

**ESTIMATION OF PHENOTYPIC AND GENETIC PARAMETERS OF MILK YIELD,
CONFORMATION AND FERTILITY TRAITS IN DAIRY CATTLE: A MULTI-
GENOTYPE AND MULTI-LOCATIONAL STUDY**

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**A THESIS SUBMITTED TO THE SCHOOL OF POSTGRADUATE STUDIES,
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**DEPARTMENT OF ANIMAL SCIENCE
FACULTY OF AGRICULTURE
AHMADU BELLO UNIVERSITY
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APRIL, 2017

DECLARATION

I declare that this thesis entitled **“ESTIMATION OF PHENOTYPIC AND GENETIC PARAMETERS OF MILK YIELD, CONFORMATION AND FERTILITY TRAITS IN DAIRY CATTLE: A MULTI-GENOTYPE AND MULTI-LOCATIONAL STUDY”** have been carried out by me in the Department of Animal Science under the supervision of Professor G.N Akpa, Professor B.I, Nwagu and Professor P.P. Barje. The information derived from the literature have been duly acknowledged in the text and a list of references provided. No part of this thesis was previously presented for another degree or diploma at any University.

Oludayo Michael, Akinsola

Signature

Date

CERTIFICATION

This thesis titled “**ESTIMATION OF PHENOTYPIC AND GENETIC PARAMETERS OF MILK YIELD, CONFORMATION AND FERTILITY TRAITS IN DAIRY CATTLE: A MULTI-GENOTYPE AND MULTI-LOCATIONAL STUDY**” by OLUDAYO MICHAEL, AKINSOLA meets the regulations governing the award of the degree of Doctor of Philosophy of Ahmadu Bello University, Zaria and is approved for its contribution to scientific knowledge and literary presentation

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Chairman, Supervisory Committee

..... Prof. B.I. Nwagu Sign..... Date
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Dean, Postgraduate School

DEDICATION

This thesis is specially dedicated to all the people who lost their lives in the fight against Boko Haram insurgency and to my sweet mother, Mrs Sherifat Akinsola.

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ABSTRACT

This study aimed to estimate the phenotypic and genetic parameters of milk yield, conformation, and fertility traits in multi-genotype cows across diverse environments. Data were collected from six genotypes: Holstein Friesian, Friesian×Bunaji, Jersey, Jersey×Bunaji, Brown Swiss, and Simmental cows, reared on three commercial farms: Shonga Dairy Holdings in Kwara State, Integrated Dairies Limited in Plateau State, and Sebore Farm in Adamawa State, Nigeria. Milk production traits assessed included 305-day fat-corrected milk yield, daily milk yield, 100-day fat-corrected milk yield, total fat yield, total protein yield, and lactation length. Six efficiency indices were evaluated: fat-corrected milk yield per kilogram weight (FCM Kg W), per kilogram metabolic weight (FCM Kg MW), per day per kilogram weight (FCM/day/kgW), per day per kilogram metabolic weight (FCM/day/kgMW), net energy efficiency, and dairy merit. Additionally, four lactation traits (initial yield, peak yield, peak day, last day yield), body weight, seven body traits (body condition score, stature, chest width, body depth, heart girth, rump width), five udder traits (central ligament, rear udder height and width, udder clearance, teat length), and six fertility traits (age at first calving, calving interval, days open, services per conception, calving rate, herd life) were analyzed. The effects of genotype, breed improvement, and year of calving on fertility traits were also examined. Multi-trait animal models using the average information restricted maximum likelihood (AIREML) method were employed to estimate (co)variance components, with basic descriptive and regression analyses performed in R 3.0.3 and computational modeling conducted in MATLAB. The average milk production metrics were 2496.4 kg for 305-day fat-corrected milk yield, 7.2 kg/day for daily milk yield, 1549.2 kg for 100-day fat-corrected milk yield, 63.3 kg for fat yield, 58.7 kg for protein

yield, and 344.9 days for lactation length. Efficiency indices included 4.8 kg FCM Kg W, 22.7 kg FCM Kg MW, 0.02 kg FCM/day/kgW, 0.07 kg FCM/day/kgMW, 42.4% net energy efficiency, and 61.8% dairy merit. Fertility traits were significantly ($P < 0.05$) affected by genotype, breed improvement, year of calving, and their interactions. Milk production, lactation traits, and conformation traits were significantly ($P < 0.05$) influenced by genotype and location. Heritability estimates were moderate to high for milk yield ($h^2 = 21\text{--}44\%$), low to high for conformation traits ($h^2 = 2\text{--}61\%$), and low to moderate for fertility traits ($h^2 = 1\text{--}28\%$). Genetic and environmental correlations among milk yield, milk components, conformation, and fertility traits were less than unity across environments. Breeding value estimation accuracy ranged from moderate to high for 305-day fat-corrected milk yield and from low to high for reproductive traits. The effect of inbreeding on milk production and fertility traits was minimal overall but showed considerable severity in Jersey herds in Kwara State. All lactation models (Wood, Wilmink, Dijkstra, MilkBot, and Neural Network) effectively reconstructed the ascending, peak, and descending phases of lactation, except for the Wilmink model, which produced atypical curves for Friesian×Bunaji cows in Kwara State (Adj $R^2 = 62\%$), and the Dijkstra model for Holstein Friesian cows in Adamawa State (Adj $R^2 = 56\%$). The Genetic Function Algorithm (GFA) was identified as the most efficient and economical model for predicting 305-day fat-corrected milk yield in Nigerian herds ($FCM_{305d} = 1036.1 - 98.3RP + 22FY + 15.92UC - 0.07RUH$; Adj $R^2 = 0.997$; RMSE = 30.07; BIC = 1997.28). Neural Network models demonstrated the highest prediction accuracy across environments, with the optimal architecture for predicting 305-day fat-corrected milk yield being a 6-2-1 multilayer perceptron using backpropagation with an 88% learning rate and 2% bias. Holstein Friesian cows showed the highest dairy merit for

milk production in Plateau and Adamawa States, while Jersey cows exhibited optimal milk yield in Kwara State. These findings highlight substantial genetic variation for milk production, conformation, fertility, and lactation traits among multi-genotype cows across different environments.

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CHAPTER ONE

1.0

INTRODUCTION

1.1 Background of the Study

Dairy cattle exhibit tremendous phenotypic diversity, including a greater variation in milk yield than any other mammal due to selective pressure to improve milk production (Akpa *et al.*, 2007). Milk yield is the most important economic trait that determines productivity and profitability in dairy cattle (Adebayo and Oseni, 2016). The introduction of improved-grade exotic breeds (Friesian, Brown Swiss, Jersey and Simmental) by government and private farm is one of the options for upgrading milk production in Nigeria. Exotic dairy cattle have been imported to Nigeria in large numbers during the last 25 years to enhance and optimize milk production. Milk production will need to nearly double in the world over the next decade to follow population and income growth (Hammami *et al.*, 2009). The strongest demand for milk and milk products is anticipated for developing countries where population growth is expected (Tollens *et al.*, 2004).

Breeding programmes in cattle are primarily focused on milk yield (Xuefeng *et al.*, 2017). It is then obvious that accurate measurement and prediction of milk yield is also essential for the economy of the dairy industry. A deterministic and stochastic model may be a good instrument for on-the-spot assessment and forecasting of milk yield. Such a model is expected to provide the farmers, researchers and policy makers some valuable information for genetic evaluation of dairy cattle.

Genetic architecture refers to the organization of the whole genome and its connection to the expression of complex phenotypes rather than single locus traits (Boone *et al.*, 2007). It is synonymous with the “genotype-environment map” for a trait. Hansen (2006) defined

genetic architecture as “the pattern of genetic effects that build and control a given character and its variation properties”. Taking account of these traits by fitting the herd as a fixed effect when modeling milk yield will decrease the residual variance, therefore decreasing phenotypic variance and increasing the heritability estimate. This will lead to an increase in the accuracy of the predicted breeding value which directly increases genetic gain. Accurate estimation of an individual’s breeding value is critical for increasing genetic improvement of milk and fertility traits in dairy cattle (Hayes *et al.*, 2009; Luan *et al.*, 2009).

Eurostat (2016) reported that milk production, including fat and protein yield, has been the main objective for selection in the dairy industry of most countries. However, continued selection for higher milk production has been questioned on several accounts as it has been widely associated with deleterious effects on the health, fertility, conformation and welfare of cows (Pryce *et al.*, 2001; Pryce and Veerkamp, 2001; Miglior *et al.*, 2005). Declining fertility seems to be caused by a combination of various physiological and management factors, which start at calving, and which all have an additive effect on reproductive efficiency.

The determination of genetic parameters for reproductive traits is a prerequisite for the construction of selection index. It may be assumed that genetic selection for improved female fertility is hampered by the dairy industry’s strive for high milk production levels. There is overwhelming evidence that increasing genetic merit for yield, without considering genetic merit for fertility reduces fertility (Pryce *et al.*, 2001; Veerkamp *et al.*, 2003). Also, genetic selection for yield may change the energy partitioning in lactating dairy cows, causing a genetically induced negative energy balance and a lower body condition score (Veerkamp *et al.*, 2003; Gutierrez *et al.*, 2006). However, genetic associations between yield

and fertility are such that conjoined improvement for milk yield and reproductive performance is feasible (Jamrozik *et al.*, 2005) while maintaining 70–80 % of the yearly increase in yield (Veerkamp *et al.*, 2000).

1.2 Justification

Nigeria spends an estimated amount of \$1.3 billion on the importation of dairy products and the government's target is to double milk production over the next three to four years to meet up with domestic consumption and export (FAOSTAT, 2013). With a population higher than 180 million people, the country is currently going through low local milk production while importing more than 70 percent of its dairy products (National Agricultural Sample Survey, 2011). An average cow in Nigeria is said to produce 1 kg of milk a day, showing there is a long way to go before reaching self-sufficiency (Yahuza, 2001). Unfortunately, the domestic output of about 503,000 metric tonnes of milk (FAOSTAT, 2013) from an estimated 14 million cattle can hardly satisfy the dairy demands of an ever-increasing population of Nigerians (Ibeawuchi *et al.*, 2000).

The thinking is that with the ongoing diversification agenda and the push for industrialization to mitigate the effects of the economic recession, an initiative in the mode of this research could not have come at a better time than this which will help prioritize a robust institutional framework and necessary policy formulations geared towards genetic improvement of milk yield to bridge the gap for protein sufficiency. These attempts are aided by increased computing power and software capability available today that have facilitated the use of more appropriate models and more sophisticated statistical procedures to estimate variance components and to predict breeding values.

A comprehensive understanding of milk yield and composition is imminent to bridge the gap in protein insufficiency. The use of novel tools such as genetic algorithm programs for optimization of the estimates of milk yield in Nigeria dairy industry have not been conceived. However, these tools have been used in many fields to solve complex problems such as prediction of bank failure, object categorization, pattern recognition, prediction of oil extraction, crime detection, and pipeline modeling among others. There are some fields in which the use of genetic function algorithm models and artificial neural networks in prediction and optimization study is still scarce. This lack of intelligent model applications in Animal Science especially the dairy sector is quite paradoxical, as large data sets are usually generated from production records and data analyses are done using classical statistical methods. Intelligent models however have shown to be more powerful than classical statistical methods to carry out this kind of task (Bishop, 1995; Ripley, 1996; Arbib, 2003).

To this end, this study aims to achieve the following hypotheses:

Hypotheses

Null Hypothesis (H_0): Estimation of phenotypic and genetic parameters for milk yield, conformation, and fertility traits has no significant effect in multi-genotype and multi-location in this study

Alternative Hypothesis (H_a): Estimation of phenotypic and genetic parameters for milk yield, conformation, and fertility traits has a significant effect in multi-genotype and multi-location in this study.

1.3 Objectives

1.3.1 Main objective

To estimate the phenotypic and genetic parameters of milk yield, conformation and fertility traits in a multi-genotype and multi-locational study

1.3.2 Specific objectives:

These are to:

1. Determine an appropriate model for predicting 305 day fat corrected milk yield from milk indices and conformational traits (body and udder) among genetic groups of cows in different environments using multiple linear regression, neural network and genetic function algorithm
2. Test the significant effects of genetic groups in addition to other non-genetic factors in influencing milk production, conformational (body and udder) and female fertility traits in different environments
3. Estimate the genetic (heritability, repeatability and genetic correlations) and environmental relationships among milk production, conformational (body and udder) and female fertility traits in genetic groups of cows in different environments
4. Estimate the magnitude of predicted breeding values and inbreeding coefficients for both milk production and reproductive traits in exotic purebred cows in different environments
5. Quantify the shape of lactation curves using different computational models (empirical, mechanistic and artificial intelligence) among genetic groups of cows in different environments

CHAPTER TWO

2.0

LITERATURE REVIEW

2.1 Genotype by Environment Interaction in Dairy Cattle

In recent decades, dairy cattle breeding has become an increasingly international business and a substantial exchange of Holstein semen has taken place worldwide (Powell *et al.*, 1994). On the other hand, performances of daughters of artificial by inseminated bulls are recorded in various environments in the world. However, Banos and Smith (1991) cited in Hammami *et al.* (2009) reported that across-country selection is more profitable under the globalization of dairy industries. Currently, the multiple-trait across-country evaluation (MACE) procedure (Schaeffer, 1994) is used by Interbull. This routine evaluation incorporates information on daughters of bulls from different Interbull country members.

The international bull breeding values can then be converted to National scales. Thus, using the international evaluation, foreign bulls can be reliably selected for national use. Lohuis and Dekkers (1998) estimated that global selection can increase rates of genetic response up to 17 % compared to within-country selection. In the absence of genotype by environment interaction ($G \times E$), the expected genetic correlation across environments is unity. Cooper and Delacy (1994) reported that only when the genetic correlation among environments is less than one does the $G \times E$ impede response to selection. With the current international genetic evaluation of bulls, the national trait measures are viewed as different traits depending on the location of herds and using the country member borders as the criterion for differing among environments. Such procedures ignore the differences between herds in the same country especially in large countries. It also ignores the similarities between many herds within and between countries (Fikse *et al.*, 2003; Zwald *et al.*, 2003).

Tropical and developing countries often rely on exotic germplasm for breeding purposes. They however have climatic conditions, production systems, and markets different from those where animals were evaluated. Thus, the $G \times E$ can cause reduced efficiency of their genetic improvement programmes.

Genotype can refer to a genotypic unit (breeds, crossbreeds, individuals), but also to a genotypic value (individuals with certain phenotypic or genotypic performances). The usual elementary unit for the definition of environment in dairy cattle is the herd. Using individual characteristics of each herd as a different environment will lead to great difficulties in comparing different environments. Experiments on dairy cattle reported in the literature dealt mainly with genotype by feeding level and system interactions. Two different diets varying in the dry matter proportion of concentrates, brewers' grains and silage were fed to a herd of two genetically distinct groups based on merit (Veerkamp *et al.*, 1994; Pryce *et al.*, 1999). In general, the $G \times E$ interaction exhibited was mostly a scaling effect and there was no significant interaction between diets and lines.

McCarthy *et al.* (2007) studied the effect of three Holstein-Friesian strains (high production North American, high durability North American, and New Zealand Holstein-Friesian) and feeding system (high grass allowance feed system, increased stocking rate system, and increased concentrate supplementation) on body weight and body condition score. These authors found that the New Zealand strain remains the most suitable to low-cost grass-based system, a predominant system in Ireland. Their study extended previous results found on a subset of the same data and confirmed significant effects of the strain of Holstein-Friesian and feed system on reproduction performance (Horan *et al.*, 2004), milk production (Horan *et al.*, 2005), grass dry matter intake (Horan *et al.*, 2006) and somatic cell scores

(McCarthy *et al.*, 2007). All these studies reported important genotype by environment interactions. Cows of New Zealand origin produced less milk than North American ones but had better reproductive performances. Kolver *et al.* (2002) reported also a re-ranking of New Zealand and North American genotypes between grazing and mixed ration. Macdonald *et al.* (2008) compared growth parameters between three different strains of Holstein-Friesian cows grazed on pasture in New Zealand.

They concluded that differences in growth parameters and puberty exist among the different genetic strains studied when grazed on pasture. In more comprehensive studies (large-scale studies), the number of factors differing across environments is large compared to controlled experiments. This is the case in large countries with diverse climatic conditions and production systems. Within-country analyses of $G \times E$ have been based on modeling data using essentially multi-trait models. Correlations between different environments were used to estimate $G \times E$ interactions.

Stratification of herds varied by studies and was based on: within herd year mean for mature equivalent milk yield (Castillo Juárez *et al.*, 2000; Ceron-Munoz *et al.*, 2004), within herd-year standard deviation for mature equivalent milk yield (Raffrenato *et al.*, 2003), regions (Carabaño *et al.*, 1990; Rekaya *et al.*, 2003; König *et al.*, 2005), production level (Calus *et al.*, 2002; Kolmodin *et al.*, 2002), herd size (Gernand *et al.*, 2007), test-day production levels (Veerkamp *et al.*, 1998; Hayes *et al.*, 2003). Estimates of genetic correlations between environments as defined above were high (> 0.80) showing little or no evidence for strong $G \times E$ interactions. The latter authors concluded a lack of presence of $G \times E$ between grazing and conventional management systems. In consequence, they

reported that selection of sires on grazing systems can be accurate using the national breeding values applied for conventional systems.

Most of the cross-country analyses estimated the genetic parameters of traits for each environment studied. However, relationships between traits may also differ by environment. Thus, selection for high production in one environment may lead to different changes in correlated traits under different environments. To avoid this problem, the best way will be to model the relationship between several traits in different environments (Oseni *et al.*, 2004). Recently, $G \times E$ has been observed for the correlation of milk yield with protein, fat yield and somatic cell score (Castillo-Juárez *et al.*, 2000; Raffrenato *et al.*, 2003), milk yield with fitness traits (Castillo-Juárez *et al.*, 2000; Windig *et al.*, 2005), milk yield with age at first calving (Ruiz-Sánchez *et al.*, 2007). Castillo-Juárez *et al.* (2000) reported changes in correlations between milk production and somatic cell score and conception rate with specific environments. These correlations were small between pairs of traits in favorable environments and were high in less favorable environments. These authors suggested that an improvement of the management in low environments can reduce the unfavorable correlation found between milk yield and somatic cell score and conception rate. The use of germplasm selected in regions with differing climatic conditions and production systems may result in $G \times E$ that could reduce the efficiency of genetic improvement programs in the area where animals will be produced.

König *et al.* (2005) summarized genetic correlations for production traits estimated between countries reported in most studies investigating $G \times E$. Genetic correlations between the Northern hemisphere group (Canada, USA and Western Europe) ranged between 0.85 and 0.90 (Fikse *et al.*, 2003). Genetic correlations of less than 0.8 were found between North and

South America (Ceron-Munoz *et al.*, 2004) and between some eastern European countries (Rekaya *et al.*, 2001). Low genetic correlations were obtained between countries that differ considerably in climate, management and production system. The genetic correlation between Mexico and the USA was 0.63 (Cienfuegos-Rivas *et al.*, 1999) and 0.49 between Kenya and the United Kingdom (Ojango and Pollot, 2002). Most of these studies pointed out the existence of a scaling effect of $G \times E$, where the response to selection was smaller in low-input environments than in high-input ones. Selection responses to the use of selected US Holstein sires for milk production in Latin America were estimated to range from 53 % to 78 % of the response observed in the USA (Stanton *et al.*, 1992). In Kenya, the response to selection based on UK breeding values was only 44 % (Ojango and Pollot, 2002).

Weigel *et al.* (2001) found high genetic correlations (> 0.80) between milk yields across seventeen Interbull country members. Estimates reported were higher than 0.90 between countries with predominantly grazing systems (Ireland, Australia and New Zealand). Correlations were also greater than 0.91 between countries with high milk production (US, Canada, Belgium, The Netherlands, and Italy). Correlations between remaining Interbull members ranged between 0.8 and 0.9. Regardless of the approach applied, the scaling effect of $G \times E$ was frequently reported. However, some studies did report the re-ranking effect (Cienfuegos-Rivas *et al.*, 1999; Kolver *et al.*, 2002). In case of the scaling effect, animals will maintain their ranking among environments but only differences in the magnitude of breeding values were observed.

Togashi *et al.* (2001) reported that when sire by country interaction exists, selection of candidate animals in the country with the highest genetic variance should be more effective than selection in the country with the lowest genetic variance. Togashi *et al.* (2001) also

reported that when GxE interaction is important, an international optimum index becomes more efficient than a within-country index as a means to select candidate animals. When considering only sire selection, James (1961) reported that when genetic correlation among two environments was greater than 0.70, testing progeny in both environments and applying a unique index selection was more appropriate than applying separate selection following testing in both environments or selecting and testing in only one of the two environments. Mulder (2007) concluded that a single breeding program with progeny test bulls in both environments was more appropriate when the genetic correlation was higher than 0.60. In contrast, when the genetic correlation was less than or equal to 0.60, it was more opportune to have a specific breeding program and progeny testing in each environment.

2.2 Milk Production in Dairy Cattle

Nyamushamba *et al.* (2014) have reported the significant effects of calving interval, parity and month of calving on milk, milk fat and protein yields of Red Dane and Jersey cattle in Zimbabwe, their observation was consistent with earlier reports by several researchers (Makuza, 1995; Missanjo, 2010; Nyamushamba *et al.*, 2013). Hatungumukana *et al.* (2007), Missanjo *et al.* (2011) and Nyamushamba *et al.* (2013) reported that calving intervals significantly affect milk yield and composition of dairy cattle. The ideal calving interval is 365 days for both breeds in milk production whereby the producer is assured of one calf from each cow per annum. This would also ensure that the cows can replenish its body reserves and regenerate secretory tissue without necessarily leading to over-conditioning. Missanjo (2010) reported that herd-year-season significantly affects milk yield and composition of dairy cattle in Zimbabwe. It is expected that different herds have different levels of production because of variations in the level of management. Parity tends to cause

milk yield to increase along with an increase in parity till decline sets in. This suggests that milk yield increases as parity proceeds because large cows produce more milk than small cows due to large body size and increased udder development that comes with repeated pregnancies as well as full development of tissues of the udder. Also, multiparous cows reach their peak earlier in the lactation than first parity cows and consume more feed, eat larger meals and drink more water therefore their persistency will be longer than that of the first calvers leading to less milk yield produced by first calvers. The milk yield was also lower in early parities because the feed that was provided to the heifers was also channeled to their growth as they were still growing. As the parity proceeded, milk yield increased because the feed requirements for growth were declining (Keown and Everett, 1986). Amimo *et al.* (2007) reported a similar trend in Ayrshire and Holstein's breeds studied in Kenya.

2.3 Genetic Parameter Estimates

2.3.1 Heritability for milk production and reproductive traits

Reviewed estimates of heritability for milk production traits (305-day milk yield; length of lactation period; dry period length) in Holstein cattle indicated that magnitude of heritability ranged from 0.05 to 0.66 for 305-day milk yield, from 0.03 to 0.23 for length of lactation period and from nearly zero (0.0003) to 0.20 for dry period length, while reproductive traits such as calving interval, age at first calving showed that estimates ranged from 0.0003 to 0.58 for calving interval and from 0.04 to 0.38 for age at first calving (Alhammad, 2005; Safaa, 2006; Salem *et al.*, 2006).

2.3.2 Genetic correlation coefficients of milk production and reproductive traits

Genetic correlation coefficient between any two traits measures the correlation between the breeding values of these two traits (Falconer, 1981). The reviewed estimates of genetic correlation coefficients for different milk production and reproductive traits revealed in general, strong positive genetic correlation between 305-day milk yield (standard measure of milk yield per lactation) in dairy cattle and length of lactation period (Shitta *et al.*, 2002; Salem *et al.*, 2006). Most estimates of genetic correlation coefficients were of moderate to high magnitudes. Positive genetic correlation between 305- day milk yield and length of lactation period was also reported by Morad (1967) cited in Safaa (2006) and Ragab *et al.* (1973) cited in Safaa (2006). Genetic correlation coefficients between 305-day milk yield and dry period length were negative in some cases (EL-Arian *et al.*, 2003; Salem *et al.*, 2006) and positive as reported by some researchers (Shahrودي *et al.*, 2001; Alhammad, 2005). Safaa (2006) reported that cows with a very long dry period has improper body conditions for lactation and its lifetime milk production is not increased. Estimates of genetic correlation coefficients between 305- day milk yield and calving interval reveal that milk yield is positively genetically correlated with calving interval (Hussein, 2004; Ulutas *et al.*, 2004). These findings were confirmed by Safaa (2006) who stated that cows with long calving interval tend to produce more milk than those with short ones ($r_g = -0.56$). Values of genetic correlation coefficients between 305-day milk yield and age at first calving indicates that age at first calving was negatively correlated with 305-day milk yield.

Genetic correlation coefficients given evidenced by Polastre *et al.* (1988) cited in Safaa (2006) showed high positive genetic correlation between length of lactation period and

calving interval ($r_g = 0.47$ and 0.98 , respectively). Reviewed results gave evidence that dry period length was often genetically positively correlated with calving interval (Shereen-Genena, 1998). Shereen-Genena (1998) when analyzing data across all available lactations found that the genetic correlation coefficient between dry period and calving interval was -0.52 indicating a high negative genetic correlation between the two correlated traits. The genetic correlation between age at first calving and calving interval was negative and ranged between -0.09 and -0.64 .

2.3.3 Genetic correlations for conformation and economic traits

Jairath *et al.* (1998) reported genetic correlations of conformation traits with functional herd life to be moderately high for mammary system (0.57) but lower for capacity, feet and legs, and rump (0.19 to 0.23). Conformation traits were more closely associated with functional herd life in registered herds compared to grade herds. Most of the body traits had a slightly positive relationship with functional herd life. Results from Samoré *et al.* (2010), in a study on Italian Brown Swiss, indicated that cows with higher stature, greater strength, deeper body and more angularity had a short herd life. Low to moderate negative genetic correlations (-0.07 to -0.22) were reported for most of the structural type traits, except for rear legs set (-0.56). Rump angle was positively correlated with functional length of productive life (0.21). Most of the udder traits were positively correlated with functional length of productive life, with a strong correlation of 0.42 for udder depth. In a study on Czech Fleckvieh cows by Zavadilová *et al.* (2009), body measurements negatively correlated with length of productive life as well as functional length of productive life were wither height (stature), chest width, dairy character (dairy strength) and body depth. The correlations for wither height and body depth were almost similar for both longevity traits.

Concerning the mammary traits, rear udder attachment and central ligament (udder support) showed positive genetic correlations with length of productive life, while the genetic correlation for udder depth was negative and low (-0.02). In contrast, the genetic correlations with functional length of productive life for rear udder attachment and central ligament were negative and lower as with length of productive life.

Weigel *et al.* (1998) reported that udder traits (0.24 to 0.32), teat placement (0.22), and dairy form (0.41) had the largest correlations with length of productive life, which was consistent with the results of previous studies using independent data (Boldman *et al.*, 1992). Udder traits have an important influence on involuntary culling decisions, mainly because of their influence on susceptibility to injuries and mastitis infections. The importance of the genetic correlations (especially for fore udder attachment and udder depth) were very large. Continued selection pressure for improved udder characteristics appears justified in Jerseys despite indications that udder problems may be less prevalent than in Holsteins (Rogers *et al.*, 1991b). Buenger *et al.* (2001) reported the strongest relationships between conformation traits and longevity were found for udder traits, namely udder depth, fore udder attachment, suspensory ligament, and front teat placement. Foot angle also seemed to be important, whereas most of the other body traits on longevity were less important.

2.4 Effect of Genetic Purging on Economic Traits

Inbreeding depression per 1 % increase of inbreeding was predicted to be up to -30 kg milk, -1.0 kg fat and -1.5 kg body weight (Panicke *et al.*, 1975). This prediction was confirmed by an extensive study based on individual level within the population, carried out by Smith *et al.* (1998) in the USA. The estimated inbreeding depression on milk yield in first lactation amounted to -27 kg, fat yield and protein yield -0.9 and -0.8 kg. For the whole life time the depression was - 177 kg milk, - 6 kg fat and -5.5 kg protein, per 1% increase of inbreeding.

Further, the inbreeding depression in age of first calving was +0.55 days, -6 days of productive life and -4.8 milking days. There was no large effect on conformation traits.

2.5 Application of multiple linear regressions for prediction of milk production

Samanta *et al.* (1992) constructed prediction equations for lifetime milk production up to six lactations based on different early traits in Holstein Friesian x Harijana cow crosses and observed that five first lactation traits (FLTMY, AFC, FLPY, FL100DMY (First Lactation 100 Days Milk Yield) and FLL) explained 87.76 percent of the total variation in lifetime milk production. Pundir and Raheja (1995) predicted lifetime milk yield in Sahiwal cows based on different early traits and they reported that an equation including AFC, FLL, FSP and SLTMY in the model explained 47.11 percent of total variation in lifetime production. Gandhi and Bhattacharjya (2001) used a multiple linear regression method to predict the milk yield up to the age of 6 (LTP6) and 8 (LTP8) years of age based on first lactation traits e.g. AFC, FL305DMY, FCI, FSP, FLL in Karan Fries Cattle. The maximum R^2 found for LTP6 and LTP8 were 0.59 and 0.32 when all the above traits were included in the model. Gahlot (2003) developed 32 regression equations for the prediction of lifetime milk yield and 25 regression equations for the prediction of herd life from different combinations of 9 independent traits viz. AFC, TMY (total milk yield), 305DMY (305 days milk yield) FL305DMY in Sahiwal cattle and observed that these traits explained 50.68, 51.12 and 39.92 percent of total variation in 6, 8 and 10 years of age of animals respectively. Chander (1977) predicted the milk yield at different years of age (6, 8 and 10 years) in Tharparkar cattle on the basis of AFC and FL305DMY and reported that 87, 57 and 67 percent of total variation was explained due to these early traits in 6, 8 and 10 years lifetime milk production, respectively.

Rao (1977) constructed prediction equations for 3 lactations lifetime production in crossbred cattle (1/8 Friesian x 7/8 Zebu cattle) and concluded that 75.22 percent variation was attributed to AFC, WFC (Weight at First Calving) and FLMY (First Lactation Milk Yield). Gupta (1980) predicted milk production for different levels of lifetime production (6, 8 and 10 years of age) in Tharparker cattle. It was reported that only AFC alone explained 48.97, 35.60 and 26.42 percent of total variation in 6, 8 and 10 years of lifetime production; lactation length, peak yield, daily milk yields, dry period, service period and calving interval for prediction of breeding value of lifetime milk yields in Tharparkar cows. The maximum R^2 was 0.82 when all the traits were included in the model. Dalal *et al.* (2004) used the multiple linear regression method (Backward elimination procedure) to predict lifetime milk production up to third and fifth lactations in Haryana cattle and concluded that early lactation and reproductive traits were more effective in predicting lifetime milk production as compared to efficiency traits alone. Singh and Rana (2008) predicted 305 days milk yield based on first to ninth-month test day values in Murrah buffaloes. The R^2 was in the range of 0.42 to 0.67. The highest R^2 value was for the sixth month test day followed by the seventh month test day. When different combinations of monthly test days were included in the model the R^2 was in the range of 0.85 to 0.94.

2.6 Application of Artificial Neural Network for prediction of milk production

Grzesiak *et al.* (2006) studied the capabilities of artificial neural networks to forecast milk yield in dairy cows. Using the actual data on daily milk yields and the data recorded on official milk recording test days, a number of neural network models were designed and parameters of Wood's model were estimated. Performance neural network and regression model were compared using coefficient of determination, relative approximation errors and

root mean square errors and found that ANN were better than Wood's model. Hosseinia (2007) used feed forward back propagation error correction learning rules of ANN in dairy farms in Iran and stated that artificial neural network can be used as a decision making support system in animal and dairy research. It can help breeders to predict future yield of dairy cows based on uncorrelated and orthogonalized available information.

