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RESEARCH ARTICLE

Indirect selection decision making for production and reproduction traits using multi-variate Markov chain Monte Carlo (MCMC) algorithm in Sahiwal cattle

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Abstract: The prosperity in livestock productivity can be achieved by properly emphasizing both the analytical approach and traits of economic importance that affect present and future generations in a herd *viz*. reproduction and production. The study was planned to explore genetic parameters and correlation components for reproduction traits (AFC: Age at First Calving, FSP: First Service Period), milk production traits (FLMY: First Lactation Milk Yield) and milk composition traits (FLSNFY: First Lactation SNF Yield, FLFY: First Lactation Fat Yield) in Sahiwal cattle of Livestock farm unit from ICAR-NDRI Karnal, Haryana, India. A comparative analytic approach (LSML v/s Bayesian) was considered by using LSML Harvey and Gibbs sampler Animal model approach of Bayesian application with a mixed model equation and estimated breeding values (EBVs) for production traits. Marginal posterior means for heritability varied between 0.17±0.0148-0.51±0.0114 by univariate, bivariate, and trivariate analysis while between 0.12±0.003-0.49±0.002 by multi-trait analysis. Heritability estimate was higher for FLSNFY (0.51±0.01) followed by FLFY, AFC, FLMY (0.45±0.01, 0.29±0.04, 0.20±0.01) and lowest for FSP (0.17±0.01). High and positive genetic and phenotypic correlation (0.99±0.0001 and 0.98±0.004) was observed for FLFY-FLSNFY by multi-trait analysis. AFC has a moderate positive correlation with considered traits, while FSP has a negative genetic correlation (FSP-FLMY: -0.15±0.02; FSP-FLSNFY: -0.11±0.02; FSP-FLFY: -0.04±0.02). High correlations of reproduction traits suggest earlier age selection and directly reflect the production potential of the herd. Gibbs sampling was advantageous for genetic analysis with heterogeneous (reproduction traits) and homogenous (production traits) factors. Our work revealed improvement in the genetic gain of dairy cattle by indirect selection through AFC for FSP, FLMY, FLSNFY, and FLFY. High correlations of reproduction traits suggested earlier age selection could bring better production potential of the herd through a balanced selection decision.

Keywords: Bayesian approach Breeding value, Correlation, Multivariate Gibbs sampler, Zebu cattle,

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Introduction

Indian cattle genetic resources are contributed by some of the best milch breeds including Sahiwal, Gir, Rathi, Tharparkar, and Red Sindhi. Zebu cattle breeds carried forward the better adaptive capacities to successive generation which were gained during evolution in different spatial-temporal conditions (Hansen 2004; Silpa et al. 2021; Das et al. 2016). Climate resilient zebu breeds such as Sahiwal are raised, selected and utilized to evolve hybrids (Karan Swiss) for their outrageous performance in changing global habitats (Kumar et al. 2016; Kumar and Gandhi 2011). Sahiwal breed is originated from Punjab province of Pakistan and synonymously known as Lambi Bar, Lola, Montgomery, Multani and Teli (NBAGR, 2023). This breed is third (2^{nd} among top milch breeds) after Gir and Lakhimi in population with 59,49,674 animals in India. It is also reared for its lean carcass with desirable fat cover in Australia but well known for its dairy potential in Indian sub-continent. Sahiwal is heavy, parasite-resistant, heat-tolerant, produce milk with high fat content and better calving potential than other breeds. Scientific rearing and management can improve the production potential of cattle farms. Cattle production system will be economically profitable by considering the complex phenomenon of reproduction, regular breeding and timely calving. Reproduction traits vary with species, breeds and also among the animals within the same breed as these traits are affected by both genetic and non-genetic factors (climate, nutrition, and level of management). Reproduction traits are very important to reduce the cost of production by reducing calving interval to alter current and subsequent lactations. Desirable genetic gain can be achieved without reducing productive and reproductive performance considering TMI (total merit index) under breeding and selection programs to improve the genetic potential of dairy herd. Reproduction traits are good indicators of production potential for genetic improvement through breeding programs of Sahiwal cattle (Singh et al. 2020; Ratwan et al. 2022).

Milk is the primary source of protein and vital for nutritional security in India and worldwide, its production had been increased by 2% globally. India is largest producer of milk in world due to an increase in Compounded Annual Growth Rate (CAGR) from two decades, which is majorly contributed by cattle and buffalo breeds. Recently, cows surpassed the share in milk production as increase (+1.8 per cent) was noticed from 49.2 per cent (2016-17) to 51 per cent (2020-21) (FAO 2022). Milk of Sahiwal breed is rich in desirable proteins such as Alpha, Beta, and Globin proteins and A2 allele includes proline rather than histidine protein among A1 and A2 alleles of beta protein. Milk is used as remedy and treatment of cholesterol, diabetes, cancer and heart disease (Davoodi et al. 2013; Akram et al. 2020). Sahiwal is efficient dairy cattle breed due to its fast-growing calves, high productivity, better reproduction performance and hardiness under unfavorable climatic conditions. The evaluation of improvement in the rearing of our productive herd can be done by estimation of the true genetic potential of present herd for direct and indirect selection of the traits. Along with this the prediction of performance of the progeny generations based on heritability 0of the traits. Reproduction and production traits were considered for genetic analysis using conventional methods viz. Harvey, derivative free restricted maximum likelihood (DFREML), best linear unbiased prediction (BLUP), Regression, maximum likelihood (ML) and restricted maximum likelihood (REML) approaches in Sahiwal cattle (Ratwan et al. 2019; Banik and Gandhi 2010; Choudhary et al. 2003; Kaiser et al. 2018; Ilatsia et al. 2007; Kothekar et al. 2004). The genetic analysis from Frequentist approaches includes likelihood values of the given data structure.

