	496.14	189.32	4134.96	14.26
Coefficient of variation (%)	27.39	21.75	21.96	7.80	31.00	20.05

Table 2. Bi-Variate animal model approach for genetic (below diagonal) and phenotypic (above diagonal) correlation in production traits

Traits	305DMY	PY	LL	DP	LMY	WA
305DMY	-	0.23**±0.02	0.77**±0.02	0.22**±0.05	0.96**±0.12	-0.29**±0.03
PY	0.15±0.11	-	0.07±0.03	0.12**±0.07	0.86**±0.09	0.82**±0.05
LL	0.79±0.15	0.69±0.31	-	0.02±0.05	0.86**±0.11	-0.32**±0.04
DP	0.16±0.02	0.17±0.06	-0.79±0.12	-	0.09*±0.05	-0.09*±0.05
LMY	0.89±0.11	0.82±0.02	0.76±0.11	-0.06±0.05	-	0.71**±0.02
WA	-0.62±0.09	-0.78±0.12	-0.81±0.21	-0.08±0.07	0.86±0.25	-

Where *P<0.05, **P<0.01

Table 3. Annual genetic and phenotypic trends with coefficient of determination of production traits

Traits	Phenotypic trends (R^2_P)	Genetic trends (R^2_G)
305DMY (kg)	60.110**±7.611 (74.3%)	1.510±0.960 (9.2%)
PY (kg/day)	0.199**±0.028	0.011±0.005

	(65.5%)	(13.3%)
LL (days)	1.412**±0.610 (19.2%)	-0.220±0.114 (14.1%)
DP (days)	-2.310**±0.502 (47.3%)	-0.290*±0.130 (18.4%)
LMY (kg)	64.132**±8.106 (74.3%)	0.759±0.778 (4.6%)
WA (kg/day)	0.192**±0.020 (81.4%)	0.011±0.007 (13.2%)