Gandhi *et al.* (2009) compared neural networks and multiple linear regression models for the prediction of lifetime milk production based on early lactation traits in Sahiwal cattle. The traits considered were age at first calving, first lactation 305 day yield, first lactation length, first service period, and first dry period. The constructed network was a feed forward back propagation ANN with three layers of input, hidden and output with 5, 3 and 1 neurons respectively. The hyperbolic tangent sigmoid transformation was used for hidden layer and pureline linear transfer function was used for output layer. The root mean square error estimated from ANN method was lower than that estimated from multiple regression and suggested ANN method to be an alternative method for prediction in Sahiwal cattle. Sharma (2009) proposed a feed forward connectionist model to predict milk yield in dairy cattle for an organized herd. Ruhil *et al.* (2011) predicted 305 days lactation milk yield (LMY) of Sahiwal cows using feed forward back propagation networks based on partial lactation records of 10 test days milk yield to rank the sires at younger age to improve the quality of milking animals and reducing generation intervals. The data set was divided into two training and test data sets at 2:1 and 3:1. Results showed that the prediction accuracy of the models increased with the addition of test-days milk yield as input variable and neural network models were able to predict LMY with more than 80 % of explained variation by the model based on partial lactation records at an early stage.

Gorgulu (2012) focused on the capability of ANNs to predict 305 day milk yield in early lactation of Brown Swiss cattle, based on a few test-day records, age, number of lactation and season of calving and compared with multiple linear regressions. The various ANNs were constructed based on number of neurons in hidden layer. It was found that the optimum number of hidden layer neuron is 8 with four input neuron and one output neuron.

2.7 Mathematical Description of Lactation Curve

2.7.1 Lactation curve modelling

Lactation curve modelling means to express main features of the lactation shape in few terms with biological and technical meaning. It is widely accepted that the trajectory of milk production during lactation, or what is commonly known as the standard lactation curve, follows an increasing curvature from calving to a peak followed by a decreasing curvature. The trajectory of the lactation curve has been the centre of attention of farmers and breeding organisations for decades as they have worked on increasing milk yield by moving the lactation curve upwards through improved genetics and improved management routines. Wood (1967) developed a mathematical equation in for comparison of cattle, goat and sheep (See Table 2.1 and 2.2).

Table 2.1: Estimated parameters of the Wood's model in different breeds of Cattle, Goat and Sheep

Species	Parity	A	b	c	References
Cattle					
Holstein	1	13.89	0.25	0.0036	Rekik and Ben Gara (2004)
	2	17.46	0.24	0.0046	
Holstein	1	13.46	0.22	0.0041	Tekeri <i>et al.</i> (2000)
	2	15.79	0.21	0.0046	
Reggiana	1	20.26	0.19	0.026	Sabbioni <i>et al.</i> (2003)
	2				
Simmental	-	18.43	0.05	0.06	Cilek and Keskin (2008)
Goat		1.338	0.16	0.005	Giaccone <i>et al.</i> (1995)
Sheep (Awassi)		0.42	0.33	0.012	Dag <i>et al.</i> (2005)

a = scaling factor; b = increasing slope of yield or rate of increase to peak; c = decreasing slope of yield or rate of decline after the peak production

Table 2.2: Time at peak yield (Tm), Peak milk yield (Ym) and lactation persistency (S) calculated from parameters estimated by Wood's model in different breeds of Cattle, Goat and Sheep

Species	Parity	Tm(days)	Ym(Kg)	S	Reference
Cattle					
Holstein	1	69.4	26.5	7.15	Rekik and Ben Gara (2004)
	2	52.2	30.8	6.76	
Holstein	1	53.7	26.6	6.85	Tekerli <i>et al.</i> (2000)
	2	45.7	30.3	6.63	
Reggiana	1	44.5	22.2	4.37	Sabbioni <i>et al.</i> (2003)
	2	37.8	26.8	4.07	
Simmental	-				Cilek and Keskin (2008)
Goat		64.4	3.22	7.04	Giaccone <i>et al.</i> (1995)
Sheep (Awassi)		27.6	0.91		Dag <i>et al.</i> (2005)

Tm-Time in milk; Ym-Milk yield; S-persistency

2.8 Multiple Breeding (Crossbreeding) effect on Economic Traits

Crossbreeding is known as a type of a larger class of mating systems called outbreeding. It is the mating of animals from different breeds (Falconer and Mackay, 1996) or the mating of individuals less related than the average pair of animals in a population (Cassell, 2007). Taneja *et al.* (1980) also observed that there was no linear increase in production level above 50 % with the increase in the level of inheritance of the exotic parent and it cannot be assumed that grading up to a total replacement of genes will lead to higher levels of production, at least in cattle. Brown Swiss × Red Sindhi half breeds produced 53 % more milk than Red Sindhi cows. Bhasin *et al.* (1967) observed 188 % improvement in milk production in Friesian × Haryana half breeds. Heterotic effect of 34 % had been reported by Katpatal (1977) in Holstein × Sahiwal crossbreds at Military Dairy Farm, Jabalpur that was gradually declined as the fraction of Holstein inheritance deviated from 50 %. Taneja and Bhat *et al.* (1974) based on large volume of data reported 4.97 % heterosis for 1st lactation milk yield in Sahiwal × Friesian crosses at different Military Dairy Farms. He also observed beneficial heterosis of -4.63% for age at 1st calving, -11.4% for service period, -22.4% for number of dry days and -8.53% for calving interval. Brown Swiss × Sahiwal crosses at NDRI excelled in milk production by 56% in F1 that was dropped by 24.5% in F2. The data generated at Kerala under field conditions reflected 146% rise of milk production in Jersey × local half-bred. Holstein Friesian × Sahiwal half-bred had lower age at 1st calving by 14 months and produced 3.5 times more milk than Sahiwal cows (Parmar and Jain, 1986). The increased variation in F2 over F1 is expected theoretically when the differences among parental breeds are large. The results obtained from various crossbreeding experiment have

revealed that performance of crossbreds was undoubtedly better as compared to native breeds.

Singh *et al.* (2008) collected data from history sheet of crossbred cattle maintained at Instructional dairy farm, Pant. University of Agriculture and Technology, Pantnagar. The data pertained to 1170 crossbred cattle from 65 sires were distributed over a period of 35 years from 1970 to 2004. The overall mean of age at first calving, first lactation milk yield, first lactation period, first dry period, first calving interval, first service period, herd life, productive life, total lactation length, lifetime milk yield and lifetime milk yield/day of productive life were found as 1350.52 ± 13.48 (days), 3093.65 ± 37.17 (days), 361.42 ± 3.61 (days), 177.20 ± 6.47 (days), 538.60 ± 6.66 (days), 271.32 ± 0.75 (days), 1633.22 ± 20.56 (days), 1515.75 ± 20.56 (days), 1305.18 ± 20.37 (days), 9234.45 ± 133.75 (kg) and 6.85 ± 0.14 (kg) respectively.

Singh (2005) evaluates the performance of crossbreds for lifetime parameters, economics of crossbreds, decline in performance of crossbreds over generations and constraints in performance recording and sire evaluation. The lifetime performance in crossbreds was much higher than indigenous breeds. The Friesian crosses had higher lifetime milk yield, longer herd and productive life and completed more number of lactations than other breed crosses. The lifetime milky yield and number of lactations completed in 75% (two- and three- breed) crosses was relatively low. Variability in performance of crossbreds under field conditions could be ascribed to different availability of inputs, agro-ecological conditions, type of farmer and the indigenous and exotic breeds used in crossbreeding.

Daughters of Haryana dams produced more milk than daughters of nondescript (Indigenous) dams, and Holstein crosses more than Jersey crosses. Both differences were highly

significant. Chaudhary *et al.* (1984) studied lifetime performance of 101 Rathi cows and Red Danish × Rathi crosses in Rajasthan. The crosses were about 15 months younger at first calving and produced 70% more milk in their first lactation (2319 vs. 1418 kg), but their superiority decreased with increasing age. A least squares analysis, taking account of year and season effects, but based on smaller numbers of records, led to similar results. Kaikini *et al.* (1981) studied reproductive traits of 96 Friesian × Gir and 84 Jersey × Gir crosses in the Rahuri unit in more detail. Incidences of repeat breeding and reproductive disorders did not differ much in the two crosses (22.0 vs. 19.9% and 36.5 vs. 32.1%, respectively). Differences were slight also for age at maturity (413 vs. 402 days) and age at first service (454 vs. 444 days). However, at first calving Holstein Friesian crosses were about 1 month older than Jersey crosses (812 and 766 days, respectively). Among F1 crosses Friesian had the highest and Jersey had the lowest milk yield and their daughters sired by Friesian bulls ranked similarly. Milk yield decreased and calving interval increased when the proportion of exotic inheritance increased from 50 to 75%. Jadhav *et al.* (1983) compared dairy merits of different crossbred groups in the NDRI herd. The groups compared were Holstein × Harparkar (HT), Holstein × Sahiwal (HS), Brown Swiss × Harparkar (BT), Brown Swiss × Sahiwal (BS) and Jersey × Harparar (JT). Dairy merit was defined as energy in milk produced in per cent of energy consumed, the latter being predicted from fat-corrected milk yield, body weight, and change in body weight during lactation. The overall least squares means obtained were 28.8 ± 0.3 , 28.8 ± 0.5 , 26.0 ± 0.4 , 26.6 ± 0.1 , and 26.2 ± 0.3 , for HT, HS, BT, BS, and JT, respectively. It was concluded that Holstein crosses (HT and HS combined) were significantly superior to Brown Swiss crosses (BT and BS combined) and JT crosses in dairy merit.

CHAPTER THREE

MATERIALS AND METHODS

3.1 Location of the Study

This study of multi genotype cattle was carried out in Adamawa, Kwara and Plateau States in Nigeria (Fig. 3.1)

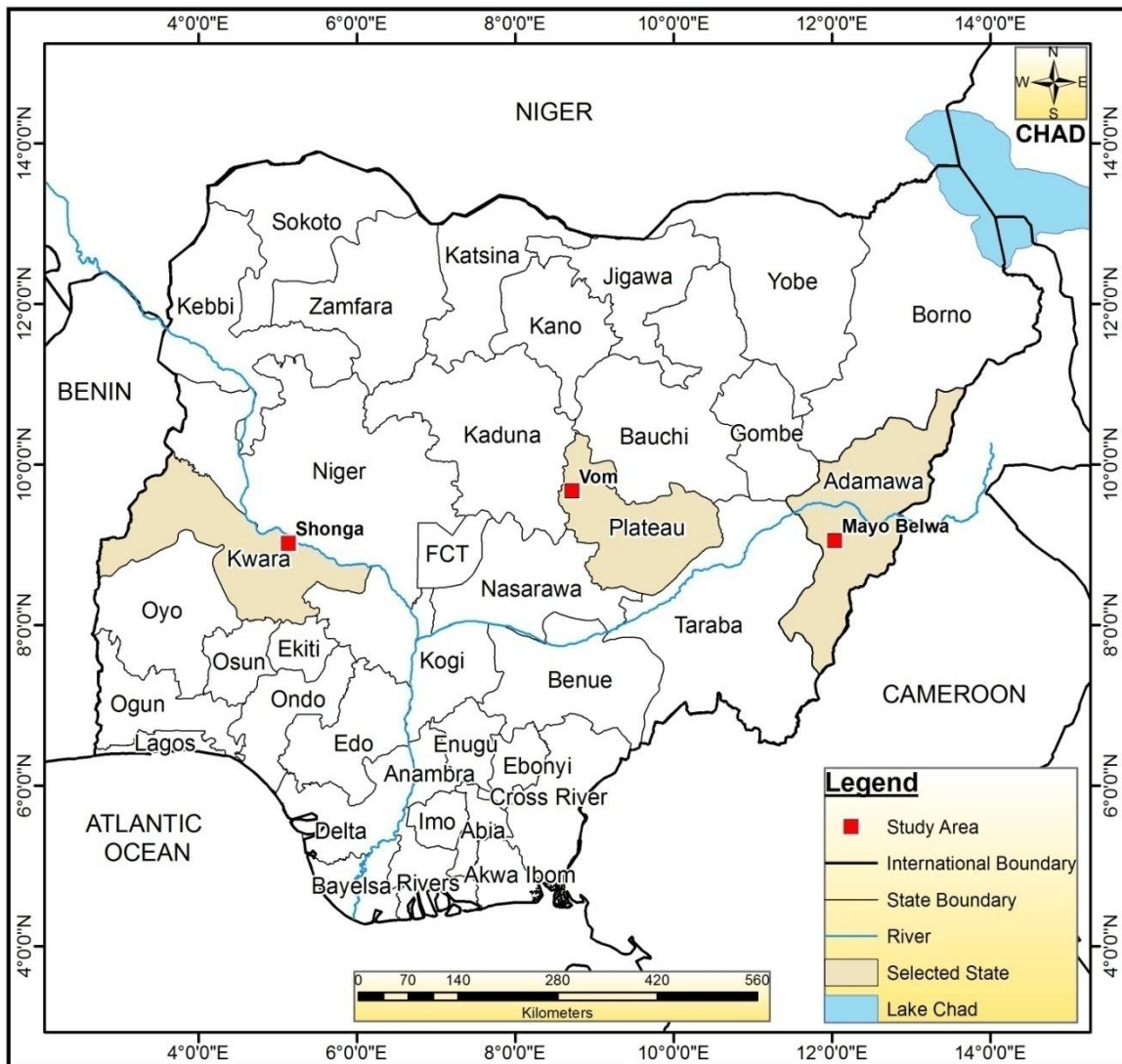


Figure 3.1: Map of Nigeria showing Study Area

Source: Modified from the Administrative Map of Nigeria (2016)

3.1.1 Adamawa State

Sebore Farm in Adamawa State is situated at an elevation ranging from 200 to 300 meters, within the coordinates 9°20' to 9°33'N latitude and 12°30' to 12°50'E longitude. The farm is bordered by Borno State to the northwest, Gombe State to the west, Taraba State to the southwest, and shares an eastern boundary with the Republic of Cameroon. The region experiences average daily temperatures ranging from a minimum of 23.2°C to a maximum of 35.2°C, with an annual rainfall average of 718.1 mm and relative humidity at 44.2%. Covering an area of 39,742.12 square kilometers, the area is characterized by numerous rivers, the most prominent being the Benue River, which originates from the highlands of Cameroon and flows southward to join the Niger River (Climate-Data, 2015).

3.1.2 Plateau State

Integrated Dairies Limited (IDL) is located on the Plateau at an elevation of 1,280 meters above sea level. The farm lies at 9°43' east longitude and 8°45'43" north latitude. The area experiences approximately seven months of rainfall, starting in April and ending in October. The dry season spans from November to March, with peak rainfall and cooler temperatures occurring in July and August. Annual rainfall averages between 1,300 mm and 1,500 mm, while ambient temperatures range from 21.8°C to 22.8°C. The harmattan winds typically occur from late December to January. Relative humidity peaks in August at 82.28% and drops to its lowest in November at 43.78% (Climate-Data, 2015).

3.1.3 Kwara State

Shonga Dairy Holdings is situated in Edu Local Government (Kwara State, Nigeria). The farm is located in the tropical climate of Nigeria, with pronounced wet and dry seasons and

steady high temperatures. Its geographical coordinates are 9° 1' north, 5° 9' East at an altitude 305m. The nearest meteorological station showed maximum rainfall in month of September which drops to zero in December. The rainy season with a duration of about 218 days, starts in April and ends in October (Climate-Data, 2015).

3.2 Experimental Animals and Breeding Plan

This study was conducted on three commercial farms: Shonga Dairy Holdings, Integrated Dairies Limited, and Sebore Farm. Six cattle genotypes, including four purebred breeds (Holstein Friesian, Jersey, Brown Swiss, and Simmental) and two crossbred types (Friesian x Bunaji and Jersey x Bunaji), were utilized. Sebore Farm in Adamawa State housed all four purebred breeds, while Shonga Dairy Holdings in Kwara State managed both purebreds (Holstein Friesian and Jersey) and crossbreds (Friesian x Bunaji and Jersey x Bunaji). Integrated Dairies Limited maintained Holstein Friesian and Friesian x Bunaji cattle. The females were imported as pregnant heifers, and artificial insemination (AI) was employed before importation in their country of origin. Post-calving in Nigeria, AI continued using imported frozen semen from purebred bulls sourced from the U.S.A., with measures in place to avoid full-sibling and sire-daughter matings.

The breeding strategies across the farms primarily involved pure breeding through AI, though Shonga Dairy Holdings transitioned to full-time natural mating in 2010 using fifteen Fowler-grade bulls. Records of abnormal lactations, including those without breeding dates, abortions, or cases of mastitis or other udder disorders, were excluded from the dataset before statistical analysis (Tables 3.1). Additionally, data from cows sold for production purposes were omitted from the analysis.

3.3 Animal Management

3.3.1 Animal Management in West Africa Milk Company Integrated Dairy Farm

The cows were allocated to paddocks sized between 1 and 2.5 hectares, grouped by breed, age, and lactation stage. They remained outdoors throughout the year, except during morning and afternoon milking sessions in a herringbone parlor, when they were provided with hay (primarily *Digitaria exilis* or 'acha') and maize silage during the dry season (October to April). During the wet season (May to September), the cows grazed rotationally in paddocks planted with *Hyparrhenia rufa*, *Digitaria* species, *Andropogon guyanus*, *Stylosanthes gracilis*, Bermuda grass, and Rhodes grass, alongside naturally occurring grasses such as *Eleusine indica* and *Pennisetum purpureum*. Salt blocks and water were available on pasture ad libitum.

Milking cows were also given a daily concentrate supplement consisting of 70% maize, 15% groundnut cake, 10% cottonseed cake, 4.9% churn mineral, and 0.1% vitamin and trace mineral premix. Molasses was included in their ration, which was divided into two equal portions and fed during the morning (7:30 AM) and afternoon (3:00 PM) milking sessions. Stubborn cows were culled from the milking group. Calves were allowed to suckle their dams for the first three days postpartum, after which they were fed milk from a bucket until weaning at 42 days of age.

Table 3.1: Structure of the data used in the genetic analyses of sire, daughter and progeny records in Shonga Dairy Holdings, Integrated Dairies Limited and Sebore farm.

Animals and Herd	Holstein Friesian	FRxBJ	Jersey	JxBJ	Brown Swiss	Simmental
Kwara						
Sire	17	26	15	20	-	-
Dams	100	114	300	201	-	-
Female progeny	308	187	622	488	-	-
Plateau						
Sire	75	49	-	-	-	-
Dams	896	341	-	-	-	-
Female progeny	1146	680	-	-	-	-
Adamawa						
Sire	92	-	38	-	16	23
Dams	292	-	50	-	78	70
Female progeny	583	-	168	-	200	142

JxBJ-JerseyxBunaji; FRxBJ-Holstein FriesianxBunaji

Deworming was done three times in the year. Routine inoculations were carried out against rinderpest, contagious bovine pleuro pneumonia, anthrax and black quarter diseases. Cows were inseminated when they are on heat. Fourteenth day before calving, pregnant animals are separated from the paddock to the steaming. Calving was done at anytime of the year. Heifers are bred when they are 18-24 months of age. Stubborn cows were culled from milking.

3.3.2 Animal Management in Sebore Farm

Same as in Integrated Dairies Limited excepting that molasses was not added in their rations.

3.3.3 Animal management in Shonga Dairy Holdings

The farm was subdivided into seven paddocks. As cows displayed signs of approaching parturition they were moved to the steaming paddock. All cows in this camp were regularly checked daily. Morning milking was done between 6.00 am and 9.30 am daily while the evening milking took place between 3.30 pm and 7.00 pm daily and it varies according to the number of lactating cows. Cows were disbudded using caustic soda, which is done at 5 days of age. Female calves with supernumerary teat have the teat removed with scissors or a blade. Calves were usually weaned at around 7 days. Following weaning, calves were vaccinated against certain bacterial or viral diseases and be given treatment for parasites. Vaccination usually requires a course of injections. Cows were impregnated either naturally by a bull in the herd, or via artificial insemination (AI). Cows were fed total mixed ration (TMR) which includes hay, fermented grass (silage), maize silage and high energy grains

like brewers grains, soy bean and cotton seed. Cows were milked twice a day in DELAVAL computerized milking parlour.



Plate I: Milk component Analysis at Integrated Dairies Limited, Plateau State

3.4 Qualitative and Quantitative Measurements

3.4.1 Milk yield measurement

Cows were milked using an automatic DELAVAL suction milking machine with teat cups which was used to collect raw milk produced from the cows' udders. Measurement was taken twice a day (06:00 hrs and 13.00 hrs) and was recorded in litres.

3.4.2 Milk component measurements

Butter fat and protein percentages were measured by infrared spectroscopy, using a Lactoscan analyser in the quality control laboratory of Shonga Dairy Holdings in Kwara State. Three (3) mls of raw milk from the bulk milk tank were injected into the automated lactoscan milk analyzers for determination of butterfat, protein and total solids in Shonga and Sebore farms while in Integrated Dairies Limited, analysis were done using the conventional method. For the determination of total solids content (milk solid with fat), two (2) mls of fresh cows raw milk sample were thoroughly mixed and 5 g was transferred to a pre-weighed and dried flat bottom crucible (AOAC, 1990). The milk samples were dried in a hot air oven (Serial No-96H203, Model-EDSC made in England) at 102 °C for 3 hours. Finally, the dried samples were taken out of the oven and placed in desiccators to cool to room temperature. Then samples were weighed again and total solids was calculated by the following formula (Richardson, 1985).

Total solids = $\frac{\text{Crucible weight} + \text{Oven dry sample weight} - \text{Crucible weight}}{\text{Sample weight}} \times 100$

3.4.2.1 Butter fat content of milk

The fat content was determined by the Gerber method according to Richardson (1985). Ten ml of sulphuric acid (density 1.815 gm/ml at 20 °C) was pipetted into a butyrometer. Then eleven ml of milk sample was added into the butyrometer and mixed with the sulphuric acid. This was followed by addition of one ml amyl alcohol into the butyrometer which was then closed with a lock stopper. Then the mixture was shaken and inverted several times until the milk was completely digested by the acid. Finally, the butyrometer was kept in water bath for 5 minutes at 65 °C and centrifuged in a Gerber centrifuge for 5 minutes. The butyrometer was placed in water bath again at 65 °C for 5 minutes. At the end, the butyrometer reading was recorded.

3.4.2.2 Crude protein content of milk

The crude protein content of milk samples was determined by the Kjeldahl method (AOAC, 1990). 5 g of milk sample was warmed in water bath at 38 °C and poured into a Kjeldahl tube. A mixture of 15 g potassium sulphate, one ml of copper sulphate solution and 25 ml of concentrated sulphuric acid were added to the tube and mixed gently. The digestion was carried out for 120 minutes at 35 °C using micro-Kjeldhal digester in the presence of catalyst (1 ml of copper sulphate and 15 g potassium sulphate) where sulphuric acid was used as an oxidizing agent. Then it was allowed to cool at room temperature over a period of 25 minutes. The digested solution was diluted with 250 ml of distilled water. The Kjeldahl tube was placed in the distillation equipment. Then, 75 ml of 40 % sodium hydroxide solution was added into the tube. Then ammonia was distilled using 50 ml of 4 % boric acid solution with bromocresol green/methyl red as indicators until blue color appears. Finally, the sample was titrated with 0.1N hydrochloric acid solution until a faint pink color is

formed and the burette reading was taken to the nearest 0.01 ml. Blank test was carried out using the above procedure except that water was used instead of the test sample. The percentage of nitrogen in the milk samples was calculated using the formula provided by AOAC (1990). % N = 1.4007x (vs-vb) X N HCl x 100 Weight of sample % CP = % N x 6.38 Where: % N = percentage of nitrogen by weight; Vs = volume of HCl used for titration of sample; Vb = volume of HCl used for titration of the blank; % CP = percent of crude protein. Butterfat and protein yields were calculated by multiplying each percentage by the average between morning and evening milk yield.

3.4.3 Milk Yield Characteristics

Initial yield (kg): measured as milk yield at day 7 postpartum

Peak yield (kg): measured as optimal test day yield during the lactation period

Peak day (d): measured as the day of the highest milk yield within the lactation period

Last test day yield (kg): measured as the last test day yield before production drops below 2 litres

Lactation length (days): measured as the number of days from the beginning of lactation to the drying period

3.4.4 Measures of Milk Yield Efficiency

Fat corrected milk (FCM) = [(0.4*milk yield (kg) + [(15*fat yield (kg)] (Gains, 1928)

$$FCM / kgW = \frac{FCM}{W}, \quad \text{where } w = \text{body weight (kg)}$$

$$FCM / kgMW = \frac{FCM}{M^{0.75}}, \quad \text{where } MW = \text{Metabolic body weight (kg) and 0.75 is the power function for calculating MW (Kleiber, 1967)}$$

$$FCM / day / kgW = \frac{FCM / day}{W}$$

$$FCM / day / kgMW = \frac{FCM / day}{W^{0.75}}$$

$$Net\ energy\ efficiency\ (NEE)(\%) = \frac{750 * FCM / day * 100}{(750 * FCM / day) + 70W^{0.75}}, \text{ where } 750 = \text{kilocalories of} \\ \text{/energy per kg of FCM and} \\ 70 = \text{Basal metabolic rate}$$

$$Dairy\ Merit\ (DM)(\%) = \frac{NEE * FCM / day}{FCM / day + 0.173W^{0.75}} \quad (\text{Brody, 1945})$$

3.4.5 Body weight measurement

Body weight was measured by firmly positioning the animal on the Avery weighbridge scale (Tronix Model E1010) without agitation. The weight was expressed in kilograms (kg). The weights of the animals were recorded at monthly intervals for 12 months. The conformation traits measurements are subsumed in Table 3.2.

3.4.6 Body Condition Scores

Body condition scoring was assessed using a subjective visual evaluation based on a threshold scale ranging from 1 to 5, following the methodology outlined by Banos *et al.* (2010). The scoring system is defined as follows:

- 1: Severe under conditioning (emaciated)
- 2: The frame is visible
- 3: Frame and covering are well-balanced
- 4: Fat, with no discernible bony processes
- 5: Severe over conditioning (grossly fat)

Table 3.2: Definition of Conformation traits of dairy cattle

No	Measurements	Description	Instruments
1	Chest ligament	Measured as the depth of cleft at the base of the rear udder	Flexible tape
2	Chest width	Measured as the inside surface distance between the top of the front legs	Flexible tape
3	Body depth	Measured as the distance between the top of the spine and the bottom floor of the abdomen at the last rib	Flexible tape
4	Stature	Measured from the top of the spine in between hips to the ground	Measuring stick
5	Rump width	Measured between the inner walls of the two ischial tuberosities (i.e. pin bones)	Flexible tape
6	Heart girth	Measured behind the front legs and shoulder blades	Flexible tape
7	Udder clearance	Measured from the ground to the bottom of the udder	Measuring stick
8	Rear Udder height	Measured as the distance from the bottom of the vulva to the top of the rear udder	Flexible tape
9	Rear Udder width	Measured as the udder width at the point where the rear udder is attached to the body.	Flexible tape
10	Teat length	Measured as the distance from base to tip of the front teat.	Flexible tape

Source: International Committee on Animal Recording (2007)

3.4.7 Fertility Traits

For fertility, traits were computed using fertility charts and calculators using the VAMMP dairy management software interface. The traits were:

Age at first calving (AFC) is defined as the (in days) at which the cow first had its first calf

Calving Interval (CI) is defined as the period (in days) between the first and the next calving.

Day open (DO) is defined as the period (in days) from calving to the next conception.

Number of Service per Conception (NSC) is defined as the number of services or matings to effect a pregnancy.

Calving rate (CR) is defined as the number of calves born per 100 services.

Herd life is defined as the number of days a cow spends in the herd before culling

3.5 Lactation Models

Five lactation models (Wood, Wilkink, Djisktra, MilkBot, Neural network) were constructed from the actual test day milk yield data.

Total milk yield was estimated as:

$$TMY = \sum_{t=1}^{350} 7(Y_t)$$

Where, t is the days of lactation

Y_t = average milk yield in day t of lactation

3.5.1 Wood Model

Woods (1967) incomplete gamma function method is an empirical model where

$$Y = at^b e^{-ct}$$

$$\text{Peak day} = \frac{b}{c}$$

$$\text{Peak yield} = a \left(\frac{b}{c} \right)^b e^{-b}$$

a = scaling factor

b = increasing slope of yield or rate of increase to peak

c = decreasing slope of yield or rate of decline after the peak production

$$\text{Persistence (S)} = -(b+1)\ln c$$

3.5.2 Wilmink Model

The Wilmink (1987) model is a modification of the model by Cobby and Le Du (1978)

$$Y = a + bt + ce^{-kt}$$

where a = production level

b = related to milk production before lactation peak

c = correlated to the peak day

d = decrease in production after the lactation peak

$$\text{Persistence (S)} = \frac{y_p}{t} - \frac{y_p}{t} \ln \left[\frac{e^t + e^{t^1}}{1 + e^{t^1}} \right] + b_3 \ln \left[\frac{e^t + e^{t^1+p}}{1 + e^{t^1+p}} \right]$$

3.5.3 Dijkstra Model

Dijkstra *et al.* (1993) model is a mechanistic model where:

$$Y_t = a \exp \left(\frac{b(1 - \exp^{-ct})}{c - dt} \right)$$

a = theoretical initial milk production and is a product of the number of differentiated parenchyma cells and milk production per cell that is assumed as being constant during lactation

b = cell proliferation rate at birth

c = rate of decrease in cell proliferation during lactation

d = cell death rate during lactation.

Persistency (S) = c

3.5.4 MilkBot Model

MilkBot model is an empirical model

$$Y(t) = a \left(1 - \frac{\exp\left(\frac{c-t}{b}\right)}{2} \right) \exp(-dt)$$

Peak milk production was estimated using this formula:

$$t_{peak} = -b \ln\left(\frac{2db}{db+1}\right) + c$$

Total milk yield was estimated as:

$$TMY_{305} = \frac{a}{b} e^{-305d} + \frac{a}{2} \frac{b}{db+1} e^{\frac{c-305}{b}} e^{-305d} + \frac{a}{d} - \frac{a}{2} \frac{b}{db+1} e^{\frac{c}{b}}$$

a = scaling (determines the overall magnitude of milk production)

b = ramp (controlling the rate of rise in milk production in early lactation)

c = offset (the time of maximal creation of productive capacity)

d = decay (controlling the loss of productive capacity, and analogous to the first-order decay constant common in pharmacokinetics)

The constant e is Euler's number (i.e. the root of natural logarithms, approximately 2.718)

$$\text{Persistency (S)} = \frac{0.693}{decay}$$

3.5.5 Neural Network Model

Neural network model is an artificial intelligent model where a , b , c are parameter vectors and also a universal approximator

$$Y(t) = \sum_i C_i 1(a_i < x < b_i)$$

a = Inclining phase of lactation

b = increasing slope of yield

c = declining phase of lactation

The equations for persistency of the different lactation curve model which was defined as the ability to sustain peak milk production was subsumed in Table 3.4. Best predict algorithm was used to estimate the peak day, peak time, total yield and last day yield for each of the models.

Persistency (S) = Best predict algorithm

Optimization of milk yield for Lactation curve

Gosing solver was used to optimize the model parameter by initializing the starting values at non zero positives of 1 to simulate the relationship among a, b, c and d parameters. Model equation was solved when there was convergence and the sum of square deviations was minimized.