The paradigm shifts in analytical methods (viz. from Frequentist to Bayesian) leads to betterment in decision making process for selective breeding programs of livestock species. Bayesian approach was recently used for breeding data analysis of various cattle breeds (Tharparkar, Sahiwal, Karan Fries and Japanese Black cattle) and Murrah buffalo (Yadav et al. 2023; Yadav et al. 2022; Worku et al. 2021; Setiaji et al. 2021; Dahiyta et al. 2022). Bayesian approach provides appropriate estimates for parameters by including priori with likelihood values in analysis. Approach also provides validation, automation and cross examination of the resulted estimates by defining iterations and visualization of graphs. The studies on heterogeneous bivariate (Age at First Calving and First Service Period) and trivariate (First Lactation Milk Yield, First Lactation Fat Yield and First Lactation Solid Not Fat Yield) analysis using Gibbs sampler (MTGSAM) in Sahiwal cattle were lacking. The underlying hypothesis for this work was that the Bayesian approach provide accurate estimation for breeding value. Under this proposed hypothesis the present study was aimed to obtain comparative genetic evaluation using Harvey and Gibbs sampling approach while considering reproduction and production traits as selection criteria and to estimate the breeding values of sires for milk production and composition traits in Sahiwal.

Materials and Methods

Sampling structure and data curation

Records of 802 Sahiwal cows for reproduction, production and milk composition were collected over a period of 30 years (1990-2019) from history-cum-pedigree sheet from ICAR-National Dairy Research Institute (ICAR-NDRI) herd maintained at Karnal, Haryana. The information collected in order to get or generate the data related to various production and reproduction traits were given as below:

- Animal number
- Sire number
- Dam number
- Date of birth
- Date of calving
- Date of successful insemination
- Milk yield in first lactation
- Fat %
- SNF %

Data for normally calved and lactating animals were sequentially pre-processed for analysis as compiling, normalization and standardization steps. Outlier animals with suboptimal records viz. lactation length less than average days (<100 days) milk yield less than average yield (<500 kg) and fat% (<3.5%) were excluded from the present analysis.

Considered traits: The research work was undertaken while considering the economically important traits of milch animals.

Reproduction traits

Reproductive traits include age at first calving and first service period which have direct as well as indirect effect on productivity of animal in terms of milk yield and milk composition.

- ***Age at First Calving (AFC):*** AFC is age of the animal in days at the time of first calving and was calculated by taking the difference (days) between the date of birth and date of first calving.

- ***First Service Period (FSP):*** Trait was calculated by taking the difference between date of calving and subsequent date of successful conception.

Production traits: Production traits include milk production and composition traits such as milk yield, fat yield and solid not fat yield which have direct effect on life time production performance of animal.

- ***First lactation 305 days / Less milk yield (FLMY):*** FLMY was taken as milk yield (kg) from the day of first calving to the day on which cows dried off.

- ***First Lactation SNF (Solid Not Fat) yield (FLSNFY):*** Trait was calculated by taking the average records of percent SNF from date of calving to date of dry taken at regular intervals and multiplying this by number of days in milk in first lactation.

- ***First Lactation Fat yield (FLFY):*** Trait was calculated by taking the average of fat% records taken at different intervals in first lactation and multiplying this by number of days in milk from date of calving to date of dry for that lactation.

Statistical analysis: Data was statistically analyzed for estimation of descriptive statistics, least squares mean and posterior densities by Bayesian approach using software packages such as R software (version 4.2.0), Harvey and BLUPF90 family of program, respectively (R Core Team 2022; Harvey 1990; Misztal and Perez-Enciso 1998). Sire evaluation was also done after estimation of breeding value by both methods Harvey and BLUPF90 software for production traits.

Model specifications

Model considered various fixed and random effects on traits in proposed work. Year of calving/birth had been classified into four seasons e.g., summer (April to June), rainy (July to September), autumn (October to November) and winter (December to March). Seasonal variations were based on meteorological factors at ICAR-Central Soil Salinity Research Institute (ICAR-CSSRI), Karnal for temperature fluctuations, relative humidity and prevalent geo-climatic conditions. The region is specified at an altitude of 235 to 252 meters from the sea level, latitude 29.43^{0}N and longitude 77.2^{0}E with 10^{0}C-45^{0}C temperature range.

Collected data had been classified into six periods by taking five years in a group based on year of birth/calving. Age has important influence on economic traits in cattle. Age at First Calving (AFC) is taken as covariate for all traits except for age at first calving as a continuous trait. Covariate age at first calving has been classified in eleven classes (Sturges 1926) as:

$$\text{Number of age group} = \frac{\text{Range}}{1 + 3.322\log_{10}\text{N}}$$

Where, N = No. of observations; Range = Maximum – Minimum

Following mixed model equation was used for analysis of various reproduction and production traits:

For FSP, FLMY, FLFY and FLSNFY

$Y_{ijklm} = \mu + P_i + Sn_j + Ag_k(cov) + S_l + e_{ijklm}$

Where,

Y_{ijklm} = Observation of mth animal having lth sire effect, kth age group at first calving, calved in jth season, ith period

μ = Overall mean

P_i = Effect of ith period of calving (i=1 to 6)

Sn_j = Effect of jth season of calving (j=1,2,3,4)

$Ag_k(cov)$ = Effect of kth age group in first calving (k=1 to 11)

S_l = Effect of lth sire (l= 41)

e_{ijklm} = Random error, N (0, σ^2e)

For AFC

$Y_{ilkl} = \mu + P_i + Sn_j + S_k + e_{ijkl}$

Where,

Y_{ijkl} = Observation of lth animal having kth sire effect, calved in jth season, ith period

μ = Overall mean

P_i = Effect of ith period of birth (i=1 to 6)

Sn_j = Effect of jth season of birth (j=1,2,3,4)

S_k = Effect of kth sire

e_{ijkl} = Random error, N (0, σ^2e)

Least Squares Maximum Likelihood (LSML) approach

The effects of genetic (sire) and non-genetic factors (periods, season of birth/calving and age at first calving) were assessed by LSML method.

