

**GENETIC EVALUATION OF PRODUCTION AND LIFETIME TRAITS
IN MURRAH BUFFALO THROUGH BAYESIAN APPROACH**



THESIS SUBMITTED TO THE
**ICAR-NATIONAL DAIRY RESEARCH INSTITUTE, KARNAL
(DEEMED UNIVERSITY)**

IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE OF

MASTER OF VETERINARY SCIENCE

IN

ANIMAL GENETICS AND BREEDING

BY

ASHISH YADAV

B.V.Sc. & A.H

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(DEEMED UNIVERSITY)

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Approved by:



(Dr. M.K Singh)
External Examiner

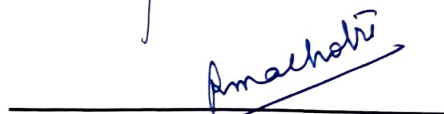
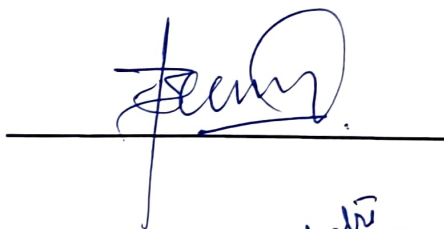
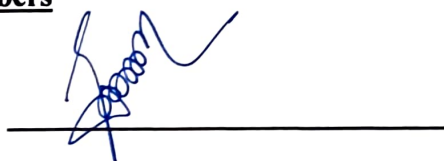


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CERTIFICATE

This is to certify that the thesis titled “**GENETIC EVALUATION OF PRODUCTION AND LIFETIME TRAITS IN MURRAH BUFFALO THROUGH BAYESIAN APPROACH**” submitted by **Ashish Yadav** towards the partial fulfillment of the requirements for the award of the degree of **Master of Veterinary Science in Animal Genetics and Breeding** of the **ICAR- National Dairy Research Institute (Deemed University)**, Karnal (Haryana), India, is a *bona fide* research work carried out by him under my supervision and guidance and no part of the thesis has been submitted for any other degree or diploma.

Date: 11 August, 2022

(Dr. Raja K N)

Major Advisor & Chairperson,
Advisory Committee

I dedicate this thesis

*To my
Mother, Father,
& Sister*

Roots and Wings

*If I had two wishes, I know what they would be
I'd wish for Roots to cling to, and Wings to set me free;*

*Roots of inner values, like rings within a tree,
and Wings of independence to seek my destiny.*

*Roots to hold forever to keep me safe and strong,
To let me know you love me when I've done something wrong;*

*To show me by example, and help me learn to choose,
To take those actions every day to win instead of lose.*

*Just be there when I need you, to tell me it's alright,
To face my fear of falling when I test my wings in flight;*

*Don't make my life too easy, it's better if I try,
And fail and get back up myself, so I can learn to fly.*

*If I had two wishes, and two were all I had,
And they could just be granted, by my Mom and Dad;*

*I wouldn't ask for money or any store-bought things.
The greatest gifts I'd ask for are simply Roots and Wings.*

Denis Waitley

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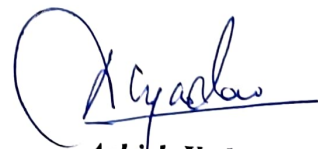
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*"The woods are lovely, dark and deep. But I have promises to keep,
And miles to go before I sleep, And miles to go before I sleep" -Robert Frost*


Ashish Yadav

Date: | | August 2022

Karnal

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Abbreviations

305MYAP	:	305 Day Milk Yield Across Parity
AFC	:	Age at First Calving
AI-REML	:	Average Information Restricted Maximum Likelihood
ANOVA	:	Analysis of Variance
BAIF	:	Bharatiya Agro Industries Foundation
BLUP	:	Best Linear Unbiased Prediction
BV	:	Breeding Value
CC	:	Contemporary Comparison
DF-REML	:	Derivative-Free Restricted Maximum Likelihood
EM-REML	:	Expectation Maximisation Restricted Maximum Likelihood
EPA	:	Expected Producing Ability
<i>et al.</i>	:	Co-Workers
FL305MY	:	First Lactation 305 Day Milk Yield
h²	:	Heritability (direct)
h²_t	:	Heritability (total)
ICAR	:	Indian Council of Agricultural Research
kg	:	Kilogram
LL	:	Lactation Length
LSM	:	Least Squares Mean
M.C.E	:	Monte Carlo Error
m²	:	Maternal proportion in heritability
NDDB	:	National Dairy Development Board
NDRI	:	National Dairy Research Institute
NID	:	Normally and Independently Distributed
NS	:	Non-significant
p<0.001	:	Significant at 1% level
p<0.005	:	Significant at 5% level
PL	:	Productive Life
PY	:	Peak Yield
r	:	Repeatability
REML	:	Restricted Maximum Likelihood
S	:	Significant
S. E	:	Standard Error
SLRS	:	Simple Regressed Least-Squares

TMY	:	Total Milk Yield
σ^2_e	:	Random error variance
σ^2_m	:	Maternal genetic variance
σ^2_{mpe}	:	Maternal permanent environment variance
σ^2_p	:	Phenotypic variance
σ^2_{pe}	:	Permanent environment variance
$\sigma_{cov Am}$:	Covariance between A & m
σ^2_a	:	Additive genetic variance

Abstract

The aim of the present study was to genetically evaluate Murrah buffaloes for various production traits recorded throughout their lifetimes. The study relied on lactation records of Murrah buffalo, maintained at the record room (AGB Division) of ICAR-NDRI, Karnal from the period 1971 to 2020. Through Bayesian analysis utilising the BLUPF90 family of programmes, genetic analysis was carried out using animal models with a combination of random factors, such as the direct additive genetic effect of the animal, the direct maternal genetic effect, and the maternal permanent environmental effect. Using the most appropriate models (based on DIC value) that account for direct and maternal influences fitted to the majority of the traits, (co)variance components and genetic parameters were estimated. The heritability estimates of FL305MY, TMY, LL, PY, PL and 305 MYAP in the most appropriate models were 0.49 ± 0.007 , 0.20 ± 0.011 , 0.04 ± 0.001 , 0.10 ± 0.001 , 0.10 ± 0.009 and 0.21 ± 0.003 respectively with repeatability estimates of TMY, LL, PY, and 305MYAP as 0.40, 0.20, 0.21 and 0.34. In comparison to the animal model with only additive genetic effects of the animal in each trait, lower error variance and higher additive variance were found for production and lifetime traits through various models based on partition of variance, indicating that it is crucial to use the best statistical model for elucidating genetic parameters that incorporate suitable random and fixed effects. The comparison of sires based on their breeding value (obtained from AIREML as well as the Bayesian approach) and ranking them, the correlation of which obtained using spearman's rank correlation revealed that both approaches provide similar results as these all were normally distributed traits, with the best BV estimates for FL305MY, TMY, LL, PY, PL and 305 MYAP as 404.40, 415.99, 20.43, 1.39, 221.89 and 398.19 respectively using Bayesian approach. AIREML revealed estimates of BV of the given traits as 401.22, 409.02, 18.11, 1.37, 111.82, and 393.55. In terms of the accuracy of breeding values based on the standard error predicted, the Bayesian method provides a slightly better outcome with relative efficiency over the AIREML method as 0.73 %, 1.2 %, 7.2 %, 1.2 %, 42.94 %, and 0.78 % in respective traits. It is recommended to use the Bayesian method to estimate the breeding values of Murrah sires for production traits, which in turn can be used for ranking and selection of bulls.

बायेसियन दृष्टिकोण के माध्यम से मुर्हाह भैंसों में उत्पादन और जीवनकालीन लक्षणों का आनुवंशिक मूल्यांकन

सार

वर्तमान अध्ययन का उद्देश्य मुर्हाह भैंसों के जीवनकाल में दर्ज विभिन्न उत्पादन लक्षणों के लिए आनुवंशिक रूप से मूल्यांकन करना था। यह अध्ययन 1971 से 2020 की अवधि के दौरान भा. कृ. अनु. प.- राष्ट्रीय डेयरी अनुसंधान संस्थान, करनाल के रिकॉर्ड रूम (पशु आनुवंशिकी एवं प्रजनन विभाग में स्थित) में संग्रहित मुर्हाह भैंस के उत्पादन रिकॉर्ड पर निर्भर था। BLUPF90 सॉफ्टवेयर कार्यक्रमों का उपयोग करते हुए बायेसियन विश्लेषण के माध्यम से आनुवंशिक विश्लेषण किया गया। यादृच्छिक कारकों के संयोजन के साथ पशु मॉडल, जैसे कि पशु का प्रत्यक्ष योगात्मक आनुवंशिक प्रभाव, प्रत्यक्ष मातृ आनुवंशिक प्रभाव और मातृ स्थायी पर्यावरणीय प्रभाव। सबसे उपयुक्त मॉडल का उपयोग करना (डीआईसी मूल्य के आधार पर) जो कि अधिकांश लक्षणों के लिए प्रत्यक्ष और मातृ प्रभावों के लिए जिम्मेदार है, (सह) विचरण घटकों और आनुवंशिक मापदंडों का अनुमान लगाया गया। FL305MY, TMY, LL, PY, PL और 305 MYAP की आनुवंशिकता अनुमान, सबसे उपयुक्त मॉडल में 0.49 ± 0.007 , 0.20 ± 0.011 , 0.04 ± 0.001 , 0.10 ± 0.001 , 0.10 ± 0.009 , 0.21 ± 0.003 क्रमशः TMY, LL, PY, और 305MYAP के 0.40, 0.20, 0.21 और 0.34 के रूप में दोहराव के अनुमान थे। प्रत्येक विशेषता में पशु के केवल योगात्मक आनुवंशिक प्रभावों वाले पशु मॉडल की तुलना में, विभिन्न मॉडलों के माध्यम से उत्पादन और आजीवन लक्षणों के लिए कम त्रुटि विचरण और उच्च योगात्मक विचरण पाए गए, यह दर्शाता है कि आनुवंशिक को स्पष्ट करने के लिए सर्वोत्तम सांख्यिकीय मॉडल का उपयोग करना महत्वपूर्ण है। पैरामीटर जो उपयुक्त यादृच्छिक और निश्चित प्रभाव शामिल करते हैं। उनके प्रजनन मूल्य (AIREML के साथ-साथ बायेसियन दृष्टिकोण से प्राप्त) के आधार पर प्रजनन सांडों की तुलना और उनको श्रेणीबद्ध 404.40, 415.99, 20.43, 1.39, 221.89, 398.19 बायेसियन दृष्टिकोण का उपयोग करना। AIREML ने दिए गए लक्षणों के BV के अनुमानों को के रूप में प्रकट किया, 401.22 409.02, 18.11, 1.37, 111.82 तथा 393.55 | अनुमानित मानक त्रुटि के आधार पर प्रजनन मूल्यों की सटीकता के संदर्भ में, बायेसियन विधि AIREML विधि पर सापेक्ष दक्षता के साथ 0.73 %, 1.2 %, 7.2 %, 1.2 %, 42.94 %, और 0.78 % के रूप में थोड़ा बेहतर परिणाम प्रदान करती है। उत्पादन लक्षणों के लिए मुर्हाह सांडों के प्रजनन मूल्यों का अनुमान लगाने के लिए बायेसियन पद्धति का उपयोग करने की सिफारिश की जाती है, जिसका उपयोग सांडों को श्रेणीबद्ध और चयन के लिए किया जा सकता है।

CHAPTER -1

Introduction

Introduction

Livestock is seen as a vital resource for a nation like India as it provides food, nutrition, health, and economic security to meet the ever-increasing dietary demands of great geographical, and social diversity and a steadily increasing human population. According to the 20th Livestock Census (2019), India has 535.78 million livestock heads of various indigenous, crossbred, and exotic origins. The presence of a zebu bull on Indus valley civilisation seals found during the Harappa Archaeological Research Project demonstrates how much value livestock has held in the Indian lifestyle since ancient times. This shows how the role and importance of livestock in the Indian subcontinent extends beyond social, economic, and environmental utilities to traditional, cultural and ritual contexts.

India, the top milk producer in the world, is home to some of the best milch cattle and buffalo breeds, as well as the highest population of buffalo in the world. In the last three decades, India's milk output has expanded by around 3.7 times, from 54 million tons in 1990 to 198.44 million tons in 2020-21 (DAHD, 2021), whereas the global milk production has increased by about 59 per cent, from 530 million tonnes to 843 million tonnes. The boost in milk production can be attributed to the excellent milch breeds that exist in India, as well as Operation Flood and all of the selection, breeding, and development strategies employed for livestock.

One great genetic resource is Indian buffalo. FAO (2013) estimates that buffaloes generate 49 per cent of the total milk produced in India, but only 15.14 per cent of the total milk produced globally. India has the largest population of buffaloes in the world (about 53 per cent of all buffaloes), with a total of 19 registered breeds (NBAGR, 2021) which are well adapted to the country's climatic conditions. In the dairy industry, Murrah breed of buffalo is well-known and its breeding grounds can be found in Delhi, Gurgaon, Hisar, Rohtak, and the central part of Haryana. As one of the best breeds utilised in upgrading programmes, the Murrah breed has been widely used as an improver breed across the nation. Nearly 20 per cent of India's 109.85 million total buffaloes are of the Murrah breed or its grades.

Animal productivity and reproductive efficiency are key factors in the success of dairy industry since they are crucial from an economic standpoint. For genetic improvement programmes to predict breeding values and select animals with high genetic merit, it is crucial to continuously monitor them, collect adequate data, and make interventions. The fundamental objective of any selection experiment is to identify elite animals that may be

employed to create the subsequent generation of offspring to maximise the genetic development of desired phenotypic traits. To maximise a population's potential for growth, the best breeding animals must be identified. The most crucial element in enhancing yield and reproductive traits simultaneously is the genetic relationship between the traits.

Milk production, a widely variable quantitative trait, the genetic make-up of the animal as well as the environment in which it is raised both have an impact on this trait. As a result, a variety of variables influencing the characteristic, the most significant of which is genetic potential, combine to determine the economics of dairy industry. This variability is used by breeders to create effective methods for enhancing quantitative traits. Developing the finest breeding programmes can be aided by understanding the type and degree of genetic variability present in traits utilised for selection. In this way, additive genetic variation has helped to improve the genetics of commercially significant traits in populations of dairy animals.

Traditional methods like maximum likelihood and the least square method are used to predict genetic variables and estimate (co)variance components for quantitative traits. Later, restricted maximum likelihood method (REML) was utilised to counteract selection bias and small sample nuisance effects. Two analytical techniques that are frequently utilised for the estimation of (co)variance components and genetic parameters in animal breeding are REML and Bayesian methodology (Malhado *et al.*, 2012). According to Carneiro *et al.* (2007), the Bayesian methodology has some benefits over REML-based processes and is well justified for analysing small populations or datasets (Silva *et al.*, 2013, Lopes *et al.*, 2017). The statistical method known as Bayesian inference expresses all uncertainty in terms of probability. The formulation of a model that is suitable to describe the situation of interest is the first step in a Bayesian approach to a problem. Then, a prior distribution is created over the model's unknown parameters in order to represent pre-data opinions about the situation. Bayes' rule is used after certain data have been observed to produce a posterior distribution for these parameters that account for both the prior and the observed data. For the purpose of estimating parameters using random sampling, the Gibbs sampling process produces posterior distributions (Magnabosco *et al.*, 2000).

To elucidate the genetic factors with high accuracy, which may then be employed in breeding programmes to improve animal performance, statistical modelling of breeding data for a variety of phenotypes is required. It is crucial to utilize optimal statistical models with the appropriate random and fixed effects that are applied to large populations when

elucidating genetic factors (Wolf and Wade, 2016; Ahmad *et al.*, 2021). Repeatability estimates of productive parameters are especially useful in the context of the buffalo's lifetime. Additionally, getting parameter estimates of performance traits throughout the buffalo's lifetime (repeatability) has received relatively little attention. Effective breeding plans can be designed with the support of accurate genetic parameter estimations, which in turn depend on the methods and models used for estimating the (co)variance components and consequent genetic parameters. Keeping given considerations in mind regarding statistical model, variability and repeatability of traits, this study was undertaken with the following objectives:

- **Estimation of (co)variance components for lactation and lifetime traits using repeatability model in Murrah buffalo.**
- **Comparison of Bayesian and AIREML approach for breeding value estimation and rank correlation in Murrah buffalo.**

CHAPTER -2

Review of literature

Previous studies on production and lifetime traits using traditional approaches for genetic evaluation as well as a comparison study on genetic parameter estimation in Murrah buffalo using a variety of approaches, including Bayesian, have been thoroughly reviewed. The information gathered is presented in the following sequence:

2.1 Historical background of Murrah buffalo breeding

2.2 Bayesian approach to animal breeding

2.3 AIREML approach in animal breeding

2.4 The Animal model

2.5 Performance of production and lifetime traits in Murrah buffalo

2.6 Effect of non-genetic factors on production and lifetime traits in Murrah buffalo

2.7 Genetic parameters estimation

2.8 Previous works implementing Bayesian approach in animal breeding

2.9 Estimation of breeding value

2.1 Historical background of Murrah buffalo breeding

In India, 56.63 per cent of all buffalo fall into the descript category, with the remaining 43.37 per cent falling into the non-descript category. One of the best breeds of Indian buffaloes is the Murrah, which accounts for 44.39 percent of the total (of which only 24.22 percent are pure, while the remaining 75.78 percent are graded Murrah buffaloes) (DAHD, 2013). The Murrah breed of buffalo in India is the exclusive dairy breed. Haryana is Murrah buffalo's home tract, although graded Murrah buffaloes are widespread in the nation due to their superior milk production capacity, adaptability to a variety of environmental situations, and feed conversion efficiency. In addition to India, the Murrah breed has expanded throughout Asia and Europe. Numerous nations, such as China, Brazil, Egypt, Bulgaria, Bangladesh, and so on, have used the Murrah breed as an enhanced one for improving their indigenous buffaloes.