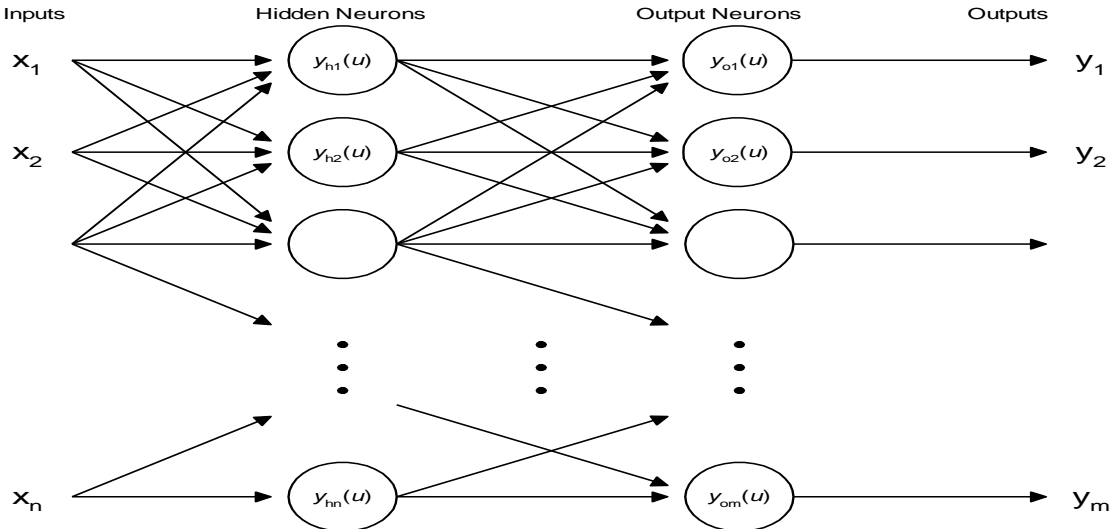


Fig 3.2. Topology/ Architecture of the Neural Network for Monthly Milk Extraction

X_{1-n} = coefficient of the independent variables (day 0 through day 360), Y_m – Daily milk yield. *U-weights of the coefficients*

3.6 Genetic Analysis

Predicted Breeding Value Estimation

The estimation of genetic parameters and prediction of estimated breeding values were solved in ASReml 3.0 (Gilmour *et al.*, 2009). Accuracy (r_{TI}) of EBVs was calculated as:

$$r_{TI} = \sqrt{1 - \frac{SE^2}{(1+f)\sigma_a^2}}$$

Where SE^2 is the squared standard error of the EBV, f represents the inbreeding coefficient (derived from the diagonal element of the additive genetic numerator relationship matrix) and σ_a^2 is the additive genetic variance of the specific trait estimated from the data.

Inbreeding Coefficient Estimation

Best Linear Unbiased Estimation Method

The inbreeding coefficient for each animal (F_i) in the pedigree was calculated using the *ainv* tool of the ABTK. The *ainv* tool implements the algorithm of Meuwissen and Luo (1992) to compute the inbreeding coefficients. Individual inbreeding coefficients were used to compute the individual rate of inbreeding (ΔF_i) according to the methodology described by Gutiérrez *et al.* (2009). The ΔF_i is an alternative measure of inbreeding which is adjusted for the depth of known pedigree. Therefore, the individual rate of inbreeding makes it possible to distinguish between two animals with the same inbreeding coefficient, but different number of generations in which inbreeding was accumulated (González-Recio *et al.*, 2007; Gutiérrez *et al.*, 2009). The individual rate of inbreeding was calculated as $\Delta F_i = 1 - t^{-1} (1 - F_i)$ where t is the number of known equivalent generations for the i th individual.

The t was calculated using the ENDOG v4.3 computer program (Gutiérrez and Goyache, 2005). The MTDFREML software package was used to estimate the effect of inbreeding (Boldman *et al.*, 1995).

Path Analysis Method

The level of inbreeding – inbreeding coefficient F_x , was calculated as follows (Wright, 1922):

$$F_x = \sum 0.5^{n+n'+1} (1 + F_a)$$

Where: Σ =summation over all paths through to common ancestor, n =the number of generations from the sire to the common ancestor, n' =the number of generations from the dam to the common ancestor, F_a =the inbreeding coefficient of the common ancestor.

3.7 Statistical Model and Analysis

3.7.1 Data preparation

Data preparation entailed the entry of data into an excel worksheet and statistical manipulation of the data to compute some of the indices that were not directly measured on the cows. Edits were performed to remove records that were incomplete or had obvious errors.

3.7.2 Statistical model

The statistical model describing regression for 305day fat corrected milk yield was given as;

$Y = \beta_0 + \beta_1 100dFCM + \beta_2 FY + \beta_3 PY + \beta_4 BW + \beta_5 BD + \beta_6 BCS + \beta_7 UC + \beta_8 TL + \beta_9 RW + \beta_{10} RUW$; where Y = 305day fat corrected milk yield, β_0 =intercept, β_{1-10} =coefficient of the independent variables (100dFCM, FY, PY, BW, BD, BCS, UC, TL, RW and RUW are the

fat corrected milk yield (100dFCM), fat yield, protein yield, body weight, body depth, body condition score, udder clearance, teat length, rump width and rear udder height).

Model selection for regression analysis

Selection of traits was done using backward elimination regression method. The Backward elimination method begins by placing all the predictor variables in the model and then removing the predictor variable which contributes the least to the model. The procedure is repeated with the left over predictor variables and for the predictor variable having least contribution is removed. The process is continued until a model in which all of the remaining predictor variables are statistically significant ($P < 0.05$) is obtained.

Model describing the ANOVA was given as; $Y_{ijkl} = \mu + \alpha_i + \delta_k + e_{ijkl}$, where Y_{ijkl} = observed measure, μ = the overall mean, α_i = i^{th} fixed effect of genotype, δ_k = k^{th} covariate effect of days in milk and e_{ijkl} = residual random error.

(Co) variance components were estimated by Derivative free Restricted Maximum Likelihood Method using the MTDFREML software (Boldman *et al.*, 1995), which estimates fixed and random effects by solving the mixed models equations (MME), described by Henderson (1949). Variance components for milk component, fertility and conformation were estimated through univariate analysis using an animal model considering the effects of herd, number of calving and contemporary group as fixed, and the permanent environmental, animal additive genetic and residual effects as random. The contemporary group included herd, year of calving and calving season.

The repeated records model used (Mrode, 1996) can be described as:

$$y = Xb + Wpe + Za + e$$

in which y = vector of observations; b = vector of fixed effects (herd, number of calving, and season). pe = vector of random permanent environmental effects; a = vector of random animal effects; e = vector of random residual effects; X , W , and Z = incidence matrices that establish relationships between the records and the effects. It is assumed that permanent environmental, animal, and residual effects are independently distributed with mean zero and constant variance:

$$V \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

Considering that A = relationship matrix, $I\sigma_e^2 = R$, then $V(y) = ZAZ'\sigma_a^2 + WI\sigma_{pe}^2W' + R$.

Thus, the mixed model equations for the best linear unbiased estimator (BLUE) of estimable functions of b and for the best linear unbiased prediction (BLUP) of pe and a are:

$$\begin{bmatrix} b \\ a \\ pe \end{bmatrix} = \begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + A_{\alpha_1}^{-1} & Z'W \\ W'X & W'Z & W'W + I_{\alpha_2} \end{bmatrix}^{-1} = \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}$$

in which A = relationship matrix; and $\alpha_1 = \sigma_e^2 / \sigma_a^2$ and $\alpha_2 = \sigma_e^2 / \sigma_{pe}^2$. Heritability was estimated as the ratio of the additive genetic variance to total phenotypic variance; and repeatability, as the ratio of the sum of the additive genetic variance plus permanent environmental variance to phenotypic variance, as described by Falconer and Mackay (2001):

To estimate genetic and environmental correlations, a bivariate model was used including herd, number of calving and contemporary group (year of calving and calving season) as the fixed effects, and the permanent environmental and additive genetic direct effects as random. The matrix model used was:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

in which y_i = vector of N observations; b_i = vector of fixed effects (herd, number of calving, contemporary group); p_{ei} = vector of random permanent environmental effects; a_i = vector of random animal effects; e_i = vector of random residual effects; X , W , and Z = incidence matrices establishing relationships between the records and the fixed and random effects, respectively. It is assumed that random permanent environmental, animal and error effects are independently distributed with a mean of zero and variance:

$$V \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} G_0 \otimes A & 0 & 0 \\ 0 & Q_0 \otimes I & 0 \\ 0 & 0 & R_0 \otimes I \end{bmatrix}$$

in which \otimes = direct or Kronecker product; I = identity matrix equal to number of observations; A = relationship matrix among all animals in the pedigree; G_0 = variance and covariance matrix of random animal effects; $\sigma_{a_{ii}}^2$ = animal additive genetic variance for trait i ; $\sigma_{a_{jj}}^2$ = animal additive genetic variance for trait j ; $\sigma_{a_{ij}} = \sigma_{a_{ji}}$ = animal additive genetic covariance between traits i and j ; Q_0 = variance and covariance matrix of random permanent environmental effects; $\sigma_{pe_{ii}}^2$ = permanent environmental variance for trait i ; $\sigma_{pe_{jj}}^2$ = permanent environmental variance for trait j ; $\sigma_{pe_{ij}} = \sigma_{pe_{ji}}$ = permanent environmental covariance between traits i and j ; R_0 = variance and covariance matrix of residual effects; $\sigma_{e_{ii}}^2$ = residual variance for trait i ; $\sigma_{e_{jj}}^2$ = residual variance for trait j ; and $\sigma_{e_{ij}} = \sigma_{e_{ji}}$ = residual covariance between traits i and j . The mixed model equations for the best linear unbiased estimator (BLUE) of estimable functions of b and the best linear unbiased prediction (BLUP) of a and ap are:

$$G_0 = \begin{bmatrix} \sigma_{a_{ii}}^2 & \sigma_{a_{ij}}^2 \\ \sigma_{a_{ji}} & \sigma_{a_{jj}}^2 \end{bmatrix}, Q_0 = \begin{bmatrix} \sigma_{pe_{ii}}^2 & \sigma_{pe_{ij}} \\ \sigma_{pe_{ji}} & \sigma_{pe_{jj}}^2 \end{bmatrix}, R_0 = \begin{bmatrix} \sigma_{e_{ii}}^2 & \sigma_{e_{ij}} \\ \sigma_{e_{ji}} & \sigma_{e_{jj}}^2 \end{bmatrix}$$

$$\begin{bmatrix} \hat{b} \\ \hat{a} \\ \hat{pe} \end{bmatrix} = \begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & X'R^{-1}W \\ Z'R^{-1}X & Z'R^{-1}Z + k_1 & Z'R^{-1}W \\ W'R^{-1}X & W'R^{-1}Z & W'R^{-1}W + I * Q^{-1} \end{bmatrix}^{-1} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \\ W'R^{-1}y \end{bmatrix}$$

in which $k_1 = G_0 * A^{-1}$, $\hat{b} = \begin{bmatrix} \hat{b} \\ \hat{b}_2 \end{bmatrix}$, $\hat{a} = \begin{bmatrix} \hat{a}_1 \\ \hat{a}_2 \end{bmatrix}$ and $\hat{pe} = \begin{bmatrix} \hat{pe}_1 \\ \hat{pe}_2 \end{bmatrix}$

The estimates of genetic (r_g), permanent environmental (r_{pe}) and residual (r_e), correlations were obtained from the estimation of covariance components using the following equations:

$$r_g = \frac{\sigma_{aij}}{\sqrt{\sigma_{ait}^2 \sigma_{ajt}^2}}, r_{pe} = \frac{\sigma_{peij}}{\sqrt{\sigma_{peit}^2 \sigma_{pejt}^2}}, r_e = \frac{\sigma_{eij}}{\sqrt{\sigma_{eit}^2 \sigma_{ejt}^2}}$$

3.7.3 Data Analysis

Preliminary descriptive statistical analyses were done before statistical modelling and analysis to test the significance of fixed effects. All descriptive statistical analyses (Mean, coefficient of variation and standard error of mean) were done using R commander (2016) Software. The interaction between genotype, breed improvement and year of calvings was analysed using a factorial layout. The Tukey's procedure for mean comparison was used to rank the means after a significant effect ($P < 0.05$) was observed. The ordinary least squares method using PROC REG in Statistical Analysis Software (S.A.S 9.4, 2014) was used to compute the regression analysis. Components of (co)variance were estimated by fitting an animal model using the AI-REML algorithm (Johnson and Thompson, 1995). Genetic correlations were estimated using bivariate analyses. Lactation curves were fitted in MATLAB (2014) using days in milk as a numerical variable. Genetic function algorithm was modelled in Material studio software. Genetic algorithm system as a selection tool was incorporated into Material studio 7 program (Acclerys Material Studio, 2014) and utilized in this study. The Genetic algorithm method (GA) begins with the formation of a populace of randomly produced parameter sets. The probability of a given parameter from the active set is 0.5 in any of the initial population sets. The parameters set used for the genetic algorithm incorporates the boundaries for mutation (0.1), hybrid (0.9), population (10000), number of model generation (1000), R^2 floor limit (50%), and target capacity ($R^2/\text{Number of}$

parameters). The calculation keeps running until the wanted number of generations is achieved. Equations were generated between the experimental biological activity and the descriptors. The best mathematical statement was taken in light of statistical parameters such as adjusted coefficient of multiple determination ($\text{Adj } R^2$), root mean square error and Bayesian information criterion.

CHAPTER FOUR

4.0

RESULTS

4.1 Variations in Measures of Efficiency of Milk Production Traits in Genotypes of Cows in different Environment

4.1.1 Least squares means and coefficients of variation in measures of efficiency of milk production traits among genotypes of cows in Shonga Dairy Holdings in Kwara State.

The least squares means and coefficients of variation of the thirteen milk measures across the four genotypes are presented in Table 4.1. Milk production and efficiency traits were greatly influenced ($P < 0.01$) by the genotypes of cows in Kwara State, except total solid. There were highly significant ($P < 0.01$) differences across the genetic groups. The mean fat corrected milk yield ($N = 2320$) for all the genotypes determined on the 305th day of milk production was 2208.7 ± 39.79 kg, with the highest (2411.8 ± 56.66 kg) recorded by Jersey cows, while JerseyxBunaji and FriesianxBunaji had the least yield (1810.5 ± 18.34 kg and 1937.6 ± 13.14 kg), respectively. The 305dFCM accounted for 36.76 % of the total variation in milk yield. The Jersey cows yielded 11.50 %, 24.47 % and 33.21 % more milk for 305dFCM than Holstein Friesian, FriesianxBunaji and JerseyxBunaji respectively while HolsteinxBunaji was 7.02 % higher in milk yield than JerseyxBunaji. 305 FCM /cows/per day was similar ($P > 0.05$) for the genotypes but statistically different ($P < 0.05$) from JerseyxBunaji. The genetic group effect was significant ($P < 0.05$) on 100dFCM, with each of the four genotypes being highly significantly ($P < 0.01$) different from the other three genetic groups. Holstein had the highest volume of milk while the least was recorded in the Jersey breed during the part period of milk production. The 100dFCM from Holstein was 13.88 % more than the Jersey breed respectively, while FriesianxBunaji was 3.51 % higher than JerseyxBunaji. The effect of genotypes was significant ($P < 0.05$) on 305 d fat yield, protein

yield and lactation length accounting for 37.03 %, 41.13 and 8.84 % of the total source of variation. The genetic group effect was highly significant ($P < 0.01$) for milk efficiency traits (FCMKgW, FCMKgMW, FCM/day/kgW, FCM/day/kgMW, net energy efficiency and dairy merit). The mean FCMKgW, FCMKgMW, FCM/day/kgW, FCM/day/kgMW, net energy efficiency and dairy merit for the combined genotypes were 4.2 ± 0.14 kg, 19.6 ± 0.55 kg, 108.1 ± 0.85 kg, 0.01 ± 0.001 kg, 39.7 ± 0.61 % and 58.3 ± 0.46 %, respectively. The characteristics estimating the efficiency of milk production in genotypes of dairy cows were highly variable ($CV = 23.91 - 50.17$ %).

Table 4.1: Least squares means (\pm standard error) and coefficient of variation of milk production and efficiency traits among different genetic groups of cows in Shonga Dairy Holdings in Kwara State.

Traits	Holstein Friesian (n=408)	Friesian x Bunaji (n=301)	Jersey (n=922)	Jersey x Bunaji (n=689)	Overall (n=2320)	CV %	SEM
305 FCM (kg)	2163.0 \pm 13.11 ^b	1937.6 \pm 13.14 ^c	2411.8 \pm 56.66 ^a	1810.5 \pm 18.34 ^c	2208.7 \pm 39.79	36.76	102.84
305 FCM /cow/per day(kg)	6.6 \pm 0.25 ^a	6.1 \pm 0.22 ^a	7.2 \pm 0.31 ^a	5.3 \pm 0.16 ^b	6.7 \pm 0.51	20.12	0.85
100d FCM (kg)	1085.9 \pm 12.12 ^a	888.1 \pm 11.61 ^b	758.5 \pm 10.81 ^d	812.1 \pm 14.72 ^c	840.4 \pm 9.93	33.72	25.56
305d Fat yield (kg)	41.2 \pm 0.66 ^a	32.3 \pm 0.62 ^b	52.2 \pm 2.29 ^a	33.2 \pm 0.92 ^b	44.5 \pm 1.60	37.03	6.48
305d protein yield (kg)	42.2 \pm 0.68 ^a	36.2 \pm 0.75 ^b	33.1 \pm 1.27 ^b	28.6 \pm 1.16 ^c	35.6 \pm 0.58	41.13	1.50
Total solid (g/100g)	12.2 \pm 0.08	12.6 \pm 0.09	12.5 \pm 0.09	12.6 \pm 0.09	12.4 \pm 0.05	6.48	0.40
Lactation length (days)	329.6 \pm 0.08 ^b	319.9 \pm 1.18 ^c	335.6 \pm 2.25 ^b	341.9 \pm 4.16 ^a	331.9 \pm 1.16	8.84	3.40
FCM Kg W	3.9 \pm 0.05 ^b	3.2 \pm 0.04 ^c	4.8 \pm 0.20 ^a	3.4 \pm 0.12 ^c	4.2 \pm 0.14	50.17	0.30
FCM Kg MW	18.5 \pm 0.17 ^b	15.4 \pm 0.15 ^c	22.1 \pm 0.78 ^a	15.8 \pm 0.42 ^c	19.6 \pm 0.55	45.06	1.21
FCM/day/kgW	0.04 \pm 0.01 ^b	0.06 \pm 0.01 ^a	0.02 \pm 0.01 ^c	0.06 \pm 0.01 ^a	0.01 \pm 0.003	50.17	0.01
FCM/day/kgMW	0.01 \pm 0.001 ^b	0.01 \pm 0.001 ^b	0.02 \pm 0.01 ^a	0.02 \pm 0.001 ^a	0.01 \pm 0.001	45.06	0.005
NEE (%)	39.3 \pm 0.20 ^{ab}	35.1 \pm 0.24 ^b	42.6 \pm 0.80 ^a	35.4 \pm 0.60 ^b	39.7 \pm 0.61	33.06	2.45
Dairy Merit (%)	57.7 \pm 0.16 ^a	54.6 \pm 0.17 ^b	60.6 \pm 0.64 ^a	54.8 \pm 0.25 ^b	58.3 \pm 0.46	23.91	2.19

^{abcd} Means of the same trait across genetic groups with different superscripts differ significantly (P<0.05); d-days; FCM-Fat corrected milk; kg-kilogram; MW-Metabolic weight; W-Weight; NEE –Net energy efficiency; CV-Coefficient of variation; SEM-Standard error of mean

4.1.2 Least squares means and coefficients of variation in measures of efficiency of milk production traits among genotypes of cows in Integrated Dairies Limited in Plateau State

Table 4.2 shows the least squares means and coefficients of variation of the thirteen milk measures of the two genetic groups. Milk production and efficiency traits were greatly influenced ($P<0.01$) by the genotypes of cows in Plateau State, except total solid. There were highly significant ($P<0.01$) differences between the two genetic groups. The mean fat-corrected milk yield ($N=3063$) for the combined genotypes determined on the 305th day of milk production was 4040.0 ± 74.92 kg, with the highest (4996.8 ± 92.64 kg) recorded by Holstein Friesian cows, while FriesianxBunaji had the least milk yield of 3322.8 ± 29.16 kg. The 305dFCM accounted for 37.64 % of the total variation in milk yield. The Holstein breed had an increment of 50.38 % for 305dFCM as compared to HolsteinxBunaji respectively. 305 FCM /cow/per day was statistically different ($P<0.05$) between the two genetic groups. The genetic group effect was significant ($P<0.05$) on 100dFCM, with each of the two genotypes being highly statistically ($P<0.01$) different from the other group.

Holstein had significantly higher values for milk yield than HolsteinxBunaji. The 100dFCM from Holstein Friesian was 29.77 % heavier than FriesianxBunaji. The effect of genotypes was significant ($P<0.05$) on 305d fat yield, protein yield and lactation length accounting for 37.83 %, 51.30 % and 19.52 % of the total source of variation. Genetic group effect was highly significant ($P<0.01$) on milk efficiency traits (FCMKgW, FCMKgMW, FCM/day/kgW, FCM/day/kgMW, net energy efficiency and dairy merit). The mean FCMKgW, FCMKgMW, FCM/day/kgW, FCM/day/kgMW, net energy efficiency and dairy merit for the combined genotypes were 6.9 ± 0.16 kg, 33.3 ± 0.74 kg, 0.02 ± 0.005 kg, 0.1 ± 0.02 kg, 52.6 ± 0.55 % and 73.0 ± 0.47 %, respectively.

respectively. The efficiency estimation of milk production in genotypes of cows were highly variable (CV=14.75- 42.45 %).

4.1.3 Least squares means and coefficients of variation in measures of efficiency of milk production traits among genotypes of cows in Sebore herd in Adamawa State

Milk production and efficiency traits were greatly influenced ($P<0.01$) by the genotypes of cows in Adamawa State, except 305FCM per cow per day protein yield and lactation length (Table 4.3). The results indicate that overall mean effect for 305 day fat corrected milk yield (305dFCM) was 1650.8 kg; 305 fat corrected milk yield per cow per day (305FCM/cows/day) 4.8 kg; 100-day fat-corrected milk yield (100dFCM) 728.5 kg; fat yield (305dFY) 33.6 kg; (305dPY) 22.1 kg; total solid (TS) 12.8 g/100 g; lactation length (LL) 343.1 days; fat corrected milk yield per bodyweight (FCM/kgW) 3.5 kg; fat corrected milk yield per metabolic bodyweight (FCM/kgMW) 95.9 kg; fat corrected milk yield per day per bodyweight (FCM/day/kgW) 0.05 kg; fat corrected milk yield per day per metabolic bodyweight (FCM/day/kgMW) 0.05 kg; net energy efficiency (NEE) 34.7 % and dairy merit (DM) 54.34 %. 305dFCM accounted for 17.54 % of the total variation in milk yield. Holstein and Brown Swiss had the heaviest milk weights and fat yield, respectively while the least was recorded in Simmental cows for part and full-period milk production (100dFCM and 305dFCM). The efficiency of milk production was best in Holstein Friesian except for fat-corrected milk per day per kg metabolic weight. Holstein Friesian differed significantly ($P<0.05$) from all the genotypes which were similar ($P>0.05$) for total solid. However, except for dairy merit (CV=8.14 %), the characteristics estimating the efficiency of milk production in genotypes of cows in Adamawa State were highly variable (CV=22.79 - 51.78 %).

Table 4.2: Least squares means (\pm standard error) and coefficient of variation of milk production and efficiency traits among different genetic groups of cows in Integrated Dairies Limited in Plateau State

Traits	Holstein Friesian (n=2042)	Friesian x Bunaji (n=1021)	Overall (n=3063)	CV %	SEM
305 FCM (kg)	4996.8 \pm 92.64 ^a	3322.8 \pm 29.16 ^b 8 9+0 06 ^b	4040.0 \pm 74.92	37.64	224.82
305 FCM /cow/per day(kg)	14.0 \pm 0.37 ^a		11.06 \pm 0.51	25.05	1.88
100d FCM (kg)	1585.3 \pm 20.34 ^a	1221.6 \pm 13.46 ^b	1345.7 \pm 46.94	50.42	50.47
305d Fat yield (kg)	186.8 \pm 7.34 ^a	110.3 \pm 3.44 ^b	115.3 \pm 4.09	51.30	21.91
305d protein yield (kg)	151.6 \pm 3.94 ^a	84.1 \pm 1.37 ^b	116.2 \pm 3.04	37.83	14.16
Total solid (g/100g)	12.2 \pm 0.07	12.4 \pm 0.08	12.3 \pm 0.05	6.33	0.39
Lactation length (days)	357.3 \pm 5.35 ^b	372.6 \pm 4.72 ^a	365.3 \pm 3.58	19.52	5.52
FCM Kg W	7.7 \pm 0.20 ^a	4.4 \pm 0.10 ^b	6.9 \pm 0.16	42.45	0.49
FCM Kg MW	37.1 \pm 0.89 ^a	21.22 \pm 0.42 ^b	33.3 \pm 0.74	40.62	2.17
FCM/day/kgW	0.01 \pm 0.001 ^a	0.3 \pm 0.001 ^b	0.02 \pm 0.005	41.45	0.002
FCM/day/kgMW	0.1 \pm 0.02 ^a	0.2 \pm 0.01 ^b	0.1 \pm 0.02	40.62	0.01
NEE (%)	55.7 \pm 0.66 ^a	42.27 \pm 0.49 ^b	52.6 \pm 0.55	25.96	2.96
Dairy Merit (%)	75.6 \pm 0.61 ^a	63.18 \pm 0.31 ^b	73.0 \pm 0.47	14.75	2.56

^{ab}Means of the same trait across genetic groups with different superscripts differ significantly (P<0.05); d-days; FCM-Fat corrected milk; kg-kilogram; MW-Metabolic weight; W-Weight; NEE –Net energy efficiency; CV-Coefficient of variation; SEM-Standard error of mean.

Table 4.3: Least squares means (\pm standard error) and coefficient of variation of milk production and efficiency traits among different genetic groups of cows in Sebare herd in Adamawa State

Traits	Holstein Friesian (n=875)	Jersey (n=218)	Simmental (n=278)	Brownswiss (n=212)	Overall (n=1583)	CV %	SEM
305 FCM (kg)	1788.2 \pm 39.35 ^a	1668.4 \pm 50.41 ^b	1475.7 \pm 23.17 ^c	1780.4 \pm 54.61 ^a	1650.8 \pm 25.59	17.54	86.71
305 FCM /cow/per day(kg)	5.1 \pm 0.28	4.9 \pm 0.25	4.2 \pm 0.23	5.3 \pm 0.35	4.8 \pm 0.20	22.35	1.21
100d FCM (kg)	934.6 \pm 10.96 ^a	669.8 \pm 8.07 ^c	719.5 \pm 10.64 ^b	642.8 \pm 8.88 ^d	728.5 \pm 24.84	13.76	10.45
305d Fat yield (kg)	40.2 \pm 2.23 ^a	30.4 \pm 2.04 ^b	24.0 \pm 1.18 ^b	35.2 \pm 2.22 ^a	33.6 \pm 0.83	40.03	3.85
305d protein yield (kg)	27.6 \pm 2.22	24.3 \pm 2.35	19.7 \pm 0.76	21.7 \pm 1.46	22.1 \pm 0.78	40.02	4.46
Total solid (g/100g)	11.9 \pm 0.08 ^b	12.8 \pm 0.16 ^a	12.9 \pm 0.13 ^a	12.9 \pm 0.11 ^a	12.8 \pm 0.07	6.29	0.32
Lactation length (days)	348.1 \pm 3.44	342.3 \pm 6.84	350.5 \pm 3.61	334.5 \pm 4.15	343.1 \pm 2.38	11.09	9.60
FCM Kg W	7.7 \pm 0.32 ^a	3.7 \pm 0.24 ^b	2.8 \pm 0.15 ^c	2.7 \pm 0.10 ^c	3.5 \pm 0.16	51.78	0.35
FCM Kg MW	61.7 \pm 1.76 ^d	102.8 \pm 4.1 ^c	117.2 \pm 3.52 ^b	133.0 \pm 2.16 ^a	95.9 \pm 0.55	39.41	3.33
FCM/day/kgW	0.02 \pm 0.002 ^a	0.01 \pm 0.001 ^b	0.01 \pm 0.002 ^b	0.01 \pm 0.002 ^b	0.01 \pm 0.005	51.78	0.01
FCM/day/kgMW	0.1 \pm 0.001 ^a	0.1 \pm 0.003 ^a	0.01 \pm 0.001 ^b	0.01 \pm 0.002 ^b	0.05 \pm 0.002	39.41	0.002
NEE (%)	50.5 \pm 0.91 ^a	36.7 \pm 1.18 ^b	31.3 \pm 0.81 ^c	31.9 \pm 0.72 ^c	34.7 \pm 0.70	22.79	1.67
Dairy Merit (%)	61.2 \pm 0.69 ^a	54.4 \pm 0.74 ^b	51.5 \pm 0.37 ^c	54.9 \pm 0.63 ^b	54.34 \pm 0.39	8.14	1.65

^{abcd} Means of the same trait across genetic groups with different superscripts differ significantly (P<0.05); See table 4.1 for abbreviation

4.1.4 Least squares means and coefficients of variation in measures of efficiency of milk production traits among genotypes of dairy cows in Nigeria after correcting for environmental effect

Table 4.4 shows the least squares means and coefficients of variation of the thirteen milk measures across the six genetic groups. Except for lactation length and total solid that were similar ($P>0.05$) all other traits showed highly significant differences ($P<0.01$) across the genetic groups. However, except for total solid (CV = 6.5 %), all the measures of efficiency of milk production traits were variable (CV=15.2 - 48.5 %). The mean fat-corrected milk yield (N=6966) for all the genotypes determined on the 305th day of milk production was 2496.4 ± 45.41 kg, with the highest (3199.8 ± 104.8 kg) recorded by Holstein Friesian cows, while Simmental had the least value (1475.7 ± 23.17 kg). Holstein dairy cows were more efficient in yield than other genotypes for 305d FCM (3199.8 ± 104.8 kg), 305MY/cow/d (9.3 ± 0.08 kg), 305d fat yield (92.5 ± 4.20 kg) and FCM KgMW (28.9 ± 0.90 kg).

