



Genetic and Phenotypic Correlations between Production and Reproduction Traits in Frieswal Cattle under Field Progeny Testing Programme

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Authors' contributions

This work was carried out in collaboration among all authors. Author OS managed the literature and wrote the manuscript, Author RSB carried out the interpretation of result and editing of the manuscript, Author MAR performed the statistical analysis and wrote material and methods, Authors CBS and ST provided the data to perform the study. All authors read and approved the final manuscript.

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ABSTRACT

Aim: To estimate the genetic and phenotypic correlations in production and reproduction traits in Frieswal Cattle under FPT.

Place and Duration of Study: G B Pant University of Agricultural and Technology, Pantnagar, Uttarakhand, India, Between March, 2023 to March, 2024.

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Methodology: The present study was conducted on Frieswal cattle, a synthetic breed, using data from 1163 first lactation records, progenies of 67 sires, spread over period of nine years (2013-2021) as part of an ongoing field progeny testing programme at GBPUA&T, Pantnagar, Uttarakhand. The study aimed to estimate genetic and phenotypic correlations among various production and reproduction traits, such as test day peak yield (TDPY), first lactation 305-days milk yield (FL305D-MY), fat percentage (FP), first lactation length (FLL), age at sexual maturity (ASM), age at first calving (AFC), gestation period (GP), first calving interval (FCI), first service period (FSP), and number of services per conception (NSPC). The data were analyzed using WOMBAT software.

Results: The study revealed that age at first service (ASM) and age at first calving (AFC) had very high genetic (0.99) and phenotypic (0.99) correlations, suggesting they were influenced by the same genes. A strong genetic correlation (0.71) between ASM and gestation period (GP) indicates a close association, while the negative correlation between ASM and total days to peak yield (TDPY) (-0.76) suggests younger cows reach higher peak yields. ASM's negative genetic correlation (-0.57) with first lactation 305-days milk yield (FL305D-MY) implied that selecting for earlier maturity could enhance milk production. Positive correlation between ASM and reproductive traits (FCI, FSP, NSPC, and FDP) were observed, while FL305D-MY showed high negative correlation with traits like FLL and FP but positive phenotypic correlation with FLL, FCI, and FSP. Additionally, there were varied genetic correlation among FCI, FSP, NSPC and FDP, highlighting complex inter-trait relationships.

Conclusions: The present study highlighted the potential of Frieswal herd for selective breeding to improve both milk production and reproductive efficiency. By focusing on traits like age at sexual maturity (ASM), age at first calving (AFC), and milk yield indicators such as test day peak yield (TDPY) and first lactation 305-days milk yield (FL305D-MY), breeders can target genetically associated traits for enhanced overall productivity. These findings provide a valuable foundation for future genetic improvement strategies in Frieswal cattle.

Keywords: Correlations; frieswal; genetic; phenotypic; traits.

1. INTRODUCTION

India has experienced a significant transformation in its dairy sector, commonly referred to as the "white revolution," during the 1980s and 1990s of the previous century, which can be primarily ascribed to a substantial increase in milk production, predominantly resulting from the utilization of crossbred cattle. The practice of crossbreeding indigenous bovines (*Bos indicus*) with exotic breeds (*Bos taurus*) was initiated to augment the genetic capacity for enhanced milk yield. The analysis of genetic parameters is critically important in the field of animal genetics and breeding. These parameters are uniquely associated with certain location and time periods and it may not be appropriate to apply estimates across varied populations (Chaudhari et al., 2013). Understanding the genetic parameters, such as heritability and correlations, allows breeders to implement effective selection strategies that can lead to significant improvements in these economically important traits. Correlation represents the association between different traits and is valuable for predicting the correlated response to selection. Genetic and phenotypic correlations elucidate the extent of association

between different traits at both genetic and phenotypic level. Phenotypic correlations arise from genetic influences as well as the shared environmental conditions in which animals are raised. Conversely, genetic correlations among various traits predominantly result from pleiotropic effects and the linkage of genes that influence multiple traits. Moreover, reproductive traits, often overlooked in favor of production traits, are crucial for ensuring herd sustainability and profitability. The genetic correlations between production and reproduction traits can significantly impact selection strategies, as improvements in one area may inadvertently affect another (García-Ruiz et al., 2020). Therefore, the present investigation was undertaken to study the genetic and phenotypic correlation of various production and reproduction traits in Frieswal cattle under field progeny testing programme.