Murrah buffalo have a deep, imposing physique, a short, broad back, and a somewhat long neck and head. Its short, distinctive horns are tightly curled, and its udder is fully formed. The fore and rear quarters of Murrah buffalo are drooping, its hips are broad and long tail extends up to the fetlocks. Jet black with white tail markings is a popular colour. Unquestionably, the most critical factors in determining the profitability of a buffalo dairy farm are production and reproduction performance. Dairy animals' reproductive and productive abilities ought to

be assessed using a variety of factors. By connecting rural farmers in villages to districts, state federations, and dairy cooperatives, the National Dairy Development Board (NDDB) is credited with bringing a white revolution to the nation through its ongoing projects for improving Murrah buffaloes. Currently, the National Dairy Plan-I, a project of NDDB in collaboration with central government, is focused on improving several buffalo breeds, including Murrah. The Murrah and Mehsana breeds are being improved through progeny testing programme. The enhancement of the buffalo breeds, especially Murrah, is being worked on by a number of NGOs, including the Bharatiya Agro Industries Foundation (BAIF). An integrated Murrah development scheme (2018–19) is being carried out by the Haryana government. The long-term goals of this plan include raising milk output, and overall productivity, and conservation, as well as upgrading valuable germplasm that is already present in the state. The identification of superior germplasm and their insemination with superior semen for sustainable genetic improvement, the acquisition and rearing of pedigreed young Murrah calves as breeding bulls for supply to other states and panchayats, as well as encouraging farmers to raise high-yielding animals of superior genetic merit are among the medium-term goals.

2.2 Bayesian approach to animal breeding

Thomas Bayes (1702–1761), proved a special case of what is now known as the Bayes theorem used in statistics. After the discovery of Bayes theorem, Pierre-Simon Laplace (1749–1827) presented a general version of it and used it to solve issues with reliability, medical statistics, and astronomical mechanics (Stigler, 1986). There are two main methods for drawing conclusions in statistics: conventional (or frequentist) and Bayesian. The frequentist school of thought developed in the 1930-1940s and is based on the previous writings of Karl Pearson and Ronald Fisher. The frequentist method of inference is based on the idea that if a large number of samples are acquired or the experiment is performed an unlimited number of times, a huge number of estimates would be spread around the true value. For a frequentist, the true value is fixed while the sample is variable, whereas for a Bayesian, the sample is fixed while the parameter of interest is a random variable. On the other hand, Bayesians consider the probability distribution of the true value of given information. That is not to suggest that the parameter does not have a true value; a Bayesian just does not know what that value is, thus the Bayesian speaks about the probability that the parameter has a particular value. Essentially, Bayesians see any inference as an update from

the prior belief in the parameters to the posterior belief in the values that are now more likely as a result of the analysis of the evidence.

Contrary to frequentism, the Bayesian paradigm for statistical inference treats parameters (referred to as θ) as random variables. Bayesians are more interested in deriving a posterior distribution $P(\theta | Y)$ from data Y than a point estimate (based on maximum likelihood, for example). This is accomplished by using the Bayes' inferential theorem, which reads

$$P(\theta | Y) = \frac{P(Y | \theta) P(\theta)}{P(Y)}$$

where $P(Y | \theta)$ is the likelihood of the data given the model and the parameters, $P(\theta)$ is the prior distribution on the parameters, and $P(Y)$ is a scaling constant.

In animal breeding, Gianola and Foulley started using Bayesian methods in 1982. Shortly after, Gianola and Fernando (1986) highlighted other Bayesian possibilities. The majority of quantitative genetics analyses have typically been performed using frequentist (also known as classical) ANOVA techniques. In this case, probability is viewed through the hypothetical lens of repeatedly conducting an experiment under the same conditions. ANOVA techniques have been largely replaced by REML procedures for the estimation of (co)variance components and the prediction of breeding values using (approximate) best linear unbiased predictors (BLUP).

Given the complexity of many genetic problems, Bayesian methods may undoubtedly considerably enhance studies. The development of Gibbs sampling strategy enabled the introduction of Bayesian Markov chain Monte Carlo (MCMC) methods in quantitative genetics in the first half of the 1990s (Wang *et al.*, 1994; Sorensen *et al.*, 1994). When computing issues were resolved and MCMC methods were used to estimate marginal posterior distributions, interest in Bayesian techniques was revived (Blasco, 2001). By selecting samples from the conditional distributions of each parameter in a model, the Gibbs sampler creates a random sample of the marginal posterior distribution, which is the goal of Bayesian inference.

Conclusions in the form of posterior distributions greatly enhance the capacity to assess uncertainty of estimate and, more importantly, to spread such uncertainty in a series of subsequent studies. A second benefit that is regrettably sometimes overlooked is the capability to include previous, state-of-the-art knowledge into prior distributions to improve the capacity to fit models successfully. A third technological benefit is the accessibility of

general-purpose, flexible, and reliable algorithms: Markov Chains in Monte Carlo (de Villemereuil, 2019). The use of Bayesian estimation methods, especially MCMC, is highly recommended for researching non-Gaussian features for two main reasons: no asymptotic assumptions or approximations are necessary since the behaviour of the estimates follows the model and prior utilised; hence, standard errors and related credible ranges are always a meaningful measurement of the estimate's imprecision (Morrissey, 2013). Because each large or small data set has an exact posterior distribution from which inferences may be made, Bayesian inference using the Gibbs sampling technique is well preferred when the amount of data is comparatively small (Worku *et al.*, 2021).

2.3 AIREML approach in animal breeding

Johnson and Thompson (1995) and Gilmour *et al.* (1995) presented the average information (AI) approach for efficient variance component estimation by REML in the linear mixed model. They applied the mixed model equations and took use of sparsity. They discovered that their method, which uses a sparse matrix inversion, is an efficient alternative for the expectation-maximization (EM) and derivative-free algorithms (DF) methods. With great success, the method was quickly extended to larger models, such as multivariate data (Jensen *et al.*, 1997). The emergence of AI-based technology is to credit for the sudden rise in REML applications. In research and applications involving animal breeding, the restricted maximum likelihood (REML) approach is widely used to estimate genetic parameters and variance components. For the REML estimation, well-known algorithms exist, such as the EM and DF algorithms., while the so-called average information (AI) approach has later gained popularity due to its desired computational property (Ashida and Iwaisaki, 1998).

2.4 The Animal Model

The "animal model" enables simultaneous use of data from all sorts of relatives in a complicated pedigree and immediately calculates causal variance estimates while optimally weighing contributions from individual sources. This has evolved into the industry standard for quantitative genetic analysis when coupled with likelihood-based estimates (Meyer, 2007). Utilizing REML procedures in sophisticated statistical models, particularly animal models, has made it possible to accurately estimate genetic variance for each component, including sire, dam, and animal covariance. In India, the use of animal models for genetic assessment ensued relatively late. Jain and Sadana (1998) provided the first report on genetic parameter estimates using REML for the Murrah buffalo.

In the past, the model of choice for genetic research was paternal half-sib; however, more lately, animal models for genetic analysis of economically significant traits have been documented. The theory of maternal influence on the phenotype of an offspring is composed of genes acquired from the sire and dam, with equal contribution from both sides. In sexually reproducing animals, the phenotype of the progeny is most likely to be influenced by both parents. Dams can adjust their phenotype in response to their environment, and they can also influence the phenotype of their offspring in the same way. For instance, inadequate nutrition during the latter trimester of pregnancy causes low birth weight. Dams transfer information about the environment to their offspring by doing so (Maestripieri and Mateo, 2009).

Some maternal effects may last a lifetime for the offspring and next generations. Understanding maternal effects should be a major health concern due to the significant consequences of effects that depend on the brief period of pregnancy (Cooney, 2006). The ability to assess the genetic basis of the traits can be affected by maternal influences. Estimates of additive genetic variance and genetic correlations can be greatly biased by correlations of variables between mothers and offspring caused by maternal effects. As a result, understanding maternal effects is essential to understand the genetic basis of the traits. It has also been shown that heritability estimates inflated or biased upward when maternal influences were excluded. To prevent biased results, it is therefore essential to assess the maternal effect's impact on genetic parameter estimations.

2.5 Performance of production and lifetime traits in Murrah buffalo

2.5.1 Production traits

Production traits are the attributes of animals, like quantity or quality of the milk produced that add directly to the worth of the animals for the farmer, and are distinguishable or measurable at the individual level. They are quantitatively inherited, *i.e.*, they are affected by many genes and environmental factors have their influence on the expression of such traits.

2.5.1.1 First lactation 305 day milk yield (FL305MY)

The milk yield produced in 305 days in the first lactation is very important criteria for a profitable dairy enterprise, since the optimum period of lactation maintains the reproductive cycle and yields one calf per year. More duration of lactation length will lead to increase in calving interval which ultimately affects the breeding efficiency and milk production per day. Thus, 305 days duration of lactation length is considered as optimum and for buffaloes, this is the best indication of their production potential.

Table 2.1 lists the results of a survey of the literature on the FL305MY in Murrah buffalo. According to several researchers, the FL305MY in Murrah buffalo ranged from 1351.70 ± 43.97 (Suresh *et al.*, 2004) to 2258.17 ± 95.73 (Kaur *et al.*, 2020).

Table 2.1: Estimates of FL305MY (kg) of Murrah buffalo

Mean \pm S.E(kg)	Number of observations	References
1627.78 ± 27.26	450	Gajbhiye (1987)
1457.60 ± 09.10	1926	Ipe and Nagarcenkar (1992)
1648.00 ± 20.00	404	Dass and Sharma (1994)
1784.90 ± 16.70	628	Nath (1998)
1794.87 ± 22.12	518	Banik (2001)
1704.51 ± 25.41	1214	Kumar <i>et al.</i> (2003)
1351.70 ± 43.97	624	Suresh <i>et al.</i> (2004)
2063.66 ± 13.1	997	Jain (2009)
1818.06 ± 22.46	326	Chakraborty <i>et al.</i> (2010)
1706.52 ± 17.85	395	Thiruvekadan (2011)
1750.91 ± 28.62	707	Patil <i>et al.</i> (2012)
1866.41 ± 28.66	522	Jamuna (2012)
1853.49 ± 15.88	961	Sahoo <i>et al.</i> (2014)
1806.45 ± 16.99	965	Singh <i>et al.</i> (2014)
2078.20 ± 31.12	154	Jamuna <i>et al.</i> (2016)
2060.93 ± 20.22	1637	Jakhar <i>et al.</i> (2016)
2045.30 ± 52.15	162	Kumar <i>et al.</i> (2017)
1977.9 ± 36.2	315	Chitra <i>et al.</i> (2018)
2258.17 ± 95.73	445	Kaur <i>et al.</i> (2020)
1893.7 ± 20.9	659	Kour and Narang (2021)

1834.86 ± 41.97	1858	Kumar (2021)
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2.5.1.2 Total milk yield (TMY)

The total lactation milk yield is the total of milk yield obtained from date of calving till the cow dried off in the lactation. Overall total milk yield in first lactation of Murrah buffalo ranged from 1429.17 (Suresh *et al.*, 2004) to 2934.4 ± 95.9 (Dahiya *et al.*, 2020) as shown in Table 2.2.

Table 2.2 Estimates of Total milk yield (kg) in Murrah buffalo

Mean ± S.E. (kg)	No. of observations	References
1564.86 ± 23.60	392	Yadav <i>et al.</i> (1983)
1784.00 ± 69.82	224	Prakash (1984)
1654.05 ± 44.21	478	Hatwar and Chawla (1988)
1869.70 ± 27.91	424	Sahana (1993)
1844.99 ± 21.31	628	Nath (1998)
2095.67 ± 27.73	491	Saha (1998)
1429.17	624	Suresh <i>et al.</i> (2004)
1997.9 ± 66.2	1479	Singh <i>et al.</i> (2011)
1942.75 ± 53.79	330	Gupta <i>et al.</i> (2012)
1855.6 ± 16.1	698	Thiruvankadan <i>et al.</i> (2014)
2465.48 ± 130.72	445	Kaur <i>et al.</i> (2020)
2934.4 ± 95.9	54	Dahiya <i>et al.</i> (2020)
1957.28 ± 48.00	1858	Kumar (2021)

2.5.1.3 Lactation length (LL)

Animals' lactation duration has an impact on the amount of milk produced at a particular parity. Table 2.3 lists the length of lactation in Murrah buffalo as reported in various studies.

According to published data, Murrah buffaloes' lactation periods ranged from 278.26 3.19 (Geetha, 2005) to 357.90 12.99 (Shabade *et al.*,1993).

Table 2.3: Estimates of Lactation length (days) in Murrah buffalo

Mean \pm S.E (days)	No. of observations	References
311.33 \pm 4.25	413	Gajbhiye (1987)
324.20 \pm 2.54	716	Raheja (1992)
357.90 \pm 12.99	114	Shabade <i>et al.</i> (1993)
289.55 \pm 3.68	683	Dhara (1994)
306.00 \pm 4.00	404	Dass and Sharma (1994)
324.99 \pm 3.36	628	Dass (1995)
295.00 \pm 2.10	1164	Dutt <i>et al.</i> (2001)
306.63 \pm 3.53	518	Banik (2001)
303.74 \pm 5.92	1003	Yadav <i>et al.</i> (2002)
319.49 \pm 5.62	259	Kumar <i>et al.</i> (2002)
291.52 \pm 2.53	311	Kundu <i>et al.</i> (2003)
278.26 \pm 3.19	176	Geetha (2005)
323.62 \pm 3.73	441	Katneni (2007)
286.06 \pm 1.72	795	Jamuna (2012)
297.8 \pm 1.9	698	Thiruvankadan <i>et al.</i> (2014)
313.16 \pm 0.43	116	Pandey <i>et al.</i> (2015)
311.68 \pm 3.35	2107	Jakhar <i>et al.</i> (2016)
340.48 \pm 14.14	445	Kaur <i>et al.</i> (2020)
343.8 \pm 3.5	659	Kour and Narang (2021)
309.45 \pm 4.57	1858	Kumar (2021)

2.5.1.4 Peak yield (PY)

When a buffalo reaches peak yield, it has produced the most milk over the whole lactation.

Table 2.4 provides Murrah buffaloes' average peak production after evaluation.

Table 2.4: Estimates of Peak yield (kg) in Murrah buffalo

Peak yield (kg)	References
10.16 ± 0.26	Chakraborty <i>et al.</i> (2010)
8.87 ± 0.05	Thiruvankadan <i>et al.</i> (2014)
9.96 ± 0.11	Dev <i>et al.</i> (2015)
10.08 ± 0.96	Jakhar <i>et al.</i> (2016)
11.13 ± 0.44	Kumar <i>et al.</i> (2017)
13.17 ± 0.45	Kaur <i>et al.</i> (2020)
10.5 ± 0.1	Kour and Narang (2021)

2.5.2 Lifetime traits

The lifetime performance of dairy animals determines the economic return. The establishment of selection schemes for genetic improvement in lifetime traits and the prediction of correlated response to selection based on early performance are probably more advantageous. According to Cady *et al.* (1983) and Ahmad *et al.* (1992), buffaloes are typically culled because of reproductive failures, low output, mastitis, and other health issues. Thus, lifetime milk output is a feature that is frequently researched to record lifetime performance (Bashir *et al.*, 2007)

2.5.2.1 Productive Life (PL)

The duration of productive life is defined as the number of days in milk produced between the first calving and the last lactation or culling (Kalsi and Dhillon, 1982; Umrikar and Deshpande, 1985; Ali, 1989; Dutt and Taneja, 1994).

Table 2.5: Estimates of Productive life (days) of Murrah buffalo

Mean \pm S. E	Number of observations	References
1261.79 \pm 24.48	351	Chander (2002)
1138 \pm 20	1037	Bashir <i>et al.</i> (2007)
1520.7 \pm 46.2	664	Thiruvankadan <i>et al.</i> (2015)
1009.90 \pm 26.59	479	Dev <i>et al.</i> (2017)

2.6 Effect of non-genetic factors on production and lifetime traits in Murrah buffalo

2.6.1 First lactation 305 day milk yield

According to several researchers, the period of calving had a significant effect on Murrah buffaloes' milk production for 305 days (El-Arian, 1986; Gajbhiye, 1987; Tomar and Tripathi, 1988; Hatwar and Chawla, 1988; Singh *et al.*, 1990; Dass and Sharma, 1994; Dhara, 1994; Dass, 1995; Jain, 1996; Saha, 1998; Nath, 1998; Wakchaure, 2008; Gupta, 2009). Shabade *et al.* (1993) and Sharma and Singh (1988) found no statistically significant relationship between the calving period and the FL305MY in Murrah buffalo. FL305MY was shown to be significantly affected by the calving season, according to several researches (El-Arian, 1986; Gajbhiye, 1987; Hatwar and Chawla, 1988; Singh *et al.*, 1990; Sahana, 1993; Dass and Sharma, 1994; Dass, 1995; Nath, 1998). Lathwal (2000) found that Murrah buffalo at the Karnal farm produced more milk throughout the summer (April to June) than during other seasons.

2.6.2 Total milk yield

Rohilla *et al.* (1992), Chhikara *et al.* (1994), and Gupta (2009) found a significant relationship between the period of calving and total milk output, however Sharma and Singh (1988) and Sarkar (2002) found no relationship. Significant effects on milk yield were seen by Prakash (1984), Chhikara *et al.* (1994), while Sharma (1982) and Sarkar (2002) found no significant effects of season of calving on milk yield.

2.6.3 Lactation length

Several researchers have noted that the calving period has a significant effect on the length of the lactation in Murrah buffalo (Dhara, 1994; Dass, 1995; Nath, 1998; Wakchaure, 2008;

Gupta, 2009). Shabade *et al.*,1993 found no statistically significant relationship between lactation length and the period of calving (1993). Nath (1998) identified a substantial relationship between calving season and lactation length in Murrah buffalo, but other researchers found no such relationship (Dhara, 1994; Dass, 1995; Wakchaure, 2007; Gupta, 2009).

2.6.4 Peak yield

Das *et al.* (2015) observed significant influence of period on peak yield in swamp buffalo whereas influence of season of calving was found to be non-significant.

2.6.5 Productive life

Bashir *et al.* (2007) found that year of birth significantly ($p < 0.01$) affected the productive life whereas AFC did not affect the trait. The AFC had highly significant effect in findings of Thiruvekadan *et al.* (2015).

2.7 Genetic parameters estimation

2.7.1 Heritability estimates of production, lifetime traits in Murrah buffalo

2.7.1.1 Heritability estimates of First lactation 305 day milk yield

Information on heritability estimates raises the prospect of genetic progress through animal selection or culling. According to published researches, heritability estimates for FL305MY (Table 2.6) in Murrah buffalo ranged from 0.023 ± 0.005 (Ipe and Nagarcenkar, 1992) to 0.65 ± 0.12 (Wakchaure, 2007).