Bayesian approach

Data were subjected to analysis using suitable software packages from BLUPF90 family. Alpha-numeric values were removed from data file by using RENUMF90 software initially to get renumbered data file for further analysis. Breeding Values were estimated by using blupf90 software. Multiple iterative trails were used in GIBBS2F90 software for standardization of Gibbs sampler in Markov chain. Generated binary files act as input to invoke POSTGIBBSF90 application to estimate posteriori of the (co)variance component, genetic parameters and correlations. These results were than validated till normalization and cross checked by visualization of trace plot and histogram (Gianola and Foulley 1990; Garcia-Cortés et al. 1998). Final point estimates were obtained by marginalization process and automated statistically for accuracy by Monte Carlo error (MCE) and convergence diagnostic methods.

Standardization of Gibbs Sampler

Gibbs samples were standardized by various measures for i) the steps of automation viz. total Gibbs sampling chain, burning samples, thinning interval ii) and cross examination by observing the resulted measures for MCE, Standard deviation (SD), trace plot and histogram for posterior distribution. Initial non converging samples were discarded in standardized sampling rounds. Final effective samples give the desired point estimates for genetic analysis. Standardized sampling parameters after various trials were considered as, 35000 iterative cycles with 25000 burn-in cycles and 10 cycles thinning interval to achieve 1000 Gibbs samples for bivariate analysis of reproduction traits (AFC and FSP). Meticulous Gibbs sampler string to accomplish final 900 samples from 10000 overall cycles with a burn-in of 1000 cycles and 10 cycles thinning break were considered for trivariate analysis of production traits (FLMY, FLFY and FLSNFY). Multi-trait Gibbs Sampling Animal Model (MTGSAM) approach with a total of 18000 Gibbs samples were finalized while each 10th cycle to be stored after discarding initial 20000 cycles from overall sampling chain of 200000 for all reproduction and production traits in Sahiwal. The difference in standardizing parameters is due to number of considered traits as well as sampling size till desired distribution for each trait in bivariate, trivariate and multivariate analysis.

Results and Discussion

Descriptive Statistics

Descriptive statistics of data is presented by Mean ± SE, Coefficient of Variation (C.V.), Standard deviation and lower, higher values (Table 1). Coefficient values explain the large variability in data distribution for this sampling structure and ranged between 14.17 and 79.45 for AFC (least varying) and FSP (most varying) traits respectively. FLSNFY and FLMY was the most varying and the least varying production traits, respectively. Genetic analysis uses priori for calculating joint probability distribution of (co)variance component in Bayesian statistics.

Least-squares Mean and affecting factors

Least-squares Mean values and effect of various genetic and non-genetic factors were estimated by Harvey LSML approach for Sahiwal cattle (Table 2). Average age at first calving and first service period was valued as 1145.19±10.81 and 189.58±22.95 days respectively. All non-genetic and genetic factors are found to be non-significant for reproduction traits while period of birth has significant effect at P<0.01 on AFC. The significance was due to different feeding, managemental practice and environmental condition over these years. Average first lactation milk yield, first lactation solid not fat yield and first lactation fat yield was found as 2191.43±143.43 kg, 1500.28±123.23 kg and 829.01±67.61 kg respectively. Period of calving was showing highly significant effect while other non-genetic and genetic factors were found to be non-significant for production traits.

All the genetic components differ from one population to another because they are influenced by gene frequencies. The similarity in the results was found for the age at first calving (Chawla and Mishra 1982; Raja 2010; Narwaria et al. 2015; Pathak 2018) and for first service period (Rehman et al. 2008). Average first lactation milk yield was found quite lower from the present work as 1716.04±78.47 kg (Girimal et al. 2020). However, there was some differences with the previous reports in the results for production traits while effect of factors for the considered traits was in association (Kumar and Gandhi 2011; Raja and Gandhi 2015; Verma et al. 2016).

Bayesian posterior densities and genetic evaluation

Marginal posterior mean estimates for heritability ± MCE were found as 0.29±0.0401, 0.17±0.0148, 0.20±0.0125, 0.51±0.0114 and 0.45±0.0112 for AFC, FSP, FLMY, FLSNFY and FLFY respectively (Table 3 and 4).

Phenotypic variance was higher for all traits among all other sources of variances by bivariate and trivariate analysis through GS (Gibbs Sampling). The estimates of variability and range of posterior densities were lower and narrow for additive genetic variance of AFC (1560.5±345) as indicated in descriptive statistics. Higher phenotypic variance was noticed for FLMY (832930 and 883750) followed by environmental and genetic variance. Phenotypic variance was followed by FLSNFY and FLFY (686640 and 201610) in our work. The genetic variance was higher for FLSNFY followed by FLMY and FLFY (354940, 170750 and 92353). Higher variability was noticed for additive genetic variation of FLSNFY (109390±9983.3) while less variability was observed for phenotypic variation of FLFY (19659±1228.6).