Table 4.4: Least squares means (\pm standard error) and coefficient of variation of milk production and efficiency traits among different genetic groups of cows in Nigeria

Traits	Holstein Friesian (n=3325)	FRxBJ (n=1322)	Jersey (n=1140)	JxBJ (n=689)	Simmental (n=212)	Brownswiss (n=278)	Overall (n=6966)	CV %	SEM
305 FCM (kg)	3199.8 \pm 104.8 ^a	2552.5 \pm 51.07 ^b	2151.9 \pm 50.98 ^c	1710.5 \pm 18.3 ^d	1475.7 \pm 23.17 ^e	1780.4 \pm 54.61 ^d	2496.4 \pm 45.41	46.3	290.26
305MY/cow/d (kg)	9.3 \pm 0.08 ^a	7.2 \pm 0.06 ^b	6.4 \pm 0.05 ^b	5.0 \pm 0.03 ^c	4.4 \pm 0.02 ^d	5.1 \pm 0.03 ^c	7.2 \pm 0.04	30.0	1.15
100d FCM (kg)	1817.9 \pm 30.9 ^a	1708.2 \pm 54.3 ^{ab}	1269.2 \pm 14.13 ^b	1312.1 \pm 24.72 ^b	1119.5 \pm 18.64 ^c	1042.8 \pm 11.88 ^c	1549.2 \pm 21.26	34.7	87.90
305d FY (kg)	92.5 \pm 4.20 ^a	65.1 \pm 2.11 ^b	50.5 \pm 2.03 ^b	33.9 \pm 0.92 ^c	24.0 \pm 1.18 ^c	35.2 \pm 2.22 ^c	63.3 \pm 1.81	32.7	12.42
305d PY (kg)	92.8 \pm 4.81 ^a	62.2 \pm 2.19 ^{ab}	32.4 \pm 1.14 ^b	28.6 \pm 1.16 ^b	19.7 \pm 0.76 ^b	21.7 \pm 1.46 ^b	58.7 \pm 2.06	39.3	15.75
TS (g/100g)	12.3 \pm 0.05	12.5 \pm 0.06	12.4 \pm 0.08	12.6 \pm 0.09	12.9 \pm 0.13	13.0 \pm 0.11	12.5 \pm 0.03	6.5	0.40
LL (305 d)	343.7 \pm 2.71	353.3 \pm 2.66	337.4 \pm 2.04	341.9 \pm 4.16	334.5 \pm 4.15	350.5 \pm 3.60	344.9 \pm 1.48	15.4	17.90
FCM Kg W	6.1 \pm 0.19 ^a	4.5 \pm 0.11 ^a	3.4 \pm 0.12 ^b	5.2 \pm 0.20 ^a	2.8 \pm 0.15 ^b	2.7 \pm 0.10 ^b	4.8 \pm 0.09	48.5	0.8
FCM Kg MW	28.9 \pm 0.90 ^a	21.9 \pm 0.48 ^b	23.1 \pm 0.73 ^b	15.8 \pm 0.42 ^c	13.2 \pm 0.54 ^c	13.5 \pm 0.47 ^c	22.7 \pm 0.42	46.5	3.42
FCM/day/kgW	0.02 \pm 0.006 ^a	0.02 \pm 0.004 ^a	0.02 \pm 0.001 ^a	0.01 \pm 0.003 ^b	0.01 \pm 0.001 ^b	0.01 \pm 0.003 ^b	0.02 \pm 0.002	48.5	0.003
FCM/day/kgMW	0.09 \pm 0.003 ^a	0.07 \pm 0.00 ^a	0.08 \pm 0.002 ^a	0.05 \pm 0.001 ^b	0.04 \pm 0.002 ^b	0.04 \pm 0.002 ^b	0.07 \pm 0.001	46.5	0.01
NEE (%)	42.6 \pm 0.53 ^a	47.9 \pm 0.74 ^a	43.7 \pm 0.75 ^a	35.4 \pm 0.60 ^b	31.3 \pm 0.81 ^b	31.9 \pm 0.72 ^b	42.4 \pm 0.39	23.6	3.10
Dairy Merit (%)	66.9 \pm 0.78 ^a	63.0 \pm 0.52 ^a	54.8 \pm 0.25 ^b	60.7 \pm 0.56 ^b	51.5 \pm 0.37 ^b	54.9 \pm 0.63 ^b	61.8 \pm 0.37	15.2	2.41

^{abcde} Means of the same trait across genetic groups with different superscripts differ significantly ($P < 0.05$); d-days; TS-Total solid; FCM-Fat corrected milk; kg-kilogram; PY-Protein yield; NEE-Net energy efficiency; MW-Metabolic weight; W-Weight; CV-Coefficient of variation; SEM-Standard error of mean; FRxBJ-Friesian x Bunaji; JxBJ-Jersey x Bunaji

4.1.5 Spatial effect on the efficiency of milk production traits

Except for 305MYper cows per day and total solids that were similar ($P>0.05$) all other traits showed highly significant differences ($P<0.01$) across the locations (Table 4.5). Higher milk yields were obtained for cows in Plateau State for 305d FCM, 100d FCM, fat yield, FCM Kg W, FCM Kg MW, FCM/day/kgW, FCM/day/kgMW, net energy efficiency and dairy merit. This could be linked to the higher altitude effect in Plateau State which makes the cows less aware of heat stress. The coefficients of variation was highly variable ($CV=15.21-89.20\%$) with the exception of 305MY/cows/d ($CV=8.31\%$) and total solid ($CV=6.53\%$).

4.2 Variation in Bodyweight and Udder Conformation in Genotypes of Cows in Different Climatic Gradients

4.2.1 Least squares means and coefficients of variation in body weight and udder conformation traits among genotypes of cows in Shonga Dairy Holdings in Kwara State

Genotype had a significant ($P<0.05$) effect on body weight and conformation traits (Table 4.6). All the traits were significant across genotypes except body condition score, chest ligament, chest width, stature, rump and udder clearance, respectively. The CV % had a minimum value of 7.56 % in body depth (BD) and a maximum value of 31.45 % in body condition scores (BCS). The results indicated that overall ($N=1592$) mean for body weight (BW) was 517.33 kg; body condition score (BCS) 3.0; central ligament (CL) 4.3 cm; chest width (CW) 23.1cm; body depth (BD) 210.5 cm; stature (ST) 149.9 cm; rump (RP) 13.1 cm; heart girth (HG) 201.7 cm; udder clearance (UC) 42.6 cm; rear udder height (RUH) 35.7 cm; rear udder width (RUW) 13.9 cm and teat length (TL) 5.06 cm. FriesianxBunaji had a heavier body weight (633.5 kg) and deeper body depth (225.8 cm) which differed significantly across the genetic groups. The highest value for heart girth (223.9 cm) was recorded in JerseyxBunaji cows. Rear udder height in Jersey and

Holstein dairy cows was similar and higher (35.7 and 41.2 cm) than the other genotypes, respectively.

Table 4.5: Spatial effect on milk production and efficiency traits in multi-genotype cows

Traits	Adamawa (n=2320)	Plateau (n=3063)	Kwara (n=1583)	CV %	SEM
305 FCM (kg)	1650.8±25.59 ^c	3840.0±74.92 ^a	1939.7±21.0 ^b	72.62	102.64
305MY/cow/per day(kg)	4.8±0.23	10.5±0.55	5.8±0.12	8.31	2.44
100d FCM (kg)	1109.6±13.50 ^c	2047.5±45.24 ^a	1394.7±11.59 ^b	34.90	89.34
Fat yield (kg)	44.87±1.09 ^b	116.2±3.04 ^a	41.02±0.86 ^b	72.66	15.99
Protein yield (kg)	42.2±0.68 ^a	36.2±0.75 ^b	33.1±1.27 ^b	89.3	4.99
Total solid (g/100g)	12.8±0.07	12.3±0.05	12.4±0.05	6.53	0.46
Lactation length (305 d)	343.3±2.38 ^b	365.3±3.58 ^a	331.9±1.16 ^c	15.41	3.12
FCM Kg W	3.9±0.16 ^b	6.9±0.16 ^a	3.9±0.07 ^b	48.46	1.05
FCM Kg MW	15.9±0.55 ^b	33.3±0.74 ^a	18.4±0.29 ^b	46.54	4.39
FCM/day/kgW	113.3±2.53 ^b	118.0±1.09 ^a	108.1±0.85 ^c	48.46	0.01
FCM/day/kgMW	0.05±0.001 ^b	0.11±0.002 ^a	0.06±0.002 ^b	46.54	0.01
NEE (%)	34.74±0.70 ^b	52.55±0.55 ^a	38.66±0.32 ^b	23.57	4.01
Dairy Merit (%)	54.34±0.39 ^b	72.97±0.47 ^a	57.4±0.25 ^b	15.21	3.04

^{abde} Means of the same trait across genetic groups with different superscripts differ significantly (P<0.05); d-days; TS-Total solid; FCM-Fat corrected milk; kg-kilogram; PY-Protein yield; NEE-Net energy efficiency; MW-Metabolic weight; W-Weight; CV-Coefficient of variation; SEM-Standard error of mean; HxB-Holstein x Bunaji; JxB-Jersey x Bunaji

Table 4.6: Least squares means (\pm standard error) and coefficient of variation for body and udder conformation traits among different genetic groups of cows in Shonga Dairy Holdings in Kwara State

Conformation Traits	Holstein Friesian (n=367)	FRxBJ (n=360)	Jersey (n=510)	JxBJ (n=355)	Overall (n=1592)	CV %	SEM
Body weight (kg)	610.2 \pm 13.5 ^b	633.5 \pm 14.6 ^a	522.24 \pm 13.94 ^c	531.3 \pm 10.49 ^c	517.3 \pm 5.35	18.21	18.84
BCS (1-5)	2.9 \pm 0.05	2.8 \pm 0.06	3.3 \pm 0.12	3.2 \pm 0.15	3.0 \pm 0.06	31.45	0.45
Central ligament (cm)	4.4 \pm 0.07	4.4 \pm 0.13	4.3 \pm 0.04	4.3 \pm 0.05	4.3 \pm 0.04	15.54	0.34
Chest width (cm)	43.3 \pm 0.38	43.6 \pm 0.40	43.4 \pm 0.17	41.9 \pm 0.15	42.1 \pm 0.15	11.71	1.32
Body depth(cm)	223.3 \pm 0.15 ^a	225.8 \pm 0.54 ^a	191.2 \pm 0.99 ^c	203.6 \pm 0.68 ^b	210.5 \pm 0.90	7.56	3.03
Stature (cm)	145.9 \pm 1.26	152.6 \pm 8.23	152.5 \pm 1.53	149.9 \pm 1.60	149.9 \pm 1.80	21.12	15.85
Rump (cm)	14.0 \pm 0.15	12.7 \pm 0.27	12.7 \pm 0.07	12.7 \pm 0.09	13.1 \pm 0.08	11.29	0.68
Heart girth (cm)	198.0 \pm 1.54 ^b	176.4 \pm 1.40 ^c	207.6 \pm 1.11 ^b	223.9 \pm 0.51 ^a	201.7 \pm 1.10	9.56	5.68
Udder clearance (cm)	41.2 \pm 0.91	43.1 \pm 1.37	44.1 \pm 0.51	41.9 \pm 0.70	42.6 \pm 0.45	18.45	3.90
Rear Udder height (cm)	41.8 \pm 1.05 ^a	28.2 \pm 0.06 ^b	35.7 \pm 0.60 ^a	28.9 \pm 1.27 ^b	35.7 \pm 0.52	25.44	3.54
Rear Udder width (cm)	15.1 \pm 0.05 ^a	15.0 \pm 0.04 ^a	12.7 \pm 0.07 ^b	12.8 \pm 0.08 ^b	13.9 \pm 0.07	9.33	0.58
Teat length (cm)	4.7 \pm 0.08	5.1 \pm 0.10	5.2 \pm 0.02	5.2 \pm 0.06	5.06 \pm 0.04	14.53	0.36

^{abc} Means of the same trait across genetic groups with different superscripts differ significantly ($P < 0.05$); BCS-Body condition score; CV-Coefficient of variation; SEM-Standard error of mean; FRxBJ-FriesianXBunaji; JxBJ-JerseyxBunaji

4.2.2 Least squares means and coefficients of variation in body and udder conformation traits among genotypes of cows in Integrated Dairies Limited in Plateau State.

Table 4.7 shows the effect of genotypes on body and udder conformation traits in cows. Most of the traits were similar ($P>0.05$) except body weight, heart girth and udder clearance which differed significantly ($P<0.05$) across the genetic groups. The highest BW (600.1 kg) between the genotypes was found in FriesianXBunaji which differed significantly ($P<0.05$) from the Holstein Friesian (560.6 kg) genotype. Heart girth (HG) (cm) differed significantly ($P<0.05$) between the genotypes with FriesianXBunaji having a broader HG (212.2 cm). Udder clearance differed significantly ($P<0.05$) between the two genetic groups. Coefficients of variation ranged from 5.42 % in heart girth to 32.59 % in udder clearance.

4.2.3 Least squares means and coefficients of variation in body and udder conformation traits among genotypes of dairy cows in Sebore herd in Adamawa State.

The effect of genotypes on the body and udder conformation traits of dairy cows is depicted in Table 4.8. All measured characteristics varied significantly ($p<0.05$) between genotypes with the exceptions of body condition score, chest ligament, stature, and udder clearance. The weights of Simmental and Brown Swiss were similar and heavier (578.6 kg and 580.7 kg) respectively than other genetic groups. The rump was correctly sloped and wide in Holstein Friesian (13.2 cm) and differed significantly ($P<0.05$) from other genetic groups. Teat length was similar and longer in Holstein and Jersey dairy cows but differed statistically ($P<0.05$) from other genetic groups. The rear udder was high and similar for Holstein Friesian (39.9 cm), Simmental (39.0 cm) and Brown Swiss (39.3 cm) but differed significantly ($P<0.05$) from Jersey dairy cows (38.4 cm). Most of the traits were less variable except body weight and body condition score which were highly variable (32.47 and 32.29 %).

Table 4.7: Least squares means (\pm standard error) and coefficient of variation for body and udder conformation traits among different genetic groups of cows in Integrated Dairies Limited in Plateau State

Conformation Traits	Holstein Friesian (n=941)	FriesianxBunaji (n=682)	Overall (n=1623)	CV %	SEM
Body weight (kg)	560.6 \pm 8.33 ^b	600.1 \pm 11.28 ^a	581.3 \pm 7.22	17.96	18.26
BCS (1-5)	2.5 \pm 0.03 ^b	2.9 \pm 0.05 ^a	2.6 \pm 0.03	14.04	0.04
Central ligament (cm)	4.1 \pm 0.04	4.0 \pm 0.08	4.1 \pm 0.03	10.72	0.44
Chest width (cm)	44.8 \pm 0.16	41.9 \pm 0.18	42.9 \pm 0.12	7.94	2.74
Body depth(cm)	196.7 \pm 0.73 ^a	185.1 \pm 1.40 ^b	191.1 \pm 0.87	6.56	8.13
Stature (cm)	149.8 \pm 1.39	151.7 \pm 0.95	150.7 \pm 0.86	8.23	12.39
Rump (cm)	12.8 \pm 0.22	12.0 \pm 0.07	12.4 \pm 0.12	13.60	1.64
Heart girth (cm)	195.2 \pm 0.61 ^b	212.2 \pm 0.74 ^a	204.1 \pm 0.76	5.42	3.02
Udder clearance (cm)	48.9 \pm 1.45 ^b	70.7 \pm 1.72 ^a	60.3 \pm 1.36	32.59	6.39
Rear Udder height (cm)	25.9 \pm 0.73	28.1 \pm 0.45	27.0 \pm 0.44	23.59	6.29
Rear Udder width (cm)	12.1 \pm 0.07	12.1 \pm 0.08	12.1 \pm 0.05	6.40	0.78
Teat length (cm)	5.21 \pm 0.04	4.99 \pm 0.08	5.1 \pm 0.04	11.34	0.57

^{ab}Means of the same trait across genetic groups with different superscripts differ significantly (P<0.05); BCS-Body condition score; CV-Coefficient of variation; SEM-Standard error of mean; FRxBJ-FriesianxBunaji

Table 4.8: Least squares means (\pm standard error) and coefficient of variation for body and udder conformation traits among different genetic groups of cows in Sebore farm in Adamawa State

Conformation Traits	Holstein Friesian (n=220)	Jersey (n=390)	Simmental (n=250)	Brownswiss (n=204)	Overall (n=1064)	CV %	SEM
Body weight (kg)	585.4 \pm 26.6 ^a	344.5 \pm 9.34 ^b	578.6 \pm 22.7 ^a	580.7 \pm 22.8 ^a	456.3 \pm 15.96	32.47	61.50
BCS (1-5)	3.4 \pm 0.26	3.9 \pm 0.34	3.8 \pm 0.20	3.3 \pm 0.16	3.1 \pm 0.11	32.29	0.62
Central ligament (cm)	4.3 \pm 0.08	4.3 \pm 0.13	4.3 \pm 0.06	4.2 \pm 0.07	4.1 \pm 0.04	10.23	0.22
Chest width (cm)	47.7 \pm 0.25 ^a	42.4 \pm 0.38 ^b	47.6 \pm 0.22 ^a	42.2 \pm 0.04 ^b	43.6 \pm 0.11	5.73	0.59
Body depth(cm)	213.8 \pm 1.24 ^a	199.4 \pm 0.43 ^b	190.6 \pm 1.04 ^c	214.7 \pm 1.48 ^a	203.7 \pm 1.15	6.59	3.78
Stature (cm)	153.0 \pm 3.34	153.4 \pm 3.51	155.5 \pm 1.86	154.7 \pm 2.48	154.5 \pm 1.29	9.46	7.38
Rump width (cm)	13.2 \pm 0.23 ^a	12.9 \pm 0.15 ^b	10.5 \pm 0.11 ^c	12.5 \pm 0.12 ^b	12.6 \pm 0.06	6.73	0.41
Heart girth (cm)	234.7 \pm 1.50 ^a	216.4 \pm 0.51 ^b	208.5 \pm 0.96 ^b	233.0 \pm 1.76 ^a	221.7 \pm 1.20	6.52	4.21
Udder clearance (cm)	44.7 \pm 0.85	44.4 \pm 1.41	43.7 \pm 0.71	43.8 \pm 0.64	44.0 \pm 0.40	10.28	2.28
Rear Udder height (cm)	39.9 \pm 0.10 ^a	34.4 \pm 0.14 ^b	39.0 \pm 0.21 ^a	39.3 \pm 0.10 ^a	36.2 \pm 0.09	2.68	0.49
Rear Udder width (cm)	15.6 \pm 0.30 ^a	12.4 \pm 0.14 ^b	15.2 \pm 0.09 ^a	12.5 \pm 0.12 ^b	13.8 \pm 0.14	11.71	0.38
Teat length (cm)	5.6 \pm 0.01 ^a	5.9 \pm 0.09 ^a	3.8 \pm 0.03 ^b	3.1 \pm 0.01 ^b	4.4 \pm 0.05	11.10	0.40

^{ab} Means of the same trait across genetic groups with different superscripts differ significantly ($P < 0.05$); BCS-Body condition score; CV-Coefficient of variation; SEM-Standard error of mean

4.2.4 Least squares means and coefficients of variation in body and udder conformation traits among genotypes of cows in Nigeria after correcting for environmental effect

The least squares means and coefficients of variation of the twelve body and udder conformation traits across the six genotypes are presented in Table 4.9. Body and udder conformation traits were greatly influenced ($P < 0.001$) by the genotypes of cows in Nigeria, except body condition score, chest ligament, chest width, stature, rump and teat length. Genotype was a significant ($P < 0.05$) source of variation in body weight, body depth, heart girth, udder clearance, rear udder height and width, respectively. The mean body weight ($N=5324$) for all the genotypes determined was 517.3 ± 5.35 kg, with the highest (580.4 kg) recorded by HolsteinxBunaji, while Jersey and JerseyxBunaji had the lowest (457.4 and 444.3 kg). The HolsteinxBunaji was 9 %, 17.2 %, 17.5 %, 21.2 % and 23.4 % heavier than Holstein, Brown Swiss, Simmental, Jersey and JerseyxBunaji, respectively. HolsteinxBunaji had the highest value for udder (60.6 cm) and differed significantly ($P < 0.05$) from other genetic groups. Body depth was deeper and similar in Holstein, HolsteinxBunaji and Brown Swiss. Heart girth was broader and similar in JerseyxBunaji (223.9 cm) and Brown Swiss (232.8 cm) but differed significantly ($P < 0.05$) across the genetic groups. Rear udder height was similar for all the genotypes except HolsteinxBunaji and JerseyxBunaji. Simmental had a high rear udder and differed significantly ($P < 0.05$) across the genetic groups.

Table 4.9: Least squares means (\pm standard error) and coefficient of variation for body and udder conformation traits among different genetic groups of cows in Nigeria

Conformation Traits	Holstein Friesian (n=1528)	FRxBJ (n=1042)	Jersey (n=1400)	JXBJ (n=900)	Simmental (n=250)	Brownswiss (n=204)	Overall (n=5324)	CV %	SEM
Body weight (kg)	527.9 \pm 5.36 ^b	580.4 \pm 7.66 ^a	457.4 \pm 13.5 ^d	444.3 \pm 17.46 ^d	478.6 \pm 22.73 ^c	480.7 \pm 14.8 ^c	517.3 \pm 5.35	22.4	9.5
BCS (1-5)	2.0 \pm 0.05	2.9 \pm 0.03	3.4 \pm 0.12	4.2 \pm 0.15	3.8 \pm 0.20	4.3 \pm 0.16	3.3 \pm 0.06	30.7	2.4
Central ligament (cm)	4.3 \pm 0.04	4.2 \pm 0.06	4.3 \pm 0.04	4.3 \pm 0.04	4.3 \pm 0.06	4.2 \pm 0.07	4.3 \pm 0.04	13.4	0.29
Chest width (cm)	22.5 \pm 0.18	22.5 \pm 0.19	23.4 \pm 0.16	21.9 \pm 0.15	23.1 \pm 0.22	22.2 \pm 0.04	23.1 \pm 0.15	10.0	1.10
Body depth (cm)	204.5 \pm 1.39 ^a	207.3 \pm 1.19 ^a	192.4 \pm 0.90 ^c	203.6 \pm 0.68 ^b	190.5 \pm 1.04 ^c	214.7 \pm 1.48 ^a	210.5 \pm 0.90	8.2	5.39
Stature (cm)	149.3 \pm 0.81	150.9 \pm 3.13	152.6 \pm 1.40	149.9 \pm 1.60	155.5 \pm 1.86	154.7 \pm 2.48	150.0 \pm 1.80	15.9	12.0
Rump (cm)	13.3 \pm .13	12.3 \pm 0.11	12.7 \pm 0.07	12.7 \pm 0.09	12.5 \pm 0.11	12.5 \pm 0.12	12.9 \pm 0.08	11.5	0.70
Heart girth (cm)	200.3 \pm 1.02 ^b	199.1 \pm 1.49 ^b	208.9 \pm 0.99 ^b	223.9 \pm 0.51 ^a	208.5 \pm 0.96 ^b	232.8 \pm 1.75 ^a	201.7 \pm 1.10	8.6	7.23
Udder clearance (cm)	45.1 \pm 0.82 ^b	60.6 \pm 1.57 ^a	44.1 \pm 0.48 ^b	41.9 \pm 0.70 ^b	43.7 \pm 0.71 ^b	43.8 \pm 0.64 ^b	42.6 \pm 0.45	30.8	6.10
Rear Udder height cm)	35.3 \pm 0.67 ^{ab}	28.6 \pm 0.53 ^b	36.1 \pm 0.52 ^a	28.9 \pm 1.27 ^b	39.0 \pm 0.21 ^a	39.3 \pm 0.09 ^a	35.7 \pm 0.52	25.8	3.42
Rear Udder width (cm)	13.4 \pm 0.11 ^b	13.2 \pm 0.12 ^b	13.1 \pm 0.12 ^b	12.8 \pm 0.08 ^c	15.2 \pm 0.09 ^a	12.5 \pm 0.12 ^c	13.9 \pm 0.07	11.2	0.54
Teat length (cm)	5.0 \pm 0.05	5.1 \pm 0.06	5.2 \pm 0.05	5.2 \pm 0.02	4.8 \pm 0.03	5.9 \pm 0.09	5.06 \pm 0.04	13.1	0.63

^{abcd}Means of the same trait across genetic groups with different superscripts differ significantly (P<0.05); BCS-Body condition score; CV-Coefficient of variation; FRxBJ-FriesianxBunaji; JxBJ-JerseyxBunaji; SEM-Standard error of mean

4.2.5 Spatial effect on bodyweight and udder conformation traits

The spatial effect was a highly significant ($P<0.01$) source of variation in body weight, body depth, udder clearance, teat length, rear udder height, and width (Table 4.10). The coefficients of variation ranged from 8.21 % in body depth to 30.76 % in udder clearance. Cows in Plateau State recorded the heaviest and wider udder clearance which differed significantly ($P<0.05$) from Kwara and Adamawa States. Cows in Kwara and Adamawa States had longer rear udder height which was statistically different ($P<0.05$) from Plateau State.

4.3 Variations in Reproductive Traits in Genotypes of Cows in Different Environments

4.3.1 Least squares means of genetic and non-genetic factors on reproductive traits of cows in Shonga Dairy Holdings in Kwara State

Table 4.11 shows the Least squares means of reproductive traits across genetic and nongenetic factors in Kwara State. The genotype effect was highly significant ($P<0.01$) for all the reproductive traits. The average AFC, NSC, DO, CI, CR and HL (N=2320) for all the genotypes were 1134.9 ± 18.91 d, 2.4 ± 0.03 , 185.4 ± 1.56 d, 409.2 ± 5.87 d, 47.3 ± 0.48 % and 37.8 ± 0.94 months, respectively. However, Holstein Friesian and FriesianxBunaji were highly significantly ($p<0.01$) younger than Jersey and JerseyxBunaji at first calving in Kwara State.

Jersey had the highest number of insemination per conception, which differed significant ($P<0.01$) from other genotypes. NSC was similar for Holstein Friesian and FriesianxBunaji and JerseyxBunaji. CI in Holstein (330 ± 13.19 d) was 63 d shorter than HolsteinxBunaji (393.8 ± 11.30 d) which differed significantly ($P<0.01$) between the genotypes.

Table 4.10: Spatial effect on body and udder conformational traits of multi-genotype cows

Traits	Adamawa (n=928)	Plateau (n=2209)	Kwara (n=2256)	CV %	SEM
Body weight (kg)	556.3±15.20 ^b	581.3±7.22 ^a	517.3±5.33 ^c	22.44	10.91
BCS (1-5)	3.1±0.11	2.9±0.03	3.3±0.06	30.68	0.53
Central ligament (cm)	4.3±0.04	4.1±0.03	4.3±0.04	13.40	0.32
Chest width (cm)	22.6±0.11	21.9±0.12	23.1±0.15	10.01	1.27
Body depth(cm)	203.7±1.15 ^a	191.1±0.87 ^b	210.5±0.90 ^a	8.21	8.29
Stature (cm)	154.5±1.29 ^a	150.7±0.05 ^a	132.4±0.05 ^b	15.86	3.84
Rump (cm)	12.6±0.06	12.4±0.12	13.1±0.08	11.53	0.83
Heart girth (cm)	221.7±1.20 ^a	204.1±0.76 ^b	201.7±1.10 ^b	8.56	4.21
Udder clearance (cm)	44.02±0.40 ^b	60.3±1.36 ^a	42.6±0.45 ^b	30.76	7.27
Rear Udder height (cm)	39.2±0.09 ^a	27.0±0.44 ^b	35.7±0.51 ^a	25.83	4.20
Rear Udder width (cm)	13.8±0.14 ^a	12.1±0.05 ^b	13.9±0.07 ^a	11.16	0.71
Teat length (cm)	5.4±0.05	5.1±0.04	5.1±0.04	13.05	0.38

^{abc}Means of the same trait across genetic groups with different superscripts differ significantly (P<0.05); BCS-Body condition score; CV-Coefficient of variation

The HxB, Jersey and JerseyxBunaji were similar in CI. Holstein, HolsteinxBunaji and Jersey cows had similar and shorter day open but differed significantly ($P<0.05$) from JerseyxBunaji cows which was longer. Calving rate was similar in Holstein, Jersey and JerseyxBunaji but differed significantly ($P<0.01$) from HolsteinxBunaji. Jersey purebred cows significantly ($P<0.01$) stayed longer in the herd as compared to other genotypes. Breed improvement strategies had highly significant ($P<0.01$) effect on all the reproductive traits with the exception of NSC, CR and HL. The AI prolonged AFC but a converse trend was observed for NSC and C1. AFC, DO and CI were the only reproductive traits that differed significantly ($P<0.01$) by year of calving.

Table 4.11: Least squares means (LSM) and SE for the effect of genetic and non-genetic factors on reproductive traits of cows in Shonga Dairy Holdings in Kwara State

Traits/Factors	N	AFC (days)	NSC	DO (days)	CI (days)	CR (%)	Herd life (months)
Overall mean	2320	1134.9±18.91	2.4±0.03	185.4±1.56	409.2±5.87	47.3±0.48	37.8±0.94
Genotype	2320	**	**	**	**	**	**
Holstein Friesian	408	1021.9±19.94 ^a	2.5±0.07 ^b	176.2±2.48 ^a	330.0±13.19 ^a	46.4±0.65 ^a	36.6±0.96 ^b
Friesian xBunaji	301	1083.5±15.69 ^a	2.7±0.06 ^b	177.4±1.21 ^a	393.8±11.30 ^b	41.3±0.46 ^b	29.9±1.18 ^b
Jersey	922	1220.0±16.84 ^b	2.1±0.09 ^a	175.4±1.52 ^a	375.4±4.52 ^b	56.8±0.64 ^a	54.2±1.57 ^a
JerseyxBunaji	689	1231.5±25.36 ^c	2.0±0.01 ^a	213.5±4.09 ^b	376.2±8.49 ^b	45.9±1.05 ^a	36.6±0.96 ^b
Breed improvement	2320	**	NS	**	**	NS	NS
AI	2016	1138.1±23.04 ^b	2.8±0.05	176.4±1.71 ^a	390.3±10.83 ^a	46.7±0.77	36.2±1.01
NSS	304	1133.2±11.57 ^a	2.6±0.04	190.1±2.14 ^b	419.7±6.77 ^b	47.7±0.61	38.8±1.18
Breeding Year	2320	*	NS	**	*	NS	NS
2008-2012	1688	1085.5±30.41 ^a	2.7±0.08	173.4±2.60 ^a	420.4±11.29 ^b	47.7±1.01	38.50±1.45
2012-2015	632	1130.7±23.16 ^b	2.6±0.07	183.6±2.99 ^b	382.1±12.56 ^a	48.8±1.14	44.32±1.76

^{abc}Means of the same trait across genetic groups with different superscripts differ significantly (P<0.05); AFC-Age at first calving, NSC-Number of service per conception rate, CI-Calving interval, DO-days open, CR-Calving rate, AI-Artificial insemination, NSS-natural service, SE-Standard error; *P<0.05-significant; **P<0.01-Highly significant; NS-not significant; N-sample size.

4.3.2 Least squares means of genetic and non genetic factors on reproductive traits of cows in Integrated Dairies Limited in Plateau State

The least squares means of reproductive traits across genetic groups and non genetic factors in Plateau State are presented in Table 4.12. Genotype has highly significant ($P<0.01$) effect on AFC, DO, CR and HL with the exceptions of NSC, CR and CI. The average AFC, NSC, DO, CI, CR and HL ($N=3063$) for all the genotypes were 1020.9 ± 12.59 d, 2.8 ± 0.03 , 147.1 ± 1.44 d, 423.1 ± 3.15 d, 49.3 ± 0.13 % and 66.7 ± 0.45 months, respectively. However, Holstein Friesian was significantly ($p<0.01$) younger than FriesianxBunaji at first calving in Plateau State. FriesianxBunaji cows had the highest number of insemination per conception, which differed significantly ($P<0.01$) from Holstein Friesian cows. Holstein Friesian cows significantly ($P<0.05$) stayed longer in the herd as compared to FriesianxBunaji. Breed improvement strategies had highly significant ($P<0.01$) effect on AFC while NSC, DO CI, CR and HL were similar ($P>0.05$). The AI had significant ($P<0.05$) effects on AFC. AFC and DO were the only reproductive traits that differed highly significantly ($P<0.01$) across the year of calvings.