Table 2.6: Heritability estimates FL305MY in Murrah buffalo

Heritability \pm S.E	References
0.046 ± 0.136	El-Arian (1986)
0.122 ± 0.168	Tien and Tripathi (1990)
0.023 ± 0.005	Ipe and Nagarcenkar (1992)
0.27 ± 0.16	Sahana (1993)
0.43 ± 0.19	Dhara (1994)
0.38 ± 0.18	Dass (1995)
0.152 ± 0.097	Nath (1998)
0.18 ± 0.07	Kumar <i>et al.</i> (2002)

0.65 ± 0.12	Gupta (2009)
0.25	Chakraborty <i>et al.</i> (2010)
0.29 ± 0.25	Singh <i>et al.</i> , 2011
0.17 ± 0.13	Jamuna (2012)
0.24 ± 0.15	Sahoo <i>et al.</i> (2014)
0.25 ± 0.09	Gupta <i>et al.</i> (2015)
0.33 ± 0.16	Jamuna <i>et al.</i> (2015)
0.15 ± 0.03	Godara <i>et al.</i> (2015)
0.29 ± 0.31	Dev <i>et al.</i> (2015)
0.50 ± 0.08	Jakhar <i>et al.</i> (2016)
0.18 ± 0.08	Singh <i>et al.</i> (2016)
0.26 ± 0.18	Patil <i>et al.</i> (2018)
0.30 ± 0.18	Chitra <i>et al.</i> (2018)

2.7.1.2 Heritability estimates of Lactation length

Heritability estimates of lactation length obtained from available literature ranges between 0.043 ± 0.03 (Kour and Narang, 2021) to 0.267 ± 0.169 (Gupta *et al.* 2015), which is of low to moderate heritability as presented in Table 2.7

Table 2.7 Heritability estimates of lactation length in Murrah buffalo

Heritability ± S.E	References
0.23 ± 0.14	Sachan <i>et al.</i> (2006)
0.09 ± 0.07	Wakchaure <i>et al.</i> (2008)
0.10 ± 0.10	Thiruvenkadan <i>et al.</i> (2010)
0.15	Malhado <i>et al.</i> (2013)
0.21 ± 0.15	Pareek and Narang (2014)

0.11 ± 0.22	Godara <i>et al.</i> (2015)
0.267 ± 0.169	Gupta <i>et al.</i> (2015)
0.043 ± 0.03	Kour and Narang (2021)

2.7.1.3 Heritability estimates of Peak yield

Heritability estimates of peak yield obtained from available literature ranges between 0.19 ± 0.11 (Chakraborty *et al.* 2010) to 0.52 ± 0.08 (Jakhar *et al.* 2016), which is of moderate to slight high heritability as compared to the other production traits as presented in Table 2.8.

Table 2.8 Heritability estimates of Peak yield (kg) in Murrah buffalo

Heritability± S.E	References
0.19 ± 0.11	Chakraborty <i>et al.</i> (2010)
0.48 ± 0.17	Pareek and Narang (2014)
0.37 ± 0.13	Dev <i>et al.</i> (2015)
0.35 ± 0.32	Godara <i>et al.</i> (2015)
0.52 ± 0.08	Jakhar <i>et al.</i> (2016)

2.7.1.4 Heritability estimates of Productive life

Heritability estimates of peak yield obtained from available literature ranges between 0.05 ± 0.06 (Patro and Bhat, 1979) to 0.53 ± 0.08 (Alli *et al.*, 2000) as presented in Table 2.9.

Table 2.9 Heritability estimates of productive life in Murrah buffalo

Heritability± S.E	References
0.05 ± 0.06	Patro and Bhat (1979)
0.17 ± 0.11	Kalsi and Dhillon (1984)
0.53 ± 0.08	Alli <i>et al.</i> (2000)
0.21 ± 0.11	Chander (2002)
0.133	Bashir (2007)

2.8 Previous works implementing Bayesian Approach in animal breeding

The previous works related to the application and use of Bayesian approach on animal breeding data have been thoroughly reviewed and briefed in Table 2.10. Studies listed in the below table belong to analysis of various species and breeds of livestock animals.

Table 2.10 Previous works implementing Bayesian Approach in animal breeding

Species/Breed	Objective(s)	References
Nelore cattle	Genetic parameters for growth traits	Faria <i>et al.</i> (2007)
		Lopes <i>et al.</i> (2017)
	Selection for fertility using stayability	Silva <i>et al.</i> (2003)
Brown Swiss	Genomic evaluations of sires with intergenomics	Croiseau <i>et al.</i> (2012)
Holstein cattle	Genetic parameters for milk traits	Krag <i>et al.</i> (2013)
		Mosharraf <i>et al.</i> (2014)
	Selection ranking of sire	Unalan and Cebeci (2005)
	Comparison of ABC and CBA using MCMC	Arpanahi <i>et al.</i> (2018)
Sahiwal and Tharparkar cattle	Variance components and heritability estimation	Yadav (2020)
Karan Fries cattle	Evaluation of production and fertility traits and sire ranking	Gujral (2021)
	Evaluation of production and fertility traits using repeatability model	Worku <i>et al.</i> (2021)
Murrah buffalo	Genetic parameter estimates for buffalo milk yield, milk quality and mozzarella production	Aspilcueta-Borquis <i>et al.</i> (2010)

	Estimation of genetic parameters for milk yield in Murrah buffalo	Breda <i>et al.</i> (2010)
Jaffarabadi buffalo	Genetic parameters estimation of Jaffarabadi buffalo	Malhado <i>et al.</i> (2012)
Landlly pigs	Influence of maternal effect on pre-weaning body weights in Landlly piglets	Ahmad <i>et al.</i> (2022)

2.9 Estimation of breeding value

Most breeding programmes for genetic enhancement include the prediction of breeding values as a necessary element. The availability of performance records is essential for the precise estimation of breeding value. Data on a population are often first accessible for individual animals, some of which may or may not be linked, and then subsequently for offspring and other relatives. Thus, the records of a few individuals and their close relatives may initially serve as the basis for the prediction of breeding values. Therefore, the progeny's breeding value is equal to the total of both parents' transmitting abilities. The only component that can be chosen for and hence the major component of importance is the additive genetic value, which is a function of the genes passed down from parents to offspring. Any breeding programme must incorporate an accurate estimate of breeding value because genetic improvement through selection depends on accurately identifying the individuals who have the highest true breeding value (Banik and Gandhi, 2006). The kind and quantity of information provided about potential individuals for selection affects the approach used to forecast breeding value.

When an animal is subjected to multiple measurements of the same trait, such as milk production during several lactations, its breeding value may be estimated from the mean of these measures. With repeated measurements, it is considered that there is an increased resemblance between an individual's records because of environmental factors or situations that have a permanent impact on those records (Singh and Singh, 2011). In other words, non-genetic long-term environmental effects provide more covariance between an individual's records. Thus, genetic and environmental factors contribute to the between-individual variation (permanent environmental effect). The differences between the individual's subsequent measures that result from temporary environmental changes from one parity to the next are attributed for the within-individual variance.

Bajetha *et al.*, 2015 compared estimated breeding values of crossbred cattle using simple daughter's average, least squares method and simplified regressed least squares (SLRS) method. Banik and Gandhi (2007) compared DFREML with conventional methods to evaluate Sahiwal sires. Kumar *et al.*, 2015 compared contemporary comparison (CC) method, least- squares (LS) method, simple regressed least-squares (SRLS) method and best linear unbiased prediction (BLUP) method in their study. Raja et al., 2012 compared least square methods (LSM), simple regressed least squares (SRLS), best linear unbiased prediction (BLUP), and the derivative-free restricted maximum likelihood (DFREML) for sire evaluation in Sahiwal cattle.

CHAPTER -3

Materials and Methods

3.1 Source of data

In the present study, the production and lifetime traits of Murrah buffalo reared at Livestock Research Centre, ICAR -National Dairy Research Institute, Karnal, Haryana, India, were analysed. The information was obtained from milk yield registers and history cum pedigree sheets maintained in the record room of the NDRI's Animal Genetics and Breeding division. The study was designed to compare breeding values generated using AIREML and Bayesian approach as well as to genetically assess animals by calculating (co)variance components of production and lifetime traits. Based on the lactation records of the Murrah buffalo herd, the parameters developed in this study can be used to establish sustainable breeding plans.

3.2 Location of the farm and the environment

ICAR-NDRI livestock farm is situated 240 meters above sea level in the Indo-Gangetic alluvial plains at latitudes 29.68°N and 76.98°E. The farm has a subtropical climate. In winter, the minimum temperature is quite close to freezing, while in summer, the maximum temperature may reach about 45°C. The average yearly rainfall is about 828 mm, with July and August receiving the most of it. The relative humidity ranges from 41percent to a maximum of 85 percent. Due to the large variation in temperature and relative humidity, it is clear that buffaloes kept at the NDRI farm are exposed to harsh weather.

3.3 Feeding management practices

A standardised, balanced ration of green, dry, and concentrate fodder was used to fulfill the nutritional needs of buffaloes. The calves were weaned at birth and given their own mother's colostrum for the first four to five days, followed by whole milk for the next 30 days. From one month of age, the calves were given access to minerals, concentrates, and roughages, and they were fed in accordance with their body weights as per dietary guidelines. Later in life, feeding plans are established based on the age group of the buffaloes. After seven months of pregnancy, pregnant heifers and/or buffaloes were given an extra concentrate of 1-1.5 kg. The extra concentrate was also administered at the time of milking, along with a let-down ration of 0.25 kg of concentrate.

3.4 Housing management practices

The buffaloes were kept in a system of loose housing. Each group of buffaloes—young, dry, nursing, and down calvers had their own shelter. The young stock was maintained in separate sheds according to age groups, with buffaloes kept in one shed from birth to six months, six months to two and a half years, and heifers from two and a half years until conception. The calves were housed loosely after being housed in covered calf enclosures for the first six months of their lives.

3.5 Milking management practices

At calving, the buffalo calves were weaned. The buffaloes were milked twice a day beginning on the sixth day after calving and continuing until the day of drying. Depending on the buffaloes' milk production and their level of machine milking adaptability, both hand milking and machine milking were used.

3.6 Health care and culling management practices

The NDRI cattle yard's animal health facility provided care for sick animals. All groups of buffalo were subjected to routine adoption of standard disease preventative measures. At the farm, all of the buffaloes were kept in hygienic conditions and received the necessary veterinary health care treatment. Two types of buffalo categories were created using the normal culling methods. Category one listed the buffaloes below the farm standard in terms of milk production based on the expected producing ability (EPA) of animals. The second category of buffalo was listed for culling based on poor growth, congenital defects, reproductive problems, teat defects, and poor health. The culling practices are followed twice a year.

3.7 Breeding information recorded on Murrah buffaloes

General information

- a) Animal number
- b) Sire number
- c) Dam number
- d) Date of birth
- e) Number of services per conception
- f) Date of successful service
- g) Service bull
- h) Number of lactations

- i) Gestation length
- j) Date of calving
- k) Sex of calf
- l) Calf number
- m) Date dried
- n) Days in lactation
- o) Peak yield

3.8 Traits considered for the study

3.8.1 Production traits recorded/generated

- a) First lactation 305-day milk yield (FL305MY)
- b) Total milk yield (TMY)
- c) Lactation length (LL)
- d) Peak yield (PY)

3.8.2 Lifetime traits generated

- a) Productive life (PL)
- b) 305-day milk yield across parity (305MYAP)

3.9 Data structure

The information on Murrah buffalo production records spanning across 50-year period from 1971 to 2020, was recorded and collated.

3.10 Normalisation and standardization of data

The study used Murrah buffaloes with known pedigrees and normal lactations. Animals were considered to have normal lactation when they calved and dried under physiologically normal circumstances. In addition to abnormal calving, lactating animals with lactation lengths of fewer than 100 days or milk yields of less than 500 kg recorded were removed (stillbirth abortion, dystocia, etc.). Data were adjusted for each trait according to the mean \pm 2 standard deviation.

3.11 Classification of data

To evaluate the effect of non-genetic factors on the traits taken into consideration in the current study, non-genetic effects such as the season, period, number of parities, and age group at first calving were divided into separate fixed sub-class effects.

3.11.1 Classification of seasons of birth/calving

Seasons are assumed to be one of the key environmental elements that influence the economic traits of Murrah buffaloes. A breeder must assess and adjust these effects on the traits they are considering since doing so would standardise the apparent variability. Based on the regional climate as documented in ICAR-CSSRI, Karnal, a year was divided into four birth/calving seasons (Singh, 1983). For production traits, season of calving is taken as a non-genetic factor, whereas for lifetime traits it is the season of birth of animals.

Table 3.1: Classification of seasons of birth/calving

S. No.	Season	Months	Season code
1	Winter	December to March	1
2	Summer	April to June	2
3	Rainy	July to September	3
4	Autumn	October to November	4

3.11.2 Classification of periods of birth/calving

Differences in management practices, availability of fodder and feed, and environmental factors affect different traits observed from year to year. However, these fluctuations may not be large enough to discern the effects of each year separately on specific traits. A period was defined as a group of years to analyse the impact of period on different qualities. Additionally, study demonstrated the impact of a group of bulls used for artificial insemination throughout a specific time period. For production traits, period of calving is taken as non-genetic factor whereas for lifetime traits it is the period of birth.

Table 3.2: Classification of periods of birth/calving

S. No.	Years	Period code
1	1971-1980	1
2	1981-1990	2

3	1991-2000	3
4	2001-2010	4
5	2011-2020	5

3.11.3 Classification of Age at first calving

Each Murrah buffalo had its first calving date recorded; the age at first calving (AFC) was then determined in number of days. In this study, the AFC was another significant factor that could have an effect on production and lifetime traits. One standard deviation above and below the mean of AFC was used to categorise Murrah buffaloes based on age at first calving. Based on their AFC, the distribution of Murrah buffaloes in various age groups has been depicted in Table 3.3.

Table 3.3: Classification of Age at first calving

S. No.	Age (in days)	Code
1	<1116	1
2	1116-1622	2
3	>1622	3

3.11.4 Classification of parity

In previous studies, parity was also one of the main factors that affected the various economic traits of buffaloes. In present study, dams with four parities and above were taken for analysis for lifetime traits. For production traits, all parities from 1 to 12 were taken into study but with systematic coding in view of obtaining conclusive and clear results.

Table 3.4: Classification of parity for production traits

S. No.	Parity of dam	Code
1	1	1
2	2	2
3	3	3

4	4	4
5	5 and above	5

Table 3.5: Classification of parity for lifetime traits

S. No.	Parity of dam	Code
1	4	1
2	5	2
3	6	3
4	7	4
5	8 and above	5

3.12 Statistical analysis

3.12.1 Measure of descriptive statistics

The data was analysed using software Harvey (1990). Using the conventional statistical methods outlined by Snedecor and Cochran (1994), the means, standard deviation, and errors of milk yield traits and lifetime traits were calculated.

3.12.2 Least squares analysis

Least square analysis was done to study how non-genetic factors such as the period of calving, the season, the number of parities of dam, and the age groups at calving affect the production and lifetime traits of Murrah buffalo and to overcome the effects of non-orthogonality as a result of unequal and disproportionate subclass frequencies. For the study of the data, least square analysis of fitting constants was used as per Harvey (1990). With the understanding that the various elements being incorporated into the model are linear, independent, and additive, the following models were taken into account.

For production traits:

$$Y_{ijklm} = \mu + P_i + S_j + Pa_k + Ag_l + e_{ijklm}$$

Y_{ijklm} = Observation of m^{th} animal having, l^{th} age group at first calving, k^{th} parity, calved in j^{th} season, i^{th} period

μ = Overall mean

P_i = Effect of i^{th} period of calving ($i=1,2,3,4,5$)

S_j = Effect of j^{th} season of calving ($j=1,2,3,4$)

Pa_k = Effect of k^{th} parity ($k=1,2,3,4,5$)

Ag_l = Effect of l^{th} age group in 1st calving taken as covariate ($l=1,2,3$)

e_{ijklm} = Random error, $N(0, \sigma^2_e)$

For FL305MY:

$$Y_{ijkl} = \mu + P_i + S_j + Ag_k + e_{ijkl}$$

Y_{ijkl} = Observation of l^{th} animal having, k^{th} age group at first calving, calved in j^{th} season, i^{th} period

μ = Overall mean

P_i = Effect of i^{th} period of calving ($i=1,2,3,4,5$)

S_j = Effect of j^{th} season of calving ($j=1,2,3,4$)

Ag_k = Effect of k^{th} age group in 1st calving ($l=1,2,3$)

e_{ijkl} = Random error, $N(0, \sigma^2_e)$

For lifetime traits:

$$Y_{ijklm} = \mu + P_i + S_j + Pa_k + Ag_l + e_{ijklm}$$

Y_{ijklm} = Observation of m^{th} animal having, l^{th} age group at first calving, k^{th} parity, calved in j^{th} season, i^{th} period

μ = Overall mean

P_i = Effect of i^{th} period of birth ($i=1,2,3,4,5$)

S_j = Effect of j^{th} season of birth ($j=1,2,3,4$)

Pa_k = Effect of k^{th} parity ($k=1,2,3,4,5$)

Ag_l = Effect of l^{th} age group in 1st calving ($l=1,2,3$)

e_{ijklm} = Random error, $N(0, \sigma^2_e)$

3.13 Various animal models under study

Various animal models with or without the combination of maternal effects, their covariance, and the environmental variance used for fitting the data on production and lifetime traits of Murrah buffalo are presented below:

3.13.1 Models for repeatable traits

- For TMY, LL, PY, 305MYAP

Model I: Animal model with direct additive genetic effect

$$Y = Xb + Z_{1a} + e$$

Model II: Animal model incorporating direct additive genetic effect with permanent environment effect of animal

$$Y = Xb + Z_{1a} + Z_{2pe} + e$$

Model III: Animal model incorporating direct additive genetic, maternal genetic effects along with covariance between them and permanent environment effect of animal

$$Y = Xb + Z_{1a} + Z_{2m} + Z_{3pe} + e, \text{Cov}_{(a,m)} = A\sigma_{am}$$

Model IV: Animal model incorporating direct additive genetic, maternal genetic effects along with covariance between them as zero and permanent environment effect of animal

$$Y = Xb + Z_{1a} + Z_{2m} + Z_{3pe} + e, \text{Cov}_{(a,m)} = 0$$

Model V : Animal model incorporating direct additive genetic, maternal genetic along with covariance between these two, permanent environment effect of animal and permanent environment effect of the dam

$$Y = Xb + Z_{1a} + Z_{2m} + Z_{3pe} + Z_{4mpe} + e, \text{Cov}_{(a,m)} = A\sigma_{am}$$

3.13.2 Models for non-repeatable traits

- For FL305MY, PL

Model I: Animal model with direct additive genetic effect

$$Y = Xb + Z_{1a} + e$$

Model III: Animal model incorporating direct additive genetic, maternal genetic effects along with covariance between them and permanent environment effect of animal

$$Y = Xb + Z_{1a} + Z_{2m} + e, \text{Cov}_{(a,m)} = A\sigma_{am}$$

Model IV: Animal model incorporating direct additive genetic, maternal genetic effects along with covariance between them as zero and permanent environment effect of animal

$$Y = Xb + Z_{1a} + Z_{2m} + e, \text{Cov}_{(a,m)} = 0$$

Model V: Animal model incorporating direct additive genetic, maternal genetic along with covariance between these two, permanent environment effect of animal and permanent environment effect of the dam

$$\mathbf{Y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_{1a} + \mathbf{Z}_{2m} + \mathbf{Z}_{3mpe} + \mathbf{e}, \mathbf{Cov}_{(a,m)} = \mathbf{A}\boldsymbol{\sigma}_{am}$$

\mathbf{Y} = Vector of observations

\mathbf{b} = Vector of fixed effects

\mathbf{a} = Vector of direct additive animal genetic effect, $\sim N(0, A\sigma_a^2)$

\mathbf{m} = Vector of maternal additive genetic effect, $\sim N(0, A\sigma_m^2)$

\mathbf{pe} = Vector of permanent environmental effects of the animal, $\sim N(0, I\sigma_{pe}^2)$

\mathbf{mpe} = Vector of permanent environmental effects of the dam, $\sim N(0, I\sigma_{mpe}^2)$

\mathbf{e} = Vector of residual effects, $\sim N(0, I\sigma_e^2)$

\mathbf{A} = Numerator relationship matrix between animals

$\boldsymbol{\sigma}_{am}$ = Covariance between direct additive animal genetic effect and maternal additive genetic effects

$\mathbf{X}, \mathbf{Z}_1, \mathbf{Z}_2, \mathbf{Z}_3, \mathbf{Z}_4$ = Association matrices

A normal distribution with a zero mean and a variance-covariance matrix was used to sample random effects. For Bayesian analysis, it was anticipated that the systemic effects and the (co)variance components would follow a uniform prior Gaussian distribution. The inverse Wishart distribution was presumptively followed by the conditional distributions of the direct additive genetic, direct maternal genetic, permanent environmental, and residual variances (Sorensen and Gianola, 2002).