The posterior densities and genetic evaluation for (co)variance estimation includes marginalization process. The marginalization process for each standardized Gibbs cycling approach in present investigation is similar to bootstrapping phenomenon of normalization. Posterior densities by joint probability distribution of priori and likelihood values from data distribution are more informative for genetic components. These results explain the 95% HPD, SD and convergence from mixed heterogeneous two-trait (AFC and FSP) model; homogenous three-trait (FLMY, FLFY and FLSNFY) model and for all five traits from multi-trait model analysis. Higher genetic variance for FSP indicated high scope for selection as compared to AFC for which phenotypic variance was higher as compared to genetic variance. While higher environmental variability as compared to genetic components for AFC and FSP explain their moderate heritability. Conclusively, low AFC and FSP are profitable in Sahiwal herd. First lactation traits are indicative of production potential of animal in subsequent lactations. Phenotypic and genetic variance was the highest and the lowest, respectively for each trait. However, overall estimates for genetic and phenotypic variations were the lowest for FLFY. More scope of improvement through management and environmental factors as compared to genetic factors for FLMY and FLFY can be revealed. More phenotypic influence was indicated for selection from our work followed by genetic and least influence with environmental factors for FLSNFY. Higher variability in genetic variance for FLSNFY indicates high heritability estimates but variance components suggest very less scope for improvement by genetic influence. More disperse pattern of variability for FLSNFY indicate less stabilized population and more scope for selection in Sahiwal.

Comparative heritability estimates for Harvey and Bayesian methods

Results were subjected for comparison to generalize this application in animal breeding data as aligning with conventional method (LSML v/s Bayesian) and different trait combinations (bivariate, triavriate and multivariate) for reproduction and production traits in Sahiwal. Heritability estimates were moderate (0.21±0.299-0.29±0.352) from LSML while moderate to higher (0.17±0.0148-0.51±0.0114) from Bayesian approach and estimates were more reliable for all considered traits with later (Table 4). Heritability estimate was moderate for reproduction traits by both methods. Medium heritability was observed by LSML (0.28±0.236 and 0.24±0.260) and Bayesian (0.29±0.0401 and 0.17±0.0148) analysis for AFC and FSP. Moderate heritability estimates valued as 0.21±0.299, 0.22±0.282 and 0.29±0.352 for FLMY, FLSNFY and FLFY respectively from LSML approach. Moderate to higher heritability estimated as 0.20±0.0125, 0.45±0.0112 and 0.51±0.0114 for FLMY, FLFY and FLSNFY from Bayesian approach.

Heritability estimate varies with sampling structure and with different climatic condition (macro and micro) for which animals were exposed in herd(s). Bayesian approach does not have any assumption about sample size as approach is effective for varying sampling structure and parameters for different traits. For some traits the estimated heritability by both methods was not similar, even comparatively higher in Bayesian estimates. Especially for FLSNFY and FLFY traits, Bayesian analysis provide higher estimate with limited data due to the fact that Bayesian estimate takes into account prior information of variance components into the analysis through a prior distribution. Another reason might be that Bayesian approach naturally accounts for uncertainty in the parameters by providing a full posterior distribution, rather than a single point estimate (as in LSML). Very low MCE indicated precise estimates by underlying Bayes theorem from Bayesian method by considering the iterative cycles using combined information of priori and likelihood values which also takes care of all uncertainty and small sampling structure in unbalanced data. Pattern of heritability estimate in bivariate and trivariate analysis as moderate estimate for AFC, FSP and FLMY and higher estimate for FLSNFY and FLFY can be explained by comparatively higher variability (among source of variation) of environmental (for earlier traits) and genetic component (for later traits) from Bayesian approach while no such explanation can be given by analysis of LSML approach. Conclusively heritability estimate was medium to high in Sahiwal for reproduction and production traits. Moderate to higher heritability was noticed from multi-trait analysis also as similar to bivariate and trivariate analysis of reproduction and production traits. Heritability estimates for reproduction traits were low to moderate while moderate to high for production traits. Direct selection was indicative for FLFY and FLSNFY due to high heritability while less effective for AFC, FLMY and FSP but with vice-versa genetic influence.

Heritability estimates for reproduction traits was in the range of previous estimates for Sahiwal cattle but not in complete agreement as values for AFC were 0.048±0.001 and 0.159, 0.43±0.168 by earlier researchers (Sivamani et al. 2013; Singh et al. 2017; Bansal et al. 2018). Varying estimates were reported as 0.193 and 0.5 under different multi-trait analyses model in Sahiwal cattle (Banik and Gandhi 2010).

Table 1: Descriptive statistics for reproduction and production traits in Sahiwal cattle

Parameters	Mean ± SE	CV	SD	Lower Values	Higher Values
		Reproduction Traits			
AFC	1135.24±9.58	14.17	160.90	776	1775
FSP	178.17±8.43	79.45	141.56	33	944
		Production Traits			
FLMY	2292.44±69.65	40.76	937.75	501.1	4991.3
FLFY	1998.92±103.07	69.18	792.08	180.01	5718.41
FLSNFY	1090.93±57.93	71.24	1424.75	101.03	3139.04

AFC: Age at First Calving; FSP: First Service Period; FLMY: First Lactation Milk Yield; FLFY: First Lactation Fat Yield; FLSNFY: First Lactation Solid-not Fat Yield; SD: Standard Deviation; CV: Coefficient of Variation (%); N= no. of records; SE=Standard Error.