2. MATERIALS AND METHODS

2.1 Data Collection

A total of 1163 lactation records of Frieswal cattle, sired by 67 bulls, spread over nine years (from 2013-2021) under field progeny testing (FPT) programme maintained at GBPUA&T,

Pantnagar, Uttarakhand were collected. Data pertaining to atypical lactation due to certain factors such as abortion, culling and premature birth were not included in the analysis.

2.2 Traits Studied

Various production and reproduction traits viz., test day peak yield (TDPY), first lactation 305-days milk yield (FL305D-MY), fat percentage (FP), first lactation length (FLL), age at sexual maturity (ASM), age at first calving (AFC), gestation period (GP), First calving interval (FCI), first service period (FSP) and number of services per conception (NSPC) were considered for the study with the aim to identify genetic and phenotypic correlations among production and reproduction traits in Frieswal Cattle.

2.3 Statistical Analysis

The sire components of variances and co-variances were used to estimate genetic and phenotypic correlations between different production and reproduction traits (Becker, 1975). The genetic correlation between two traits was estimated using the following equation:

$$r_{g(x,y)} = \frac{Cov_{s(x,y)}}{\sqrt{\sigma_{s_x}^2 \sigma_{s_y}^2}}$$

Where,

x, y = Two different characters under study

$Cov_{s(x,y)}$ = Sire components of covariance between characters x and y

$\sigma_{s_x}^2$ = Sire component of variance of trait x

$\sigma_{s_y}^2$ = Sire component of variance of trait y

The standard error of genetic correlation (r_g) has been estimated by using the following formula (Panse and Sukhatme, 1967):

$$S.E.(r_g) = (1 - r_g^2) \cdot \sqrt{\frac{S.E.(h_x^2) \cdot S.E.(h_y^2)}{2(h_x^2) \cdot (h_y^2)}}$$

Where,

(h_x^2) and (h_y^2) are the heritability of the characters x and y, respectively.

The phenotypic correlation between characters x and y were estimated by using the following formula:

$$r_{p(x,y)} = \frac{Cov_{s(x,y)} + Cov_{e(x,y)}}{\sqrt{[2(\sigma_{s(x)}^2 + \sigma_{e(x)}^2)(\sigma_{s(y)}^2 + \sigma_{e(y)}^2)]}}$$

Where,

$Cov_{s(x,y)}$ = Sire component of covariance between traits x and y

$Cov_{e(x,y)}$ = Error component of covariance between traits x and y

$\sigma_{s(x)}^2$ = Sire component of variance for trait x

$\sigma_{e(x)}^2$ = Error component of variance for trait x

$\sigma_{s(y)}^2$ = Sire component of variance for trait y

$\sigma_{e(y)}^2$ = Error component of variance for trait y

The standard error of phenotypic correlation was obtained as per the following formula (Snedecor and Cochran, 1967):

$$S.E.(r_p) = \sqrt{\frac{[1 - r_{p(x,y)}^2]}{N - 2}}$$

Where,

$r_{p(x,y)}^2$ = Phenotypic correlation between traits x and y

N = Total number of observations

The statistical significance of phenotypic correlation was determined by using the 't' test with degrees of freedom (Snedecor and Cochran, 1967).

3. RESULTS AND DISCUSSION

The estimated genetic and phenotypic correlations between various production and reproduction traits in a Frieswal cattle population

under field progeny testing programme are presented above and below diagonal, respectively (Table 1).

3.1 Genetic and Phenotypic Correlations of ASM with AFC

The very high genetic and phenotypic correlations between ASM and AFC suggesting that these traits might be governed by same set of gene and gene loci. The very high genetic correlation between AFC and ASM was in consonance with the findings of (Ali et al., 2019) who reported genetic correlation of 0.77 among AFC and ASM.

3.2 Genetic and Phenotypic Correlations of ASM with GP

The high genetic correlation (0.71 ± 0.44) between ASM and GP suggests a significant genetic association between these two traits in this cattle population, implying that they may be influenced by shared genetic factors. However, on a phenotypic level, no significant relationship was observed between ASM and GP, indicating that despite the genetic connection, the traits do not exhibit a noticeable association in practice. In contrast to these findings, (Uddin et al., 2008) reported much lower genetic correlation for indigenous, Frieswal, Sahiwal and Sindhi crossbred cattle, with values of -0.050, 0.080, 0.191, and -0.017, respectively.