3.14 Estimation of phenotypic and genotypic variance and covariance of traits

The BLUPF90 suite of programmes was the software algorithm used for estimation. In the current study, a number of BLUPF90 algorithms were used to analyse the data, identify (co)variance components, and determine genetic parameters. BLUPF90 is a set of Fortran 90/95 software that are often used for genetic data analysis in animal breeding. Data were first renumbered using the BLUPF90 program's RENUMF90 process. GIBBS2F90 was used to conduct Gibbs sampling for univariate linear mixed models in the study and generate samples for variance components. The POSTGIBBSF90 tool was used to compile these samples and obtain post-statistics. Based on Murrah buffalo production and lifetime traits data, various models were evaluated according to the deviation information criterion (DIC) (Spiegelhalter *et al.*, 2002). The parameter files

employed the `se_covar` function to calculate heritability and associated standard error estimates using various algorithms.

3.15 Bayesian inference

The given traits under study were analysed through Bayesian approach using MCMC and Gibbs sampling methods in the BLUPF90 suite of programs. The genetic improvement of milk yield traits through selection heavily relies on the accurate estimate of genetic parameters and covariance estimation of traits in various combinations of animal models including or excluding maternal effects. The accuracy of estimation of genetic parameters is influenced by the quantity and quality of data gathered and collated about the animal, observable records, pedigree information, the type of co-variance estimation utilised, and the statistical model used. The analysis, model, and choice of MCMC with GS depend on reliable estimations; standardisation of parameter variables is necessary for uniform and normalised data. The following methodologies were used to enhance the analysis and inference:

- A. The number of iterations
- B. Length of burn-in or warming-up period
- C. Thinning interval

The number of parameters that must be calculated determine the length of the burn-in or warming-up phase and the number of effective samples. The number of parameters increases with the time of burn-in and decreases with the number of effective samples. In the current study, the univariate animal models were used, which allowed to incorporate all the data and information on a single trait that were available for an animal, thus improving the accuracy of the estimate of the genetic parameters of that trait. Results depend on data standardisation, which varies on different analytic variables.

3.15.1 Warming-up period or burn-in length

According to Resende *et al.*,2001, the burn-in period controls how many samples are discarded in the Bayesian method of analysis, which is a crucial factor. Another crucial factor is the serial correlation that is formed between samples in the Markov chain. The evaluation of the posterior distribution densities derived from Gibbs chain samples was done in order to determine the genetic parameters and (co)variance components. After the burn-in, one sample was taken from every fifty samples in order to prevent any potential association between the following samples. Gibbs sampling is a Monte Carlo method for

numerical integration that enables us to draw conclusions about joint or marginal distributions even when it is difficult to generate the proper densities directly (Geman and Geman, 1984). Using this technique, it is possible to deliver more accurate estimates. The convergence is the next thing that need to be concentrated on and standardised after selecting the warming-up interval.

3.15.2 Number of iterations

Every 50th sample was saved when the single trait analysis using Gibbs chains was first begun with 500000 with burn-in as 50000 iterations. Subsequently, by examining the graphical analysis output and diagnosis tests (Geweke algorithm), the convergence of chains produced by the Gibbs sampler was verified. Then, using graphs and plots produced by POSTGIBBSF90 and Gnuplot, appropriate convergence and normalisation were confirmed. The resulting trace plot and histogram showed how the data had been normalised. In order to ensure that the data adequately converged for parameter estimate, the appropriate number of iterations and burn-in was regarded optimal. Additionally, it was discovered in the current investigation that the burn in and iterations for each attribute and population size are explicit. It should be evaluated in this way for each experiment.

3.15.3 Convergence

Using the Gnuplot (version 5.4) software, the output of the Bayesian technique of analysis also incorporates graphical representations. After executing POSTGIBBSF90, these graphical outputs essentially act as an index for tracking the convergence of the chains produced by Gibbs Sampler. The convergence was verified using the trace plots for the production and longevity qualities that were derived using the Bayesian technique of analysis. By creating a trace plot and using iterations on the X-axis and variance on the Y-axis, the normalisation of data for the various traits under consideration was examined. The trace plots are expected to not form any trend in a normally distributed data analysis and histograms produced are in a bell-shaped curve.

The number of effective sample sizes for the production and lifetime traits was sufficient to get the mean, median, mode, and highest posterior density of each parameter. Trace plots and histograms exhibited the appropriate convergence and normal form. The outcome of the current investigation demonstrated the normalising of data following chain convergence.

3.15.4 Deviance information criteria (DIC) values

The traditional method of model comparison usually includes a trade-off between the degree of complexity and how well the model fits the data. In a somewhat similar manner, Spiegelhalter *et al.* (2002) developed the DIC, a selection criterion based on Bayesian measures of model complexity and data fit.

3.16 Estimation of breeding value

Breeding value of sires were found out using an animal model with both the approaches, AIREML as well as Bayesian. For the purpose of estimating the breeding value of sires, the mixed model equation is shown below.

$$\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\mu} + \mathbf{e}$$

\mathbf{Y} = Vector of observations

\mathbf{X} = Incidence matrix for fixed effect

$\boldsymbol{\beta}$ = Vector of fixed effect

\mathbf{Z} = Incidence matrix for random effect

$\boldsymbol{\mu}$ = Vector of random effect

\mathbf{e} = Random error, $N(0, \sigma^2\mathbf{e})$

BLUP algorithm

Breeding values are estimated using BLUP methodology using the following algorithm in an animal model

$$\begin{pmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{u}} \end{pmatrix} = \begin{pmatrix} \mathbf{X}'\mathbf{X} & \mathbf{X}'\mathbf{Z} \\ \mathbf{Z}'\mathbf{X} & \mathbf{Z}'\mathbf{Z} + \lambda\mathbf{A}^{-1} \end{pmatrix}^{-1} \begin{pmatrix} \mathbf{X}'\mathbf{y} \\ \mathbf{Z}'\mathbf{y} \end{pmatrix}$$

Where \mathbf{A} = Numerator relationship matrix

$$\lambda = \frac{V_E}{V_A}$$

Here, V_E is environmental variance and V_A is additive genetic variance

3.17 Accuracy and reliability of BV

$$r^2 = 1 - \left(\frac{\text{SEP}^2}{\sigma_a^2} \right)$$

r^2 = Reliability of the estimates

SEP = Standard error of prediction

σ^2_a = Additive genetic variance of the trait

3.18 Rank correlation

Estimation of rank correlation was done by the following formula given by Steel and Torrie (1960)

$$r(s) = 1 - \frac{6 \sum d_i^2}{n(n^2 - 1)}$$

r = Rank correlation coefficient

n = Number of sires under evaluation

d_i = Difference of rank between paired items under two methods

3.19 Test of significance of rank correlation

The test of significance was performed by using t-test with the formula as given below:

$$t = r \sqrt{\frac{n - 2}{1 - r^2}}$$

t = Test statistic

r = Correlation coefficient

$n-2$ = Degrees of freedom

CHAPTER -4

Results and Discussion

The present study explored covariance components estimation of productivity and lifetime traits in Murrah buffaloes using various variance combinations of animal model. To achieve the goals of this study, the obtained data were analysed using Harvey (1990), Wombat (2007), BLUPF90 suite of programs (2018), and Gnuplot 5.4. The non-orthogonality of data recorded and collated for the suggested study was overcome using Harvey's least squares method of analysis to estimate the least squares mean for the traits. Least Squares analysis was used to determine the effect of various genetic and non-genetic factors in the study. The Bayesian inference method was also used for the same data set to estimate other genetic parameters. Estimates for the genetic parameters and covariance components were derived after using a Bayesian approach to the data. The examination of posterior distribution densities was done using Gibbs chain sampling. The outcomes of current investigation were summarised, and addressed in relation to the published literature that was available.

4.1 Performance of production and lifetime traits in Murrah buffalo

4.1.1 First lactation 305 day milk yield

The FL305MY (Table 4.1) in the present study was 1962.93 ± 12.91 kg in Murrah buffalo. However, greater FL305MY was reported in Murrah buffalo by Jamuna *et al.* (2016), Jakhar *et al.* (2016), Kumar *et al.* (2017), and Kaur *et al.* (2020). Jamuna (2012), Chitra *et al.* (2018), and Kour and Narang (2021) observed comparable FL305MY. In comparison to the current study, Kumar *et al.* (2003), Patil *et al.* (2012), and Thiruvekadan (2011) reported a lower FL305MY. Given that many studies relied on few and varying numbers of observations, farm-to-farm variations, or differences that have occurred over time depending on the time period for which data were considered, it is possible that the differences in estimates of milk yield when compared to other workers are due to sampling variations.

4.1.2 Total milk yield

In the current study, the TMY in all the parities ranged from 2004.49 ± 21.23 to 2238.1 ± 34.33 kg (Table 4.1) with overall least squares mean of 2156.24 ± 15.81 kg. Although Kaur *et al.* (2020) and Dahiya *et al.* (2020) reported higher values of first lactation total milk yield, the total milk yield during the first lactation that was observed in this study is comparable to the total milk yields reported by Singh *et al.* (2011) and Gupta *et al.* (2012) in Murrah buffalo.

4.1.3 Lactation length

In the current study, lactation length ranged from 287.63 ± 2.98 to 318.26 ± 2.24 days with overall least squares mean of 303.66 ± 1.67 days (Table 4.1). The first parity experienced the longest lactation period, whereas the fifth parity experienced the shortest period. Gajbhiye (1987), Raheja (1992), Kumar *et al.* (2002), Pandey *et al.* (2015), Jakhar *et al.* (2016), and Kaur *et al.* (2021) noted similar first lactation length in Murrah buffalo, while Kaur *et al.* (2020) noted longer lactation length in Murrah buffalo and Dhara (1994), Geetha (2005), Jamuna (2012), Thiruvankadan *et al.* (2015) reported lower value of first lactation length.

4.1.4 Peak yield

In the present study, it is clear that peak yield in Murrah buffalo ranged from 10.49 ± 0.07 to 12.76 ± 0.12 kg in various parities with overall least squares mean of 11.99 ± 0.05 as presented in table 4.1. The fourth parity showed the highest peak yield, whereas the first parity showed lowest. The peak yield in Murrah buffaloes that Thiruvankadan *et al.* (2014) and Dev *et al.* (2015) observed was significantly lower, whereas Suresh (2013) and Kaur *et al.* (2020) reported comparably higher peak yield.

4.1.5 Productive life

Productive life ranges from 1690.45 ± 46.29 to 2008.04 ± 64.98 days with overall least squares mean of 1774.85 ± 37.53 days (Table 4.1). Chander (2002), Bashir *et al.* (2007), Thiruvankadan *et al.* (2015) and Dev *et al.* (2017) have reported lesser PL values as compared to the present study. This difference in PL may be because all animals with complete records from 4th to 12th parity were taken into consideration for the analysis of lifetime traits.

4.1.6 305 day milk yield across parity

In Murrah buffalo, the 305MYAP ranged from 1910.94 ± 17.24 kg to 2061.02 ± 23.36 kg across fourth to twelfth parities with overall least squares mean of 2104.82 ± 12.91 kg was observed during the study with the highest range observed around 6th to 7th parity (Table 4.1).

Table 4.1: Parity wise least squares mean and standard errors of production and lifetime traits

Traits	Overall mean	Number of parities of dam				
	L.S.M \pm S. E	1	2	3	4	5
FL305MY	1962.93 \pm 12.91 kg	1962.93 \pm 12.91	-	-	-	-
No. of observations	1555	1555	-	-	-	-
TMY	2156.24 \pm 15.81	2004.49 \pm 21.23	2218.02 \pm 23.7	2261.58 \pm 27.73	2238.09 \pm 34.33	2059.02 \pm 28.24
No. of observations	5084	1647	1249	861	523	804
LL	303.66 \pm 1.67	318.26 \pm 2.24	304.75 \pm 2.51	306.66 \pm 2.95	301 \pm 3.66	287.63 \pm 2.98
No. of observations	5114	1664	1258	858	518	816
PY	11.99 \pm 0.05	10.49 \pm 0.07	12.13 \pm 0.08	12.54 \pm 0.09	12.76 \pm 0.12	12.01 \pm 0.1
No. of observations	4668	1529	1159	792	470	718
PL	1774.85 \pm 37.53	1690.45 \pm 46.29	1696.07 \pm 54.99	1741.42 \pm 57.83	1738.26 \pm 75.40	2008.04 \pm 64.98
No. of observations	635	212	138	129	63	93
305 MYAP	2104.82 \pm 12.91	1910.94 \pm 17.24	2146.4 \pm 19.32	2206.55 \pm 22.62	2199.18 \pm 28.09	2061.02 \pm 23.36
No. of observations	635	212	138	129	63	93

4.2 Effect of non-genetic factors on production and lifetime traits in Murrah buffaloes

Numerous non-genetic factors affect production and lifetime traits in Murrah buffalo, and it is crucial to evaluate their effect on the performance traits in order to provide accurate and unbiased estimations of genetic parameters. Following are some effects of non-genetic factors on various productivity and lifespan attributes as seen in this study.

4.2.1 Production traits

Analysis of variance (ANOVA) for the production and lifetime traits in Murrah buffaloes are presented in Table 4.2 showing effect of non-genetic factors as significant and non-significant.

4.2.1.1 First lactation 305 day milk yield

Age at first calving had no significant effect on FL305MY in the current study, but the effect of calving period, season, and parity of animals were shown to be highly significant ($p < 0.01$). Numerous studies found that the period of calving greatly influenced FL305MY, which is consistent with the given findings (El-Arian, 1986; Gajbhiye, 1987; Tomar and Tripathi, 1988; Singh *et al.*, 1990; Dhara, 1994; Dass, 1995; Dass and Sharma, 1994; Nath, 1998; Lathwal, 2000; Gupta, 2009). In contrast to the current study, Dass and Sharma (1994), Singh *et al.* (1990), Sahana (1993), and Lathwal (2000) observed a substantial influence of calving season on FL305MY. Tables 4.3, 4.4, and 4.5 represent the respective non-genetic factor-wise value of FL305MY.

4.2.1.2 Total milk yield

Parity of animal and calving season had a highly significant ($p < 0.01$) effect on TMY, whereas calving period had a significant ($p < 0.05$) effect. AFC had no appreciable effect on TMY. Similar effects of calving period on TMY were detected by Rohilla *et al.* (1992), Chhikara *et al.* (1994), and Gupta (2009); however, Sharma and Singh (1988) and Sarkar (2002) found the effect to be non-significant. Sharma (1982) and Sarkar found effect of season of calving on milk yield as non-significant, but Chhikara *et al.* (1994)

reported significant effect of calving season on milk output. Tables 4.3, 4.4, and 4.5 represent the respective non-genetic factor-wise value of TMY.

4.2.1.3 Lactation length

While AFC was having no significant effect on lactation length, the effects of parity of animal, period of calving, and season of calving were highly significant ($p < 0.01$). In Murrah buffaloes, the influence of non-genetic variables such as calving season, calving period, and age group was of significant variation. Other researchers' findings (Dhara, 1994; Dass, 1995; Nath, 1998; Wakchaure, 2008; Gupta, 2009) were consistent with the current study. Tables 4.3, 4.4, and 4.5 represent the respective non-genetic factor-wise value of LL.

4.2.1.4 Peak yield

Das *et al.* (2015) found a significant influence of period on peak yield in swamp buffaloes, whereas the effect of season of calving was found to be non-significant. In the present study, non-genetic factors like parity of animal, period of calving, and season of calving were found to have a highly significant effect ($p < 0.01$) on PY. Tables 4.3, 4.4, and 4.5 represent the respective non-genetic factor-wise value of PY.

4.2.2 Lifetime traits

4.2.2.1 Productive life

Period of birth, total number of parities of an animal, and season of birth had a highly significant effect ($p < 0.01$) on the productive life of Murrah buffalo under study. Table 4.3, 4.4 and 4.5 represent the respective non-genetic factor-wise value of PL.

4.2.2.2 305 day milk yield across parity

Period of birth is the only non-genetic factor taken in this study that had highly significant effect ($p < 0.01$) on 305MYAP of Murrah Buffalo. Season of birth, total number of parities of an animal and AFC were found to have no significant effect. Tables 4.3, 4.4 and 4.5 represent the respective non-genetic factor-wise value of 305MYAP.