Table 2: Least-squares Mean for reproduction and production traits in Sahiwal cattle

Traits	LSM±SE
AFC (days)	1145.19±10.81
FSP (days)	189.58±22.95
FLMY (kg)	2191.43±143.42
FLSNFY (kg)	1500.28±123.23
FLFY (kg)	829.01±67.61

LSM±SE= Least-squares Mean ± Standard Error

Table 3: Descriptive statistics for variance components and heritability estimates by bivariate and trivariate approach for reproduction and production traits

Parameters		Mean	Mode	Median	SD	HPD (95%) Lower	HPD (95%) Upper	Effective Size	MCE^{SD}	Geweke diagnos
AFC	σ^2_g	2355.8	1215.8	2006.0	1560.5	234.90	5156.0	20.4	345.00	-0.36
	σ^2_p	24075	24744	23959	2211.9	20206	28570	408.8	109.35	-0.13
	σ^2_e	21719	20976	21560	2339.1	16950	26050	125.8	208.41	0.11
	h^2	0.2914	0.1296	0.2506	0.1828	0.0328	0.6309	20.8	0.0401	-0.35
FSP	σ^2_g	3790.2	3045.7	3294.0	2144.6	719.80	8422.0	37.5	350.20	0.00
	σ^2_p	21561	20835	21494	1955.6	18034	25546	302.6	112.36	0.03
	σ^2_e	17771	18611	17820	2290.2	12960	21830	100.9	227.83	0.02
	h^2	0.1739	0.1191	0.1545	0.0917	0.0358	0.3705	38.3	0.0148	0.00
FLMY	σ^2_g	170750	120850	157400	76945	43100	329300	71.7	9082.9	0.19
	σ^2_p	832930	770190	823400	77669	679590	976200	282.4	4619.5	0.04
	σ^2_e	662180	659290	661900	80794	492500	816800	201.1	5694.6	-0.13
	h^2	0.2029	0.1626	0.1939	0.0839	0.0577	0.3764	44.7	0.0125	0.20
FLSNFY	σ^2_g	354940	331470	345300	109390	145700	566300	119.9	9983.3	-0.05
	σ^2_p	686640	642820	682700	69349	542600	807600	257.0	4323.1	-0.07
	σ^2_e	331700	317790	330900	75005	175000	471600	154.1	6039.7	0.01
	h^2	0.5107	0.4905	0.5064	0.1234	0.2824	0.7687	117.4	0.0114	-0.05
FLFY	σ^2_g	92353	93813	90360	29511	38190	149400	111.3	2795.2	0.01
	σ^2_p	201610	195770	199930	19659	167750	241770	255.8	1228.6	-0.03
	σ^2_e	109260	115230	109900	21248	64760	148100	146.6	1754.2	-0.04
	h^2	0.4528	0.3961	0.4479	0.1171	0.2402	0.7061	109.2	0.0112	0.01

σ^2_g - additive genetic variance; σ^2_p - total phenotypic variance; σ^2_e - residual variance; h^2 - heritability; SD - Standard deviation; HPD(95%) - Higher posterior density 95%; MCE^{SD} - Monte Carlo error for SD

Heritability estimates for FSP from present work was in range of previous estimates, which were reported as 0.36±0.09 and 0.25±0.09 (Singh and Dubey 2005; Singh et al. 2020). Similar heritability estimates valued as 0.27 and 0.15 were observed for AFC and FSP (Singh et al. 2005). However, similar estimates (Kumar et al. 2009), lower estimate (Rehman et al. 2008; Kathiravan et al. 2009; Rehman and Khan 2012) and moderate estimates (Mundhe et al. 2015; Verma et al. 2017) were also reported for heritability of production traits. Estimates of (co)variances for considered traits can be used as prior values in future with particular temporal data distribution to estimates more accurate and precise posterior values in Sahiwal.

Visualization by trace plot and histogram

Sample was iterated till normalization by standardized cycles. Bayesian approach allows normalization through marginalization and cross validation of estimates by visualization of graphical plots of heritability estimates (Fig.1 and 2). Convergence diagnostics was indicated by constant trace plot (iterations and variance on X-axis and Y-axis, respectively) and normal bell-shaped histogram till desired distribution to obtain point estimates.

Effective Iterative Trials and Credible Interval

The numbers of effective samples for reproduction and production traits were varied from 10 to 409 and 45 to 257 respectively (Table 3). Sufficient estimates for all measures of central tendency and the higher posterior density (HPD) region at 95% credible interval for each parameter of correlation and heritability estimates were obtained with these generated iterative samples.

Bayesian analysis provides measures of reliability and accuracy by automation and validation of results. Reliability was indicated for all estimates of (co)variance components and genetic parameters by lower and higher range of credible intervals OR highest posterior density (HPD) region. Accuracy was indicated for genetic parameters by Monte Carlo Error of estimated marginal posterior densities. Variability among considered traits was explained by range of credible interval which was higher for environmental variance in FSP (12960-21830) and lower for genetic variance in AFC (234.90-5156.0) among reproduction traits while among production traits higher for genetic variance in FLSNFY (145700-566300) and lower for phenotypic variance in FLFY (167750-241770). Overall credible interval was higher and lower for genetic variance of FLSNFY and AFC respectively.