Table 4.12: Least squares means (LSM) and SE of the effect of genetic and non genetic factors on reproductive traits of cows in Integrated Dairies Limited in Plateau State

Traits/Factors	N	AFC (days)	NSC	DO (days)	CI (days)	CR (%)	Herd life (months)
Overall mean	3063	1020.9±12.59	2.8±0.03	147.1±1.44	423.1±3.15	49.3±0.13	66.7±0.45
Genotype	3063	**	NS	*	NS	NS	*
Holstein Friesian	2042	1010.8±17.43 ^a	2.7±0.04	148.2±2.13 ^b	419.6±4.65	49.3±0.19	68.2±0.63 ^a
Friesian xBunaji	1021	1033.8±18.07 ^b	2.9±0.04	145.6±1.84 ^a	427.6±4.04	49.9±0.14	65.6±0.63 ^b
Breed improvement	3063	*	NS	**	NS	NS	NS
AI	2857	1016.0±15.16 ^a	2.8±0.03	144.6±1.52 ^a	425.5±3.47	49.3±0.15	67.1±0.51
NSS	206	1035.3±21.8 ^b	2.9±0.06	154.5±3.48 ^b	416.1±7.09	49.4±0.27	65.6±0.94
Year	3063	*	NS	**	NS	NS	NS
2000-2008	1286	956.3±14.00 ^a	2.7±0.03	151.0±1.88 ^b	421.3±3.99	49.0±0.16	66.2±0.56
2008-2016	1777	1167.8±24.00 ^b	2.1±0.05	138.2±1.92 ^a	427.1±4.93	50.1±0.23	68.0±0.76

^{ab}Means of the same trait across genetic groups with different superscripts differ significantly (P<0.05); AFC-Age at first calving, NSC-Number of service per conception, CI-Calving interval, DO-days open, CR-Calving rate, AI-Artificial insemination, NSS-natural service, SE-Standard error; *P<0.05-significant; ** P<0.01-Highly significant; NS-not significant; N-sample size

4.3.3 Least squares means of genetic and non-genetic factors on reproductive traits of cows in Sebore farm in Adamawa State.

The least squares means for the effect of genetic and nongenetic factors on reproductive traits in Adamawa are shown in Table 4.13. Genotypes had a highly significant ($P<0.01$) effect on all the reproductive traits except DO. The overall mean ($N=1583$) for AFC, NSC, DO, CI, CR and HL was 1261.6 ± 2.46 d, 2.4 ± 0.03 , 143.6 ± 0.29 d, 687.9 ± 1.31 d, 40.0 ± 0.71 % and 37.6 ± 0.05 months, respectively for all the genotypes. Jersey cows were highly significantly ($P<0.01$) younger than all the genotypes at first calving in Adamawa State. Holstein Friesian, Jersey and Brown Swiss had the highest and similar number of insemination per conception, which differed highly significantly ($P<0.01$) from Simmental cows. Longer CI were recorded in Simmental and Brown Swiss cows which differed highly significantly ($p<0.01$) from Holstein Friesian and Jersey. The calving rate was highest and similar in Jersey and Simmental but differed significantly ($P<0.01$) from Holstein Friesian and Brown Swiss, respectively. Simmental cows had similar values and significantly ($P<0.01$) stayed longer in the herd than all the genetic groups. Breed improvement strategies had a significant ($P<0.01$) effect on DO and CR, respectively. The use of AI reduced DO and improved CR as compared to cows sired through natural service. Year of calving had a significant ($P<0.05$) effect on NSC.

Table 4.13: Least squares means (LSM) and SE for the effect of genetic and non-genetic factors on reproductive traits in Adamawa State

Traits/Factors	N	AFC (days)	NSC	DO (days)	CI (days)	CR (%)	Herd life (months)
Overall mean	1583	1261.6±2.46	2.4±0.03	143.6±0.29	687.9±1.31	40.0±0.71	37.6±0.05
Genotype	1583	**	**	NS	**	**	**
Holstein Friesian	875	1243.8±4.36 ^a	2.5±0.04 ^b	143.1±0.42	677.8±2.29 ^a	26.6±0.53 ^b	37.4±0.09 ^b
Jersey	218	1227.4±2.44 ^a	2.5±0.11 ^b	144.6±0.99	674.8±1.88 ^a	55.2±0.48 ^a	37.3±0.09 ^b
Brownswiss	278	1263.4±3.05 ^b	2.6±0.07 ^b	144.6±0.58	693.9±2.09 ^b	25.2±0.21 ^b	37.7±0.07 ^b
Simmental	212	1321.3±3.33 ^c	2.1±0.02 ^a	142.5±0.51	709.2±2.26 ^c	52.8±1.39 ^a	38.4±0.08 ^a
Breed improvement	1583	NS	NS	**	NS	**	NS
AI	1454	1260.1±2.28	2.4±0.03	144.0±0.32 ^b	686.7±1.33	40.4±0.82 ^a	37.6±0.05
NSS	129	1267.1±7.22	2.5±0.06	142.3±0.63 ^a	691.8±3.46	37.4±1.36 ^b	37.7±0.13
Year	1583	**	**	NS	NS	NS	NS
2000-2008	764	1264.1±3.9	2.3±0.04 ^a	144.1±0.47	688.6±2.00	40.1±1.05	37.7±0.07
2008-2016	819	1260.1±3.2	2.5±0.04 ^b	143.2±0.36	687.5±1.75	39.4±0.96	37.6±0.06

^{abc}Means of the same trait across genetic group with different superscripts differ significantly (P<0.05); See table 4.12 for abbreviations

4.3.4 Interaction effect of reproductive traits among genotypes of cows

4.3.4.1 Interaction effect between genotypes and genetic improvement strategies in Kwara State

The interaction effect between genotypes and genetic improvement strategies is displayed in Table 4.14. There were significant differences ($P < 0.05$) between the interactions on all the reproductive measures. Breed improvement strategies and year of calving had the lowest CV in DO (4.36 %) through 16.83 % in NSC which was the highest. The NSC was similar for all the genotypes and breed improvement strategies except JxBJ which was sired through natural service (NSS). Longer DO (221.03 d) was observed for JxBJ that was sired through natural service (NSS). The FRxBJ had the shortest calving interval. Jersey cows serviced by AI and natural service had the highest calving rate (57.6 and 56.6 %). Jersey (AI and NSS) significantly stayed longer in the herd while JxBJ serviced through NSS had the shortest stay. Breed and year of calving had a significant effect ($P < 0.05$) on all the reproductive traits. Dairy cows with pure Holstein Friesian gene born in 2008 to 2012 and 2012 to 2016 significantly ($P < 0.05$) attained early reproductive maturity (1019.4 d) as compared to all other interactions. JxBJ born in 2008 to 2016 had a reduced NSC while Holstein Friesian cows born in 2012 to 2016 had the shortest CI. Cows with Holstein Friesian pure gene born in 2008 to 2012, 2012 to 2016 and Jersey cows born in 2012 to 2016 had longer stay in the herd.

Table 4.14: Least squares means of breed improvement and year of calving between genotypes of cows for reproductive traits in Shonga Dairy Holdings in Kwara State

Traits	HFxAI	HFxNSS	FRBJxAI	FRBJxNSS	JxAI	JxNSS	JBJxAI	JBJxNSS	CV	SEM
AFC	1040.3±28.15 ^b	991.9±25.00 ^a	1094.0±13.12 ^b	1073.8±27.82 ^b	1353.8±68.15 ^b	1200.5±15.34 ^c	1553.6±86.24 ^d	1548.6±86.00 ^d	14.82	18.06
NSC	2.5±0.12 ^b	2.5±0.12 ^b	3.0±0.01 ^b	3.0±0.01 ^b	3.0±0.01 ^b	2.6±0.06 ^b	3.1±0.31 ^b	2.2±0.08 ^a	16.83	0.60
DO	178.7±3.62 ^a	172.4±2.99 ^a	175.6±1.47 ^a	179.0±1.88 ^a	175.9±3.30 ^a	175.3±1.68 ^a	170.8±3.34 ^a	221.03±6.08 ^b	4.36	4.85
CI	353.5±17.09 ^c	396.4±20.10 ^b	409.6±16.25 ^b	379.0±15.57 ^a	404.9±35.85 ^b	415.2±12.66 ^b	473.5±15.42 ^c	462.9±6.82 ^c	5.75	12.78
CR	47.1±0.95 ^b	45.3±0.67 ^b	40.7±0.69 ^c	41.9±0.61 ^c	57.6±1.59 ^a	56.6±0.70 ^a	57.0±1.47 ^b	43.9±1.02 ^b	14.80	1.20
HL	54.6±1.24 ^b	59.9±1.33 ^b	53.4±1.84 ^b	46.8±1.34 ^c	69.4±3.15 ^a	64.9±1.76 ^a	52.5±1.52 ^b	40.2±1.61 ^d	7.81	2.18
	HFx(08-12)	HFx(12-16)	FRBJx(08-12)	FRBJx(12-16)	Jx(08-12)	Jx(12-16)	JBJx(08-12)	JBJx(12-16)		
AFC	1019.4±34.0 ^a	1025.2±11.97 ^a	1072.0±13.8 ^b	1098.9±30.9 ^c	1233.2±20.95 ^f	1197.0±28.23 ^d	1246.1±33.07 ^g	1211.7±39.85 ^e	8.16	5.15
NSC	2.5±0.10 ^b	2.5±0.09 ^b	3.0±0.001 ^d	3.0±0.001 ^d	2.7±0.07 ^c	2.7±0.09 ^c	2.5±0.13 ^b	2.2±0.11 ^a	14.22	0.09
DO	171.2±3.00 ^a	183.9±3.93 ^a	178.4±1.71 ^a	176.1±1.70 ^a	176.8±2.16 ^a	172.8±1.76 ^a	220.3±5.69 ^c	204.2±5.43 ^b	7.21	4.67
CI	402.9±17.33 ^c	326.2±18.02 ^a	402.8±15.52 ^c	382.4±16.48 ^b	438.4±14.66 ^c	371.3±17.5 ^b	468.9±7.37 ^c	458.6±10.8 ^c	10.28	6.04
CR	46.0±1.02 ^b	47.0±0.67 ^b	40.7±0.65 ^d	42.0±0.63 ^c	56.7±0.81 ^a	56.8±1.08 ^a	45.2±1.47 ^b	46.7±1.47 ^b	14.22	0.76
HL	57.4±1.32 ^a	55.6±1.40 ^a	40.2±1.59 ^e	49.7±1.77 ^c	52.4±1.76 ^b	57.4±2.97 ^a	40.5±2.07 ^e	44.2±2.04 ^d	5.08	1.22

^{abcdef} Means of the same trait across genetic groups with different superscripts differ significantly (P<0.05); NSS-Natural service; AI-Artificial insemination; HF-Holstein Friesian; FRBJ-FriesianxBunaji; J-Jersey; JBJ-JerseyxBunaji; CV-Coefficients of variation; AFC-Age at first calving, NSC-Number of service per conception rate, CI-Calving interval, DO-days open, CR-Calving rate;

4.3.4.2 Interaction effect between genotypes and genetic improvement indices in Plateau State

The effect of breed improvement indices of cows between the Holstein Friesian and Friesian x Bunaji are presented in Table 4.15. In the Holstein Friesian breed (AI and NSS) and FRxBJ sired through AI calved earlier and significantly ($P<0.05$) differed from the values obtained from FRxBJ sired through (natural service) NSS. Genotype effect was significant ($P<0.05$) on the NSC with the FRxBJ sired through NSS having the highest NSC. Genotype alone accounted for 12.27 % of the variation in NSC within genotype by breed improvement. The effect of genotype was highly significant ($P<0.01$) on DO with Holstein Friesian dairy cows serviced through NSS staying longer before conception while FRxBJ cows sired through NSS conceived earlier. The CR in FRxBJ sired through NSS had the least calving which differed highly significantly ($P<0.01$) from other genotypes by breed improvement categories. The FRxBJ sired through NSS stayed longer in the herd while Holstein Friesian sired through NSS had the shortest stay in the herd. The effect of genotype by years of calving differed highly significantly ($P<0.01$) within the groups among the reproductive traits.

Table 4.15: Least squares means of breed improvement, year of calving and genotypes of cows on reproductive traits in Integrated Dairies Limited.

	HFxAI	HFxNSS	FRBJxAI	FRBJxNSS	CV	SEM
AFC	1025.3±22.61 ^a	981.9±26.17 ^a	1006.7±20.20 ^a	1185.9±31.70 ^b	9.60	23.64
NSC	2.7±0.04 ^a	2.8±0.07 ^a	2.8±0.04 ^a	3.3±0.08 ^b	12.27	0.05
DO	140.8±2.20 ^b	163.0±4.44 ^d	148.3±2.08 ^c	130.5±2.76 ^a	14.21	2.91
CI	421.0±5.38 ^a	416.7±8.88 ^a	429.9±4.37 ^b	414.5±10.40 ^a	7.50	6.02
CR	49.2±0.24 ^a	49.6±0.30 ^a	49.4±0.20 ^a	48.9±0.59 ^b	12.35	0.33
HL	66.6±0.74 ^b	63.5±1.16 ^c	67.6±0.71 ^b	71.6±1.28 ^a	16.24	0.96
	HFx(08-12)	HFx(12-16)	FRBJx(08-12)	FRBJx(12-16)		
AFC	797.3±15.04 ^a	1357.8±22.87 ^c	1115.3±20.14 ^b	725.7±16.59 ^a	4.30	17.40
NSC	2.6±0.04 ^a	3.0±0.06 ^c	2.8±0.04 ^b	3.2±0.04 ^d	15.89	0.05
DO	155.1±3.00 ^c	137.1±2.54 ^a	146.9±2.24 ^b	140.8±2.45 ^a	15.00	2.60
CI	419.1±6.65 ^a	420.3±5.67 ^a	423.5±4.41 ^a	443.0±9.57 ^b	8.47	5.03
CR	49.0±0.25 ^a	49.7±0.28 ^a	48.9±0.21 ^b	50.8±0.38 ^a	5.28	0.29
HL	63.4±0.84 ^b	69.0±0.88 ^a	68.9±0.70 ^a	65.7±1.44 ^b	12.97	0.91

^{abcd} Means of the same trait across genetic groups with different superscripts differ significantly (P<0.05); AFC-Age at first calving, 08-2008; 12-2012; 16-2016; NSC-Number of service per conception rate, CI-Calving interval, DO-days open, CR-Calving rate; HF-Holstein Friesian; FRBJ-FriesianxBunaji; CV-Coefficients of variation; SEM-Standard error of mean; NSS-Natural service; AI-Artificial insemination

4.3.4.3 Interaction effect of genotypes and breed improvement strategies in Sebore farm in Adamawa State

Table 4.16 shows the basic descriptives of reproductive traits by breed improvement of cows within genotypes in Sebore farm in Adamawa State. There were highly significant differences ($P < 0.01$) across the genotypes by breed improvement interactions on reproductive measures (AFC, NSC, DO, CI, CR and HL). Jersey cows sired through AI and thereafter natural service (NSS) calved younger as heifers while Simmental had the most reduced number of services per conception (NSC). Holstein and Brown Swiss purebred cows sired through NSS with Simmental breed sired through AI had the shortest DO. Simmental breed sired through natural service (NSS) stayed longer in the herd. Simmental breed sired through AI and Holstein and Jersey cows sired through NSS and Jersey sired through AI had the shortest CI.

Breed and year of calving effect was significant ($P < 0.05$) on reproductive traits. In 2008 to 2015, Jersey cows calved younger as heifers (1224.9 d) while Jersey cows received the lowest number of service per conception in 2000 to 2008. The shortest DO was recorded in Simmental cows calved in 2000 to 2008. Jersey cows calved between 2000 and 2008, 2008 and 2016 and Holstein between 2008 and 2015 had longer CI. Calving rate was highest and similar in Brown Swiss cows calved between 2000 and 2008 (55.1 %), 2008 and 2015 (55.7 %) and Simmental cows between 2000 and 2008 (51.7 %). Holstein cows calved between 2000 and 2008 had the highest stay in the herd and differed significantly ($P < 0.05$) from the other breed and year of calving combinations.

Table 4.16: Least squares means of breed improvement, year of calving and genotypes of cows for reproductive traits in Sebore farm in Adamawa State.

Trait	HFxAI	HFxNSS	JxAI	JxNSS	BxAI	BxNSS	SxAI	SxNSS	CV	SEM
AFC	1249.9±4.25 ^d	1233.4±12.2 ^b	1229.5±2.82 ^a	1221.0±4.62 ^a	1267.6±2.99 ^c	1238.1±10.3 ^b	1299.2±2.88 ^d	1350.7±3.09 ^c	7.67	5.48
NSC	2.5±0.05 ^b	2.5±0.07 ^b	2.5±0.12 ^b	2.4±0.20 ^b	2.4±0.06 ^b	3.5±0.11 ^c	2.0±0.01 ^a	2.0±0.01 ^a	13.99	0.12
DO	143.7±0.46 ^b	140.9±0.98 ^a	144.7±1.11 ^b	144.1±2.23 ^b	145.6±0.53 ^b	138.1±2.08 ^a	140.2±0.75 ^a	145.6±0.12 ^b	4.36	1.80
CI	581.1±2.41 ^b	566.8±5.58 ^a	575.6±2.20 ^a	572.2±3.68 ^a	593.7±2.16 ^c	594.9±6.95 ^c	595.9±2.25 ^c	626.8±2.42 ^d	7.82	3.73
CR	26.2±0.58 ^d	28.1±1.24 ^d	25.3±0.27 ^e	24.7±0.24 ^e	55.1±0.54 ^b	55.7±1.05 ^b	59.8±0.69 ^a	43.6±2.47 ^c	2.94	1.04
HL	37.5±0.09 ^b	36.9±0.21 ^b	37.3±0.10 ^b	37.2±0.18 ^b	37.8±0.07 ^b	37.0±0.19 ^b	37.9±0.07 ^b	39.1±0.08 ^a	1.83	0.11
	HFx00-08	HFx08-16	Jx00-08	Jx08-16	Bx00-08	Bx08-16	Sx00-08	Sx08-16		
AFC	1252.4±7.37 ^d	1236.5±5.05 ^c	1230.5±3.59 ^b	1224.9±3.30 ^a	1265.8±4.61 ^e	1261.6±4.08 ^c	1319.3±3.91 ^f	1322.4±4.77 ^f	12.12	2.22
NSC	2.5±0.07 ^b	2.5±0.06 ^b	2.0±0.01 ^a	2.8±0.17 ^c	2.5±0.09 ^b	2.6±0.09 ^b	2.4±0.01 ^b	2.6±0.11 ^b	30.84	0.13
DO	143.6±0.60 ^c	142.7±0.59 ^b	145.4±1.70 ^c	143.9±1.31 ^c	145.3±0.99 ^c	144.0±0.69 ^c	141.9±1.04 ^a	142.9±0.53 ^b	26.52	1.28
CI	580.5±17.33 ^b	575.6±3.65 ^a	575.9±2.74 ^a	573.9±2.61 ^a	594.9±3.00 ^c	593.1±2.90 ^c	608.7±3.07 ^d	609.5±3.12 ^d	14.03	2.03
CR	28.5±0.85 ^c	25.1±0.65 ^d	25.1±0.65 ^d	25.1±0.33 ^d	55.1±0.70 ^a	55.3±0.66 ^a	54.7±2.24 ^a	51.7±1.77 ^b	11.35	1.09
HL	37.5±0.14 ^a	37.3±0.11 ^b	27.3±0.11 ^f	27.3±0.12 ^f	27.8±0.11 ^d	27.6±0.09 ^e	28.4±0.10 ^c	28.4±0.11 ^c	3.80	0.05

^{abcdef} Means of the same trait across genetic groups with different superscripts differ significantly (P<0.05); HF-Holstein Friesian; J-Jersey; B-Brown Swiss; S-Simmental; NSS-Natural service; AI-Artificial insemination; CV-Coefficients of variation; SEM-Standard error of mean; 00-2000; 08-2008; 16-2016; AFC-Age at first calving; NSC-Number of service per conception rate; CI-Calving interval; DO-days open; CR-Calving rate

4.3.4.4 Interaction effect between breed improvement indices and year of calving in the three locations

The interaction effect between breed improvement indices and year of calving is shown in Table 4.17. In Kwara State, interactions between the year of calving and breed improvement had a significant effect ($P < 0.05$) on all the reproductive traits except the number of services per conception and days open. All the interactions between breed improvement indices and year of calving for AFC were similar except for cows that were artificially inseminated in 2008. Cows artificially inseminated in 2008, 2012 and 2015 had shorter days open. The shortest CI was recorded in cows that were sired through AI. The lowest CR was recorded in 2008 for natural serviced and AI cows. The NSC, CI and HI had highly variable coefficients of variation (27.37, 22.72 and 25.87 %).

In Plateau State, all the interactions between the year of calving and breed improvement differed significantly ($P < 0.05$) except NSC. Cows that were mounted by the bulls in 2004, 2008 and artificially inseminated cows in 2012 produced heifers that calved at younger ages. Cows that were naturally sired in 2012, and 2016 and artificially sired in 2004 and 2016 had the shortest CI. Cows serviced through AI in 2004 stayed longer in the herd as compared to all other interactions. In Adamawa State, AI cows born in 2008 had the lowest number of service per conception with the highest coefficient of variation (43.7 %).

Table 4.17: Basic descriptives of reproductive traits by year of calvings and breed improvement indices in the three locations

Kwara	AIx2004	NSSx2004	AIx2008	NSSx2008	AIx2012	NSSx2012	AIx2016	NSSx2016	SEM	CV
AFC	-	-	1020.7±40.8 ^b	1154.6±30.6 ^a	1186.9±70.4 ^a	1109.4±31.02 ^a	1159.8±40.05 ^a	1168.8±15.51 ^a	35.40	12.30
NSC	-	-	2.9±0.08	2.5±0.09	2.1±0.09	2.6±0.08	2.7±0.10	2.5±0.07	0.08	27.37
DO	-	-	168.8±5.53 ^a	194.2±5.38 ^b	175.0±2.73 ^a	182.4±3.1 ^b	175.1±1.59 ^a	193.9±3.64 ^b	5.56	10.31
CI	-	-	375.6±27.63 ^b	411.2±11.27 ^b	334.1±22.66 ^a	391.8±20.02 ^b	404.5±20.86 ^b	448.0±9.44 ^c	15.60	22.72
CR	-	-	45.6±1.88 ^b	43.7±1.06 ^b	48.9±1.46 ^a	49.1±1.55 ^a	47.3±1.26 ^a	48.3±0.96 ^a	1.01	11.86
HL	-	-	42.0±0.43 ^c	33.45±0.21 ^d	49.5±0.62 ^a	48.4±1.05 ^a	42.4±0.15 ^c	45.1±0.41 ^b	0.63	25.87
Plateau										
AFC	995.5±51.6 ^b	804.8±19.0 ^a	983.5±18.3 ^b	861.4±26.0 ^a	833.2±41.8 ^a	1210.1±40.2 ^d	1150.9±28.2 ^c	1217.1±45.2 ^d	40.84	9.20
NSC	3.6±0.06	3.9±0.13	3.6±0.04	3.7±0.11	3.4±0.10	2.8±0.13	3.2±0.05	2.7±0.09	0.92	15.64
DO	132.9±5.06 ^a	184.5±8.41 ^c	147.1±2.07 ^b	173.9±7.27 ^c	148.7±7.61 ^b	135.2±4.84 ^a	140.4±2.20 ^a	131.9±3.88 ^a	5.25	5.80
CI	406.2±12.41 ^a	389.2±20.0 ^a	433.9±14.71 ^b	427.2±4.50 ^b	400.9±15.52 ^a	422.3±18.5 ^b	428.1±5.89 ^b	424.4±8.89 ^b	14.2	13.22
CR	48.9±0.59 ^a	50.1±0.72 ^a	49.4±0.39 ^a	48.8±0.20 ^b	49.4±0.58 ^a	47.9±1.07 ^b	50.3±0.27 ^a	49.4±0.41 ^a	0.61	13.01
HL	91.0±2.04 ^a	81.4±1.06 ^b	72.3±1.52 ^b	83.2±1.98 ^b	66.6±1.25 ^c	78.9±0.51 ^b	84.2±2.76 ^b	87.4±3.63 ^b	4.02	30.45
Adamawa										
AFC	1263.5±4.50	1289.7±18.24	1262.6±4.72	1259.9±11.6	1255.4±5.02	1254.4.1±14.9	1258.3±4.14	1217.1±45.2	45.53	3.61
NSC	2.4±0.07 ^b	2.6±0.16 ^c	2.2±0.06 ^a	2.4±0.09 ^b	2.6±0.09 ^c	2.6±0.09 ^c	2.4±0.06 ^b	2.4±0.13 ^b	0.02	43.7
DO	143.6±0.71	144.2±1.26	143.8±0.65	141.9±1.09	144.1±0.65	141.8±1.39	144.3±0.55	142.0±1.28	6.24	4.35
CI	686.5±2.49	698.5±8.12	686.6±2.73	690.6±5.72	688.6±3.19	685.6±7.24	685.9±2.43	694.7±7.43	26.73	3.89
CR	43.4±1.69	44.4±3.42	42.9±1.62	38.1±2.31	35.7±1.78	30.5±1.92	38.8±1.47	38.0±3.00	7.36	18.56
HL	73.5±1.09	75.0±1.30	73.5±1.10	73.4±0.21	72.7±2.63	73.7±0.11	73.4±2.82	74.0±13.5	3.96	3.47

^{abcde} Means of the same trait across genetic groups between locations with different superscripts differ significantly (P<0.05); AFC-Age at first calving, NSC-Number of service per conception rate, CI-Calving interval, DO-days open, CR-Calving rate; NSS-Natural service; AI-Artificial insemination;

4.4 Estimates of Genetic Parameters for Milk Production Traits in different Multi-genotype cows

4.4.1 Estimates of genetic parameters for milk production traits in different Multi-genotype cows in Shonga Dairy Holdings in Kwara State.

Table 4.18 shows the genetic correlations, heritabilities and repeatabilities among the milk production traits of Holstein Friesian purebred and FriesianxBunaji cows in Shonga Dairy Holdings, Kwara State. In Holstein Friesian cows, heritabilities ranged from 0.11 for lactation length to 0.41 for 305 d fat-corrected milk yield. Repeatabilities for 305 d FCM, 100 dMY, MYCD, fat yield, protein yield and lactation length, which are considered to be the upper limit of heritability, ranged from 0.14 for LL to 0.63 for 100 dMY. Genetic correlations between 305 d FCM and other milk production traits (100 dMY, MYCD, fat yield, protein yield and LL) were significant ($P < 0.05$) and ranged from moderate for LL ($r_g = 0.23$) to high ($r_g = 0.62$) for 305 d FCM. The strongest genetic correlation was recorded between 305 d FCM and 100 dMY ($r_g = 0.62$) while the correlation between protein and fat yield had the weakest correlation ($r_g = 0.14$). Fat yield had high and negative genetic correlation with 305 d FCM ($r_g = -0.43$) while other milk production traits showed positive genetic correlations indicating high genetic gain is achievable. In FriesianxBunaji cows, heritabilities estimates for 305 d FCM, 100 dMY, MYCD and LL were 53 %, 38 %, 40 %, 21 %, 19 and 15 %. Repeatability estimates were moderate for LL ($w^2 = 0.20$) to high ($w^2 = 0.61$) for 305 d FCM. 305 d FCM had significant ($P < 0.05$) and positive genetic correlation with 100 dMY, MYCD and LL. Fat yield had negative and highly significant genetic correlation ($P < 0.01$) with 305 d FCM ($r_g = -0.54$). Genetic correlations between protein yield and 305 d FCM were significant, negative and moderate ($r_g = -0.38$). Genetic Correlation between protein and fat yield was low and positive ($r_g = 0.16$).

Heritability estimates ranged from moderate for protein yield; 21% to high for 305 d FCM, 45% in Jersey cows while in JerseyXBunaji, low (9 %; LL) to moderate (PY; 36 %) estimates were recorded (Table 4.19). Repeatability for 305 d FCM, 100 dMY, MYCD, fat yield, protein yield and LL in cows with pure Jersey gene were moderate (24 %) to high (49 %) while in JerseyxBunaji crossbreds, the range obtained for the estimates was low (12 %) to high (50 %). Heritability and repeatability had higher numerical estimates in Jersey than JerseyXBunaji cows for all the milk production traits except protein yield. Genetic correlations of 305 d FCM with MYCD ($r_g = 0.77$) and fat yield ($r_g = 0.86$) were highly significant ($P < 0.01$) and positive while 100 dMY (0.16), protein yield (0.15) and LL (0.16) were low, but positive, whereas genetic correlations of 100dMY with protein yield ($r_g = -0.03$) was low and negative in Jersey cows. Genetic correlations between milk production traits were all positive and ranged from low (100 dMY and protein yield; 0.09) to high (MYCD and LL; 0.42) in JerseyXBunaji cows. The genetic correlations of 305 d FCM with 100 dMY (0.37), MYCD (0.23) and LL (0.21) were significant, positive and moderate.

Table 4.18: Genetic correlations, heritability (last column) and repeatability (along diagonal) among milk production traits of Holstein Friesian (above diagonal) and Friesian x Bunaji (below diagonal) cows in Shonga Dairy Holdings.

Milk production Traits/R(HF/FRxBJ)							Lactation	
	305dFCM	100dMY	MYCD	Fat yield	Protein yield	length	h^2 (H/HxB)	
305dFCM	0.57/0.61	0.62**	0.55**	-0.43**	0.32*	0.23*	0.41/0.53	
100dMY	0.32*	0.63/0.40	-0.53**	0.23*	-0.50**	0.28*	0.34/0.38	
MYCD	0.36*	0.33*	0.28/0.44	-0.39*	0.23*	0.50**	0.22/0.40	
Fat yield	-0.54**	0.46**	0.24*	0.31/0.39	0.14	0.55**	0.29/0.21	
Protein yield	-0.38*	-0.37*	0.26*	0.16	0.24/0.27	0.21*	0.20/0.19	
Lactation length	0.26*	-0.49**	0.23*	0.32*	0.27*	0.14/0.20	0.11/0.15	

* = P<0.05; ** = p<0.01; 305dFCM -305 day fat corrected milk yield; dMY-Day milk yield; MYCD-Milk yield per cows per day; H-Holstein Friesian (Upper); FRxBJ- FriesianxBunaji (lower), h^2 = Heritability estimates (last column); R-Repeatability (along diagonal)

Table 4.19: Genetic correlations, heritability (last column) and repeatability (along diagonal) among milk production traits of Jersey purebred (above diagonal) and Jersey x Bunaji (below diagonal) cows in Shonga Dairy Holdings

Milk production Traits R (J/JxB)	305dFCM	100dMY	MYCD	Fat yield	Protein yield	Lactation length	<i>h</i>²(J/JxB)
305dFCM	0.49/0.31	0.16	0.77**	0.86**	0.15	0.16	<i>0.45/0.22</i>
100dMY	0.37*	0.38/0.16	0.35*	0.10	-0.03	0.42**	<i>0.36/0.14</i>
MYCD	0.23*	0.21*	0.46/0.28	0.25*	0.34*	0.36*	<i>0.44/0.26</i>
Fat yield	0.19	0.34*	0.03	0.32/0.20	0.19	0.16	<i>0.27/0.19</i>
Protein yield	0.12	0.09	0.20*	0.28*	0.24/0.50	0.04	<i>0.21/0.36</i>
Lactation length	0.21*	0.34*	0.42**	0.19	0.25*	0.37/0.12	<i>0.25/0.09</i>

* = P<0.05; ** = p<0.01; 305dFCM -305 day fat corrected milk yield; dMY-Daily milk yield; MYCD-Milk yield per cows per day; J-Jersey (Upper); JxB- JerseyxBunaji (lower); *h*² = Heritability estimates (last column); **R**-Repeatability (along diagonal)

4.4.2 Estimates of genetic parameters for milk production traits among genotypes of cows in Integrated Dairies Limited in Plateau State.