3.3 Genetic and Phenotypic Correlations of ASM with TDPY

The strong negative genetic correlation of -0.76 ± 0.44 between ASM and TDPY suggests that younger cows tend to have higher TDPY. However, the very weak negative phenotypic correlation of -0.01 ± 0.03 indicates only a minimal relationship between ASM and TDPY at the phenotypic level. The result obtained suggesting that the genetic association among these traits is not fully reflected in their phenotypic expression, likely due to environmental or epigenetic influences.

3.4 Genetic and Phenotypic Correlations of ASM with FL305D-MY

The strong negative genetic correlation (-0.57 ± 0.55) between ASM and FL305D-MY found in this study suggests that selecting for earlier age at sexual maturity could lead to an

increase in FL305D-MY as a correlated outcome, thus enhancing the productive lifespan of cows. While boosting milk yield is a key goal in breeding, it may be advantageous to prioritize animals with traits linked to earlier age at first service, as long as early insemination does not negatively affect other important traits.

3.5 Genetic and Phenotypic Correlations of ASM with FLL

The genetic correlation of 0.78 ± 0.43 and a phenotypic correlation of 0.03 ± 0.03 were observed between ASM and FLL. A similar positive genetic correlation between ASM and FLL was also reported by (Uddin et al., 2008) in indigenous, Sahiwal and Red Sindhi crossbred cattle. However, the authors noted a negative genetic correlation between ASM and FLL in Frieswal and other crossbred cattle.

3.6 Genetic and Phenotypic Correlations of ASM with FCI, FSP, NSPC and FDP

ASM showed positive genetic and phenotypic correlations with FCI, FSP, NSPC and FDP, with genetic correlation coefficients of 0.58 ± 0.43 , 0.51 ± 0.38 , 0.17 ± 0.51 , and 0.23 ± 0.61 , respectively, and corresponding phenotypic correlation coefficients of 0.03 ± 0.03 , 0.02 ± 0.03 , 0.22 ± 0.03 , and 0.00 ± 0.01 . The positive genetic correlation between ASM and FCI aligns with the findings of (Uddin et al., 2008) in indigenous, Sahiwal and Red Sindhi crossbred cattle, as well as (Ali et al., 2019) in crossbred cattle. However, reported a negative correlation of -0.053 between ASM and FCI in Frieswal cattle. The observed positive genetic correlation may be due to gene linkage or pleiotropic effects of genes influencing these traits.

3.7 Genetic and Phenotypic Correlations of AFC with GP, FCI, FSP, NSPC and FDP

Positive genetic and phenotypic correlations between AFC and GP was observed. In contrast, (Vinoos et al., 2005) reported negative genetic and phenotypic associations between AFC and GP. A positive genetic relationship between AFC and FCI has been reported by (Singh, 2007, Tiwari, 2009, Getahun, 2019, Ayalew et al., 2017) in crossbred cattle. However, negative genetic associations between AFC and FCI were noted by (Chaudhari et al., 2013). A positive genetic correlation and a negative phenotypic

correlation between AFC and FCI was reported in crossbred cattle (Lodhi et al., 2019). Similarly, (Canaza-Cayo et al., 2017) found a positive genetic and negative phenotypic correlations between AFC and both FCI and FDP in crossbred cattle. (Getahun et al., 2019, Ayalew et al., 2017) also observed a positive genetic and negative phenotypic associations between AFC and NSPC in crossbred cattle, while (Ilatsia et al., 2007) reported a strong positive genetic correlation between AFC and NSPC in Sahiwal cattle. Positive correlation between AFC and FDP as well as FSP were identified by (Canaza-Cayo et al., 2018, Getahun and Beneberu, 2023). The genetic and phenotypic correlations of 0.06 ± 0.21 and -0.19 ± 0.21 , respectively, between FL305D-MY and AFC in Hardhenu cattle (Dev et al., 2021) whereas (Canaza-Cayo et al., 2018) found values of -0.49 ± 0.09 and -0.25 ± 0.01 , respectively, and (Ayalew et al., 2017) reported -0.24 ± 0.11 for both in crossbred cattle.

3.8 Genetic and Phenotypic Correlations of AFC with TDPY, FL305D-MY, FP and FLL

The present study found a positive genetic and negative phenotypic correlations between AFC and FP as well as FLL, which aligns with the findings of (Ambhore et al., 2017) in crossbred cattle. (Ambhore et al., 2017, Banik and Gandhi, 2010, Girimal et al., 2020, Singh and Singh, 2015) reported positive genetic and phenotypic correlations between AFC and TDPY in Phule Triveni, crossbred and Sahiwal cattle, respectively. Additionally, (Ambhore et al., 2017) noted a strong positive genetic relationship and a low negative genetic and phenotypic relationship between AFC and FL305D-MY, as well as positive genetic and phenotypic correlations between AFC and first lactation length in Phule Triveni cattle. The genetic associations of AFC with milk traits observed in this study suggest that selecting for improved AFC could lead to a decrease in fat percentage, an increase in first lactation length, and improvements in test day peak yield and FL305D-MY traits within this population.