Table 4.2: Effect of non-genetic factors on production and lifetime production and lifetime traits

Trait	No. of observations	LSM \pm SE	Non-genetic factors			
			SOC	POC	Parity of dam	AFC
FL305MY	1554	1962.93 \pm 12.91 kg	S**	S**	-	NS
TMY	5084	2156.24 \pm 15.81 kg	S**	S*	S**	NS
LL	5114	303.66 \pm 1.67 days	S**	S**	S**	NS
PY	4668	11.99 \pm 0.05 kg	S**	S**	S**	NS
PL	640	1774.85 \pm 37.53 days	NS	S**	S**	NS
305 MYAP	4523	2104.82 \pm 12.91 kg	S**	S**	S**	NS

*Significant at $p < 0.05$ ** Significant at $p < 0.01$

Table 4.3: Period wise least squares mean and standard errors of production and lifetime traits

Trait	Overall Mean	Period of calving				
		1	2	3	4	5
	L.S.M ± S. E					
FL305MY	1962.63 ± 12.91	1686.31 ± 30.54	1851.12 ± 29.44	2094.15 ± 31.78	2011.10 ± 25.64	2118.13 ± 29.44
	1555	229	382	327	309	308
TMY	2156.24 ± 15.81	1910.41 ± 33.65	2118.74 ± 24.76	2373.93 ± 24.54	2176.08 ± 26.11	2202.03 ± 24.38
	5084	579	1250	1218	959	1078
LL	303.66 ± 1.67	306.76 ± 3.57	294.13 ± 2.64	313.63 ± 2.6	308.70 ± 2.78	295.07 ± 2.58
	5114	583	1235	1225	982	1089
PY	11.99 ± 0.05	11.16 ± 0.11	12.11 ± 0.08	12.26 ± 0.09	11.89 ± 0.8	12.51 ± 0.07
	4668	579	1147	909	957	1076
PL*	1774.85 ± 37.53	1720.11 ± 50.61	1666.41 ± 59.76	1755.02 ± 66.10	1883.76 ± 48.21	1848.95 ± 146.18
	635	180	165	121	152	17
305MYAP*	2104.82 ± 12.91	1854.79 ± 27.41	2102.09 ± 20.18	2283.95 ± 19.95	2086.09 ± 21.28	2197.18 ± 20.16
	635	180	165	121	152	17

*Period of birth as one of non-genetic factor is taken for these traits

Table 4.4: Season wise least squares means and standard errors of production and lifetime traits

Trait	Overall Mean	Season of calving			
	L.S.M \pm S. E	1	2	3	4
FL305MY	1962.63 \pm 12.91	2047.97 \pm 25.42	1943.37 \pm 51.44	1920.6 \pm 35.99	1950.83 \pm 63.21
	1555	393	300	582	280
TMY	2156.24 \pm 15.81	2229.6 \pm 23.44	2186.31 \pm 27.63	2076.3 \pm 20.55	2132.75 \pm 25.83
	5084	1351	872	1837	1024
LL	303.66 \pm 1.67	310.52 \pm 2.49	308.49 \pm 2.93	294.8 \pm 2.17	300.83 \pm 2.74
	5114	1353	875	1857	1029
PY	11.99 \pm 0.05	12.38 \pm 0.08	11.87 \pm 0.09	11.71 \pm 0.07	11.99 \pm 0.09
	4668	1247	784	1689	984
PL*	1774.85 \pm 37.53	1680.92 \pm 52.17	1819.92 \pm 60.99	1767.90 \pm 47.78	1830.64 \pm 57.35
	635	155	112	247	121
305MYAP*	2104.82 \pm 12.91	2154.21 \pm 19.06	2120.74 \pm 22.46	2045.51 \pm 16.72	2098.78 \pm 21.32
	635	155	112	247	121

*Season of birth as one of non-genetic factor is taken for these traits

Table 4.5: Age at first calving wise least squares means and standard errors of production and lifetime traits

Trait	Overall Mean	Age at First Calving		
	L.S.M \pm S. E	1	2	3
FL305MY	1962.63 \pm 12.91	1938.96 \pm 56.61	1984.09 \pm 63.18	1922.43 \pm 56.75
	1555	305	939	311
TMY	2156.24 \pm 15.81	2172.7 \pm 30.33	2134.07 \pm 13.49	2161.95 \pm 30.5
	5084	620	3816	648
LL	303.66 \pm 1.67	287.63 \pm 2.98	306.52 \pm 3.2	302.16 \pm 1.43
	5114	633	3824	657
PY	11.99 \pm 0.05	11.92 \pm 0.1	11.94 \pm 0.05	12.1 \pm 0.1
	4668	553	3478	637
PL	1774.85 \pm 37.53	1769.44 \pm 70.79	1754.24 \pm 45.91	1800.86 \pm 64.53
	635	90	440	105
305MYAP	2104.82 \pm 12.91	2122.61 \pm 24.72	2093.89 \pm 11.06	2097.95 \pm 24.88
	635	90	440	105

4.3 Genetic and phenotypic parameters estimation

4.3.1 Bayesian inference

The accuracy of estimation of genetic parameters is influenced by quantity and quality of data gathered and collated about the animal, observable records, pedigree information, the type of co-variance estimation utilised, and the statistical model used. The analysis, model, and choice of MCMC with Gibbs Sampling depend on reliable estimations; standardisation of parameter variables is necessary for uniform and normalised data.

- A. The number of iterations
- B. Length of burn-in or warming-up period
- C. Thinning interval

4.3.2 The number of iterations, length of burn-in and thinning interval

Every 50th sample was saved when the single trait analysis using Gibbs chains was first begun with 500000 with burn-in as 50000 iterations. Subsequently, by examining the graphical analysis output and diagnosis tests (Geweke algorithm), the convergence of chains produced by the Gibbs sampler was verified. Then, using graphs and plots produced by POSTGIBBSF90 and Gnuplot, appropriate convergence and normalisation were confirmed (Fig.4.1 to 4.6). The resulting trace plot and histogram showed how the data had been normalised. In order to ensure that the data adequately converged for parameter estimate, the appropriate number of iterations and burn-in was as regarded optimal. Additionally, it was discovered in the current investigation that the burn in and iterations for each attribute and population size are explicit. It should be evaluated in this way for each experiment (Fig. 4.1 to 4.20).

4.3.3 Convergence

Using the Gnu plot (version 5.4) software, the output of the Bayesian technique of analysis also incorporates graphical representations. The convergence was verified using the trace plots for the production and lifetime traits that were derived using the Bayesian approach of analysis. By creating a trace plot and using iterations on the X-axis and variance on the Y-axis, the normalisation of data for the various traits under consideration was examined. The trace plots shown in figures (Figure 4.1, 4.2, 4.3, 4.4, 4.5 and 4.6) were used to verify proper convergence, for convergence of models there should not be any trend formation in trace plots. The bell-shaped histogram shown in figure (Figure 4.1, 4.2, 4.3, 4.4, 4.5, and 4.6)

represents normalisation for the production and lifetime traits. For trait like PL, the shape of histogram obtained is right side skewed and as per manual of the software BLUPF90 (Miszta *et al.*, 2018), median values of posterior densities obtained were taken for the study.

4.3.4 Monte Carlo error

The Monte Carlo error (MCE) refers to the error in genetic parameter estimate caused by number of samples utilised from the Gibbs chain (Tassel and Vleck, 1996). The value of MCE decreases as the Gibbs chain length increases. Nearly all of the characteristics in the current study had low MCE (Table 4.6). Low error means greater precision, which means that the number of viable samples we selected was adequate. As a result, the estimates of variance and covariance components we obtained for all relevant traits are trustworthy and of high precision, and they can be further incorporated for the purpose of genetically improving the animals.

4.3.5 Deviance information criteria (DIC) values

Deviance information criteria were used for deciding the appropriateness of different models (Spiegelhalter *et al.*, 2002). The lowest value was used as an estimate to decide the best model of fit. Hence the best models chosen for FL305MY, TMY, LL, PY, PL and 305MYAP were model number 3,3,2,2,5, and 3 respectively as shown in Table 4.7.

4.3.6 Measures of central tendency

Mean of direct heritability in the best fit model by Bayesian approach for the traits *i.e.*, FL305MY, TMY, LL, PY, PL and 305MYAP were estimated as 00.49 ± 0.007 , 0.20 ± 0.011 , 0.04 ± 0.001 , 0.10 ± 0.001 , 0.10 ± 0.009 and 0.21 ± 0.003 respectively (Table no. 4.8). The total heritability estimates in the best fit model for FL305MY, TMY, PL and 305MYAP were 0.17 ± 0.006 , 0.10 ± 0.007 , 0.09 ± 0.002 and 0.10 ± 0.001 , respectively.

There is a significant genetic potential for gains that may be achieved by selection, according to the medium heritability estimations obtained for all the production traits taken into consideration in this study. The heritability estimates for lifetime traits derived from the current study are low (Table 4.6), indicating that there are few possibilities to genetically improve the animals for these traits. Therefore, management practices are crucial for enhancing lifetime traits. In order to increase the animal's total productivity, lower maintenance costs, and eventually make the animal lucrative for the herd and a valuable asset

for the dairy business, environmental condition, and animal upkeep must be correctly maintained.

4.4 Estimation of (co)variance components

After the underlying sample burn-in is utilised to calculate the (co)variance component means, the chain's mean of estimated parameters is employed. Following the burn-in phase, the estimates of the posterior mean for heritability (direct, total, and maternal) and variance values (genotypic, phenotypic, environmental, maternal genetic, maternal permanent environment, and residual) are derived as the means of the functions using (co)variance components. The heritability for all the variables taken into account under production and lifetime traits in five statistical models with distinct partitions of variance and their covariances in the animal model in Murrah buffalo is shown in Table 4.6.

Measures of central tendency *i.e.*, mean and median for the trait PL, represented in Table 4.7, are practically comparable showing the information has been standardised and each trait through Gibbs sampling is fitting and accordingly the subsequent variance and covariance estimates are more exact and is reflected in low error component.

Table 4.6: Genetic parameters obtained for the production and lifetime traits under study

Traits	Model	σ^2_a	σ^2_{pe}	σ^2_e	σ^2_p	σ^2_m	σ^2_{mpe}	$\sigma_{cov Am}$	$h^2_{t \pm M.C. E}$	$h^2_{\pm M.C. E}$	$m^2_{\pm M.C. E}$	r
FL305MY	1	174360	-	465110	639470	-	-	-	-	0.27 ± 0.003	-	-
	2	-	-	-	-	-	-	-	-	-	-	-
	3	456050	-	302380	907120	148690	-	-245130	0.17 ± 0.006	0.49 ± 0.007	0.16 ± 0.004	-
	4	172320	-	444520	648380	31536	-	-	0.29 ± 0.002	0.26 ± 0.002	0.05 ± 0.002	-
	5	437860	-	286630	893620	137800	31338	-232870	0.17 ± 0.007	0.48 ± 0.006	0.15 ± 0.007	-
TMY	1	192520	-	344280	536800	-	-	-	-	0.36 ± 0.002	-	0.34
	2	57130	115870	329830	502830	-	-	-	-	0.11 ± 0.001	-	0.36
	3	113140	86670	330020	551890	502830	-	-44489	0.10 ± 0.007	0.20 ± 0.011	0.04 ± 0.002	0.33
	4	52254	111660	330110	504230	551890	-	0	0.11 ± 0.001	0.10 ± 0.001	0.02 ± 0.001	0.35
	5	113810	80392	329790	554480	504230	-4536.5	-45933	0.10 ± 0.002	0.11 ± 0.004	0.04 ± 0.002	0.34
LL	1	929.78		4358.4	5288.2	-	-	-	-	0.18 ± 0.003	-	-
	2	172370	245730	221740	639830	-	-	-	-	0.04 ± 0.001	-	0.65
	3	418980	176220	137950	882180	137950	-	-103.82	0.03 ± 0.006	0.05 ± 0.01	0.02 ± 0.001	0.67
	4	166250	236940	212800	647860	31871	-	0	0.05 ± 0.001	0.04 ± 0.001	0.01 ± 0.001	0.62
	5	427450	142570	154320	897430	145890	27198	-132.80	0.03 ± 0.002	0.06 ± 0.002	0.02 ± 0.002	0.64
PY	1	1.1832		4.4911	5.6743	-	-	-	-	0.21 ± 0.002	-	-

	2	0.54524	0.64052	4.3694	5.5551	-	-	-	-	0.10 ± 0.001	-	0.21
	3	0.82326	0.43275	4.3667	5.8708	0.24809	-	-0.27759	0.09 ± 0.002	0.14 ± 0.003	0.04 ± 0.002	0.21
	4	0.47599	0.57737	4.3686	5.5716	0.14968	-	0	0.1 ± 0.001	0.09 ± 0.001	0.03 ± 0.001	0.19
	5	0.82354	0.41105	4.3674	5.8735	0.22691	446500	-0.27582	0.09 ± 0.002	0.14 ± 0.004	0.04 ± 0.002	0.21
PL	1	23803	-	211600	235400	-	-	-	-	0.10 ± 0.005	-	-
	2	-	-	-	-	-	-	-	-	-	-	-
	3	23641	-	199290	247380	24444	-	-8752.5	0.09 ± 0.004	0.09 ± 0.006	0.1 ± 0.003	-
	4	24780	-	191360	240560	24419	-	0	0.15 ± 0.003	0.10 ± 0.003	0.1 ± 0.002	-
	5	25289	-	188370	250670	24424	12584	-10250	0.09 ± 0.007	0.10 ± 0.009	0.1 ± 0.013	-
305MYAP	1	129630	-	236170	365800	-	-	-	-	0.35 ± 0.002	-	-
	2	45983	73455	227650	347090	-	-	-	-	0.13 ± 0.001	-	0.34
	3	81290	48868	227460	387100	29477	-	-37231	0.10 ± 0.001	0.21 ± 0.003	0.08 ± 0.002	0.34
	4	38331	69312	217490	332180	12205	-	0	0.13 ± 0.001	0.11 ± 0.001	0.04 ± 0.001	0.32
	5	80967	5948.8	227390	386350	26237	45807	-36176	0.10 ± 0.004	0.21 ± 0.005	0.07 ± 0.002	0.22

Table 4.7: Deviance information criterion (DIC) values of production and lifetime in all the models

Traits	Model 1	Model 2	Model 3	Model 4	Model 5
FL305MY	26893.71	-	24594.01	25185.07	25114.49
TMY	97719.37	91452.90	91447.39	91455.82	91448.38
LL	70217.23	70116.24	70122.67	70121.60	70125.17
PY	25790.80	25739.46	25742.12	25743.38	25743.29
PL	9655.61	-	9650.67	9646.35	9641.54
305MYAP	92261.30	91452.90	91447.39	91455.82	91448.38

Table 4.8: Best fit models for production and lifetime traits under study

S. No.	Traits	Best fit model	Variance components
1	FL305MY	3	$Y=Xb + Z_{1a} + Z_{2m} + e, \text{Cov}_{(a,m)} = A\sigma_{am}$
2	TMY	3	$Y=Xb + Z_{1a} + Z_{2m} + e, \text{Cov}_{(a,m)} = A\sigma_{am}$
3	LL	2	$Y= Xb + Z_{1a} + Z_{2pe} + e$
4	PY	2	$Y= Xb + Z_{1a} + Z_{2pe} + e$
5	PL	5	$Y= Xb + Z_{1a} + Z_{2m} + Z_{3mpe} + e, \text{Cov}_{(a,m)}=A\sigma_{am}$
6	305MYAP	3	$Y=Xb + Z_{1a} + Z_{2m} + e, \text{Cov}_{(a,m)} = A\sigma_{am}$