Table 4.20 shows estimates of genetic correlations, heritabilities and repeatabilities for milk production traits. In Holstein Friesian cows, heritability estimates ranged from low (14 % for LL) to high (55 % for 100 dMY). Repeatability estimates of milk production traits ranged from moderate (23 %) for protein yield to high (71 %) for 100 dMY, implying that cows with high part-period milk production have a higher likelihood of having high part-period milk production after the next calving. Genetic correlations among milk production traits varied in magnitude and direction. Genetic correlation between 305 d FCM with MYCD (0.44), fat yield (0.56) and protein yield (0.86) was very strong, positive and significant. There was a moderate genetic correlation of 305 d FCM with 100 dMY (0.22) suggesting that early fat corrected milk yield could be used to predict later milk yield. The genetic correlations of milk production traits ranged from moderate (305 d FCM and 100 dMY; 0.22) to high (protein yield and MYCD; 0.94). Genetic correlations between LL and protein yield (-0.42) were highly significant ($P < 0.01$), strong and negative. In FriesianxBunaji, heritability estimates ranged from low (14 %; MYCD) to high (49 %; fat yield). Estimates were numerically higher in fat yield, protein yield and lactation length than cows with pure Holstein gene but a converse trend was recorded for 305 d FCM, 100 dMY and MYCD. Repeatability estimates of milk production traits ranged from 19 % for MYCD to 65 % for fat yield. There was a highly significant ($P < 0.01$), positive and strong genetic correlation of 305 d FCM with 100 dMY (0.54), MYCD (0.50), fat yield (0.49) and protein yield (0.40). The genetic correlations of milk production traits ranged from moderate (fat and protein yield; 0.27) to high (100 dMY and protein yield; 0.64).

Table 4.20: Genetic correlations, heritability (first right column) and repeatability (along diagonal) among milk production traits of Holstein purebred (above diagonal) and Friesian x Bunaji (below diagonal) cows in Integrated Dairies Limited in Plateau State.

Milk production Traits/R(HF/FRxBJ)	305dFCM	100dMY	MYCD	Fat yield	Protein yield	Lactation length	h^2 (HF/FRxBJ)
305dFCM	0.55/0.27	0.22*	0.44**	0.56**	0.86**	-0.12	0.34/0.18
100dMY	0.54**	0.71/0.54	0.25*	0.38*	0.83**	0.39*	0.55/0.46
MYCD	0.50**	0.59**	0.42/0.19	-0.12	0.94**	0.27*	0.31/0.14
Fat yield	0.49**	-0.16	0.57**	0.62/0.65	0.27*	0.13	0.41/0.49
Protein yield	0.40**	0.64**	0.11	0.27*	0.23/0.35	-0.42**	0.20/0.24
Lactation length	0.09	0.72**	0.49**	0.14	0.50**	0.26/0.34	0.14/0.22

* = P<0.05; ** = p<0.01; 305dFCM -305 day fat corrected milk yield; dMY-Day milk yield; MYCD-Milk yield per cow per day; HF-Holstein Friesian (upper); FRxBJ- FriesianxBunaji (lower); h^2 = Heritability estimates (last column), R-Repeatability estimates (along diagonal).

4.4.3 Estimates of genetic parameters for milk production traits on multiple genotype cows in Sebare farm in Adamawa State.

The genetic correlations, heritabilities and repeatabilities of milk production characteristics for Jersey and Brown Swiss cows are presented in Table 4.21. In the Jersey breed, low (protein yield; 10 %) to high (305 d FCM; 50 %) heritabilities was revealed. Repeatability estimates were between 15 % in 100 dMY to 52 % in MYCD. The LL was significant ($P < 0.05$), high and negatively correlated with 305 d FCM ($r_g = -0.65$) and moderately correlated with MYCD ($r_g = -0.28$). This implies that selection for an increase in 305 d FCM will cause a decrease in LL. 305 d FCM had significant ($P < 0.05$), positive and moderate correlations with 100 dMY (0.30) and MYCD (0.21). Positive, significant and very strong correlations existed between PY and 100 dMY ($r_g = 0.43$). Thus, selection for PY should result in improvement in the 100dMY.

In Brown Swiss, there were near zero heritability estimates for fat yield (7 %) which was low to moderate (39 %) in LL. Higher estimates were obtained for 305 d FCM, 100 dMY and fat yield than the Jersey breed but converse trends were recorded for MYCD, protein yield and lactation length. Repeatability estimates were between 11 % in 100 dMY to 41 % in LL. The 305 d FCM had positive, highly significant ($P < 0.01$), and high genetic correlations with 100 dMY ($r_g = 0.49$). This implies that selection for part period milk yield will cause a corresponding increase in milk volume at 305 days of the full lactation cycle. Positive, significant ($P < 0.05$) and moderate correlation was obtained between 305 d FCM and fat yield ($r_g = 0.23$) and with protein yield ($r_g = 0.26$). Strong and positive genetic correlation was obtained between protein yield and LL ($r_g = 0.56$) while genetic correlation between 100 dMY and MYCD ($r_g = 0.02$) had near zero correlation.

Table 4.21: Genetic correlations, heritability (right column) and repeatability (along diagonal) of milk production traits for Jersey purebred (above diagonal) and Brown Swiss (below diagonal) cows in Sebore farm in Adamawa State.

Milk production Traits/ R (J/B)	305dFCM	100Dmy	MYCD	Fat yield	Protein yield	Lactation length	h^2 (J/B)
305Dfcm	0.50/0.26	0.30*	0.21*	-0.12	0.17	-0.65**	0.50/0.23
100dMY	0.49**	0.15/0.11	0.10	0.26*	0.43**	-0.17	0.11/0.10
MYCD	0.10	0.02	0.52	0.09	0.10	-0.28*	0.22/0.29
Fat yield	0.23*	0.21*	0.32*	0.33/0.22	0.17	0.28*	0.26/0.07
Protein yield	0.26*	0.18	0.10	0.19	0.16/0.23	0.25*	0.10/0.21
Lactation length	-0.10	0.31*	0.55**	0.03	0.56**	0.29/0.41	0.26/0.39

* = P<0.05; ** = p<0.01; 305dFCM -305 day fat corrected milk yield; dMY-day milk yield; MYCD-Milk yield per cows per day; J-Jersey (upper); B- Brown Swiss (lower); h^2 = Heritability estimates (last column); R-Repeatability estimates (along diagonal)

In Holstein cows, heritability estimates ranged from low (fat yield; 6 %) to moderate (protein yield; 33 %) while the range obtained for the Simmental breed exhibited a similar trend (Table 4.22). Repeatability estimates were low (0.14) in fat yield to high (0.49) in protein yield while estimates obtained for Simmental cows were low (0.16) in 100 dMY and LL to moderate (0.31) in MYCD. Genetic correlations between 305 d FCM and milk production traits were highly significant ($P < 0.05$; 0.01) and positive (100dMY; 0.27, MYCD; 0.35 and FY; 0.53) except lactation length ($r_g = -0.01$) in Holstein cows. The highest, positive and significant correlation ($P < 0.05$) was observed between 305 d FCM and protein yield (0.58). A negative and significant correlation ($P < 0.05$) existed between protein and fat yield (-0.53); MYCD and lactation length (-0.34).

In Simmental cows, all the milk production traits were positively correlated with 305 d FCM (100 dMY; 0.23, MYCD; 0.56, FY; 0.17, PY; 0.33 and LL; 0.18). The associations between 100 dMY, MYCD and protein yield were significant ($P < 0.05$) with moderate to high genetic correlations (0.23, 0.56 and 0.33). The MYCD was negative, moderate and significantly ($P < 0.05$) correlated with fat yield ($r_g = -0.34$).

Table 4.22: Genetic correlations, heritability (last column) and repeatability (along diagonal) of milk production traits for Holstein Friesian purebred (above) and Simmental cows (below) in Adamawa State.

Milk production Traits/ R (H/S)	305dFCM	100dMY	MYCD	Fat yield	Protein yield	Lactation length	h^2 (HF/S)
305dFCM	0.32/0.27	0.27*	0.35*	0.53**	0.58**	-0.01	0.25/0.21
100dMY	0.23*	0.21/0.16	0.01	0.05	0.22*	0.25*	0.14/0.10
MYCD	0.56**	0.41*	0.26/0.31	0.26*	0.04	-0.34*	0.22/0.24
Fat yield	0.17	0.38*	-0.34*	0.14/0.25	-0.53**	0.27*	0.06/0.19
Protein yield	0.33*	0.35*	0.53**	0.40**	0.49/0.27	0.15	0.33/0.20
Lactation length	0.18	0.25*	0.22*	0.09	0.30*	0.22/0.16	0.14/0.10

* = $P < 0.05$; ** = $p < 0.01$; 305dFCM -305 day fat corrected milk yield; dMY-Day milk yield; MYCD-Milk yield per cows per day; HF-Holstein Friesian(upper); S-Simmental (lower); h^2 = Heritability estimates (last column); **R** = Repeatability (along diagonal)

4.5 Genetic Parameters of Conformation Type Traits and 305d FCM Yields between Genotypes of Cows

4.5.1 Genetic parameter of conformation type traits and 305d FCM yields in Holstein cows

Table 4.23 depicts the heritabilities, repeatabilities, environmental and genetic correlations between the conformation-type traits and fat-corrected 305-day milk yields. Heritability estimates revealed that stature had the lowest h^2 (0.06) estimates followed by BCS (0.07), rear udder height (0.11), chest ligament (0.12), body depth (0.17) and heart girth (0.18), respectively. The h^2 estimates for chest width, rump, udder clearance, rear udder width and teat length were moderate (0.25; TL- 0.38; RUW). The 305 dFCM and body weight had the highest heritability estimates (0.44 and 0.41). Repeatability estimates ranged from low for BCS (0.11) to high for 305 dFCM (0.61). The genetic correlations between the 305 dFCM and body conformation traits were all positive and ranged from; 0.01 to 0.72 while the genetic correlation with RUH and TL was significant ($P < 0.05$), positive and ranged from moderate (0.32) to high (0.80). UC and RUW had negative genetic correlations with 305 dFCM (-0.47 and -0.35).

The highest and positive genetic correlations for body type traits were observed between CL and BCS; rump and ST (0.97) while the highest negative correlation was recorded between ST and BD (-0.90). Udder clearance and HG had the strongest and most positive correlation for udder conformation traits (0.99) while UC and CL (-0.93) recorded the strongest and most negative correlation. Near zero relationship matrix was observed between CW and 305 dFCM (0.08), CW and BW (0.08), BD and 305 dFCM (0.01), rump and 305 dFCM (0.03), rump and BW (0.08), RUH and CL (0.06), RUH and CW (0.08), RUW and BCS (-0.04), RUW and CW (-0.09), RUW and BD (-0.04), TL and BCS (0.05) and TL and BD (0.05). Apart from these exceptions, most of

Table 4.23: Heritability (h^2), repeatability (R), genetic and environmental correlations of 305dFCM and conformation traits in Holstein Friesian cows

Traits	305dFCM	BW	BCS	CL	CW	BD	ST	Rump	HG	UC	RUH	RUW	TL
305FCM	0.44	0.72**	0.44**	0.35*	0.09	0.01	0.18	0.03	0.44**	-0.47**	0.80**	-0.35*	0.32*
BW (kg)	0.25*	0.41	0.49**	-0.60**	0.08	0.12	0.21*	0.08	0.88**	0.63**	0.96**	0.25*	-0.88**
BCS	0.41**	-0.13	0.07	0.97**	0.52**	0.39*	0.47**	0.52**	0.47**	-0.39*	0.18	-0.04	0.05
CL (cm)	0.32*	0.19	0.64**	0.12	0.80**	0.45**	0.91**	-0.33*	0.39*	-0.93**	0.06	-0.35*	-0.64**
CW (cm)	0.05	0.49**	-0.36*	0.49**	0.33	-0.79**	0.88**	0.80**	0.45**	-0.54**	0.08	-0.09	-0.14
BD (cm)	-0.44**	0.39	-0.67**	-0.83**	-0.25*	0.17	-0.90**	0.62**	-0.30*	0.34*	0.18	-0.04	0.05
ST (cm)	0.37*	-0.03	0.82**	0.57**	-0.25*	-0.15	0.06	0.97**	0.83**	-0.48*	0.93**	0.70**	-0.67**
RW(cm)	0.46**	0.44**	0.63**	0.76**	0.20*	-0.96**	0.16	0.32	0.89**	0.93**	0.88**	0.78**	-0.63**
HG(cm)	0.51**	0.19	0.95**	0.44**	0.54**	0.12	0.24*	0.49**	0.18	0.99**	0.56**	0.97**	-0.81**
UC (cm)	-0.13	0.06	-0.85**	-0.32*	0.58**	0.34*	-0.79**	-0.35*	-0.15	0.30	-0.33*	0.95**	-0.26*
RUH(cm)	0.47**	0.30*	0.34*	0.38*	0.07	-0.19	0.60**	0.19	0.34*	-0.44**	0.11	0.38*	0.48**
RUW(cm)	0.19	-0.17	0.87**	0.53**	-0.35*	-0.59**	0.44**	0.52**	0.82**	-0.67**	0.02	0.38	0.12
TL (cm)	-0.07	-0.68*	-0.63**	0.50**	-0.04	-0.09	0.03	-0.04	0.28*	-0.24*	0.01	0.22*	0.25
R	0.61	0.46	0.11	0.18	0.35	0.26	0.08	0.36	0.22	0.33	0.15	0.44	0.28

* = $P < 0.05$; ** = $p < 0.01$; h^2 = Heritability estimates (along the diagonal). Genetic correlation (above diagonal) and environmental correlation (below diagonal); R – Repeatability; FCM305-Fat corrected 305day milk yield; BW-Bodyweight; BCS-Body condition score; CL-Chest ligament; CW-Chest width; BD-Body depth; HG-Heart girth; UC-Udder clearance; RUH-Rear udder height; RUW-Rear udder width; TL-Teat length; ST-Stature; RW-Rump width

the genetic correlations were moderate and strong. Among the body conformation traits, BCS, rump and HG were the only type traits that had positive, significant, strong and environmental associated with 305 dFCM. Rump was the only udder conformation trait that had a positive, significant and strong correlation with RUH. The BCS and HG had a positive, strong and significant correlation for body type traits while UC and RUW (-0.67) had a negative, strong and significant correlation.

4.5.2 Genetic parameters for conformation type traits and 305d FCM yields in Jersey cows

The 305 d fat corrected milk yield had a moderate (0.35) heritability (Table 4.24). Regarding the linear type traits, the h^2 was between 0.02 (BW) and 0.72 (CL). However, the most heritable body measurement was CL (0.72) while rear udder width was the most heritable udder trait (0.52). BW (0.02) had the least heritability for body conformation traits while the least heritable udder conformation trait was RUH (0.38). Generally, the h^2 estimates for udder conformation traits were higher than those for body type traits except BD and CL. The 305 d fat corrected milk yield had high repeatability (0.57) estimates. The repeatability of the measurements of linear conformation traits varied between 0.03 (BW) to 0.75 (CL) for body conformation traits and from 0.40 (TL) to 0.63 (RUH) for udder measurements. The most repeatable udder and body conformation traits were CL (0.75) and RUH (0.63), respectively.

Body conformation traits had positive, significant ($P < 0.05$) correlations which ranged from moderate to high with 305 d fat corrected milk yield. Udder conformation traits were positive, significant ($P < 0.05$) and ranged from moderate to high with 305 d fat corrected milk yield but with the exception of TL (-0.13) which was low with negative correlations. The strongest and positive genetic correlations for body and udder conformation traits were between ST and BCS (0.99) and TL and RUH (0.93), respectively. The strongest and negative genetic correlation for

body and udder conformation traits were between BD and BW (-0.68) and UC and CW (-0.93), respectively. The highest, significant ($P < 0.05$) and positive environmental correlations for body and udder conformation traits with 305 d fat corrected milk yield were BD (0.38) and RUW (0.94). All the udder conformation traits had positive and significant correlations with 305 d fat corrected milk yield. Environmental correlations between BW and BCS had positive and near zero correlations while CL and CW recorded negative and near zero correlations with 305 d fat corrected milk yield. The highest and positive environmental correlations among the body type traits was between CL and BD (0.90) while correlation between BCS and ST (-0.83) was negative and highest. Environmental correlations among udder conformation traits were positive and negatively weak with the exception of the correlation between TL and RUH (0.22) with RUW (-0.22) which were positive, negative, moderate and significant ($P < 0.05$).

Table 4.24: Heritability (h^2), repeatability (R), genetic and environmental correlations of 305 dFCM and conformation traits in Jersey cows

Traits	305dFCM	BW	BCS	CL	CW	BD	ST	Rump	HG	UC	RUH	RUW	TL
305dFCM	0.35	0.86**	0.21*	0.42**	0.70**	0.67**	0.65**	0.69**	0.52**	0.42**	0.59**	0.32*	-0.13
BW (kg)	0.01	0.02	0.04	0.36*	-0.33*	-0.68**	0.71**	0.43**	-0.39*	0.36*	0.18	-0.31*	0.21*
BCS (cm)	0.05	-0.09	0.25	-0.34*	0.79**	0.23*	0.99**	-0.39*	0.53**	-0.74**	0.30*	0.23*	0.25*
CL (cm)	-0.02	0.48**	0.64**	0.72	0.67**	0.64**	0.48**	0.37*	0.14	0.26*	-0.34*	0.63**	-0.19
CW (cm)	-0.03	-0.05	-0.03	0.77**	0.23	0.10	-0.36*	-0.37*	-0.14	-0.93**	-0.18	-0.37*	-0.02
BD (cm)	0.38*	0.53**	0.56**	0.90**	0.81**	0.61	0.98**	0.87**	0.96**	0.56**	0.21*	-0.54**	0.42**
ST(cm)	0.35*	0.27*	-0.83**	0.73**	-0.17	-0.37*	0.16	0.95**	0.77**	0.57**	0.29*	-0.52*	-0.18
Rump(cm)	0.01	0.05	-0.77**	0.68**	-0.25*	-0.38*	0.08	0.04	0.02	0.04	-0.03	-0.05	0.65**
HG(cm)	0.25*	0.26*	0.54**	-0.16	0.74**	0.65**	0.06	0.08	0.09	0.25*	0.05	-0.12	-0.37*
UC (cm)	0.56**	0.45**	0.51**	0.57**	0.62**	0.78**	0.48**	-0.02	0.48**	0.44	-0.03	0.34*	0.42**
RUH(cm)	0.64**	0.47**	0.07	0.08	0.71**	0.25*	-0.35*	-0.03	-0.05	-0.03	0.38	-0.28*	-0.81**
RUW(cm)	0.94**	0.69**	0.60**	0.35*	-0.31*	-0.25*	-0.22*	-0.21*	0.30*	-0.09	-0.14	0.52	0.93**
TL (cm)	0.34*	0.10	0.44**	0.01 ^{ns}	0.64**	0.03	-0.12	0.42**	-0.34*	0.14	0.22*	-0.20*	0.34
R	0.57	0.03	0.31	0.75	0.28	0.65	0.18	0.05	0.14	0.45	0.41	0.63	0.40

* = $P < 0.05$; ** = $p < 0.01$; h^2 = Heritability estimates (along the diagonal). Genetic correlation (above diagonal) and environmental correlation (below diagonal); R – Repeatability; See table 4.23 for abbreviations.

4.5.3 Genetic parameters of conformation type traits and 305d FCM yields in FriesianxBunaji cows

Estimates of heritabilities, repeatabilities, genetic and environmental correlations of 305dFCM and conformation traits of FriesianxBunaji cows are represented in Table 4.25. Heritability estimates were all moderate for 305dFCM and conformation traits with the exception of BW (0.42) and HG (0.16). Repeatabilities ranged from moderate (0.27) to high (0.56) in body type and udder conformational traits (0.26; UC and 0.60; TL). The BW, BCS, CL, BD and HG were positive, significant and had moderate to high correlations with 305dFCM. The CW and rump had negative, moderate and significant correlation with 305dFCM. The RUH and RUW were the only udder conformation traits that had positive, significant and moderate to high correlations with 305dFCM. UC had negative, significant and strong genetic correlations with 305dFCM. Highest, significant and positive genetic correlation for body type traits was observed between ST and BCS (0.89) while RUH and UC were strongest (0.77) for udder conformation traits. Genetic correlation between UC and other udder conformation traits (RUH, RUW and TL) were all positive, significant and strong. BW, CL and HG were the only type traits that showed positive, high and significant environmental correlations with 305dFCM while UC and RUW had positive, moderate and significant correlation with 305dFCM. Thus, cows with better udder quality will have longer productive lives and are more profitable for producers because they produce more milk and calves in their lifetime. Negative and strong environmental correlations were observed between BCS and ST (-0.72). This implies that selection to improve the stature of a cows will reduced the BCS.

Table 4.25: Heritability (h^2), repeatability (R), genetic and environmental correlations of 305d FCM and conformation traits in Friesian x Bunaji cows

Traits	305d FCM	BW	BCS	CL	CW	BD	ST	Rump	HG	UC	RUH	RUW	TL
305FCM	0.30	0.29*	0.48**	0.58**	-0.23*	0.50**	0.14	-0.35*	0.61**	-0.40**	0.52**	0.21*	0.13
BW (kg)	0.45**	0.42	0.40**	0.62**	0.49**	0.47**	0.20*	0.28*	0.22*	0.34*	-0.22*	0.47**	0.07
BCS	0.07	0.31*	0.38	0.49**	0.45**	0.34*	0.89**	-0.06	-0.03	-0.21*	-0.31*	-0.29*	0.56**
CL (cm)	0.43**	0.44**	0.17	0.22	0.57**	0.29*	0.08	0.35*	0.38*	0.38*	0.44**	0.45**	0.30*
CW (cm)	0.05	0.47**	0.42**	0.04	0.31	0.43**	0.15	0.19	0.21*	0.33*	0.27*	0.48**	0.61**
BD (cm)	0.31*	0.33*	0.06	0.01	0.28*	0.37	-0.26*	0.37*	0.08	0.28*	0.37*	-0.36*	0.20*
ST (cm)	0.14	0.25*	-0.72**	0.22*	0.03	-0.15	0.32	0.54**	0.05	0.77**	0.11	0.66**	0.01
Rump(cm)	0.04	0.15	-0.09	-0.07	0.22*	0.13	0.09	0.28	-0.29*	0.15	-0.08	0.39*	-0.33*
HG(cm)	0.42**	0.17	0.14	0.33*	0.25*	0.05	0.51**	0.33*	0.16	-0.31*	0.25*	-0.28*	0.46**
UC (cm)	0.30*	0.05	-0.02	0.26*	0.61**	0.11	-0.21*	-0.31*	0.05	0.20	0.77**	0.40**	0.38*
RUH(cm)	0.18	0.02	-0.13	0.09	0.06	0.44**	0.49**	-0.13	0.09	0.08	0.29	-0.11	-0.39*
RUW(cm)	0.26*	0.08	0.16	-0.22*	-0.33*	0.38*	0.28*	-0.02	-0.11	0.30*	-0.12	0.23	-
TL (cm)	0.01	0.13	0.26*	0.28*	-0.23*	0.23*	0.17	0.04	0.22*	0.36*	0.38*	0.50**	0.55**
R	0.35	0.56	0.39	0.29	0.40	0.39	0.48	0.40	0.27	0.26	0.49	0.28	0.60

* = $P < 0.05$; ** = $p < 0.01$; h^2 = Heritability estimates (along the diagonal). Genetic correlation (above diagonal) and environmental correlation (below diagonal); R – Repeatability; See table 4.23 for abbreviations.

4.5.4 Genetic parameter of conformation traits and 305d FCM yields in JerseyxBunaji cows

Table 4.26 shows the heritabilities, repeatabilities, genetic and environmental correlation of 305dFCM and conformation traits. 305 d fat corrected milk yield had a moderate (39 %) heritability which was higher than estimates obtained for HolsteinXBunaji. The h^2 for body type traits was between 2 % (BCS) to 51 % (BD). However, the most heritable udder conformation measurement was RUW (36 %). The BCS (2 %) had the least heritability for body conformation traits while the least heritable udder conformation trait was TL (23 %). Generally, the h^2 estimates of the udder conformation traits were higher than those of the body type traits except BD and BW. However, some of the body and udder quality traits were moderate to highly heritable which indicates that genetic progress can be made through genetic selection. This implies that the first-period record for all the body and udder conformation traits is a good indication of future performance while BCS will indicate poor reliability of future performance.

The 305 d fat-corrected milk yield had high repeatability (57 %) estimates which were similar to the estimates obtained for the Jersey cows. All the 305 d fat-corrected milk yield and conformation traits were highly repeatable except BCS (10 %). The genetic and environmental correlations varied widely in magnitude and direction. All the body conformation traits had positive, significant and moderate genetic correlation with 305 d fat-corrected milk yield except BCS. Udder conformation traits had positive genetic correlations with 305 d fat-corrected milk yield. Thus, selection for one trait should result in improvement in the other traits. The strongest and most positive genetic correlation for body and udder conformation traits was between ST and BCS (0.99) and TL and RUH (0.93), respectively. The strongest and most negative genetic correlation for body and udder conformation traits were between HG and BD (0.61) and RUH and RUW (0.26), respectively. The highest and most significant environmental correlations for

body and udder conformation traits with 305 d fat-corrected milk yield were BW (0.22) and RUW (-0.22). Most of the environmental correlations of body and udder conformation traits with 305 d fat-corrected milk yield tended towards zero in both positive and negative directions except BW and RUW.

4.5.5 Genetic parameters of conformation traits and 305d FCM yields in Brown Swiss cows

The estimates of heritabilities, repeatabilities, environmental and genetic correlations of the 305d FCM and conformational traits in Brown Swiss are shown in Table 4.27. Heritability and repeatability estimates for 305d FCM were moderate (22 and 37 %). The highest heritability for body type traits was recorded for CW (0.48) while the least was CL while RUH was highest for udder traits. TL and UC had the lowest estimates (20 %) for udder conformation traits. Repeatability estimates were moderate to high for udder conformation traits but low to high for body conformation traits. Repeatability estimates for 305 d FCM were 37 %. The BD had the strongest and significant genetic correlation with 305 d FCM yield for body type traits while RUH had a similar trend for udder conformation traits. BW, BCS, ST and RW had moderate and significant genetic correlations with 305d FCM yield in body type traits while UC and RUW were the only traits that revealed similar trends in udder conformation traits. A strong, positive and significant genetic correlation was observed between HG and BD in body type traits while TL and RUW had very strong, positive and significant genetic correlation for udder conformation traits. In this case, cows with longer teats had genetics for wider rear udder attachment. Most of the environmental correlations between 305 d FCM and conformational were taped toward zero,

Table 4.26: Heritability (h^2), repeatability (R), genetic and environmental correlations of 305 FCM and conformation traits in JerseyxBunaji cows

Traits	305 FCM	BW	BCS	CL	CW	BD	ST	Rump	HG	UC	RUH	RUW	TL
305FCM	0.39	0.26*	0.06	0.32*	0.29*	0.30*	0.22*	0.35*	0.21*	0.49**	0.15	0.32*	0.31*
BW (kg)	0.22*	0.41	0.29*	0.11	0.41**	0.33*	0.24*	-0.35*	0.26*	0.33*	0.22*	0.25*	0.07
BCS (cm)	-0.05	-0.12	0.02	0.33*	0.26*	0.31*	-	0.29*	0.39*	0.24*	0.18	0.23*	0.28*
CL (cm)	-0.15	-0.15	0.13	0.21	0.07	0.01	0.29*	0.22*	0.30*	0.35*	0.04	0.18	0.13
CW (cm)	0.08	-0.18	-0.18	-0.03	0.36	0.53**	0.17	-0.30*	0.34*	0.60**	0.56**	0.22*	0.23*
BD (cm)	0.02	0.42**	-0.01	0.07	-0.25*	0.51	0.31*	0.21*	0.61**	0.13	0.58**	0.13	0.38*
ST (cm)	0.10	0.28*	-0.20*	0.30*	0.13	0.24*	0.28	0.36*	0.22*	0.53**	0.21*	0.19	0.26*
Rump(cm)	0.02	-0.04	-0.15	0.05	0.22*	0.11	0.08	0.15	0.12	0.32*	0.43**	0.16	0.15
HG(cm)	0.01	0.33*	0.14	0.25*	-0.30*	0.21*	0.18	-0.20	0.19	0.31*	0.29*	0.07	0.20*
UC (cm)	-0.13	-0.03	0.16	0.04	-0.21*	0.06	-0.25*	-0.09	-0.10	0.27	0.21*	0.24*	0.25*
RUH(cm)	-0.04	0.03	0.19	0.11	-0.29*	0.36*	0.14	0.04	0.28*	-0.12	0.34	0.26*	0.18
RUW(cm)	-0.22*	-0.42**	0.36*	0.24*	-0.25*	-0.04	-0.18	-0.17	0.10	-0.01	0.21*	0.36	0.15
TL (cm)	0.07	0.57**	0.10	0.13	-	0.57**	0.16	-0.16	0.64**	0.06	0.32*	0.04	0.23
R	0.57	0.42	0.10	0.48	0.64	0.71	0.33	0.20	0.26	0.36	0.48	0.47	0.62

* = $P < 0.05$; ** = $p < 0.01$; h^2 = Heritability estimates (along the diagonal). Genetic correlation (above diagonal) and environmental correlation (below diagonal);

R – Repeatability; See table 4.23 for abbreviations.

Table 4.27: Heritability (h^2), repeatability (R), genetic and environmental correlations of 305 FCM and conformation traits in Brownswiss cows

Traits+	305 FCM	BW	BCS	CL	CW	BD	ST	Rump	HG	UC	RUH	RUW	TL
305FCM	0.22	0.29*	0.34*	0.18	-0.16	0.49**	0.20*	0.23*	0.11	0.26*	0.45**	0.30*	0.16
BW (kg)	-0.08	0.25	0.01	-0.24*	-0.28*	0.07	-0.11	0.39*	0.29*	0.21*	0.33*	-0.15	0.12
BCS	0.10	0.05	0.15	-0.19	0.31*	0.32*	0.34*	0.34*	0.33*	0.29*	0.10	0.62**	-0.04
CL (cm)	0.16	0.11	-0.04	0.10	0.11	0.25*	0.18	0.32*	0.44**	0.31**	0.06	-0.36*	0.32*
CW (cm)	-0.02	0.16	0.18	0.14	0.48	0.33*	0.24*	0.21	0.12	0.29*	0.47*	0.34*	0.15
BD (cm)	0.04	-0.27	-0.05	0.06	-0.04	0.29	0.35*	0.47**	0.49**	0.31**	0.42*	0.45**	0.09
ST(cm)	-0.09	0.04	-0.05	0.07	-0.03	0.38*	0.35	0.44**	0.37*	0.11	0.12	0.42**	0.19
Rump(cm)	0.02	0.10	0.32*	0.12	0.30*	0.22*	0.22*	0.37	0.46**	0.30*	0.51**	-0.32*	0.14
HG(cm)	0.17	-0.28	0.08	-0.03	-0.11	0.81**	-0.10	-0.13	0.28	0.39*	0.39*	0.10	-0.33*
UC (cm)	0.08	0.37*	0.07	0.06	0.03	-0.26*	-0.12	0.31*	-0.32*	0.20	0.35*	0.31*	0.12
RUH(cm)	0.29*	0.20	-0.02	-0.04	-0.13	-0.16	0.08	0.03	-0.33*	0.06	0.39	0.19	0.26*
RUW(cm)	0.04	-0.02	-0.10	-0.08	0.23*	-0.31*	-0.17	-0.24*	-0.22*	-0.02	0.19	0.26	0.60**
TL (cm)	-0.04	-0.40*	0.04	-0.09	-0.05	0.62**	-0.27*	-0.20*	0.78**	-0.46**	-0.33*	-0.14	0.20
R	0.37	0.50	0.18	0.26	0.61	0.35	0.44	0.46	0.43	0.49	0.45	0.38	0.34

* = $P < 0.05$; ** = $p < 0.01$; h^2 = Heritability estimates (along the diagonal). Genetic correlation (above diagonal) and environmental correlation (below diagonal); R – Repeatability; See table 4.24 for abbreviations.

with the exception of rear udder height with moderate, positive, and significant correlation. The highest environmental correlation existed between BD and HG (0.81) for body type traits while UC and TL recorded the highest environmental correlation in a negative direction (-0.46).