3.9 Genetic and Phenotypic Correlations of GP with TDPY, FL305D-MY, FLL, FCI, NSPC and FDP

The study found that the GP had a negative and weak genetic correlations with test day peak yield, FL305D-MY, fat percentage, first calving interval, first service period, number of services

per conception and first dry period. Notably, no genetic association was observed between FLL and AFC. Phenotypically, the association between GP and TDPY was strong and positive, while the correlation with NSPC was low and positive. Conversely, the phenotypic correlations among GP and FP, FLL, FCI and FDP was negative and low. The negative genetic and phenotypic correlations between GP and FSP in crossbred cattle (Zelege et al., 2016). The positive genetic and phenotypic correlations between gestation period and FL305D-MY in Sahiwal cattle (Ratwan et al., 2024). The negative genetic and phenotypic correlations between GP and both FL305D-MY and FSP in Ongole cattle, as well as between gestation and lactation length (Vinoos et al., 2005). Additionally, both (Vinoos et al., 2005, Ratwan et al., 2024) reported negative genetic and phenotypic correlations among GP and FCI, FSP and FDP in Ongole and Sahiwal cattle breeds. The gestation period is a highly fixed trait in any organism, animals are rarely selected for this trait. Instead, selection in cattle typically focuses on milk production traits, with reproductive traits being selected as correlated responses.

3.10 Genetic and Phenotypic Correlations of TDPY with FL305D-MY, FLL, FCI, NSPC and FDP

The strong genetic and phenotypic correlations observed between TDPY and FL305D-MY suggesting that both traits are influenced by the same alleles and allele combinations. Negative genetic correlations between FL305D-MY and FLL have been reported by (Ambhore et al., 2017, Nikam, 2010) in crossbred cattle and Phule Triveni cattle, respectively. In contrast, (Girimal et al., 2020) reported a positive correlation in crossbred cattle. Contrary to the findings of the current study, (Bajetha, 2006) observed positive genetic and phenotypic correlations in crossbred cattle. The negative phenotypic association between TDPY and FCI aligns with the findings of (Dev et al., 2021) in Hardhenu cattle. The negative phenotypic and genetic correlations between peak yield and FDP in crossbred cattle (Verma et al., 2016) However, (Ratwan et al., 2024) reported genetic and phenotypic correlations of 0.19 ± 0.22 and 0.01 ± 0.03 , respectively, between peak yield and FSP, and correlations of 0.20 ± 0.21 and 0.01 ± 0.03 between peak yield and FCI. Additionally, (Kumar et al., 2017) found a genetic correlation of 0.173 ± 0.260 and a phenotypic correlation of -0.005 ± 0.000 between peak yield and FP in Frieswal cattle.

Table 1. Genetic and Phenotypic Correlations among production and reproduction traits in Frieswal cattle