Where *P<0.05, **P<0.01

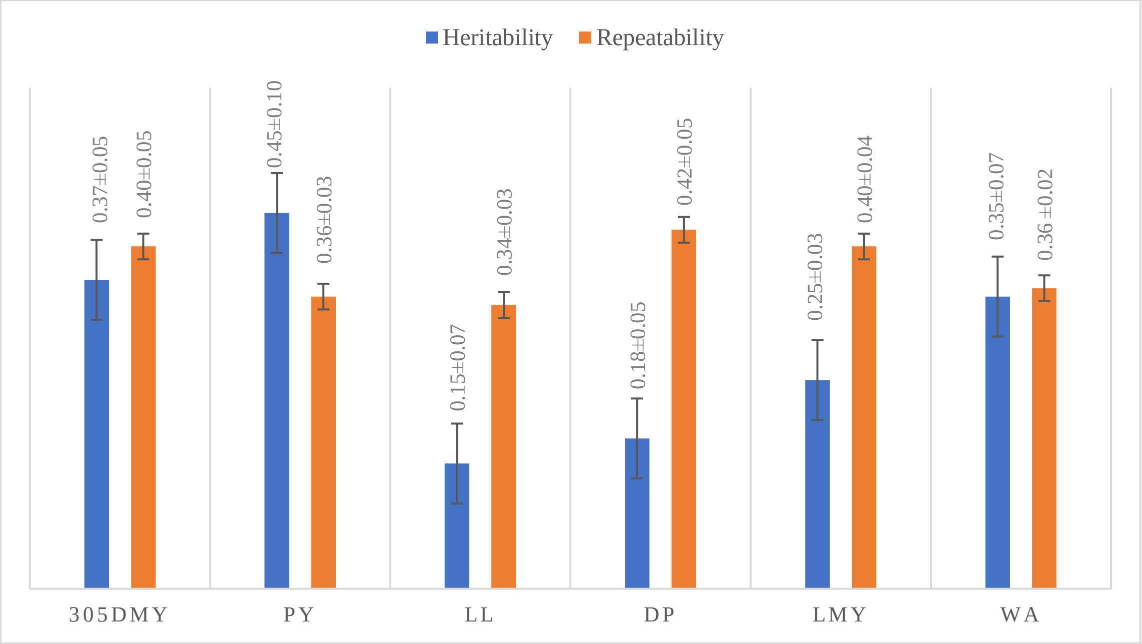
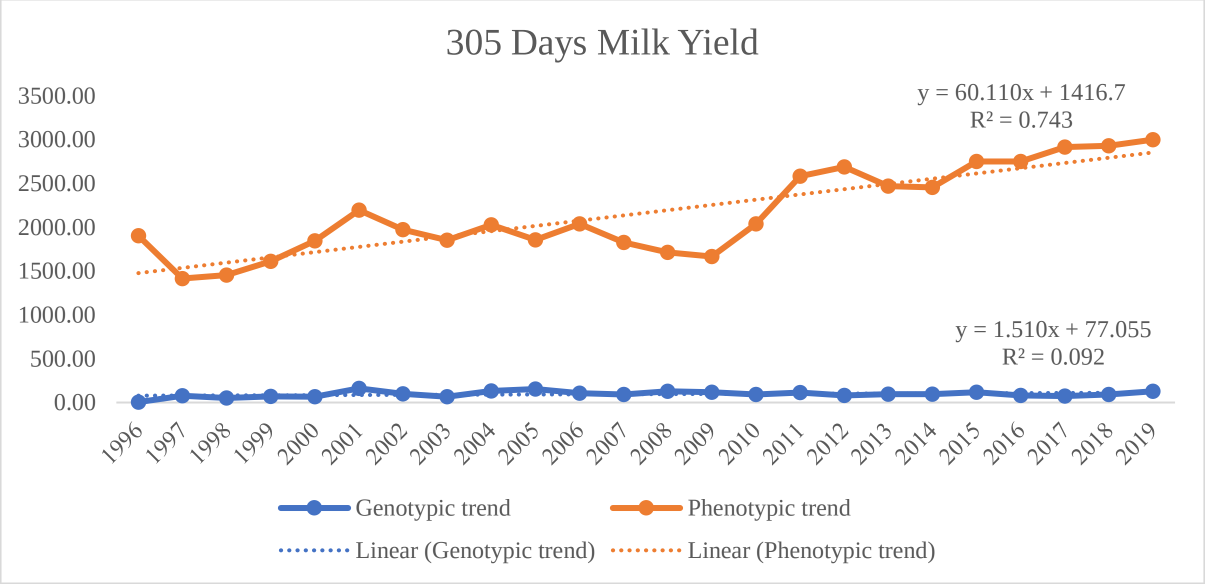
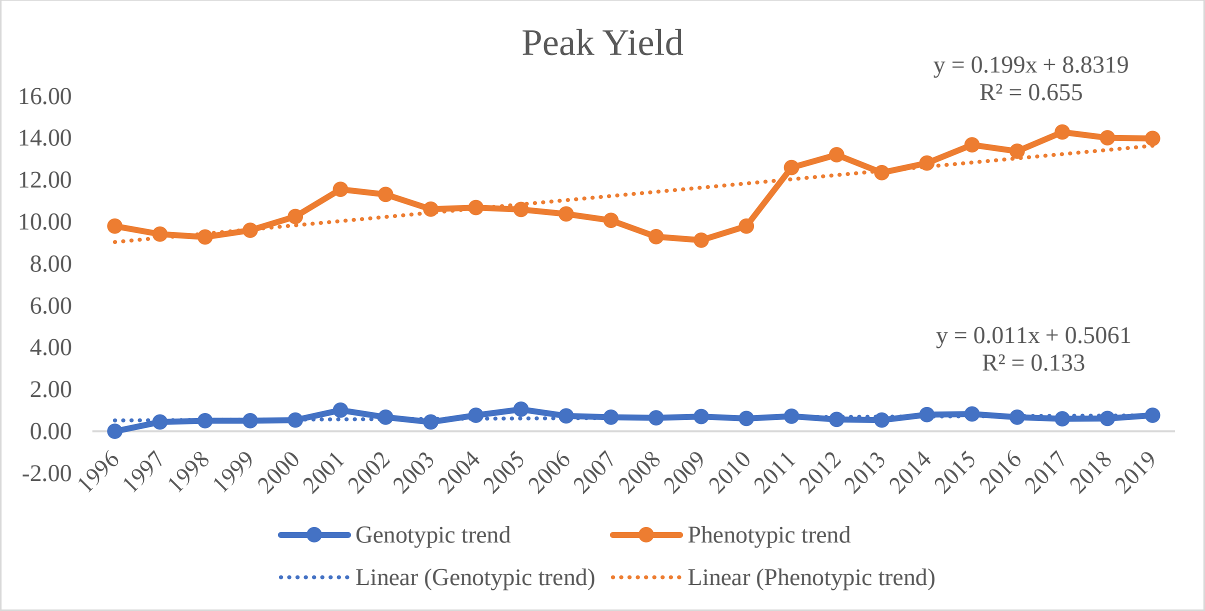