Magnitude of S.E. indicates measure of precision for heritability estimates in both approaches. Error for heritability estimate was comparatively lower for all traits in Bayesian approach ranging between 0.0112-0.0401 while higher error was noticed in LSML approach ranging between 0.236-0.352 (Table 4). Comparative heritability estimates between LSML and Bayesian also indicated accuracy and precision of estimates with later by giving low error i.e., MCE. The Monte Carlo error was low and negligible for parameters from iterated Gibbs samples (Geyer and Thompson 1992) and is inversely proportional to the length of the Gibbs chain till desired distribution. Present study revealed considerably low error with Bayesian approach then LSML approach for considered reproductive and production traits in Sahiwal. Data converged after a number of iterative trails to obtain optimized posterior densities of MCE and Geweke statistics. Convergence diagnostics was visualized by presentation of graphical plots (Fig. 1 and 2), very low (near zero) error and very low (near unity) Geweke's diagnostic values (Geweke 1992). Gibbs sampling Markov chain Monte Carlo (MCMC) approach is advantageous by including such diagnostic tools for converging results. These diagnostic tools are helpful for automation during standardizing Gibbs sampling parameters to get sufficient simulated sample size. Similarly, autocorrelation at 10 and 50 indicate significance level of within and between stationary chains for equality testing of two equal means at first 10% and last 50% part in Markov chain (Lee and Wang 2001).

Correlation component between reproduction and production traits

Genetic and phenotypic correlations were estimated using Gibbs Sampling with two-trait model, three-trait model and multi-trait Animal model (MTAM) from Bayesian analysis (Table 5 and 6). The conclusive remarks from our work are beneficial for genetic improvement by indirect selection of correlated traits of reproductive and productive importance.

Positive correlation was noticed among reproduction traits. Genetic correlation was moderately high and positive valued as 0.342±0.28 while phenotypic correlation was low and positive valued as 0.126±0.0080 between AFC and FSP. Genetic correlation was high in trivariate analysis ranging between 0.691±0.0258-0.996±0.0003 for production traits (Table 5). Our study observed very high genetic correlation for FLFY-FLSNFY (0.996±0.0003) followed by FLMY-FLFY and FLMY-FLSNFY (0.747±0.023 and 0.691±0.0258). Phenotypic correlations were moderate to very high (0.348±0.354-0.984±0.0001). Higher phenotypic correlation was noticed for FLFY-FLSNFY (0.984±0.0001) followed by FLFY-FLMY and FLMY-FLSNFY (0.373±0.0034 and 0.348±0.354) in Sahiwal.

Results of Multi-Trait Gibbs Sampling Animal Model (MTGSAM) considering reproduction and production traits are summarized in Table 6. Lower to high heritability estimates were noticed ranging between 0.12±0.003-0.49±0.002. Heritability estimate was higher for FLFY (0.486±0.0024) followed by FLSNFY, FSP, FLMY (0.427±0.0024, 0.229±0.0042, 0.196±0.0041) and lowest for AFC (0.122±0.0031).

Phenotypic correlations were positively very low to high (0.037±0.0013-0.984±0.000035) and genetic correlations were very low negative to high positive (-0.039±0.015- 0.994±0.00011). High and positive genetic correlation was observed for FLFY-FLSNFY (0.994±0.00011) followed by AFC-FLMY, AFC-FLFY, FLMY-FLSNFY, FLMY-FLFY, AFC-FSP, AFC-FLSNFY (0.584±0.018, 0.504±0.014, 0.406±0.0102, 0.399±0.0102, 0.344±0.019, 0.109±0.0015) and negative lowest for FSP-FLMY, FSP-FLSNFY, FSP-FLFY (-0.149±0.019, -0.109±0.016, -0.039±0.015). Phenotypic correlation was high for FLSNFY-FLFY (0.984±0.000035) followed by FLSNFY-AFC, FLSNFY-FLMY, FLFY-FLMY, FLMY-FSP, FSP-AFC, FLSNFY-FSP, FLFY-FSP, FLFY-AFC (0.515±0.014, 0.341±0.00097, 0.319±0.00102, 0.269±0.0013, 0.132±0.0012, 0.117±0.0016, 0.112±0.0016, 0.108±0.0015) and lowest for FLMY-AFC (0.037±0.0013).

Moderate genetic correlation indicates that traits have more influence at genetic level as compared to the environmental components when considered for indirect selection. All production traits were highly correlated and important for selection purpose. FLFY and FLSNFY are