Trait	ASM	AFC	GP	TDPY	FL305D-MY	FP	FLL	FCI	FSP	NSPC	FDP
ASM	1	0.99±0.00	0.71±0.44	-0.76±0.44	-0.57±0.55	0.71±0.42	0.78±0.44	0.78±0.43	0.51±0.38	0.97±0.51	0.23±0.61
AFC	0.99±0.00**	1	0.76±0.39	-0.72±0.38	-0.61±0.46	0.73±0.37	0.72±0.38	0.45±0.46	0.89±0.38	0.18±0.39	0.42±0.05
GP	0.001±0.03	0.90±0.01	1	-0.11±0.15	-0.22±0.14	-0.12±0.15	0.003±0.16	-0.05±0.15	-0.35±0.15	-0.09±0.23	-0.49±0.28
TDPY	-0.01±0.03	-0.02±0.03	0.95±0.02	1	0.94±0.02	-0.64±0.10	-0.76±0.09	-0.76±0.09	-0.68±0.10	-0.50±0.21	-0.24±0.26
FL305D-MY	-0.02±0.03	-0.05±0.02	0.76±0.03**	0.76±0.01**	1	-0.73±0.08	-0.72±0.09	-0.70±0.09	-0.59±0.10	-0.55±0.20	-0.11±0.25
FP	-0.04±0.03	-0.03±0.03	-0.21±0.03**	-0.27±0.03**	-0.27±0.03**	1	0.58±0.11	0.59±0.10	0.59±0.10	0.54±0.20	0.32±0.25
FLL	0.03±0.03	-0.02±0.03	-0.20±0.03**	-0.27±0.03**	0.08±0.03**	0.09±0.01**	1	0.99±0.01	0.93±0.02	0.77±0.20	0.27±0.27
FCI	0.03±0.03	-0.02±0.03	-0.20±0.03**	-0.27±0.02**	0.12±0.03**	0.95±0.01**	0.95±0.01**	1	0.95±0.01	0.61±0.20	0.36±0.25
FSP	0.02±0.03	-0.38±0.03**	-0.18±0.03**	-0.23±0.03**	0.12±0.03**	0.88±0.01**	0.93±0.01**	0.93±0.01**	1	0.61±0.20	0.49±0.24
NSPC	0.22±0.03**	0.22±0.03**	0.06±0.03*	-0.08±0.03**	-0.11±0.03**	0.03±0.03	0.03±0.03	0.04±0.03	0.05±0.03*	1	-0.30±0.40
FDP	0.001±0.01	0.001±0.01	-0.01±0.02	-0.01±0.01	-0.01±0.03	0.11±0.01**	-	0.23±0.03**	0.22±0.03**	0.02±0.03	1
							0.10±0.03**				

The genetic and phenotypic correlations are above and below the diagonal, respectively; * indicate significant at 5% level; ** indicate significant at 1% level

3.11 Genetic and Phenotypic Correlations of FL305D-MY with FP, FLL, FCI, FSP, NSPC and FDP

The genetic relationship between FL305D-MY and traits such as FP, FLL, FCI, FSP and NSPC was found to be high and negative, while it was low and negative with FDP. In terms of phenotypic associations, FL305D-MY showed a moderate positive correlation with FP, low positive correlations with FLL, FCI and FSP and low negative correlations with NSPC and FDP. In contrast to the current study, (Jayawardana et al., 2003) reported a negative genetic relationship between FL305D-MY and FP of -0.26 ± 0.27 and -0.50 ± 0.06 , respectively. The findings of the present study indicate a strong negative genetic relationship between FL305D-MY and various milk and reproductive traits, suggesting that genes associated with higher milk yield are likely to decrease FP and FLL. This indicates a significant antagonistic relationship between milk yield and other traits being studied. The genetic correlation of 0.990 ± 0.001 and a phenotypic correlation of 0.064 between FL305D-MY and NSPC in Holstein Friesian cattle (Zahed et al., 2019). Conversely, several studies, including those by (Banik and Gandhi, 2010, Ratwan et al., 2024, Ratwan et al., 2019, Dahlin et al., 1998) found positive genetic and phenotypic correlations between FL305D-MY and FLL in Sahiwal cattle. Negative genetic correlation between FL305D-MY and FDP were reported by (Ulutas and Sezer, 2009) in crossbred cattle, as well as by (Banik and Gandhi, 2010, Ratwan et al., 2014, Ratwan et al., 2019, Dahlin et al., 1998) in Sahiwal cattle. (Ratwan et al., 2019, Zahed et al., 2019, Dash et al., 2015) found positive genetic and phenotypic correlations between FL305D-MY and FSP. The positive correlation between FL305D-MY and FCI was reported in Sahiwal cattle (Ratwan et al., 2019). However, (Ayalew et al., 2017). found negative correlations between these traits, while (Dev et al., 2021, Ratwan et al., 2016) observed positive correlation between 305D-MY and FLL.

3.12 Genetic and Phenotypic Correlations of FP with FLL, FCI, FSP, NSPC and FDP

FP exhibited strong positive correlations (both phenotypic and genetic) with FLL, FCI, FSP and NSPC, while showing a low phenotypic and moderate genetic correlations

with FDP. These positive genetic and phenotypic correlations of FP with FLL, FCI, FSP, NSPC and FDP align with findings from (Ambhore et al., 2017, Girimal et al., 2020, Nikam, 2010, Lakshmi et al., 2009). Conversely, (Nikam, 2010) reported negative phenotypic correlation between FP and FLL in crossbred cattle. However, (Osman et al., 2013) mentioned genetic correlations of -0.689 , -0.562 , 0.795 , and 0.363 , along with phenotypic correlations of -0.274 , -0.143 , 0.234 , and 0.064 between FP and FSP, AFC, FDP and FCI, respectively.