Figure 1. Heritability and repeatability of production trait



305 Days Milk Yield

Figure 2. Genetic and phenotypic trends of 305DMY



Peak Yield

Figure 3. Genetic and phenotypic trends of PY

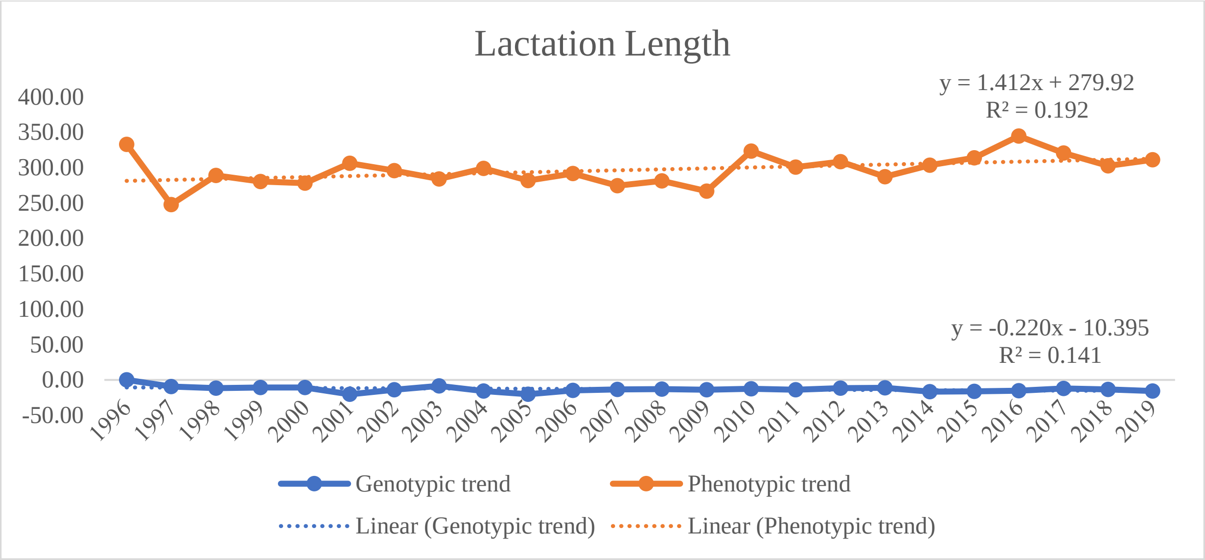


Figure 4. Genetic and phenotypic trends of LL