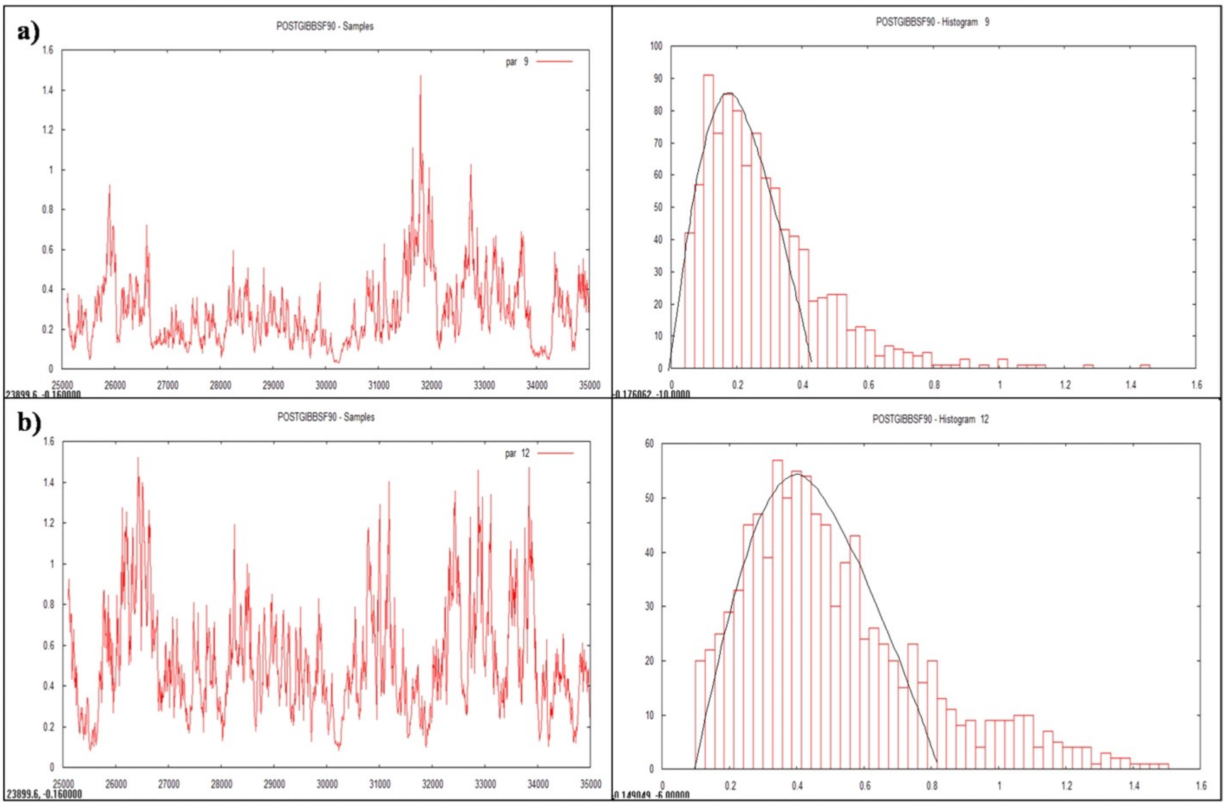

Fig. 1. Plotting of heritability estimate by trace plot and histogram a) Age at First Calving b) First Service Period.

highly correlated traits among considered production traits for indirect selection in Sahiwal. Low positive correlation between AFC and FSP suggest directional selection of early expressed reproductive trait for economic production of herd. Low to moderate improvement in production traits can be achieved from indirect selection of AFC and FSP. AFC has moderate positive correlation while FSP has negative correlation with first lactation milk production and composition traits. This positive association indicates even with short survival with less parity orders, animal still show high production within short herd life while longer survival will be more beneficial with improved production and stayability. Conclusively, AFC is more reliable due to its high correlations with production traits; indicate indirect selection for FSP, FLMY, FLSNFY and FLFY. Although FSP will proportionately change with AFC and show a negative correlation with production traits. Such contrasting effect of reproduction traits on productive performance can be sustained by reducing the higher Bayesian posterior densities of environmental variability for FSP after first parturition, indicated from which minimizes the potential change in heritability till selection limit. Indirect selection based on FSP suggests improvement in husbandry practices (feeding, breeding, housing and health care routines) to reduce days for service period for high production and survival of animals in herd. Bayesian approach does not have any assumption about sample size as approach is effective for varying sampling structure and parameters for different traits.

High genetic and phenotypic correlation for FLFY and FLSNFY was noticed by multi-trait analysis that indicates large scope for indirect selection of these traits. Reproduction traits are important for selection purpose as previous studies revealed high and positive correlation which

Table 4: Comparative Summary of heritability estimate

Traits	LSML	Bayesian
AFC	0.28±0.236	0.29±0.0401
FSP	0.24±0.260	0.17±0.0148
FLMY	0.21±0.299	0.20±0.0125
FLSNFY	0.22±0.282	0.51±0.0114
FLFY	0.29±0.352	0.45±0.0112

indicates dependence of these traits on adaptive values in animals (Chander et al. 2008; Pathak et al. 2020). Higher correlation between AFC and longevity traits in multi trait model indicated indirect selection in Kenyan Sahiwal herd (Musingi et al. 2021).

Estimation of breeding value

Sires were evaluated by both Frequentist (least squares) method and Bayesian approach to ensure dissemination of high genetic merit through the elite bulls. The sires having more than three progenies were considered in proposed study. The estimated breeding values for production traits by considering progenies of 41 Sahiwal bulls were interpreted for effectiveness of sire evaluation (Table 7).

Breeding values for sires were much higher in Bayesian approach as compared to LSML which makes more clear ranking and evaluation of sires. First rank of sires was same in both the methods for FLMY and FLSNFY in our work. However, overall ranking for all sires were not same by both the methods. Under these circumstances it was necessary to compare sire ranks. Difference in ranking was subjected to calculate