3.13 Genetic and Phenotypic Correlations of FLL with FCI, FSP, NSPC and FDP

The very high genetic correlation and low phenotypic correlation between FLL and NSPC are consistent with findings of (Ilatsia et al., 2007, Zahed et al., 2019), who reported genetic and phenotypic correlations of 0.80 and 0.30, respectively, in Sahiwal cattle, and 0.995 ± 0.009 and 0.245 , respectively, in Holstein Friesian cattle. In contrast, (Getahun and Beneberu, 2023) reported lower genetic and phenotypic correlations between FLL and NSPC in crossbred and Sahiwal cattle, respectively. A positive genetic and negative phenotypic correlations between FLL and FDP in crossbred cattle (Lodhi et al., 2016) Nearly perfect genetic correlations between FLL and FCI was reported in crossbred cattle (Ayalew et al., 2017). The positive and strong correlation between FLL and FCI have been reported by several researchers across different genetic groups of cattle, including (Ilatsia et al., 2007, Banik and Gandhi, 2010, Ulutas and Sezer, 2009, Ratwan et al., 2019). Similarly, the positive genetic relationship between FLL and FDP aligns with reports from (Singh and Singh, 2015, Lodhi et al., 2016, Nikam, 2010, Ratwan et al., 2019). in various cattle genetic resources.

3.14 Genetic and Phenotypic Correlations of FCI with FSP, NSPC and FDP

The genetic correlations of 0.95 ± 0.01 , 0.61 ± 0.20 , and 0.30 ± 0.25 were found between FCI and FSP, FCI and NSPC, and FCI and FDP, respectively. The phenotypic associations were 0.93 ± 0.01 , 0.04 ± 0.03 , and 0.20 ± 0.03 for the same pairs of traits. The high positive genetic correlation between FCI and FSP suggests that no genetic antagonism

exists between these traits. Previous studies by (Tiwari, 2009, Bajetha, 2006, Moges et al., 2009, Singh and Gurnani, 2004a) also reported positive genetic and phenotypic correlations between FCI and FSP in crossbred cattle. Additionally, (Ilatsia et al., 2007) obtained the positive genetic correlations between FCI and NSPC in Sahiwal and crossbred cattle. However, (Getahun and Beneberu, 2023) reported a negative genetic correlation and a positive phenotypic relationship between FCI and NSPC in crossbred cattle.

3.15 Genetic and Phenotypic Correlations of FSP with NSPC and FDP

Both genetic and phenotypic correlations of FSP with NSPC and FDP were found to be positive. The genetic correlation between FSP and NSPC was high, while the phenotypic correlation was low. However, the genetic and phenotypic correlations of FSP with NSPC and FDP were relatively low. The genetic correlation of 0.64 between NSPC and FSP in crossbred cattle (Fathoni et al., 2022). The positive genetic and phenotypic correlations between FSP and NSPC and FDP are consistent with findings from (Ratwan et al., 2004) in Sahiwal cattle. In contrast, (Dev et al., 2021, Ulutas and Sezer, 2009) reported negative correlations of -0.04 ± 0.105 and -0.69 ± 0.20 , respectively, in crossbred and Sahiwal cattle.

3.16 Genetic and Phenotypic Correlation of NSPC with FDP

A negative genetic correlation of -0.30 ± 0.40 was found between FDP and NSPC. However, no phenotypic correlation was observed between these traits. This negative genetic correlation suggests that as one trait increases, the other tends to decrease at the genetic level. Despite this genetic relationship, the lack of observable correlation at the phenotypic level indicates that traits can be genetically related even if they do not exhibit a phenotypic association.

4. CONCLUSION

The study on Frieswal cattle revealed important genetic and phenotypic correlations between production and reproduction traits. High correlation between age at sexual maturity (ASM) and age at first calving (AFC) suggesting

that these traits were controlled by the same genes, offering potential for selection to improve reproductive efficiency. Negative correlation between ASM and both test day peak yield (TDPY) and first lactation 305-days milk yield (FL305D-MY) indicated that selecting for earlier maturity could enhance milk production. Additionally, the study found strong genetic correlation between TDPY and FL305D-MY, emphasizing the importance of these traits in improving overall productivity. Therefore, the present study in the Frieswal herd highlighted the potential for selective breeding to improve both milk production and reproductive efficiency.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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