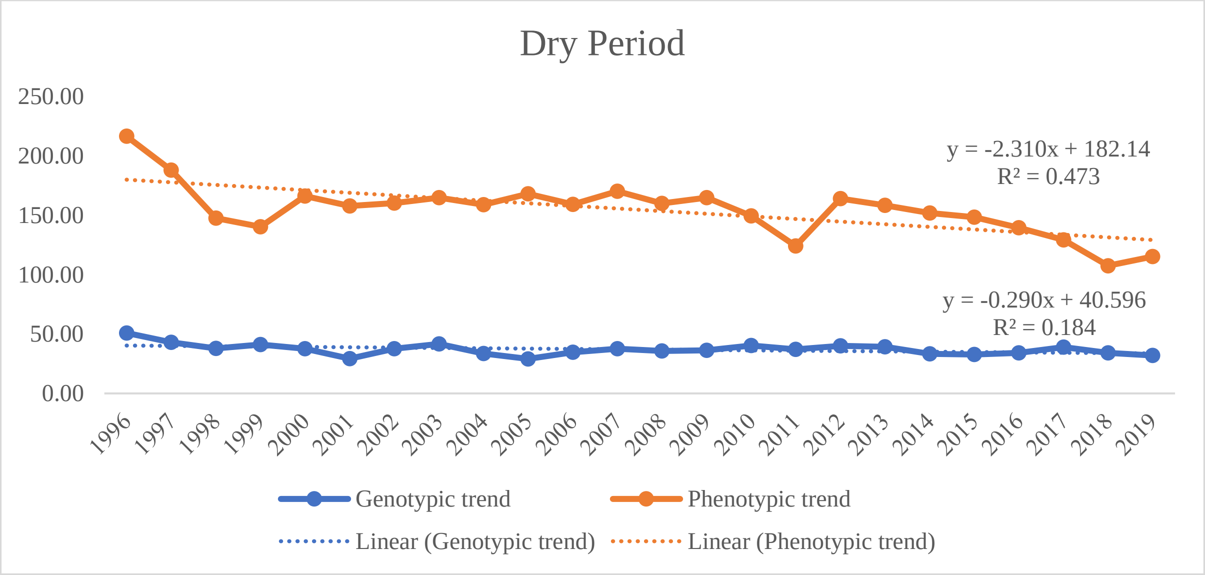


Figure 5. Genetic and phenotypic trends of DP

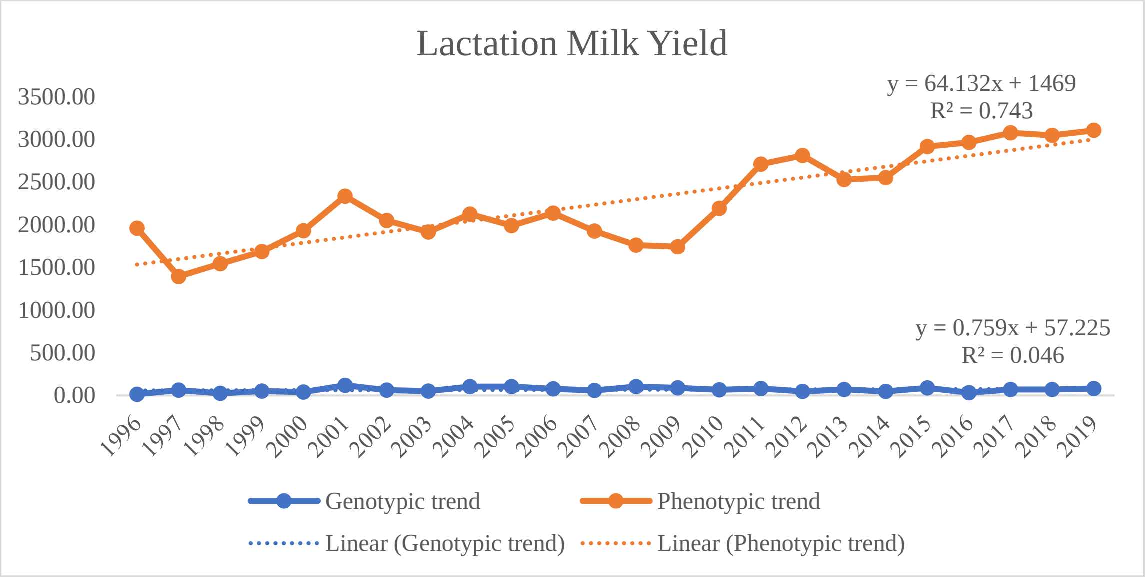


Figure 6. Genetic and phenotypic trends of LMY

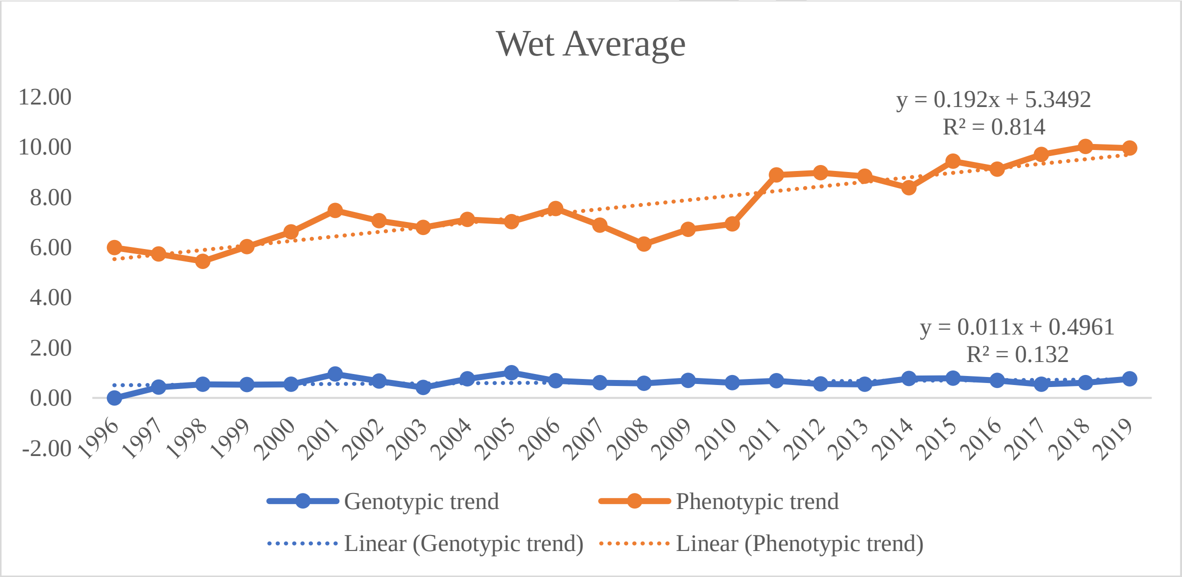


Figure 7. Genetic and phenotypic trends of WA