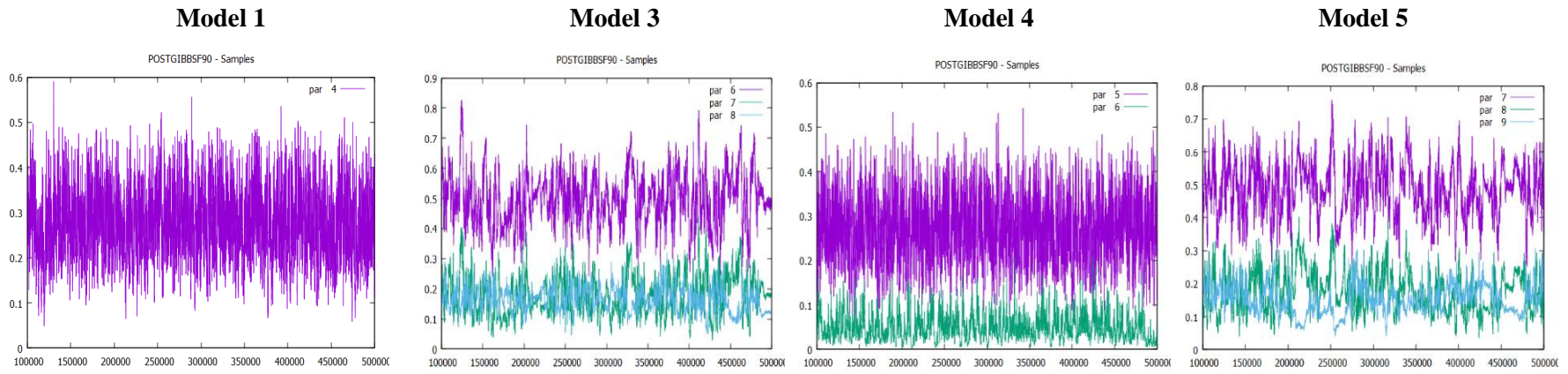


Figure 4.1 (A): Trace plots of FL305MY in various models

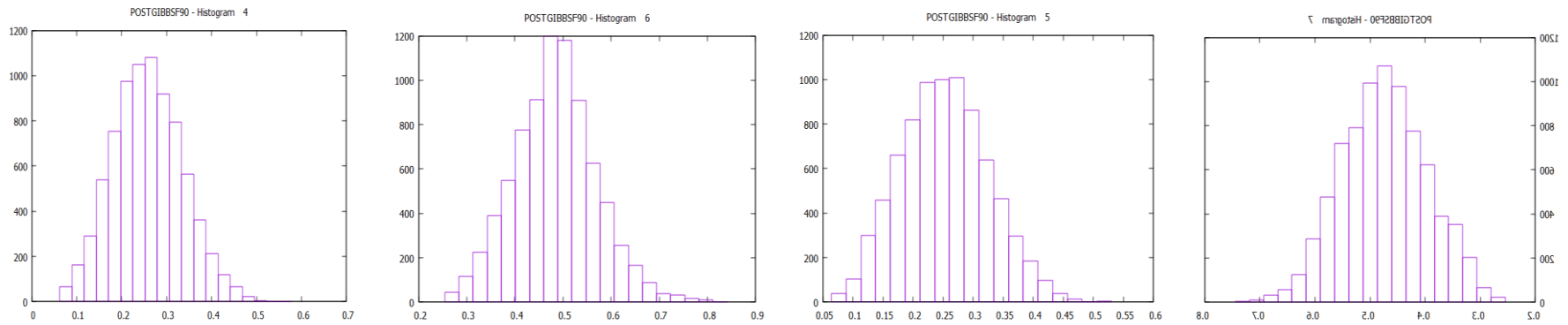


Figure 4.1 (B): Histograms of FL305MY in various models

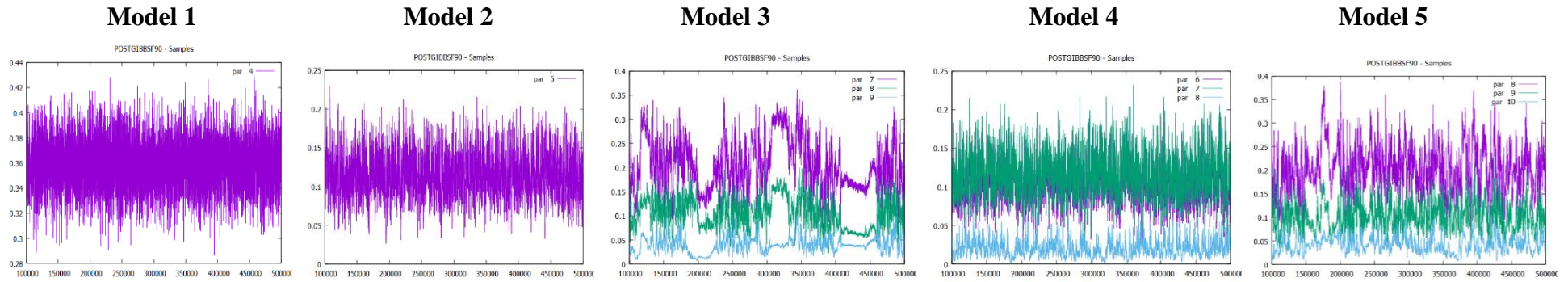


Figure 4.2 (A): Trace plots of TMY in various models

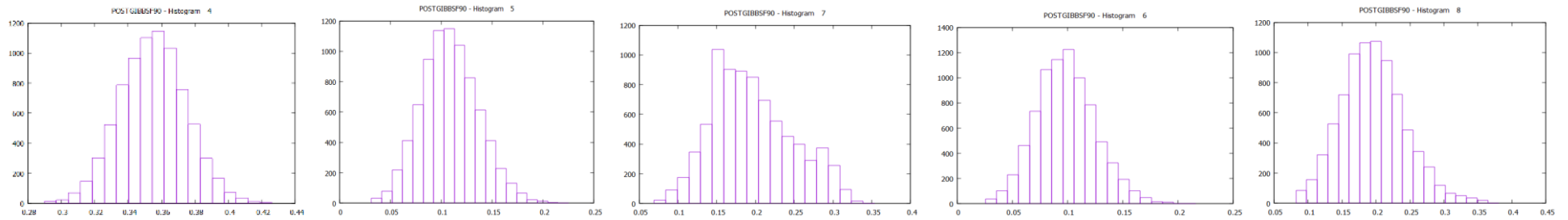


Figure 4.2 (B): Histograms of TMY in various models

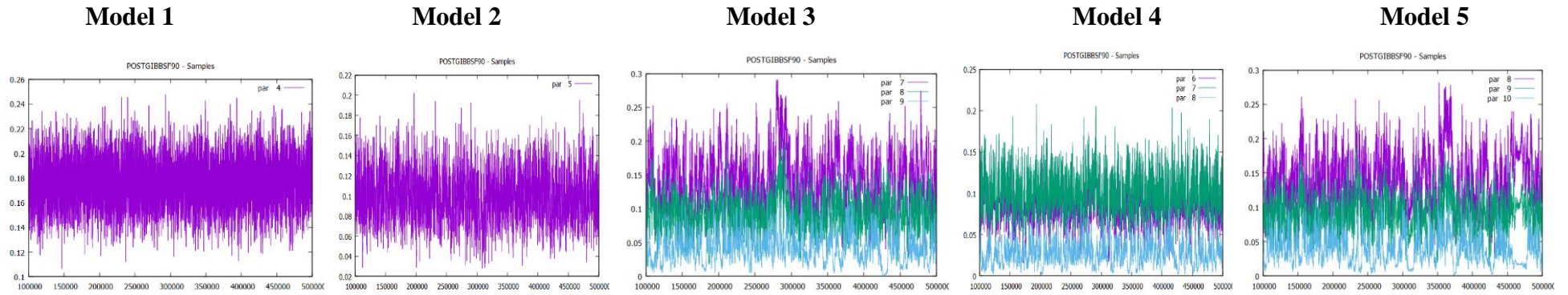


Figure 4.3 (A): Trace plots of LL in various models

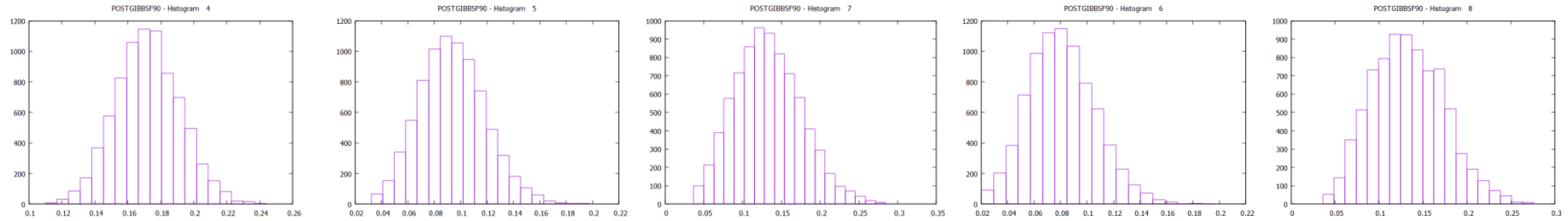


Figure 4.3 (B): Histograms of LL in various models

Model 1

Model 2

Model 3

Model 4

Model 5

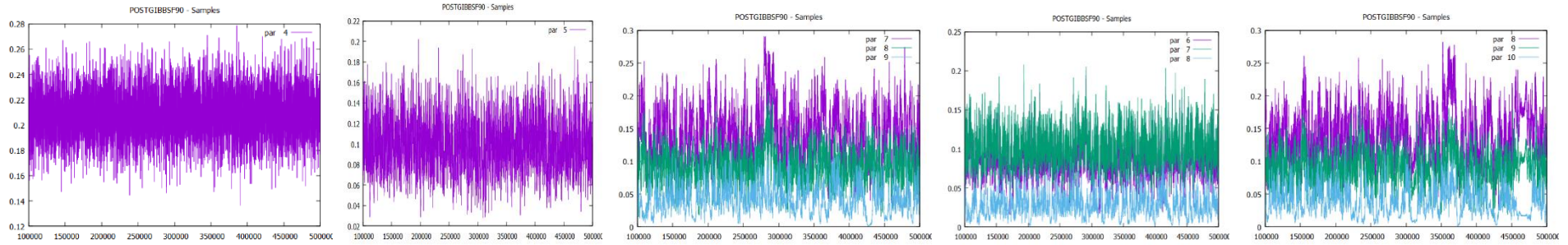


Figure 4.4 (A): Trace plots of PY in various models

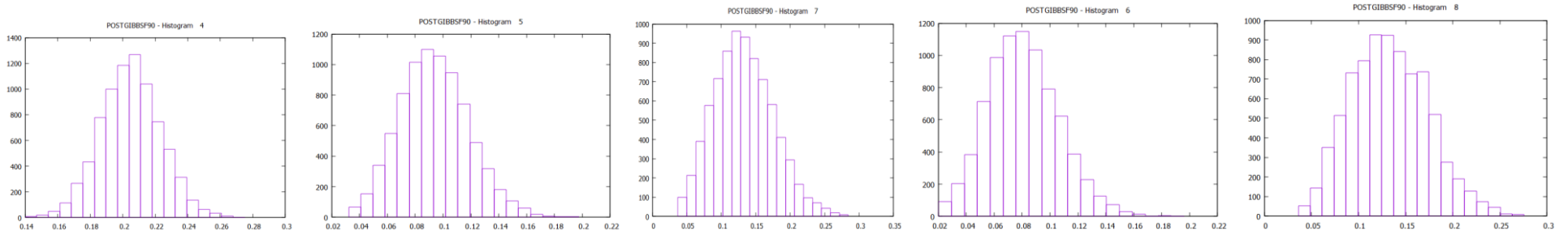


Figure 4.4 (B): Histograms of PY in various models

Model 1

Model 3

Model 4

Model 5

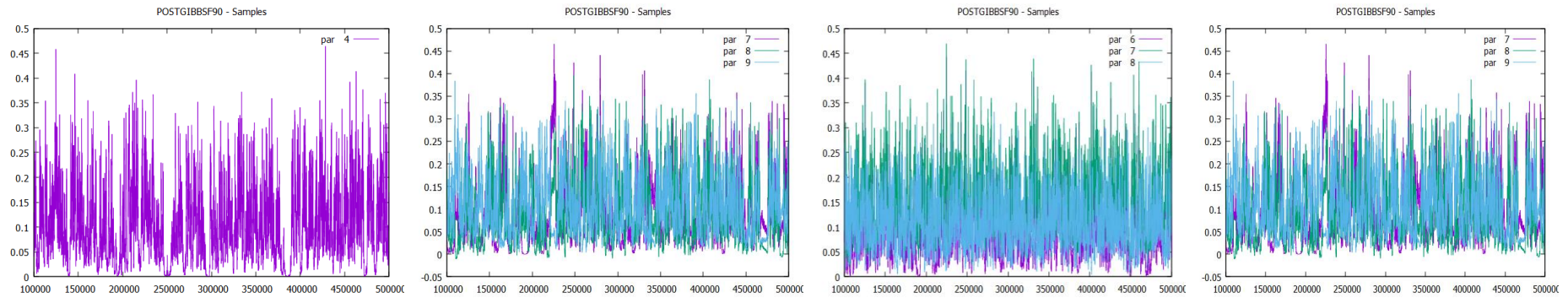


Figure 4.5 (A): Trace plots of PL in various models

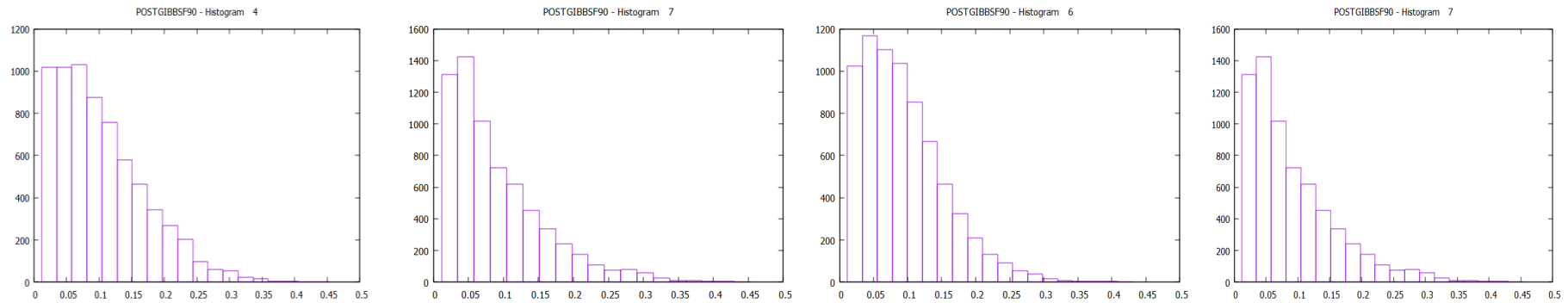


Figure 4.5 (B): Histograms of PL in various models

*skewness is observed in these histograms of PL may be due to the small sample size of the data as compared to other traits for the assumed number of iterative cycles which is not able to reflect the normal distribution of this trait in the population.

Model 1

Model 2

Model 3

Model 4

Model 5

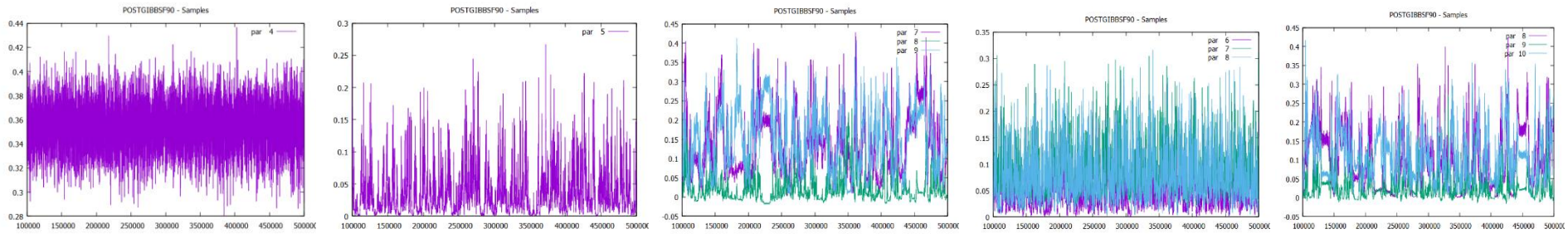


Figure 4.6 (A): Trace plots of 305MYAP in various models

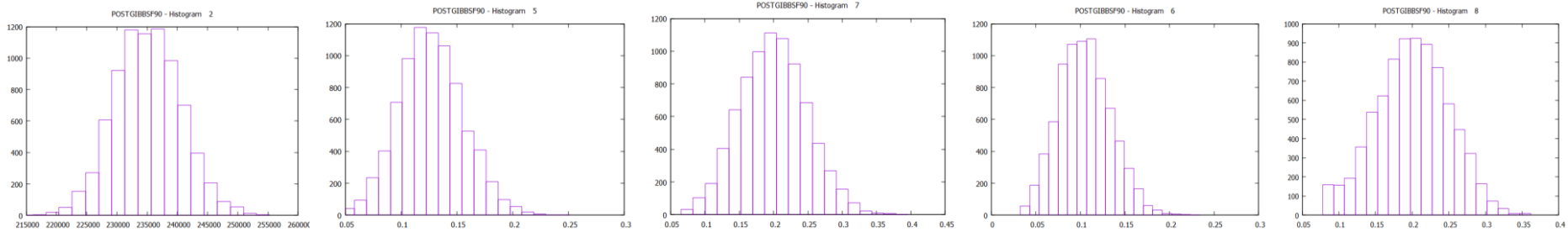


Figure 4.6 (B): Histograms of 305MYAP in various models

4.5 Breeding value estimation

Considering sires with more than three progenies, there were a total of 175-294 sires for analysis, depending on the traits under evaluation that were analysed in the study. First, AIREML method was used to estimate the breeding values of sires, and then the Bayesian approach was used with animal model in both the approaches. Banik and Gandhi (2006), Singh and Singh (2011) compared animal model with conventional methods for estimation of breeding values in Sahiwal and crossbred cattle. In this study, both methodologies ranked sires from 1 to 175-295 according to breeding value, which varied depending on the approach. The following table provides the estimated breeding value for these sires using both methods (Table 4.10 and 4.11). The same sires achieved first rank using both methodologies. However, when sires' total rankings were compared using both methodologies, few fluctuations in sires' rankings were observed. As a result, it becomes important to compare the rankings obtained by these two approaches. To do so, the significance of the results was assessed using the t-test and the Spearman rank correlation.

The calculated rank correlation was around one, indicating a very strong correlation. Additionally, compared to the AIREML methodology, the Bayesian method estimates breeding values more precisely, making it more credible.

4.5.1 Comparison of sire ranks based on AIREML and Bayesian methods

Bajetha *et al.* (2015) compared estimated breeding values of crossbred cattle using simple daughter's average, least squares method and simplified regressed least squares (SLRS) method. Banik and Gandhi (2007) compared DFREML with conventional methods to evaluate Sahiwal sires. Kumar *et al.*, 2015 compared contemporary comparison (CC) method, least-squares (LS) method, simple regressed least-squares (SRLS) method and best linear unbiased prediction (BLUP) method in their study. Raja *et al.* (2012) compared least squares method (LSM), simple regressed least squares (SRLS), best linear unbiased prediction (BLUP), and the derivative-free restricted maximum likelihood (DFREML) for sire evaluation in Sahiwal cattle. In this study ranking of sires based on BLUP values was done by both the approaches and the results obtained from both the approaches were compared using the standard error predicted. The EBV range obtained from AIREML for FL305MY, TMY, LL, PY, PL, 305MYAP were 401.22 to -353.45, 409.02 to -348.61, 18.11 to -11.68, 1.37 to -1.05, 111.82 to -44.79, 393.55 to -341.42 respectively. The range of EBV obtained

from the Bayesian method were 404.40 to -359.87, 415.99 to -354.97, 20.43 to -13.23, 1.39 to -1.07, 221.89 to -93.03, and 398.19 to -345.56 respectively for the above-mentioned traits respectively as shown in Table 4.8.

4.6 Spearman rank correlation

Ranking of sires was done through both the approaches and through Spearman's rank correlation values it was evident that there is not much difference in the ranking of sires by both these approaches as correlation was near to one for all the production and lifetime traits shown in Table 4.12.

4.7 Accuracy of the estimated breeding values

The accuracy (r) and the reliability were estimated from standard error predicted. Both values for all the traits and in both the methods are shown in Table 4.12. The accuracy of estimated breeding value is slightly better with the Bayesian methods as compared to the AIREML for production and lifetime traits in Murrah buffalo. Table 4.12 illustrates the accuracy, reliability and efficiency per cent of Bayesian method over AIREML.