4.5.6 Genetic parameters for conformation traits and 305d FCM yields in Simmental cows

Table 4.28 shows the heritability, repeatability, environmental and genetic correlations of the conformation type traits and corrected 305-day milk yields in Simmental dairy cows. Heritability estimates were 21 % for FCM305 day milk yields which was the least among the estimates obtained for the multiple breeds while the repeatability estimate was 27 %. Heritability estimates for body type traits were 26, 13, 10, 28, 20, 35, 6 and 33 % for BW, BCS, CL, CW, BD, ST, rump and HG, respectively. Repeatability estimates were all moderate and high for FCM305 day milk yields, body and udder conformational traits. Environmental and genetic correlations varied both in magnitude and direction. The BW and HG had positive, high and significant genetic correlation with 305 d FCM. The genetic correlation between 305 d FCM and CL was positive, moderate and significant. The Rump and BD had the highest and most significant genetic correlation between body type traits. All the udder conformation traits had positive, high and significant genetic correlation with 305 d FCM except for udder clearance. Estimates of genetic correlations were higher than the values recorded for environmental correlations. The BD and HG had positive, strong and significant environmental correlation with 305 d FCM for body type traits while RUW and TL showed similar trend for udder conformation traits. The BW and RUH had negative, moderate and significant environmental correlation with fat corrected 305 day milk yield. The BCS, CW, rump and UC had near zero environmental correlations with fat corrected 305 day milk yield. The RUW and TL had the strongest, positive and significant environmental correlations.

Table 4.28: Heritability (h^2), repeatability (R), genetic and environmental correlations of 305 FCM and conformation traits in Simmental cows

Traits	305dFCM	BW	BCS	CL	CW	BD	ST	Rump	HG	UC	RUH	RUW	TL
305dFCM	0.21	0.54**	0.11	0.25*	0.11	0.61**	0.17	-0.10	0.62*	0.10	0.42*	0.60**	0.74**
BW (kg)	-0.29*	0.26	0.26*	-0.30*	0.18	0.14	0.48**	0.45**	0.41**	0.18	0.29*	0.50*	0.61**
BCS	0.02	-0.15	0.13	0.16	0.14	0.40**	0.49**	0.19	0.38*	0.73**	0.06	0.27*	0.11
CL (cm)	0.17	0.20*	-0.08	0.10	0.25*	0.17	0.25*	0.13	0.22*	0.74**	0.12	0.38*	0.58**
CW (cm)	0.04	-0.11	0.31*	-0.30*	0.28	0.10	0.18	0.45**	0.56**	0.67**	-0.22*	-0.31*	0.19
BD (cm)	0.45**	0.09	-0.23*	-0.08	-0.17	0.20	0.63**	0.94**	0.23*	0.18	0.95**	0.91**	0.37*
ST(cm)	-0.06	0.06	-0.09	-0.12	-0.03	0.44**	0.35	0.20*	0.15	-0.10	0.16	0.20*	0.38*
Rump(cm)	0.03	-0.34*	0.07	0.10	-0.08	0.85**	-0.17	0.06	0.18	0.33*	0.29*	0.10	0.29**
HG(cm)	0.53**	-0.38*	-0.15	0.05	-0.14	-0.13	-0.14	-0.12	0.33	-0.40**	-0.15	0.91**	0.90**
UC (cm)	0.04	-0.05	0.02	0.16	0.07	-0.15	0.07	0.15	-0.20*	0.31	-0.30*	0.15	0.25*
RUH(cm)	-0.33*	0.05	-0.01	-0.15	-0.03	0.91**	-0.03	0.26*	-0.05	-0.18	0.20	-0.23*	0.49**
RUW(cm)	0.54**	-0.43**	-0.26*	-0.04	-0.13	0.88**	-0.13	-0.05	0.89**	-0.11	-0.15	0.18	-0.10
TL (cm)	0.46**	-0.42**	-0.24*	-0.02	-0.10	-0.30*	-0.10	-0.06	0.86**	-0.10	-0.12	0.96**	0.59
R	0.27	0.43	0.20	0.20	0.62	0.35	0.70	0.07	0.38	0.35	0.28	0.52	0.64

* = $P < 0.05$; ** = $p < 0.01$; NS = Not Significant+ See Table 4.23 for meaning of abbreviations; h^2 = Heritability estimates (between the diagonal), Genetic correlation (above) and environmental correlation (below) the diagonal. **R** - Repeatability

4.6 Genetic Parameters of Reproductive Traits and 305d FCM Yields in Genotypes of Cows

4.6.1 Heritabilities, Repeatabilities, Genetic and Environmental Correlations of Reproductive Traits and 305 d FCM yields in different Genotypes of cows in Kwara State

Table 4.29 reveals the heritability, repeatability estimates, genetic and environmental correlations of reproductive traits and 305 d FCM yields. For the Holstein Friesian breed, the heritability estimates for the reproductive indices computed for Holstein Friesian cows varied between 0.02 (CI) and 0.19 (HL). The AFC (24 %) was the only heritable fertility trait. Repeatability estimates for reproductive traits estimates varied between 9 % for NSC and 28 % for herd life. The largest positive, significant, genetic and environmental correlations were observed between CR and NSC; 0.68 (genetic) and 0.31 for CI and CR (residual). However, estimates of genetic correlations were higher than the environmental correlations. The AFC and DO had negative, moderate and significant genetic correlations with 305 d FCM yield. All environmental correlations between reproductive traits and 305 d FCM yields were positive and not significant except NSC (0.33) which was positive and moderately significant.

In FriesianxBunaji cows, all heritability estimates for the reproductive traits were less than 20 %. The AFC was the only fertility trait that was highly repeatable. Genetic correlations between fat-corrected 305-day milk yield and reproductive traits were negative and weakly correlated with AFC and DO. The CR and HL had positive, moderate and significant genetic correlations with 305 d FCM. All the reproductive traits showed low and positive environmental correlation with 305 d FCM. The HL was the only fertility trait that had positive, moderate and significant environmental correlation with 305 d FCM.

In the Jersey breed, heritability estimates for reproductive traits were all lower than 17%. Repeatability estimates ranged from 2 % for DO to 19 % for herd life. The AFC, CR and HL had positive and significant genetic correlations with 305 d FCM while NSC and HL were positive, significant and environmentally correlated with 305 d FCM. Lastly, heritability and repeatability estimates for all the reproductive traits were less than 10 % for heritability and 20 % for repeatability in JerseyxBunaji cows. Both environmental and genetic correlations varied in both magnitude and direction. The 305d FCM had negative genetic correlations with all the reproductive traits except AFC while CI had negative, moderate and significant environmental correlation with 305 d FCM yield. The AFC, DO, CR and HL had a positive and low relationship with 305 d FCM yield.

4.6.2 Heritability, repeatability, genetic and environmental correlations of reproductive traits and 305 d FCM yields in multi-genotypes cows in Integrated Dairies Limited in Plateau State

The heritability and repeatability estimates; genetic and environmental correlations for reproductive traits and 305 d FCM are shown in Table 4.30. In the Holstein Friesian breed, low to moderate estimates of heritability were recorded for all the fertility traits ($h^2=1$ to 23 %). Repeatability estimates for reproductive traits varied from 7 % for CR to 26 % for AFC. The DO and CI had positive, significant and strong genetic correlations with 305 d FCM. AFC had negative, moderate and significant correlations with 305 d FCM. Therefore, selecting cows for improved milk volume could potentially help reduce the AFC. Genetic correlations between CR and NSC were positive, significant and strong. CI had the strongest environmental correlation with 305 d FCM while AFC was positive, significant with moderate correlations.

Table 4.29: Heritability estimates (diagonal), repeatability (right column), genetic correlations (above diagonal) and environmental correlations (below diagonal) for 305d FCM and reproductive traits in multi-genotypes cows in Kwara State

Genotype/ Trait	305 dFCM	AFC	NSC	DO	CI	CR	HL	R
Holstein								
305 dFCM		-0.33*	-0.08	-0.22*	0.14	0.05	0.08	
AFC	0.14	0.24	-0.41*	0.16	-0.17	-0.13	-0.33*	0.28
NSC	0.33*	0.30*	0.08	0.27*	0.23*	0.68**	-0.18	0.09
DO	0.14	0.09	0.22*	0.10	-0.22*	0.23*	-0.22*	0.11
CI	0.08	0.12	0.20*	-0.19	0.02	-0.14	0.14	0.11
CR	0.01	0.12	0.32*	0.20*	0.31*	0.05	0.65**	0.19
Herdlife	0.06	0.15	0.12	-0.12	0.26*	0.11	0.19	0.16
FriesianxBunaji								
305 dFCM		-0.07	0.11	-0.15	0.10	0.29*	0.31*	
AFC	0.02	0.18	-0.22*	0.25*	0.09	-0.21*	-0.47**	0.25
NSC	0.03	0.05	0.06	0.11	0.51**	0.18	0.05	0.13
DO	0.03	0.01	0.33*	0.01	0.01	-0.14	0.10	0.05
CI	0.04	0.42**	0.12	0.14	0.03	-0.27*	-0.42**	0.11
CR	0.09	0.20*	0.09	0.35*	0.04	0.08	0.08	0.09
Herdlife	0.22*	0.27*	0.01	0.29*	0.11	0.12	0.003	0.02
Jersey								
305 dFCM		0.13	0.67**	-0.12	0.12	0.23*	0.54**	
AFC	0.10	0.04	0.27*	-0.38*	0.05	-0.10	-0.09	0.10
NSC	0.30*	0.20*	0.08	0.60**	-0.36*	0.28*	0.66**	0.13
DO	0.01	0.29*	0.42**	0.14	0.12	0.23*	-0.28*	0.02
CI	0.08	0.12	0.33*	0.06	0.04	-0.04	0.16	0.05
CR	0.18	0.29*	0.22*	0.10	0.02	0.02	0.29	0.04
Herdlife	0.46*	0.15	0.54**	0.17	0.12	0.16	0.17	0.19
JerseyxBunaji								
305 dFCM		0.17	-0.35*	-0.14	-0.36*	-0.09	-0.13	
AFC	0.13	0.09	0.20*	-0.37*	0.27*	0.29*	0.10	0.13
NSC	0.20*	0.06	0.04	-0.29*	-0.12	0.35*	0.36*	0.11
DO	0.12	-0.08	0.21*	0.07	0.16	-0.74**	-0.63**	0.09
CI	-0.24*	-0.15	0.05	0.10	0.02	-0.10	-0.75**	0.05
CR	0.05	0.24*	0.16	0.46**	-0.02*	0.08	0.69*	0.15
Herdlife	0.08	0.02	-0.19	0.40**	0.55**	0.56**	0.01	0.08

305 dFCM – 305 day fat corrected milk yield, AFC-Age at first calving, NSC-Number of service per conception rate, CI-Calving interval, DO-days open, CR-Calving rate, HL-Herd life; *P<0.05-Significant; **P<0.01-Highly significant, R-Repeatability (last column), h²-heritability (along the diagonal)

In FriesianxBunaji cows, AFC and CI showed moderate heritabilities among reproductive traits. Reproductive traits for repeatability estimates varied from 8 % for CR to 36 % for AFC. The CR and HL had moderate and negative genetic correlation with 305 d FCM yield. The DO had moderate and strong positive genetic correlation with 305 d FCM yield. The CI, CR and HL had positive environmental correlations that were significant and moderately correlated with 305 d FCM in a positive direction.

4.6.3 Heritabilities, repeatabilities, genetic and environmental correlations of reproductive traits and 305d FCM yields in multi-genotypes of cows in Sebore farm in Adamawa State

In Holstein Friesian cows, reproductive traits were lowly heritable and repeatable (less than 20 %) (Table 4.31). The NSC had a positive, significant and strong genetic correlation with 305 d FCM yield while moderate correlations were recorded for CR. The AFC, CI, DO and herd life were moderate, significant, and negatively correlated with 305 d FCM. The highest genetic correlation was observed between CI and AFC. The AFC, NSC, CR and HL had positive and moderate environmental correlation with 305 d FCM yield while DO showed negative moderate and significant correlation. The strongest environmental correlation was observed between AFC and DO (0.90).

In Jersey cows, most of the reproductive traits were lowly heritable except NSC. Repeatability estimates ranged from low for HL (3 %) to high for NSC (26 %). Positive, moderate and strong genetic correlations were observed between fat-corrected 305-day milk yield and reproductive traits except for DO (-0.30) and CI (-0.19). The strongest genetic correlations were observed between HL and DO ($r_g=97$ %). The CR and NSC had positive and strongest environmental correlations with fat-corrected 305-day milk yield while AFC and CI were moderately correlated with 305 d FCM yield.

Table 4.30: Heritability estimates (diagonal), repeatability (last column), genetic correlations (above diagonal) and environmental correlations (below diagonal) for 305d FCM and reproductive traits in multi-genotypes cows in IDL in Plateau State

Genotype /Trait	305d FCM	AFC	NSC	DO	CI	CR	HL	R
Holstein Friesian								
305d FCM		-0.31*	-0.04	0.40**	0.46**	-0.09	-0.12	
AFC	0.30*	0.23	0.20*	0.29*	0.33*	0.26*	0.07	0.26
NSC	0.02	-0.03	0.10	0.19	0.52**	0.63**	0.07	0.16
DO	0.45**	0.31*	0.29*	0.14	0.12	0.19	-0.13	0.18
CI	0.09	-0.19	0.08	0.40**	0.09	-0.05	0.41**	0.10
CR	0.04	0.18	0.34*	0.29*	0.16	0.01	-0.24*	0.07
Herdlife	0.08	0.05	-0.10	0.04	-0.03	0.14	0.18	0.29
FriesianxBunaji								
305d FCM		-0.14	-0.19	0.24*	-0.06	-0.29*	-0.28*	
AFC	0.08	0.28	0.37*	0.15	-0.08	0.48**	0.27*	0.36
NSC	0.11	0.30*	0.16	0.25*	-0.30*	0.32*	-0.23*	0.18
DO	-0.04	0.05	0.24*	0.10	0.68**	0.55**	-0.30*	0.15
CI	0.21*	0.20*	-0.29*	0.15	0.23	0.35*	-0.21*	0.27
CR	0.26*	0.38*	0.31*	0.24*	0.40**	0.05	-0.23*	0.08
Herdlife	0.20*	0.21*	0.12	0.18	0.24*	-0.19	0.04	0.10

305 dFCM – 305 day fat corrected milkyield, AFC-Age at first calving, NSC-Number of service per conception rate, CI-Calving interval, DO-days open, CR-Calving rate, HL-Herd life

Brown Swiss had low heritability and repeatability estimates for reproductive traits with the exception of DO which was moderate (23 and 29 %). The DO and CI had the highest genetic relatedness while the highest environmental correlations were observed between HL and NSC ($r=0.68$).

Lastly, heritability estimates for reproductive traits were all low in Simmental cows. Repeatability estimates had a similar trend with heritability with the exception of NSC and CI. The HL and CI had positive and the strongest genetic relatedness while AFC and HL had the strongest environmental correlations. The AFC, CI and HL had positive, significant and strongest genetic correlation with corrected 305-day milk yield. The DO and NSC were low, positive and moderately correlated while CR revealed the existence of moderate negative genetic correlation with fat corrected 305 day milk yield. All the reproductive traits had positive, significant and moderate to high environmental correlations with 305 day milk yield except NSC ($r=0.06$).

4.7 Effect of Genotype by Environment interaction on Predicted Breeding Values for 305 d FCM and Some Selected Reproductive Traits in Cows

4.7.1 Predicted breeding value estimates for 305 d FCM and some selected reproductive traits in genotype by environment interactions in the first and pooled lactations

The breeding value estimates and their accuracy for 305 d FCM and some selected reproductive traits are given in Table 4.32. The estimated breeding values for 305 d FCM yield from animal model was 70 kg with 50 % accuracy of estimation for Holstein Friesian cows in first lactation under low environmental conditions in Plateau State. The high accuracy of 50 % implies that there is a substantial opportunity for genetic change when more records from the progeny are considered. The corresponding values for lactation length, calving interval and day open were extended by a day, 4.6 days longer and -1.7 days shorter, respectively.

Table 4.31: Heritability estimates (diagonal), repeatability (last column), genetic correlations (above diagonal) and environmental correlations (below diagonal) for 305d FCM and reproductive traits in multi-genotypes cows in Sebore Farm in Adamawa State

Genotype/ Trait	305d FCM	AFC	NSC	DO	CI	CR	HL	R
Holstein Friesian								
305d FCM		-0.27*	0.56**	-0.36*	-0.39*	0.23*	-0.35*	
AFC	0.30*	0.14	0.49**	0.57**	0.95**	0.25*	0.94**	0.16
NSC	0.25*	-0.43*	0.11	0.14	0.06	0.30*	0.08	0.18
DO	-0.35*	0.90**	0.02	0.16	0.31	0.83**	0.24*	0.19
CI	-0.14	0.75**	-0.15	0.63**	0.12	0.87**	0.18	0.13
CR	0.25*	0.14	-0.22*	0.20*	0.73**	0.05	0.16	0.08
Herdlife	0.20*	0.88**	-0.12	-0.10	0.14	0.20*	0.10	0.13
Jersey								
305d FCM		0.50**	0.71**	-0.30*	-0.19	0.89**	0.49**	
AFC	0.29*	0.01	-0.21*	0.83**	0.91**	0.18	0.86**	0.05
NSC	0.46**	0.16*	0.24	-0.34*	-0.37*	0.86**	-0.35*	0.26
DO	-0.14	0.89**	0.30*	0.11	0.22	-0.36*	0.97**	0.25
CI	0.30*	0.50**	0.10	0.29*	0.18	0.29*	0.60**	0.07
CR	0.65**	0.14	0.56*	0.23*	0.14	0.08	-0.12	0.14
Herdlife	0.10	0.32*	-0.19	0.60**	0.77**	0.08	0.01	0.03
Brown Swiss								
305d FCM		0.80**	0.61**	-0.39*	0.68**	0.31*	-0.60**	
AFC	0.64**	0.14	-0.45**	0.30*	0.71**	-0.35*	0.84**	0.17
NSC	0.58**	0.19**	0.06	0.52**	0.34*	-0.16	-0.35*	0.11
DO	0.49**	0.58**	0.37*	0.23*	0.07	0.83**	0.58**	0.29
CI	0.05	0.61**	-0.10	0.03	0.02	-0.33*	0.56**	0.06
CR	0.20*	-0.29*	0.15	0.09	0.18	0.19	-0.34*	0.26
Herdlife	0.28*	0.61**	0.68**	0.60**	0.33*	0.22*	0.02	0.08
Simmental								
305d FCM		0.74**	0.11	0.18	0.46**	-0.32*	0.79**	
AFC	0.59**	0.06	0.18	0.31*	0.92**	-0.53*	0.92**	0.11
NSC	0.06	-0.10	0.13	0.11	0.18	0.21*	0.27*	0.23
DO	0.32*	0.41**	0.15	0.10	0.04	-0.44*	0.98**	0.06
CI	0.27*	0.07	0.07	0.39*	0.17	-0.65**	0.78**	0.21
CR	0.29*	0.29*	0.16	0.26*	-0.22*	0.09	-0.49**	0.10
Herdlife	0.63**	0.90**	-0.19	0.20*	0.75**	0.26*	0.07	0.13

AFC-Age at first calving, NSC-Number of service per conception rate, CI-Calving interval, DO-days open, CR-Calving rate, HL-Herd life, R-Repeatability; 305 dFCM – 305 day fat corrected milkyield

The accuracy of estimating the true breeding values for reproductive traits ranged from 20 % (LL and CI) to 40 % (DO). The positive value of breeding value was obtained for milk yield which implied a likelihood for moderate genetic improvements. Also, this might be an indicator that early milk yield could be used in predicting 305 d standardized lifetime milk production in Holstein Friesian cows. DO showed low estimates of negative breeding values in first and pooled lactation with moderate accuracy (0.2-0.4). All sires showed very short ranges in their breeding values for DO, which reflected low genetic differences among them. The genetic difference among individuals is a factor that determines the rate of genetic improvement that can be accomplished through selection.

Holstein Friesian cows in Adamawa State had predicted estimates of 42 kg and 101.8 kg breeding values with 30 % accuracy for 305 d FCM yield for first and pooled lactations, respectively. The difference between the 305 d FCM yield between the first and pooled lactations was 59 kg. This implies that cows in later lactations will on average produce 29.6 kg more in milk weight than the first lactation at the 305th day of milk production.

Jersey cows in Kwara State had predicted breeding values of 12.4 kg and 80.1 kg with moderate accuracy for pooled (30 %) to high (50 %) in the first lactation. Low (0.1) to high (0.9) accuracies of predicted breeding values for reproductive traits were estimated for the first lactations while moderate to high accuracies were obtained for pooled lactation. The CI showed a small genetic improvement by shortening the duration of calvings with moderate accuracy of predicted breeding values.

Jersey cows in high environmental conditions (High temperature and high humidity) in Adamawa had low genetic improvements for first lactation 305 d FCM yield with moderate accuracy of estimation while the lifetime milk production yield had high accuracies for estimated

breeding value. The CI and DO had high estimates of negative breeding values except for LL with high accuracies of prediction in the first lactation while in the pooled lactations all the predicted estimates were positives with low (0.1; CI) to high (0.8; LL) accuracy of prediction. Brown Swiss in Adamawa State had high genetic improvements for first and pooled lactations with low accuracies in the first lactation and high accuracies in the pooled lactations. The LL had significant genetic improvement in the first and pooled lactations with high accuracies (50 – 80 %). DO was shortened in the first and pooled lactations with low to moderate accuracies. Simmental cows in high environmental conditions (High temperature and high humidity) in Adamawa State showed positive genetic improvement in 305 d FCM yield with low prediction accuracy. The LL and CI had short, moderate to high accuracies while DO was longer in the first lactations but shorter in the pooled lactations.

Table 4.32: Predicted breeding values and accuracy of 305dFCM and reproductive traits when using records of first and pooled lactations in purebred multi-genotype cows in Shonga Dairy Holdings, Integrated Dairies Limited and Sebore farms

Breed and /Trait	First Lactation		Pooled Lactation	
	Breeding values (+, -)	Accuracy	Breeding values (+, -)	Accuracy
Holstein Friesian Plateau				
305d FCM (kg)	+70.0±2.34	0.5±0.09	+226.8±23.11	0.3±0.07
Lactation length (d)	+1.0±0.01	0.2±0.06	+0.6±0.04	0.3±0.09
CI	+4.6±1.15	0.2±0.17	+3.1±0.09	0.3±0.02
DO	-1.7±0.04	0.4±0.19	-0.5±0.11	0.2±0.02
Holstein Friesian Adamawa				
305d FCM (kg)	+42.0±3.17	0.3±0.08	+101.8±22.21	0.3±0.07
Lactation length (d)	+11.5±1.12	0.2±0.06	+3.8±1.33	0.3±0.06
CI	+9.6±1.01	0.1±0.05	+11.4±3.58	0.3±0.08
DO	+16.8±2.20	0.1±0.06	+6.2±2.06	0.2±0.03
Jersey Kwara				
305 FCM (kg)	+12.4±3.74	0.5±0.12	+80.1±6.84	0.3±0.03
Lactation length (d)	-3.0±0.06	0.1±0.03	-5.4±1.12	0.4±0.01
CI	-3.1±0.26	0.2±0.04	-9.4±1.20	0.3±0.07
DO	+2.6±0.03	0.9±0.39	-4.7±0.93	0.5±0.04
Jersey Adamawa				
305 FCM (kg)	+12.1±18.2	0.3±0.01	+138.3±20.3	0.4±0.02
Lactation length (d)	-7.2±2.14	0.5±0.03	-2.4±0.56	0.8±0.04
CI	-9.8±2.90	0.8±0.27	+4.7±1.16	0.1±0.01
DO	-7.7±2.23	0.5±0.03	+4.2±1.12	0.3±0.01
Brownswiss Adamawa				
305 FCM (kg)	+42.6±12.9	0.11±0.07	+134.7±14.5	0.5±0.09
Lactation length (d)	+6.8±2.72	0.2±0.10	+5.3±1.20	0.3±0.03
CI	+11.0±4.36	0.6±0.01	-5.6±2.19	0.4±0.08
DO	-6.4±2.60	0.1±0.05	-8.0±2.22	0.2±0.05
Simmental Adamawa				
305 FCM (kg)	+21.9±4.20	0.1±0.01	+185.4±20.25	0.1±0.05
Lactation length (d)	-3.2±1.60	0.4±0.08	-3.9±1.20	0.3±0.08
CI	-3.5±1.65	0.5±0.23	-13.9±5.42	0.8±0.03
DO	+4.8±1.97	0.3±0.20	-5.9±2.45	0.3±0.01

CI-Calving interval; DO-Day open; d-day; FCM-Fat corrected milk; kg-kilogram; -=depression; +=gain

4.8 Inbreeding Depression for Milk Production and Reproduction Traits in First and Pooled Lactations in Breed x Environment Interaction

4.8.1 Inbreeding depression for milk production traits in breed x environment interaction

Table 4.33 presents the inbreeding depression per 1% of inbreeding for milk production traits in Holstein Friesian cows in Integrated Dairies Limited. There was a very large difference between fixed (Wright method) and animal model analysis (BLUE) of inbreeding depression on 305 d FCM yield, with all estimates rounding to a decrease of 350 kg (4646.6 kg) in BLUE and 381 kg (4615.4 kg) for wright method per 1% increase in inbreeding. There was little difference between the fixed (Wright method) and mixed model analysis (BLUE) for fat yield, protein yield and lactation length. Lactation length was extended by 5 days in both methods of estimation.

In the Holstein Friesian cows born and bred in Adamawa State, there was a very small difference between fixed (Wright method) and animal model analysis (BLUE) of inbreeding depression on milk production traits. Inbreeding extended lactation length by 13 days in both models while a small difference was observed for 305 d FCM yield with a differential of 6 kg.

Jersey cows in Kwara State had the largest effect of inbreeding depression. Animal model estimates of inbreeding depression per 1 % increase in inbreeding for the entire data were -419.6 kg, -.15.2 kg, -13.1 kg and -12.2 d for 305 d FCM, fat yield, protein and lactation length respectively, and are lower than estimates for the fixed model (-422.1 kg, -15.2 kg, -13.0 kg and -11.4 d for 305 d FCM, fat yield, protein yield and lactation length), respectively but with the exception fat yield which was similar in both models. Inbreeding was more severe on Jersey cows in Kwara State which might be due to the small numbers (N=15) of breeding males for natural mating in the herd since 2010.

Inbreeding depression per 1% increase in inbreeding decrease 305 d FCM yield by 102.9 kg (1565.5 kg) using interactive methods of BLUE in Jersey cows born in Adamawa. Lactation length decreased approximately by 2 days in both models.

In the Brown Swiss cows born in Adamawa, LL was depressed by 2 days which was similar for both methods of estimation. 305 d FCM was decreased by 50.5 kg (1730.1 kg) using BLUE methods and 53.1 kg (1727.3 kg) in Wright methods.

Lastly, Simmental cows in Adamawa State had 305 d FCM yield loss of 89 kg and 100 kg for BLUE and Wright's method of estimation, respectively. LL was depressed for 2 days and had a similarity to the trend observed in Brown Swiss.

4.8.2 Inbreeding depression for reproduction traits under breed x environment interaction

Table 4.34 presents the means, mixed and fixed model analysis of the inbreeding depression on reproduction traits per 1 % increase in inbreeding of genotypes of cows in three production environments. Inbreeding depression of Holstein cows in Plateau State per 1% increase in inbreeding extended AFC by 1.3 vs 1.5 days, CI by 20.4 vs 15.8 days and calving rate by 3 vs 3.3 % while the NSC was reduced by 2.8 vs 2.5 % when the mixed (BLUE) and fixed model (Wright method) was used as a tool for analyzing the effects of inbreeding. The effect of inbreeding was not significant in all the reproductive traits except CI.

Tables 4.33: Means and inbreeding depression on milk production traits per 1 % increase in inbreeding of multi-genotype cows in three production environments

Breed and Environment/Trait	Mean±SE	BLUE	Wright
Holstein Friesian Plateau			
305d FCM (kg)	4996.8±92.64	-350.2 (4646.6)	-381.4 (4615.4)
Fat yield (kg)	151.6±3.94	-3.2 (148.4)	-3.4 (148.2)
Protein yield (kg)	186.8±7.34	-3.8 (183)	-4.5 (182.3)
Lactation length (d)	357.3±5.35	+5.2 (362.5)	+5.0 (362.3)
Holstein Friesian Adamawa			
305 FCM (kg)	1788.2±39.35	-220.1 (1568.1)	-225.5 (1562.7)
Lactation length (d)	348.1±3.44	-13.0 (335.1)	-12.8 (335.3)
Jersey Kwara			
305 FCM (kg)	2411.8±56.66	-419.6 (1992.2)	-422.1 (1989.7)
Fat yield (kg)	52.2±2.29	-15.2 (37)	-15.2 (37)
Protein yield (kg)	33.1±1.27	-13.1 (20)	-13.0 (20.1)
Lactation length (d)	335.6±2.25	-12.2 (323.4)	-11.4 (324.2)
Jersey Adamawa			
305 FCM (kg)	1668.4±50.41	-102.9 (1565.5)	-107.7 (1560.7)
Lactation length (d)	342.3±6.84	-2.0 (340.3)	-1.9 (340.4)
Brown Swiss Adamawa			
305 FCM (kg)	1780.4±54.61	-50.3 (1730.1)	-53.1 (1727.3)
Lactation length (d)	334.5±4.15	-2.9 (331.6)	-2.9 (331.6)
Simmental Adamawa			
305 FCM (kg)	1475.7±23.17	-89.3 (1386.4)	-100 (1357.7)
Lactation length (d)	350.5±3.61	-2.0 (348.5)	-2.0 (348.5)

d-day; kg-kilogram; SE-Standard error; FCM-Fat corrected milk; BLUE-Best linear unbiased estimate; - =depression; +=improvement

In Holstein Friesian cows born and bred in Adamawa, the inbreeding effect per 1 % increase in inbreeding had a positive effect on AFC and calving interval while the effect on NSC and calving rate were negatives when both models were used for estimation.

In Jersey cows under Kwara State climatic conditions, the inbreeding effect per 1 % increase in inbreeding extended AFC by 1 vs 1.8 days, CI by approximately 6 days for both models, reduced NSC by approximately 4 days and extended CR by 6 % for both models.

In Adamawa State, the inbreeding effect per 1 % increase in inbreeding for Jersey cows reduced AFC and NSC but extended CR (positive effect) and CI (negative effects) in both models.

The inbreeding effect per 1 % increase in inbreeding hurt AFC, CI and NSC except for the calving rate in Brown Swiss cows bred in Adamawa State. Both the fixed and mixed model methods were approximately similar for all the reproductive traits.

Lastly, AFC (3.8 vs 3.9 days), CI (3.0 vs 2.6 days) and NSC (2.9 vs 3.3) were depressed by inbreeding effect per 1 % increase in inbreeding except CR (2.5) in Simmental cows born and bred in Adamawa. The accuracy of estimating the inbreeding effect per 1 % increase in inbreeding was approximately similar in both models. Generally, the negative effect of inbreeding per 1 % increase in inbreeding was more severe in the Jersey herd in Kwara State, though genetic purging effect has not been established in the population.