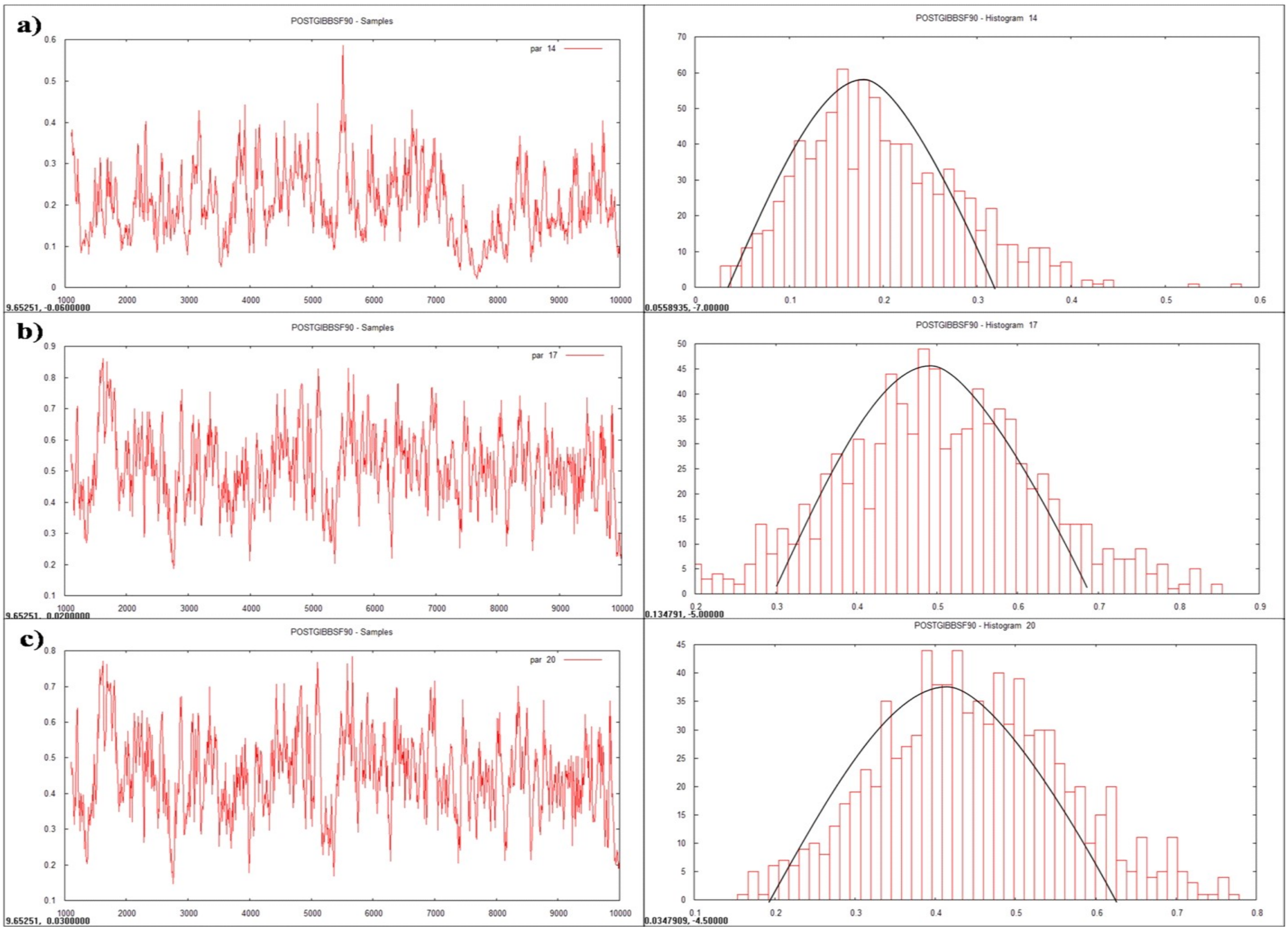

Fig. 2. Plotting of heritability estimate by trace plot and histogram a) First Lactation Milk Yield b) First Lactation SNF Yield c) First Lactation Fat Yield.

Table 5: The posterior mean of genetic (above diagonal) and phenotypic (below the diagonal) correlations with standard error for reproductive and production traits using a two-trait and three-trait models

Traits	AFC	FSP	
AFC	0.29±0.0401	0.342±0.28	
FSP	0.126±0.008	0.17±0.0148	
	FLMY	FLFY	FLSNFY
FLMY	0.20±0.0125	0.747±0.023	0.691±0.026
FLFY	0.373±0.003	0.51±0.011	0.996±0.0003
FLSNFY	0.348±0.354	0.984±0.0001	0.45±0.0112

rank correlation further useful for calculating the t-values. Due to difference in ranking the significance of rank correlation was judged by t-test. Significance was checked at 5% and 1% level for t-values (calculated v/s tabulated) at appropriate degrees of freedom. Significant difference was noticed in ranking of sires by these methods in Sahiwal.

Conclusion

In the present study, the moderate heritability of majority of production traits indicated further improvement by better feeding and managemental practices. Milk composition traits are more economical for direct selection to improve per cow production. The results revealed that indirect selection with AFC for FSP and production traits may be practised based on positive correlation. Reduced FSP suggested for indirect selection of production traits due to negative and low correlations. Sire evaluation was more effective by Bayesian approach as the estimated breeding values for sires were comparatively higher than that through the LSML method. Multiple criteria indicated that the results were more informative, precise and accurate with the Bayesian analysis compared to conventional LSML method. This study also

Table 7: Effectiveness of sire evaluation

Trait	Rank correlation	t-calculated	df	Interpretation
FLMY	0.75	7.08		
FLSNFY	0.84	9.67	40	Significant
FLFY	0.85	10.08		

Table 6: The posterior mean of genetic (above diagonal), phenotypic (below the diagonal) correlations and heritability estimates (diagonal) with standard error for reproductive and production traits using a MTGSAM approach

Traits	AFC	FSP	FLMY	FLFY	FLSNFY
AFC	0.122±0.003	0.344±0.019	0.584±0.018	0.504±0.014	0.109±0.002
FSP	0.132±0.001	0.229±0.004	-0.149±0.019	-0.039±0.015	-0.109±0.016
FLMY	0.037±0.001	0.269±0.001	0.196±0.004	0.399±0.010	0.406±0.0102
FLFY	0.108±0.002	0.112±0.002	0.319±0.001	0.486±0.002	0.994±0.0001
FLSNFY	0.515±0.014	0.117±0.002	0.341±0.001	0.984±0.00004	0.427±0.002

MTGSAM – Multi-Trait Gibbs Sampling Animal Model

showed the effectiveness of Bayesian approach based on reliable estimates for the direct and indirect selection of first lactation traits and early expressed reproduction traits (AFC, FSP), respectively in Sahiwal cattle.

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