Table 4.9: Range of Breeding Values of sires estimated from AIREML and Bayesian approach

S. No.	Traits	Method	Model (AM)	Herd Mean	No. of Sires	EBV	
				L.S.M \pm S. E		Max.	Min.
1	FL305MY	AIREML	Direct Additive Genetic	1962.93 \pm 60.69kg	151	401.22	-353.45
		Bayesian				404.40	-359.87
2	TMY	AIREML	Repeatability	2156.24 \pm 15.81 kg	245	409.02	-348.61
		Bayesian				415.99	-354.97
3	LL	AIREML	Repeatability	303.66 \pm 1.67 days	250	18.11	-11.68
		Bayesian				20.43	-13.23
4	PY	AIREML	Repeatability	11.99 \pm 0.05 kg	239	1.39	-1.05
		Bayesian				1.39	-1.07
5	PL	AIREML	Direct Additive Genetic	1704.08 \pm 35.22 days	139	111.82	-44.79
		Bayesian				221.89	-93.03
6	305MYAP	AIREML	Repeatability	2104.82 \pm 12.91 kg	175	393.55	-341.42
		Bayesian				398.19	-345.56

*Model (AM)=Animal model

Table 4.10: Best 10 sires for the traits FL305MY, TMY, LL

Rank	FL 305 MY		Sire IDs	TMY		Sire IDs	LL		Sire IDs
	AIREML	Bayesian		AIREML	Bayesian		AIREML	Bayesian	
1	401.22	404.40	2338	409.02	415.99	2704	18.11	20.43	2699
2	387.5	391.46	5054	397.35	405.16	4245	13.97	15.72	2583
3	355.54	373.51	2666	309.36	316.67	5054	13.06	15.02	4244
4	342.56	370	652	307.27	313.57	2336	12.95	14.85	4915
5	330.78	349	2801	268.97	274.09	452	11.13	12.33	452
6	315.56	327.30	6136	253.86	257.23	4523	10.6	11.89	594
7	286.45	306.65	2321	251.24	256.72	2583	9.50	10.89	4506
8	259.48	282.37	594	203.23	208.17	594	9.13	10.31	2670
9	240.89	278.76	1538	185.057	188.07	478	8.36	9.53	2338
10	205.23	265.73	4244	179.34	183.30	2666	8.21	9.50	1746

Table 4.11: Best 10 sires for the traits PY, PL, 305MYAP

Rank	PY		Sire IDs	PL		Sire IDs	305MYAP		Sire IDs
	AIREML	Bayesian		AIREML	Bayesian		AIREML	Bayesian	
1	1.37	1.39	82	111.82	221.89	888	393.55	398.19	1749
2	1.16	1.18	2583	62.08	136.19	1944	315.16	319.53	1867
3	0.86	0.88	988	58.84	117.21	2321	247.27	249.71	3226
4	0.72	0.74	594	43.77	86.71	2921	224.47	227.24	1538
5	0.67	0.69	4244	40.02	85.61	AL-5	215.89	219.62	2801
6	0.67	0.68	6044	39.98	83.87	96	192.98	195.61	3098
7	0.65	0.66	3255	35.82	71.57	34	192.23	195.09	3930
8	0.60	0.61	2801	32.54	67.7	ND1	190.92	193.58	3609
9	0.54	0.56	652	32.19	67.61	2848	186.85	190.77	1689
10	0.53	0.54	6136	30.98	67.43	658	185.38	188.44	3551

Table 4.12: Accuracy, reliability and efficiency of Bayesian method over AIREML

S. No	Trait	Method	Model (AM)	Spearman's Rank Correlation	Accuracy	Reliability	Efficiency (%)
1	FL305MY	AIREML	Direct Additive Genetic	1.00	0.562	0.317	0.73
		Bayesian			0.567	0.321	
2	TMY	AIREML	Repeatability	1.00	0.416	0.194	1.2
		Bayesian			0.421	0.198	
3	LL	AIREML	Repeatability	1.00	0.279	0.091	7.2
		Bayesian			0.299	0.104	
4	PY	AIREML	Repeatability	1.00	0.409	0.168	1.20
		Bayesian			0.414	0.172	
5	PL	AIREML	Direct Additive Genetic	0.99	0.186	0.035	42.94
		Bayesian			0.266	0.071	
6	305MYAP	AIREML	Repeatability	0.99	0.161	0.026	0.78
		Bayesian			0.207	0.043	

*Model (AM)=Animal model

CHAPTER -5

Summary and Conclusion

Summary and Conclusion

The present study was conducted using phenotypic records of production performance of Murrah buffaloes maintained at Livestock Research Centre of ICAR -National Dairy Research Institute, Karnal. The objectives were to estimate covariance components for production and lifetime traits using the repeatability model and to compare AIREML and Bayesian approach for ranking sires for production and lifetime traits. The data was collected and compiled from the record room of the Animal Genetics and Breeding division. Data of production traits throughout the lifetimes of the animals was recorded, spanning 50 years i.e., from 1971 to 2020. The data recorded were then classified into various categories of seasons of birth/calving (4), periods of birth/calving (5), parities of dams (5), and age at first calving (3). The data were normalised by removing records of abnormal lactation, lactation length less than 100 days, milk yield less than 500 kg, and then data for individual traits were standardised with mean $\pm 2\sigma$ (standard deviation) to remove the outliers. Least squares analysis was applied using different equations depending upon the trait for the assessment of non-genetic factors using Harvey (1990). Data were adjusted for significant non-genetic factors. The overall least squares mean obtained for FL305MY, TMY, LL, PY, PL, and 305MYAP were 1962.63 ± 60.69 kg, 2156.24 ± 15.81 kg, 303.66 ± 1.67 days, 11.99 ± 0.053 kg, 1774.85 ± 35.22 days and 2104.82 ± 12.91 kg, respectively.

For genetic parameters estimation, fixed effects taken in the study were the season of calving (season of birth for lifetime traits), period of calving (period of birth for lifetime traits), number of parities of the dam, and age at first calving for all traits except FL305MY, because for this trait non-genetic factors taken were season of calving, period of calving and age at first calving. The random effects included were the additive genetic effect of the animal, permanent environment effect of the animal, maternal genetic effect, and maternal permanent environment effect depending upon the type of traits. The Bayesian approach using MCMC and Gibbs sampling was used with a univariate animal model in the BLUPF90 family of programmes. Based on the partition of variance, five models were used for the estimation of genetic parameters with and without the combination of maternal effects and their covariance with the additive genetic effects of the animal. The number of Markov chain iterative runs used in GIBBS1F90 was 500,000 for all the traits with a burn-in length of 50,000 and every 50th iteration was saved (thinning interval). In POSTGIBBSF90 again 50,000 burn-in lengths were used with every 50th iteration being saved.

The convergence of statistical models where it is assumed that the data followed inverse Wishart distribution was checked using Geweke diagnostics and autocorrelations values which were nearer to zero and visual inspection of trace plots did not form any trend in most of the trace plots and histograms obtained through Gnu plot, which were bell-shaped curves mostly. Deviance Information Criterion (DIC) estimates were used to determine the best-fit models for each trait. The genetic parameters estimated were additive genetic variance, the permanent environmental variance of the animal, total residual variance, total phenotypic variance, maternal genetic effect variance, maternal permanent environment variance, the covariance between additive genetic effects of the animal and maternal genetic effects, direct heritability, total heritability and repeatability of the traits. The direct heritability estimates obtained in best models for FL305MY, TMY, LL, PY, PL, 305MYAP were 0.49 ± 0.007 , 0.20 ± 0.011 , 0.04 ± 0.001 , 0.10 ± 0.001 , 0.10 ± 0.009 and 0.21 ± 0.003 , respectively. The traits for which the best models are models with maternal effects such as FL305MY, TMY, PL, and 305MYAP are having total heritability as 0.17 ± 0.006 , 0.10 ± 0.007 , 0.09 ± 0.007 , and 0.10 ± 0.001 , respectively. The best models for traits LL and PY are models with permanent environmental effects of the animal along with the additive genetic effects of the animal.

The breeding values of sires were estimated from two approaches which are AIREML and Bayesian using BLUP methodology in a mixed model equation. The software used were RENUMF90, AIREMLF90, BLUPF90 and WOMBAT. The accuracy and reliability of EBV were found using the standard error predicted. The EBV range obtained from AIREML for FL305MY, TMY, LL, PY, PL, 305MYAP were 401.22 to -353.45, 409.02 to -348.61, 18.11 to -11.68, 1.37 to -1.05, 111.82 to -44.79, 393.55 to -341.42, respectively. The range of EBV obtained from the Bayesian method is 404.40 to -359.87, 415.99 to -354.97, 20.43 to -13.23, 1.39 to -1.07, 221.89 to -93.03, and 398.19 to -345.56 for the above-mentioned traits respectively. Ranking of sires was done through both approaches; through Spearman's rank correlation values it was evident that there is not much difference in the ranking of sires by both approaches. The accuracy and reliability estimates show that the accuracy is slightly better with the Bayesian approach when it comes to the estimation of breeding values. The efficiency of breeding value estimation for FL305MY, TMY, LL, PY, PL, and 305MYAP were 0.73, 1.2, 7.2, 1.2, 42.94, and 0.78 percent over AIREML approach.

Based on the results mentioned above, the following conclusions can be drawn from this study:

- For evaluating genetic parameters for traits such as FL305MY, TMY, and 305MYAP, the best fit model is the model with maternal genetic effect as well as covariance with the additive genetic effect of the animal.
- For evaluating genetic parameters for traits such as LL and PY, the best fit model is the model with the permanent environment effect of the animal.
- For PL, the best fit model is the model which includes maternal genetic effect and maternal permanent environmental effects with covariance between the additive genetic effect of the animal and maternal genetic effects.
- The rank correlation between ranks obtained through Bayesian and AIREML are significantly correlated.
- The BV estimation from both methods yields almost the same results in terms of sire ranking as all the traits under study are normally distributed production traits.
- Bayesian method of estimating BV provides slightly better accuracy as compared to AIREML.

Recommendations

1. For genetic parameters estimation of production traits of Murrah buffalo, a statistical model with the inclusion of maternal genetic effects may be considered.
2. Based on the high heritability of FL305MY, this trait can be used for selection of animals at the early phase of productive life for production performance.
3. Bayesian method can be used to estimate the breeding values of Murrah sires for production traits, which in turn can be used for ranking and selection of bulls.

Bibliography

Bibliography

- 20th Livestock Census All India Report (2019). Ministry of animal husbandry, dairying and fisheries. Ministry of Agriculture, Government of India. www.dahd.nic.in
- Ahmad, S.F., Gaur, G.K., Panda, S., Chauhan, A., Dutt, T., and Bhushan, B. (2022). Bayesian analysis reveals the influence of maternal effect on pre-weaning body weights in Landilly piglets. *Zygote*:1-8.
- Ahmad, S.F., Khan, N.N., Chakraborty, D., Rather, M.A., Shanaz, S., Alam, S. and Ganai, N. A. (2021). Estimation of (co)variance components and genetic parameters of fibre traits in Rambouillet sheep using multi-trait analysis. *Tropical Animal Health and Production*, **53**(1): 190.
- Ahmad, Z., P.J. Berger and M.H. Healey. (1992). Age specific probabilities of culling under different culling criteria in Nili- Ravi buffalo. *Journal of Dairy Science*, **75**(6):1715-1724.
- Alli, A. Ahmad, Z. Mohiuddin, G. and Akhtar. P. (2000). Genetic and phenotypic parameter of some lifetime performance traits in Nili Ravi buffaloes. *Buffalo Bulletin*, **17**(1): 3-6.
- Annual report 2018-19 NDDB (National Dairy Development Board), (www.nddb.coop).
- Arpanahi, R., Hosseini, F., Karimi, O. and Javaheri, N. (2018). Analysis of livestock data using approximate Bayesian computation approach. Proceedings of the World Congress on Genetics Applied to Livestock Production.
- Ashida, I., and Iwaisaki, H. (1998). A numerical technique for REML estimation of variance components using average information algorithm and its computing property. *Animal Science and Technology*, **69**: 631-636.
- Aspilcueta-Borquis, R.R., Di Palo, R., Araujo Neto, F.R., Baldi, F., De Camargo, G.M.F., Albuquerque, L.G.D., Zicarelli, L. and Tonhati, H. (2010). Genetic parameter estimates for buffalo milk yield, milk quality and mozzarella production and Bayesian inference analysis of their relationships. *Genetics and Molecular Research*, **9**(3): 1636-1644.
- BAHS. (2019). Basic Animal Husbandry Statistics. Department of Animal Husbandry, Dairying and Fisheries. Ministry of Agriculture, Government of India.
- Bajetha, G., Singh, C.V., and Barwal, R.S. (2015). Sire evaluation by different methods in crossbred cattle. *American Advances Journal of Natural Sciences*, **1**(1): 22-26.
- Banik, S. (2001). Direct and indirect effects of different characters of Murrah buffaloes- A path analysis approach. M.Sc. Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India.

- Banik, S. and Gandhi, R.S. (2006). Animal model versus conventional models of sire evaluation in Sahiwal cattle. *Asian-Australasian Journal of Animal Sciences*, **19**(9): 1225–1228.
- Banik, S. and Gandhi, R.S. (2007). Effectiveness of DFREML versus conventional methods of Sahiwal sire evaluation. *Indian Journal of Animal Sciences*, **77** (11): 1143
- Bashir, M.K., Khan, M.S., Bhatti, S.A., and Iqbal, A. (2007). Lifetime performance of Nili-Ravi buffaloes in Pakistan. *Asian-Australasian Journal of Animal Sciences*, **20**(5): 661-668.
- Blasco, A. The Bayesian controversy in animal breeding. (2001). *Journal of Animal Sciences*, **79**(8): 2023-2046.
- Breda, F.C., Albuquerque, L.G.D., Euclides, R.F., Bignardi, A.B., Baldi, F., Torres, R.A., and Tonhati, H. (2010). Estimation of genetic parameters for milk yield in Murrah buffaloes by Bayesian inference. *Journal of Dairy Science*, **93**(2): 784-791.
- Cady, R.A., Shah, S.K., Schermerhorn, E.C., and McDowell, R.E. (1983). Factors affecting performance of Nili-Ravi buffaloes in Pakistan. *Journal of Dairy Science*, **66**(3): 578-586.
- Carneiro Júnior, J.M., Assis, G.M.L.D., Euclides, R.F., Torres, R.D.A., and Lopes, P.S. (2007). Estimation of variance components using Bayesian and frequentist inferences considering simulated data under heterogeneity of variance. *Revista Brasileira de Zootecnia*, **36**(5): 1539-1548.
- Chakraborty, D., Dhaka, S.S., Pander, B.L., Yadav, A.S., Singh, S., and Malik, P.K. (2010). Prediction of lactation milk yield from test day records in Murrah buffaloes. *Indian Journal of Animal Sciences*, **80**(3): 244-245.
- Chander, R. (2002). Prediction of the breeding value of sires for lifetime performance traits in Murrah buffaloes. Ph.D. Thesis submitted at Haryana Agricultural University, Hisar.
- Chikara, S., Narendra, S., and Dhaka, S.S. (1994). Factors influencing lactation milk yield in Murrah buffaloes. *Indian Journal of Animal Sciences*, **28**(1): 43-46.
- Chitra, A., Jain, A., Kumar, M., Ratwan, P., and Gupta, A.K. (2018). Effect of genetic and non-genetic factors on milk yield and milk composition traits in Murrah buffaloes. *Indian Journal of Animal Research*, **52**(2): 304-308.
- Cooney, C.A. (2006). Maternal nutrition: nutrients and control of expression. *Nutritional Genomics. Discovering the Path to Personalized Nutrition*: 219-254.
- Croiseau, P., Guillaume, F., and Fritz, S. (2012). Comparison of genomic selection approaches in Brown Swiss within Intergenomics. *Interbull Bulletin*: (46).

- Dahiya, S.P., Kumar, M., and Dhillod, S. (2020). Relationship of linear type traits with production and reproduction performance in Murrah buffaloes. *Indian Journal of Animal Sciences*, **90**(6): 942-946.
- Dass, G. (1995). Studies on prediction of lactation yield based on test-day values in buffaloes. Ph.D. thesis submitted at ICAR-National Dairy Research Institute, Karnal, India.
- Dass, G., and Sharma, R.C. (1994). Factors affecting milk production in Murrah buffaloes. *Indian Journal of Animal Research*, **28**: 61-64.
- de Villemereuil, P. (2019). On the relevance of Bayesian statistics and MCMC for animal models. *Journal of Animal Breeding and Genetics*, **136**(5): 339-340.
- Dev, K., Dhaka, S.S., and Yadav, A.S. Manjeet. (2017). Estimates of genetic and phenotypic trends considering early and lifetime performance traits in Murrah buffaloes. *International Journal of Agricultural Science and Research*, **7**: 225-230.
- Dhara, S.K. (1994). Prediction of breeding value of milk production by multiple regression and principal component analysis in Murrah buffaloes. M.Sc. Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India.
- Dubey, P.P., Singh, C.V., and Prasad, R.B. (2006). Relationship between sire's estimated breeding values for first lactation and life time traits and ranking of sires in Sahiwal and its cross. *Indian Journal of Animal Sciences*, **76**(10).
- Dutt, T.R and Taneja, V. K. (1994). Phenotypic and genetic parameters of age of first calving, first lactation, milk yield and some measures of efficiency of production in Murrah buffaloes. *Indian Journal of Animal Sciences (India)*.
- Dutt, T., Bhushan, B., and Kumar, S. (2001). First lactation and lifetime performance traits in Murrah buffaloes. *Indian Journal of Animal Sciences*, **71**(5): 483-484.
- El-Arian. (1986). Genetic analysis of Murrah buffalo herd. Ph.D. Thesis submitted at Kurukshetra University, Kurukshetra, Haryana, India.
- Estimated livestock population breed wise (2013), DAHD. <https://dahd.nic.in/sites/default/files/Breeding%20Survey%20Book%20-%20Corrected.pdf>
- Faria, C.U.D., Magnabosco, C.D.U., Reyes, A.D.L., Lôbo, R.B., Bezerra, L.A.F., and Sainz, R.D. (2007). Bayesian inference in a quantitative genetic study of growth traits in Nelore cattle (*Bos indicus*). *Genetics and Molecular Biology*, **30**(3): 545-551.
- Gajbhiye, P.U. (1987). Evolving restricted indices for selection of buffaloes. Ph.D. Thesis submitted at Kurukshetra University, Kurukshetra, Haryana, India.

- Geetha, E. (2005). Studies on breeding values for persistency in Murrah buffaloes. M.Sc. Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India.
- Geman, S., and Geman, D. (1984). Stochastic relaxation, Gibbs distributions, and the Bayesian restoration of images. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, **6**(6): 721-741.
- Gianola, D., and Fernando, R.L. (1986). Bayesian methods in animal breeding theory. *Journal of Animal Science*, **63**(1): 217-244.
- Gianola, D., and Foulley, J.L. (1982). Non-linear prediction of latent genetic liability with binary expression: an empirical Bayes approach. Proc. 2nd World Congress on Genetics Applied to Livestock Production, **7**: 293-303.
- Gilmour, A.R., Thompson, R., and Cullis, B.R. (1995). Average information REML: an efficient algorithm for variance parameter estimation in linear mixed models. *Biometrics*, **51**(40): 1440-1450.
- Godara, A., Singh, D., and Dhaka, S.S. (2015). Genetic parameters among lactational performance traits in Murrah buffaloes. *Indian Journal of Animal Research*, **49**(5): 579-584.
- Gowane, G.R., Chopra, A., Prakash, V., and Prince, L.L.L. (2014). The role of maternal effects in sheep breeding: a review. *The Indian Journal of Small Ruminants*, **20**(1): 1-11.
- Gujral, S. (2021). Genetic evaluation of production and fertility traits in Karan Fries cattle. M.V.Sc Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India.
- Gupta, J.P. (2009). Evolving selection criteria using growth and production traits in Murrah buffaloes. M.V.Sc. Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India
- Gupta, J.P., Sachdeva, G.K., Gandhi, R.S., and Cahkaravarty, A.K. (2012). Non-genetic factors influencing growth and production performance in Murrah buffaloes. *Indian Journal of Dairy Science*, **65**(3): 252-255.
- Gupta, J.P., Sachdeva, G.K., Gandhi, R.S., and Chakaravarty, A.K. (2015). Developing multiple-trait prediction models using growth and production traits in Murrah buffalo. *Buffalo Bulletin*, **34**(3): 347-355.
- Harvey, W.R. 1990. User guide for LSMLMW and MIXMDL package. Mix model least squares and maximum likelihood computer programme, PC-2 version, Mimeograph, Columbia, Ohio, USA.

- Hatwar, R.K., and Chawla, D.S. (1988). Least-square means of various 1st lactation traits and milk constituents of Murrah buffalos. *Indian Journal of Animal Sciences*, **58**(8): 988-990.
- Ipe, S., and Nagarcenkar, R. (1992). Estimation of heritabilities and correlations of partial and 300 days first lactation milk yield in Murrah buffaloes. *Journal of Dairying, Foods and Home Sciences*, **11**: 43-49.
- Jain, A., and Sadana, D.K. (1998). A comparison of the heritability estimates obtained from least-squares ANOVA and REML methods. *Indian Journal of Animal sciences*, **68**(9): 942-945.
- Jain, A.K. (2009). Analysis of factors affecting milk production traits of Murrah buffaloes over different lactations. *Indian Journal of Dairy Science*, **62**(5): 381-385.
- Jakhar, V., Vinayak, A.K., and Singh, K.P. (2016). Genetic evaluation of performance attributes in Murrah buffaloes. *Haryana Veterinarian*, **55**(1): 66-69.
- Jakhar, V., Yadav, A.S., and Dhaka, S.S. (2017). Estimation of genetic parameters for production and reproduction traits in Murrah Buffaloes. *International Journal of Current Microbiology and Applied Sciences*, **6**(11): 4297-4303.
- Jamuna, V. (2012). Impact of progeny testing program on lifetime fertility and lifetime milk yield in Murrah buffaloes, M.V.Sc. Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India
- Jamuna, V., Chakravarty, A.K., Singh, A., and Patil, C.S. (2015). Genetic parameters of fertility and production traits in Murrah buffaloes. *Indian Journal of Animal Research*, **49**(3): 288-291.
- Jamuna, V., Gupta, A.K., Chakravarty, A.K., and Mir, M.A. (2017). Estimation of genetic parameters for milk composition traits in Indian Murrah buffaloes. *Advances in Animal and Veterinary Sciences*, **5**(5): 229-233.
- Jamuna, V., Gupta, A.K., Chakravarty, A.K., Singh, A., Patil, C.S., Kumar, M., and Vohra, V. (2016). Leptin gene polymorphism in association with Lactation milk yield in Murrah Buffaloes. *Indian Journal of Animal Sciences*, **86**(1): 95-97.
- Jensen, J., Mantysaari, E.A., Madsen, P., and Thompson, R. (1997). Residual maximum likelihood estimation of (co) variance components in multivariate mixed linear models using average information. *Journal of the Indian Society of Agricultural Statistics*, **49**(1): 215-236.
- Johnson, D.L., and Thompson, R. (1995). Restricted maximum likelihood estimation of variance components for univariate animal models using sparse matrix techniques and average information. *Journal of Dairy Science*, **78**(2): 449-456.

- Kalsi, J.S., and Dhillon, J.S. (1982). Performance of buffaloes in first three lactations. *Indian Journal of Dairy Science*, **35**(2): 213-215.
- Kapil, D., Dhaka, S.S., Yadav, A.S., and Sangwan, S.K. (2015). Genetic parameters of early performance traits in Murrah buffaloes. *Haryana Veterinarian*, **54**(2): 144-146.
- Katneni, V.K. (2007). Studies on genetic persistency of milk production in Murrah buffaloes. Ph.D. Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India.
- Kaur, R., Malhotra, P., Kashyap, N., Dash, S.K., and Kaur, S. (2020). Analysis of different non-genetic factors affecting production performance of Murrah buffaloes. *Indian Journal of Animal Research*, **54**(4): 517-519.
- Kour, G., and Narang, R. (2021). Estimates of genetic parameters of economic traits in murrah buffaloes: Genetic Parameters of Economic Traits in Murrah Buffaloes. *Journal of AgriSearch*, **8**(2): 173-176.
- Krag, K., Poulsen, N.A., Larsen, M.K., Larsen, L.B., Janss, L.L., and Buitenhuis, B. (2013). Genetic parameters for milk fatty acids in Danish Holstein cattle based on SNP markers using a Bayesian approach. *BMC Genetics*, **14**(1): 1-10.
- Kumar, A., Rana, Z.S., Dhaka, S.S., Dalal, D.S., Singh, S., and Sethi, R.K. (2002). Test day yield and lactation parameters of Murrah buffaloes. 7th World Congress on Genetics Applied to Livestock Production: 19-23.
- Kumar, D., Singh, H., Kumar, D., and Singh, C.V. (2003). Non-genetic factors affecting some production and reproduction traits in Murrah buffaloes. *Indian Journal of Animal Research*, **37**(1): 24-27.
- Kumar, M. (2021). Strategy for multi-trait selection based on production, reproduction and functional traits in Murrah Buffaloes. Ph.D. Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India.
- Kumar, M., Vohra, V., Ratwan, P., Chopra, A., and Chakaravarty, A.K. (2017). Influence of FASN gene polymorphism on milk production and its composition traits in Murrah buffaloes. *Indian Journal of Animal Research*, **51**(4): 640-643.
- Kumar, V., Chakravarty, A.K., Patil, C.S., Shivahre, P.R., and Gupta, A. (2015). Comparison among different conventional methods of sire evaluation in Murrah buffalo. *Indian Journal of Animal Sciences*, **85**(6): 670-673.
- Kundu, S., Pandey, R.S., and Singh, S.K. (2003). Non-genetic factors affecting some reproductive traits in Murrah buffaloes. *Indian Journal of Animal Sciences*, **73**(8): 928-29.

- Lathwal, S.S. 2000. Optimum levels of economic traits for maximizing the profit function in Murrah buffaloes. Ph.D. Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India.
- Lopes, F.B., Ferreira, J.L., Lôbo, R.B., and Rosa, G.J.M. (2017). Bayesian analyses of genetic parameters for growth traits in Nelore cattle raised on pasture. *Genetics and Molecular Research*, **16**(3): 1-10.
- Maestriperi, D. (2009). The role of maternal effects in mammalian evolution and adaptation. Maternal effects in mammals. *University of Chicago Press*: 1-11.
- Magnabosco, C.D.U., Lôbo, R.B., and Famula, T.R. (2000). Bayesian inference for genetic parameter estimation on growth traits for Nelore cattle in Brazil, using the Gibbs sampler. *Journal of Animal Breeding and Genetics*, **117**(3): 169-188.
- Masuda, Y. (2018). Introduction to BLUPF90 Suite Programs. University of Georgia.
- Mendes Malhado, C.H., Mendes Malhado, A.C., Amorim Ramos, A., Souza Carneiro, P.L., Siewerdt, F., and Pala, A. (2012). Genetic parameters by Bayesian inference for dual purpose Jaffarabadi buffaloes. *Archives Animal Breeding*, **55**(6): 567-576.
- Meyer, K. (2007). WOMBAT—A tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). *Journal of Zhejiang University Science B*, **8**(11): 815-821.
- Meyer, K. (2008). Estimation of genetic parameters: it takes three to tango. *Journal of Animal Breeding and Genetics*. **125**(6): 361-362.
- Meyer, K., and Smith, S.P. (1996). Restricted maximum likelihood estimation for animal models using derivatives of the likelihood. *Genetics Selection Evolution*, **28**(1): 23-49.
- Milk and dairy products in human nutrition (2013), FAO.
<https://www.fao.org/3/i3396e/i3396e>
- Misztal, I. (2002). BLUPF90 family of programs. <http://num.ads.uga.edu/pub/blupf90/>
- Misztal, I., Tsuruta, S., Lourenco, D.A.L., Masuda, Y., Aguilar, I., Legarra, A., and Vitezica, Z. (2018). Manual for blupf90 family of programs. University of Georgia.
- Morrissey, M.B., de Villemereuil, P., Doligez, B., and Gimenez, O. (2014). Bayesian approaches to the quantitative genetic analysis of natural populations. *Quantitative genetics in the wild*: 228-253.
- Mosharraf, R., Shodja, J., Bohlouli, M., Alijani, S., and Rafat, S.A. (2014). Estimation of (co) variance components and breeding values for test-day milk production traits of holstein dairy cattle via bayesian approach. *Biotechnology in Animal Husbandry*, **30**(1): 15-28.

- Nath, M. (1998). Evaluation of breeding value in Murrah buffaloes by various methods. M.Sc. Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India.
- Pandey, H., Tomar, A.K.S., and Upadhyay, D. (2015). Effect of environmental factors on first lactation milk yield in Murrah buffaloes. *Buffalo Bulletin*, **34**(4): 459-64.
- Patil, C.S., Chakravarty, A.K., Kumar, V., Sharma, R.K., and Kumar, P. (2012). Average performance of various first lactation 305 day and test day milk yield in Murrah buffaloes. *Indian Journal of Animal Research*, **46**(3): 310-312.
- Patil, H.R., Dhaka, S.S., Yadav, A.S., and Patil, C.S. (2018). Comparison of genetic parameters of production efficiency and fertility traits in Murrah buffaloes. *International Journal of Advanced Biological Research*, **8**(1): 82-85.
- Patro, B.N., and Bhat, P.N. (1979). Inheritance of production traits in buffaloes. *Indian Journal of Animal Sciences*, **49**(1): 10-14.
- Prakash, A. (1984). Performance evaluation of Murrah buffalo herd. M.Sc. Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India
- Raheja, K.L. (1992). Selection free estimates of genetic-parameters of production and reproduction traits of 1st 3 lactations in Murrah buffalos. *Indian Journal of Animal Sciences*, **62**(2): 149-154
- Raja, T.V., and Gandhi, R.S. (2012). Comparison of different methods of sire evaluation in Sahiwal cattle. *Indian Journal of Animal Sciences*, **82**(5): 530-532.
- Registered buffalo breeds of India (2021), NBAGR.
<https://nbagr.icar.gov.in/en/new-breeds-lines>
- Rohilla, P.P., Chaudhary, S.R., and Sharma, R. (1992). Influence of various environmental factors on growth, reproduction and production of Murrah buffaloes. *Indian Journal of Animal Production and Management*, **8**(1): 235-239.
- Sahana, G. (1993). Association between productive and reproductive traits in Murrah buffaloes. M.Sc. Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India.
- Sahoo, S.K., Singh, A., Gupta, A.K., Chakravarty, A.K., Singh, M., and Ambhore, G.S. (2014). Estimation of genetic parameters of weekly test-day milk yields and first lactation 305-day milk yield in Murrah buffaloes. *Veterinary World*, **7**(12): 1094-1098.
- Seno, L.O., Cardoso, V.L., El Faro, L., Sesana, R.C., Aspilcueta-Borquis, R.R., De Camargo, G.M.F., and Tonhati, H. (2010). Genetic parameters for milk yield, age at first calving and interval between first and second calving in milk Murrah buffaloes. *Livestock Research for Rural Development*, **22**(2): 38.

- Shabade, N.S., Jagtap, D.Z., and Dehle, N.D. (1993). Factors affecting production and production efficiency traits of first lactation in Murrah buffaloes. *Indian Journal of Animal Sciences*, **63**(11): 1212-1213.
- Sharma, A. 1982. Breeding and selection methods for maximizing profit function in buffaloes. Ph.D. Thesis submitted at Kurukshetra University, Kurukshetra, Haryana, India.
- Sharma, R.C., and Singh, B.P. (1990). Genetic studies on Murrah buffaloes in livestock farms in Uttar Pradesh. In Proceedings of II World Buffalo Congress, *Genetics and breeding, digestive physiology and nutrition*, **2**: 128-133.
- Silva II, J.I.V., Eler, J.P., Ferraz, J.B.S., Golden, B.L., and Oliveira, H.N. (2003). Heritability estimate for stayability in Nelore cows. *Livestock Production Science*, **79**(1): 97-101.
- Singh, M. (2014). Genetic Analysis of test-day milk yields in Murrah buffaloes. M.V. Sc. Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India.
- Singh, M., Singh, A., Gupta, A.K., Dash, S.K., Shivahre, P.R., Sahoo, S.K., and Ambhore, G.S. (2016). Genetic parameters of 305 days and monthly test-day milk yields in Murrah buffaloes. *Indian Journal of Animal Sciences*, **86**(1): 55-60.
- Singh, S., Rathi, S.S., and Sangwan, M.L. (1990). Environmental variances affecting production efficiency in Murrah buffaloes. *Buffalo Journal*, **6**(1): 105-112.
- Singh, T.P., Singh, R., Singh, G., Das, K.S., and Deb, S.M. (2011). Performance of production traits in Nili-Ravi buffaloes. *Indian Journal of Animal Sciences*, **81**(12): 1231-1238.
- Singh, V.K., and Singh, C.V. (2011). Sire evaluation using animal model and conventional methods for milk production in crossbred cattle. *Indian Journal of Animal Sciences*, **81**(1): 77-79.
- Snedecor, G.W., and Cochran, W.G. (1967). *Statistical Methods* Oxford and IBH publishing Company. New Delhi: 593.
- Sorensen, D., Gianola, D., and Gianola, D. (2002). Likelihood, Bayesian and MCMC methods in quantitative genetics: 253.
- Sorensen, D.A., Wang, C.S., Jensen, J., and Gianola, D. (1994). Bayesian analysis of genetic change due to selection using Gibbs sampling. *Genetics Selection Evolution*, **26**(4): 333-360.
- Spiegelhalter, D., Best, N.G., Carlin, B.P., and van der Linde, A. (2003). Bayesian measures of model complexity and fit. *Quality Control and Applied Statistics*, **48**(4): 431-432.

- Stigler, S.M. (1986). The history of statistics: The measurement of uncertainty before 1900. *Harvard University Press*.
- Suresh, R., Bidarkar, D.K., Gupta, B.R., Rao, B.S., and Sudhakar, K. (2004). Production and reproduction performance of Murrah buffaloes. *Indian Journal of Animal Sciences*, **74**(3): 315-318.
- Thiruvankadan, A.K. (2012). Performance of Murrah buffaloes at coastal region of Tamil Nadu. *Indian Journal of Animal Sciences*, **82**(3): 323-325.
- Thiruvankadan, A.K., Panneerselvam, S., and Murali, N. (2015). Study on ages at first mating and calving of Murrah buffaloes in hot and humid climate of Tamil Nadu, India. *Indian Journal of Animal Research*, **49**(5): 591-94.
- Thiruvankadan, A.K., Panneerselvam, S., Murali, N., Selvam, S., and Saravanakumar, V.R. (2014). Milk production and reproduction performance of Murrah buffaloes of Tamil Nadu, India. *Buffalo Bulletin*, **33**(3): 291-300.
- Thiruvankadan, A.K., Panneerselvam, S., Rajendran, R., and Murali, N. (2010). Analysis on the productive and reproductive traits of Murrah buffalo cows maintained in the coastal region of India. *Applied Animal Husbandry and Rural Development*, **3**(1): 1-5.
- Tien, N.Q., and Tripathi, V.N. (1990). Genetic parameters of body weight at different ages and first lactation traits in Murrah buffalo heifers. *Indian Veterinary Journal*, **67**(9): 821-825.
- Tomar, S.S., and Tripathi, V.N. (1988). Standardization of data on lactation performance of Murrah buffaloes affected by various diseases. *Indian Journal of Dairy Science*, **41**: 244-246.
- Umrikar, U.D., and Deshpande, K.S. (1985). Genetic studies on lactation length and dry period in Murrah buffaloes. *Indian Journal of Animal Sciences*, **55**(10): 888-892.
- Ünalán, A., and Cebeci, Z. (2004). Estimation of genetic parameters and correlations for the first three lactation milk yields in Holstein Friesian cattle by the REML method. *Turkish Journal of Veterinary and Animal Sciences*, **28**(6): 1043-1049.
- Van Tassell, C.P., and Van Vleck, L.D. (1996). Multiple-trait Gibbs sampler for animal models: flexible programs for Bayesian and likelihood-based (co) variance component inference. *Journal of Animal Science*, **74**(11): 2586-2597.
- Viana, J.M.S., Faria, V.R., and de Resende, M.D.V. (2013). Bayesian inference of mixed models in quantitative genetics of crop species. *Theoretical and Applied Genetics*, **126**(7): 1749-1761.

- Wakchaure, R.S., Sachdeva, G.K., and Gandhi, R.S. (2008). Comparison of heritability estimates from time series and least squares adjustments in Murrah buffaloes. *The Indian Journal of Animal Sciences*, **78**(10).
- Wang, C.S., Gianola, D., Sorensen, D.A., Jensen, J., Christensen, A., and Rutledge, J.J. (1994). Response to selection for litter size in Danish Landrace pigs: a Bayesian analysis. *Theoretical and Applied Genetics*, **88**(2): 220-230.
- Wolf, J.B., and Wade, M.J. (2016). Evolutionary genetics of maternal effects. *Evolution*, **70**(4): 827-839.
- Worku, D., Gowane, G R., Kumar, R., Joshi, P., Gupta, I.D., and Verma, A. (2021). Estimation of genetic parameters for production and reproductive traits in Indian Karan-Fries cattle using multi-trait Bayesian approach. *Tropical Animal Health and Production*, **53**(3): 1-9.
- Yadav, B.S., Yadav, M.C., Khan, F.H., and Singh, A. (2002). Murrah buffaloes-II. First lactation yield and first lactation period. *Buffalo bulletin*, **21**(3): 51-54.
- Yadav, K.N., Rathi, S.S., Ram, S., and Singh, R. (1983). Estimates of genetic and phenotypic trends in Murrah buffaloes under progeny testing programme. *Indian Journal of Dairy Science*, **36**(3): 330-332.
- Yadav, N. (2020). Effectiveness of Bayesian Approach in Genetic Evaluation of Lifetime traits in indigenous cattle. M.V.Sc Thesis submitted at ICAR-National Dairy Research Institute, Karnal, India.