Tables 4.34: Means and inbreeding depression on reproduction traits per 1 % increase in inbreeding of multi-genotype cows in three production environments

Breed and Environment/Trait	Mean±SE	BLUE	Wright
Holstein Friesian Plateau			
AFC (d)	1010.8±17.43	+1.3 (1012.1)	+1.5 (1012.3)
Calving interval (d)	419.6±4.65	+20.4 (440)	+15.8 (435.4)
NSC	2.7±0.04	-2.8 (-0.1)	-2.5 (0.2)
Calving rate (%)	49.3±0.19	+3.0 (52.3)	+3.3 (52.6)
Holstein Friesian Adamawa			
AFC (d)	1243.8±4.36	-12.4 (1231.4)	-11.2 (1232.6)
Calving interval (d)	677.8±2.29	-8.9 (668.9)	-9.4 (668.4)
NSC	2.5±0.04	+2.5 (5)	+2.6 (5.1)
Calving rate (%)	26.6±0.53	-13.5 (13.1)	-14.0 (12.6)
Jersey Kwara			
Age at first calving	1220.0±16.84	+1.1 (1221.1)	+1.8 (1221.8)
Calving interval (d)	375.4±4.52	+5.6 (381)	+5.9 (381.3)
NSC	2.3±0.09	-3.5 (-1.2)	-3.7 (-1.4)
Calving rate (%)	56.8±0.64	+5.8 (62.6)	+5.9 (62.7)
Jersey Adamawa			
Age at first calving	1227.4±2.44	-2.9 (1224.5)	-3.0 (1224.4)
Calving interval (d)	674.8±1.88	+11.4 (686.2)	+11.3 (686.1)
NSC	2.5±0.11	-6.4 (-3.9)	-6.3 (-3.8)
Calving rate (%)	55.2±0.48	+4.8 (60)	+4.9 (60.1)
Brown Swiss Adamawa			
Age at first calving	1263.4±3.05	+15.8 (1279.2)	+16.1 (1279.5)
Calving interval (d)	693.9±2.09	+7.1 (701)	+7.0 (700.9)
NSC	2.6±0.07	+4.4 (7)	+4.1 (6.7)
Calving rate (%)	25.2±0.21	+1.9 (27.1)	+2.4 (27.6)
Simmental Adamawa			
Age at first calving	1321.3±3.33	-3.8 (1317.5)	-3.9 (1317.4)
Calving interval (d)	709.2±2.26	-3.0 (706.2)	-2.6 (706.6)
NSC	2.1±0.02	+2.9 (5)	+3.3 (5.4)
Calving rate (%)	52.8±1.39	+2.5 (55.3)	+2.5 (55.3)

d-day; kg-kilogram; SE-Standard error; FCM-Fat corrected milk; BLUE-Best linear unbiased estimate; AFC-Age at first calving; NSC-Number of service per conception; -=depression; +=improvement

4.9 Genotype and Environment Effect on the Predicted Estimate of Lactation Yield Characteristics

4.9.1 Descriptive analysis of milk yield traits on lactation curve of multigenotype cows in Kwara State

Last day yield and total yield had significant ($P<0.05$) effect across the genetic groups in Kwara State (Table 4.35). The overall average last day was 3.2 ± 0.16 kg with FRxBJ having heavier last day fat corrected milk weight than the other genetic groups. The mean total milk yield for all the genetic groups was 2503.3 ± 26.7 kg, with Jersey cows having significantly ($P<0.05$) the heaviest milk weight as compared to other genotypes. The coefficient of variation was generally high for all the yield curve characteristics with the exception of peak time (5.4 %). Initial yield, peak yield and total yield differed significantly ($P<0.05$) between the genotypes in Plateau State. IY, PY and TY had overall means of 8.6 ± 0.94 kg, 13.1 ± 0.95 kg and 4551.3 ± 268.7 kg, respectively. Holstein Friesian cows had significantly ($P<0.05$) higher predicted milk yield characteristics than the FriesianxBunaji cows. IY, PT, LDY and TY differed significantly ($P<0.05$) among the genetic groups with the exception of PY in Adamawa State. Holstein Friesian, Jersey and Simmental cows had higher predicted IY and TY than Brown Swiss. Jersey and Brown Swiss had similar and the highest peak time which differed significantly ($P<0.05$) from the other genetic groups.

Table 4.35: Mean values (\pm s.e) for lactation curve traits of multi-genotype cows in Adamawa, Kwara and Plateau States

Location/Traits	IY(kg)	PY(kg)	PT(days)	LDY (kg)	TY(kg)
Kwara					
Holstein Friesian	4.4 \pm 0.15	9.0 \pm 1.91	62.0 \pm 2.12	3.8 \pm 0.29 ^b	2364.3 \pm 13.07 ^b
FRXBJ	7.6 \pm 1.23	8.7 \pm 1.31	64.2 \pm 0.80	4.6 \pm 0.56 ^a	2201.3 \pm 33.0 ^b
Jersey	7.4 \pm 1.73	9.8 \pm 1.76	62.3 \pm 1.31	3.6 \pm 0.15 ^b	2896 \pm 27.6 ^a
JXBJ	5.5 \pm 0.71	7.2 \pm 0.58	62.0 \pm 2.12	3.6 \pm 0.15 ^b	2151.3 \pm 35.5 ^b
Overall	6.5 \pm 0.56	8.7 \pm 0.70	62.6 \pm 0.79	3.2 \pm 0.16	2503.3 \pm 26.7
SEM	2.13	2.48	1.69	0.27	141.5
CV%	34.4	34.2	5.4	16.4	14.8
Plateau					
Holstein Friesian	12.0 \pm 0.55 ^a	16.0 \pm 0.72 ^a	65.0 \pm 3.73	3.8 \pm 0.29	5351.3 \pm 203.4 ^a
FRXBJ	5.2 \pm 0.39 ^b	10.2 \pm 0.96 ^b	60.4 \pm 3.62	4.6 \pm 0.56	3751.3 \pm 292.0 ^b
Overall	8.6 \pm 0.94	13.1 \pm 0.95	62.7 \pm 2.58	4.2 \pm 0.32	4551.3 \pm 268.7
SEM	0.95	1.68	7.35	1.89	203.2
CV%	15.5	18.3	16.6	30.4	15.6
Adamawa					
Holstein Friesian	4.8 \pm 0.64 ^a	7.5 \pm 1.96	60.5 \pm 1.43 ^b	3.5 \pm 0.18 ^a	2347.8 \pm 75.47 ^a
Jersey	5.8 \pm 0.90 ^a	8.5 \pm 0.83	62.5 \pm 1.92 ^a	2.7 \pm 0.32 ^b	2060.3 \pm 38.82 ^a
Brown Swiss	3.6 \pm 0.21 ^b	6.4 \pm 0.86	66.5 \pm 3.18 ^a	2.3 \pm 0.36 ^b	1710.0 \pm 44.60 ^b
Simmental	5.2 \pm 0.84 ^a	7.6 \pm 0.26	60.3 \pm 2.25 ^b	2.4 \pm 0.22 ^b	2242.0 \pm 54.50 ^a
Overall	4.8 \pm 0.38	7.5 \pm 0.55	62.4 \pm 1.21	2.7 \pm 0.17	2051.3 \pm 268.7
SEM	0.70	2.16	2.29	0.28	132.28
CV%	28.9	30.8	7.3	20.6	12.7

^aMeans of the same trait across genetic groups with different superscripts differ significantly ($P < 0.05$); IY-Initial yield; PY-Peak yield; PT-Peak time; LDY-Last day yield; TY-Total yield; SEM-Standard error of mean

4.10 Genotype and Environment Effect on the Model Fitting to Actual Yield on Lactation Curves

Table 4.36 shows the milk yield characteristics of computational models for the lactation curve in Kwara State. In Holstein Friesian cows under Kwara State climatic gradients, initial level of milk production was overestimated by all the models (Wood, Wilmink, Milk Bot, Djisktra, and Neural network). The actual peak yield was perfectly estimated by Wilmink and MilkBot models but overestimated by the Wood and Neural network. The neural network had perfect estimation for total yield. MB and Djisktra overestimated total yield while Wood and Wilmink models underestimated total yield. A close look at the data used in constructing the lactation curve for Holstein Friesian cows in Kwara State indicated that there were obvious over-estimations the observed by Wood model in all the days in milk except days 150 and 210 respectively, which were underestimated by 1.4 and 3.4 % decrement respectively (Figure 4.1). The wood model perfectly estimated the observed data on days 240, 270 and 330, respectively.

Wilmink overestimated the observed yield at 7, 60, 150, 240, 300 and 330 days in milk but underestimated it at 30, 180 and 270 days in milk; while perfect estimation was recorded at 90, 120 and 210 days in milk. Djisktra model overestimated the observed milk yield at day 7, 180 and 330, respectively while perfect estimation with a null deviation was recorded at 210, 300 and 360 days in milk but the remaining lactation days underestimated the observed yield. MilkBot perfectly estimated the observed yield at 90, 210 and 360 days in milk but underestimated it at 150 and 270 days by 2.7 and 2.3 % decrease while the remaining days

Table 4.36: Milk yield characteristics of the computational models for lactation curve in multigenotype cows in Shonga Dairy Holdings in Kwara State

Genotype and Environment/Trait	Observed	Wood	d	Wk	d	Dsa	d	MB	d	NN	d
Holstein Friesian Kwara											
Initial yield (kg)	4.4	5.2	+0.8	5.7	+1.3	5.6	+1.2	6.1	+1.7	5.3	+0.9
Peak yield (kg)	8.5	8.6	+0.1	8.5	00	8.2	-0.3	8.5	00	8.8	+0.3
Peak time (days)	62	60	-2.0	60.5	-1.5	60.4	-1.6	60	-2.0	61.4	-0.6
Last day yield (kg)	3.2	3.0	-0.2	3.0	-0.2	3.2	00	3.2	00	3.1	-0.1
Total yield (kg)	2364	2360	-0.4	2362	-0.2	2368	+0.4	2366	+0.2	2364	00
Friesian xBunaji Kwara											
Initial yield (kg)	5.5	5.8	+0.3	7.7	+2.2	6.4	+0.9	5.7	+0.2	5.0	-0.5
Peak yield (kg)	7.2	7.2	00	6.8	-0.4	7.3	+0.1	7.1	-0.1	7.2	00
Peak time (days)	64.2	59.9	-4.3	60	-4.2	60.1	-4.1	60.6	-3.6	63.2	-1.0
Last day yield (kg)	3.2	3.9	+0.7	3.5	+0.3	3.4	+0.2	3.7	+0.5	3.2	00
Total yield (kg)	2201	2202	+1.0	2200	+1.0	2198	-6.0	2199	-2.0	2202	+1.0
Jersey Kwara											
Initial yield (kg)	6.7	6.8	+0.1	6.7	00	6.6	-0.1	6.5	-0.2	6.7	00
Peak yield (kg)	10	10.1	+0.1	10.1	+0.1	10	00	10	00	10	00
Peak time (days)	60	60	00	61	-0.1	60	00	59.6	-0.4	60	00
Last day yield (kg)	3.5	3.7	+0.2	3.7	+0.2	3.5	00	3.6	+0.1	3.8	+0.3
Total yield (kg)	2896	2900	+4.0	2896	00	2898	+2.0	2895	-1.0	2896	00
JerseyxBunaji Kwara											
Initial yield (kg)	5.5	6.4	+0.9	5.9	+0.4	6.2	+0.7	6.4	+0.9	5.8	+0.3
Peak yield (kg)	8.6	8.6	00	8.7	+0.1	8.5	-0.1	8.6	00	8.6	00
Peak time (days)	62	61	-0.1	60	-0.2	60.5	-1.5	64	+0.2	61	-0.1
Last day yield (kg)	3.6	3.5	-0.1	3.6	00	3.4	-0.2	3.6	00	3.7	+0.1
Total yield (kg)	2151	2150	-1.0	2154	+3.0	2152	+1.0	2152	+1.0	2151	00

d=deviation; MB=Milkbot; NN=Neural network; kg=kilogram; Under =decrement in the deviation; +Over= increment in the deviation

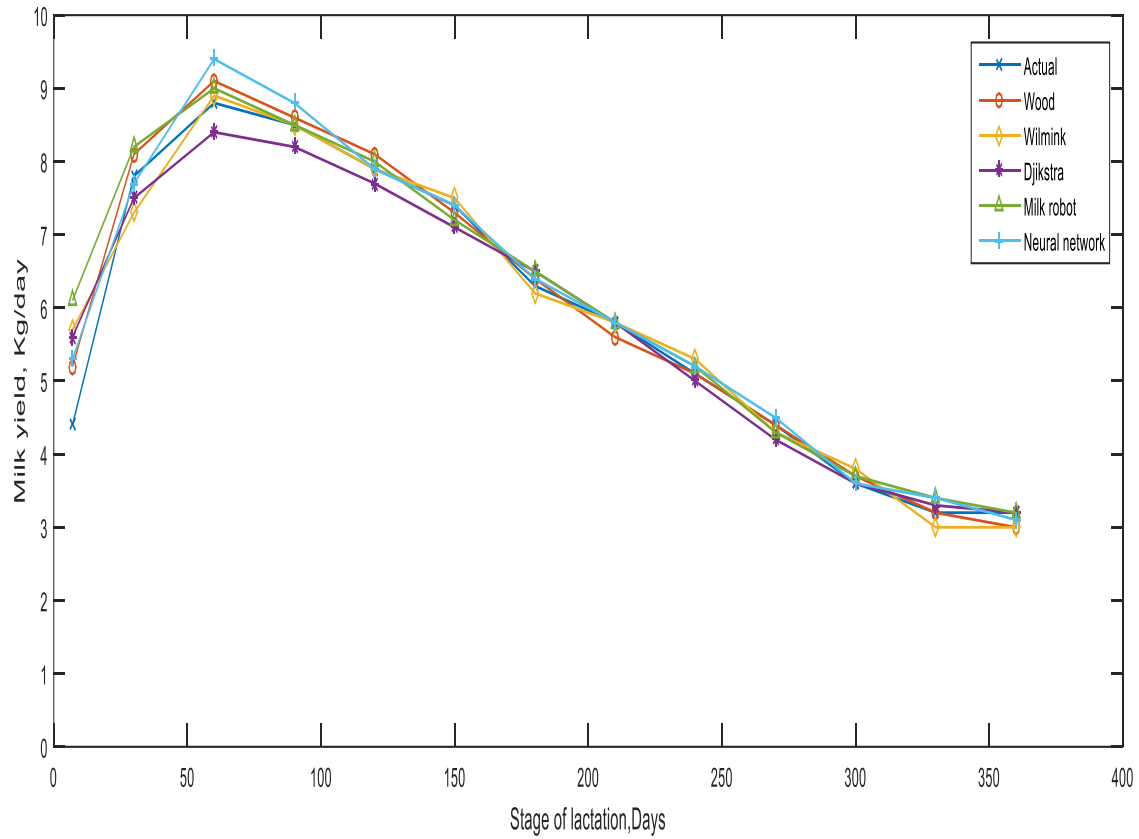


Figure 4.1: Lactation curves estimated for Holstein Friesian dairy cows in Kwara State

were overestimated on the lactation curve. Neural network underestimated the observed yield at day 30 and 360 by 1.3 and 3.1 % decrement but perfectly estimated it at 120, 150, 210 and 300 days in milk. All the models fit the lactation curve of Holstein Friesian cows in Kwara State effectively and MB model was the most accurate because it's inherent ability to minimize the deviations.

In FriesianxBunaji cows born in Kwara State, initial milk yield production was overestimated with the exception NN which was underestimated. NN and Wood had perfect accuracy of prediction for peak yield while Wood, Djisktra and MB overestimated the observed yield but was underestimated by Wilmink. Peak time was underestimated by all the computational models. NN, Wilmink and Wood models overestimated the total milk yield while the remaining models underestimated it. NN had a perfect estimation for last day yield with a null deviation of zero while the other model overpredicted it. The fitting of the lactation curves of actual and predicted models was reflected in Figure 4.2. Wood model perfectly fitted the observed yield at day 60, 300 and 330, respectively while it was underestimated by 1.5 %, 1.9 % and 2 % decrease at day 30, 240 and 270, respectively. Wilmink had perfect prediction at 300 and 330 days but was over predicted at day 7, 30, 120 and 360, respectively. Djisktra underestimated the observed milk yield by 3.8 %, 6.1 %, 11.1 % and 7.3 % decrement at day 240, 270, 300 and 330, respectively but had a perfect estimation at 200th day of lactation. MB had perfect estimation of the observed yield at day 30, 120, 150, 180, 210 and 330 while NN had perfect accuracy for all the days in milk excepting the 7th day of lactation which was underestimated. Generally, all the models were good excepting Djisktra models with poor fit. NN appears the best seems it was able to fit model more accurately by minimizing the deviations.

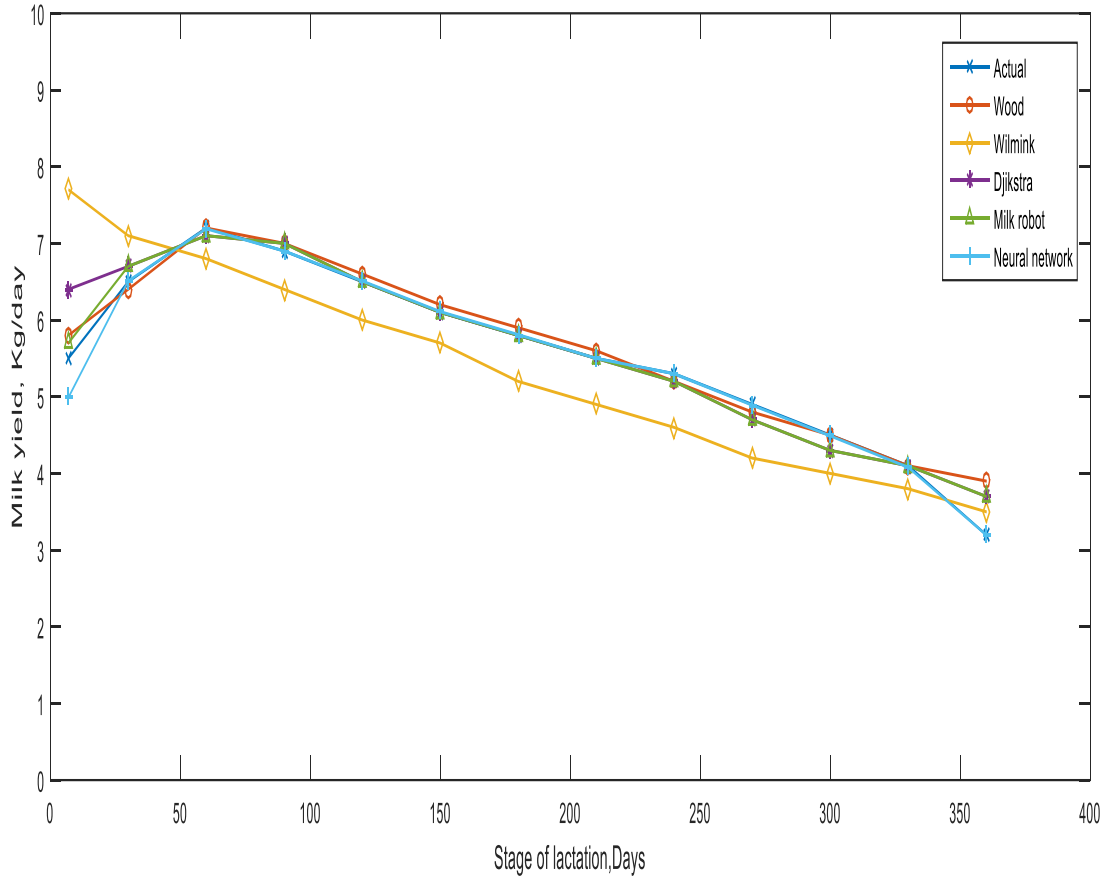


Figure 4.2: Lactation curves estimated for FriesianxBunaji dairy cows in Shonga Dairy Holdings in Kwara State

Wilmink and Neural network accurately estimated initial milk yield for Jersey cows in the New Derived Guinea Savannah Zone (Kwara State) of Nigeria while Djisktra and MilkBot closely underestimated by 1.3 and 3 % decrement, respectively but was overestimated by Wood model with 1.5 % increment. Peak yield was perfectly estimated by Djisktra, MB and NN while Wood and Wilmink models overestimated the observed yield by 1 % increase. Peak time was perfectly estimated by all the models with the exception of Wilmink and MB which underestimated the observed yield by 1.7 % and 0.7 % decrease. Last day yield was overestimated by all the models excepting Djisktra with perfect estimation. Wood and Djisktra overestimated the observed yield but MB underestimated it while Wilmink and NN had perfect accuracy. A meticulous look at the observed and predicted values used in constructing the lactation curve implied that Wood model singularly overestimated the observed yield at day 7, 60, 210, 270 and 360 while perfect estimation was observed at 30, 90, 120, 180, 240, 300 and 330 days in milk but was underestimated at day 150 (Figure 4.3). Wilmink model overestimated the observed yield at 60, 90, 330 and 360 but underestimated 120, 180, 210, 24 and 300 days while perfect estimation was observed at 7, 30, 150 and 270 days in milk. Djisktra perfectly estimated the observed yield at 60, 330 and 360 days in milk but was overestimated at 120 to 180 and 240 to 300 days, respectively while it was underestimated at day 7, 30, 90 and 210, respectively. MilkBot model perfectly estimated the observed yield at 60, 120 and 180 to 300 days in milk but overestimated it at 90, 150, 330 and 360 days, respectively; while it was underestimated at day 7, 30 and 240, respectively. NN network perfectly estimated the observed yield at day 7, 60, 150, 240, 270 and 330, respectively but overestimated at 300 and 360 days in milk and underestimated at 30, 90, 120, 180 and 210 days, respectively. Lastly in JerseyxBunaji cows, initial milk yield was

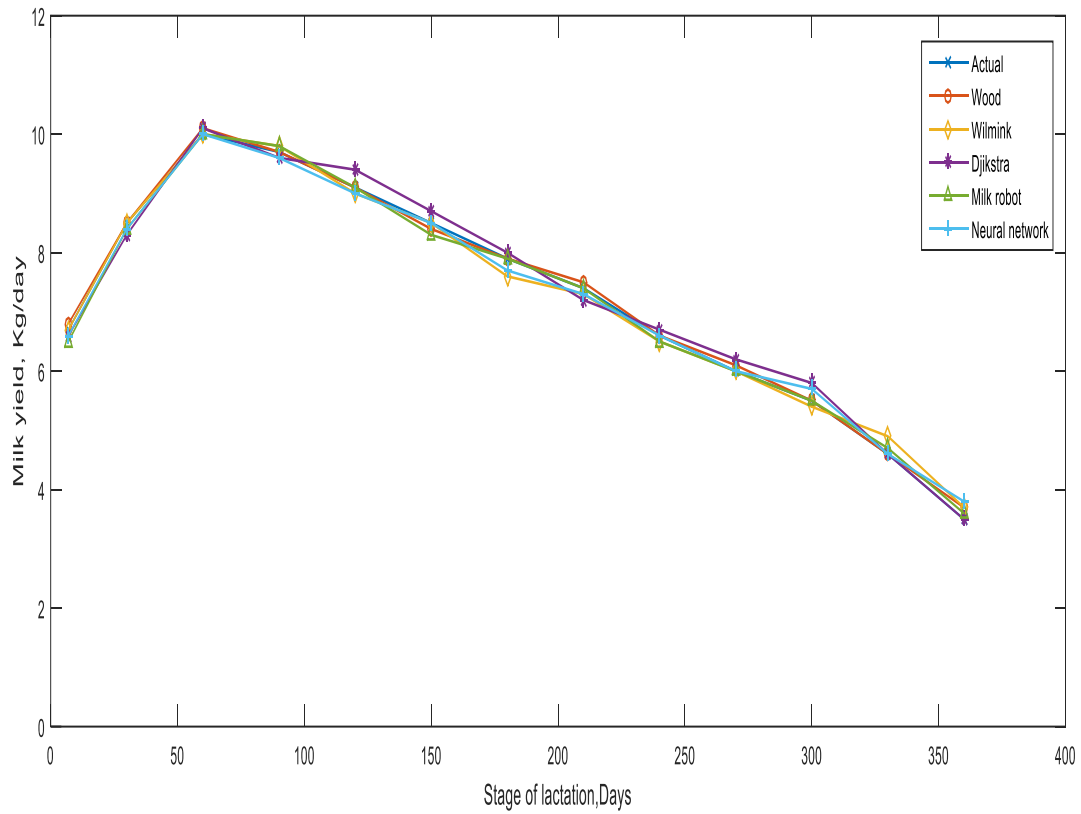


Figure 4.3: Lactation curves estimated for Jersey dairy cows in Shonga Dairy Holdings in Kwara State

overestimated by all the models. Wood, MB and neural network perfectly estimated the observed yield while Wilmink overestimated and Djisktra underestimated it. Peak time was underestimated by all the models with the exception of MB which overestimated by 3.2 % increment. Wilmink and MB perfectly estimated the last day yield while the total yield were all overestimated excepting Wood which was underestimated and NN was perfectly estimated. A close observation at the lactation curve in Figure 4.4, shows that Wood model perfectly predicted the observed yield at day 30, 90, 120, 180, 240, 300 and 330 respectively while it was under predicted at 150 days and over predicted at 7, 60, 210, 270 and 360 days in milk. Wilmink had a perfect prediction at 7, 30, 150 and 270 days, respectively but was overestimated at 60, 90, 330, 360 days and underestimated at 120, 180, 210, 240 and 300 days in milk. Djisktra model had perfect estimation of the observed yield at 60, 330 and 360 days but underestimated at 7, 30, 90 and 210 days while it overestimated at 120, 150, 180, 240, 270 and 300 days in milk. MB overestimated the observed yield at 90, 150, 330 and 360 days in milk but had a perfect estimation at 60 to 210 and 270 to 300 days while it was underestimated at 7, 30 and 240 days, respectively. NN had accurate predictions of observed yield at 7, 60, 150, 240, 270 and 330 days in milk but was over predicted at 300 and 360 days.

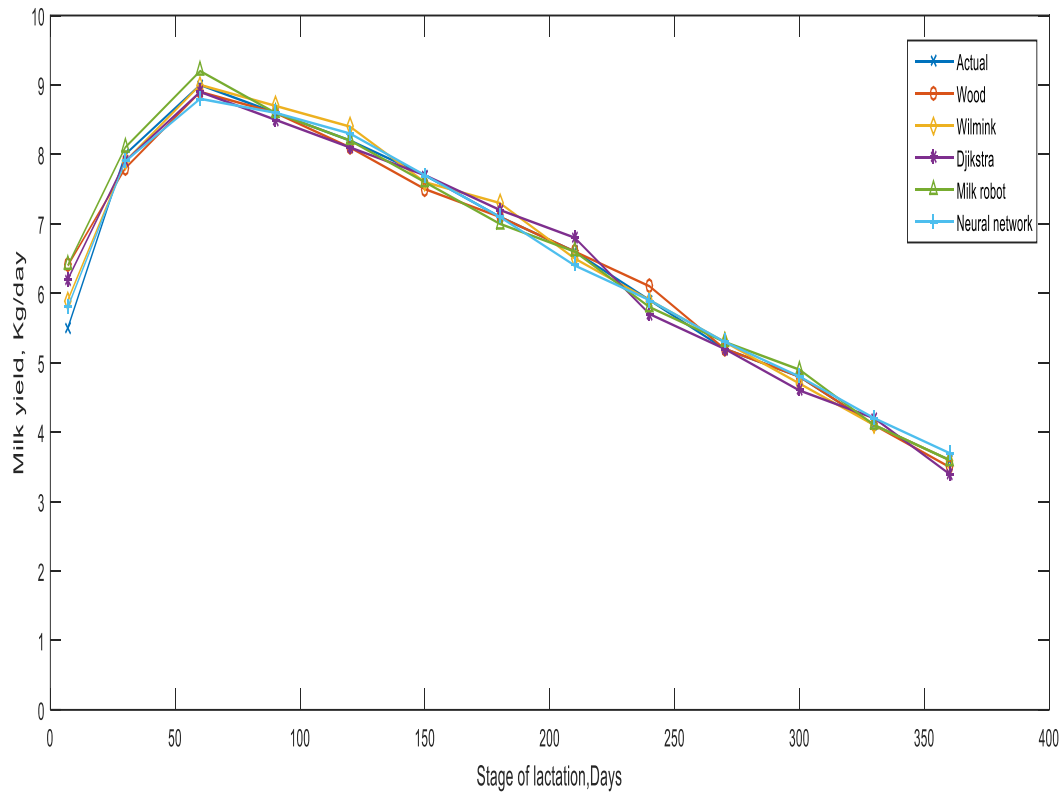


Figure 4.4: Lactation curves estimated for JerseyxBunaji cows in Shonga Dairy Holdings in Kwara State

methods while all the remaining models over predicted it. In the total yield, Wood and NN accurately predicted the observed yield but Wilmink and Djisktra model over predicted while MB under predicted it. A close glance at the data used for modelling (Figure 4.5) implied that Wood model perfectly predicted the observed yield at 30, 120, 210, 240, 300 and 330 days in milk while at 60, 150 and 180 days, respectively it was underestimated and overestimated at 7, 90, 270 and 360 days, respectively. Wilmink model accurately estimated the observed yield at 120 and 300 days, respectively while there was under prediction at 30 days through 90, 210, 270 and 330 days and over prediction at 7, 150, 180, 240 and 360 days. Djisktra model had perfect predictions at days 7 and 30 while the observed yield was overestimated at the remaining test days. MB over predicted the observed yield at 30, 330 and 360 days and underestimated at 300th test day while perfect estimation were observed at the remaining test days. NN was intelligent and perfectly estimated the observed yield for all the test days. This implies that NN is the best computational model under the Plateau State climatic gradients in optimizing the lactation curves of Holstein Friesian cows.

In Friesianx Bunaji cows, all the computational models over predicted the observed yield at initial stage of milk production (Table 4.37). Djisktra and NN perfectly predicted the observed yield for PY while Wood and MB over predicted and Wilmink under predicted it. Peak time was under predicted by all the models. NN had perfect prediction for observed yield at the last day of milk production but was over predicted by Djisktra and under predicted by the remaining computational models (Figure 4.6). Wood model predicted the observed yield accurately at 30, 270 and 300 days in milk while Wilmink was either under or overestimated with no perfect predictions.

Table 4.37: Milk yield characteristics of the computational lactation curve models in Integrated Dairies Limited in Plateau State for multi-genotypes cows

Genotype and Environment/Trait	Observed	Wood	d	Wk	d	Dsa	d	MB	d	NN	d
Holstein Friesian											
Initial yield (kg)	12.0	12.2	+0.2	12.5	+0.5	12.0	00	12.0	00	12.0	00
Peak yield (kg)	16.0	15.8	-0.2	15.8	-0.2	16.1	+0.1	16.1	+0.1	16.0	00
Peak time (days)	60.4	58.5	-1.9	60	-0.4	58	-2.4	60	-0.4	60	-0.4
Last day yield(kg)	3.5	4	+0.5	3.9	+0.4	4.7	+1.2	4	+0.5	3.5	00
Total yield (kg)	5557	5557	00	5561	+4.0	5566	+9.0	5556	-1.0	5557	00
FriesianxBunaji											
Initial yield (kg)	5.2	6.8	+1.6	6.1	+0.9	5.8	+0.6	6.3	+1.1	7.2	+2.0
Peak yield (kg)	10.2	10.5	+0.3	10.0	-0.2	10.2	00	10.3	+0.1	10.2	00
Peak time (days)	65	62	-0.3	60	-0.5	58.5	-6.5	60	-5.0	61.5	-3.5
Last day yield(kg)	4.6	4.3	-0.3	4.0	-0.6	3.7	-0.9	3.6	-1.0	4.6	00
Total yield (kg)	3609	3605	-4.0	3600	-9.0	3615	+6.0	3602	-7.0	3609	00

d-deviation; MR-Milkbot; NN-Neural network; kg-kilogram; -=decrement in deviation +=Increment in deviations; Wk-Wilmink; Dsa-Dijkstra

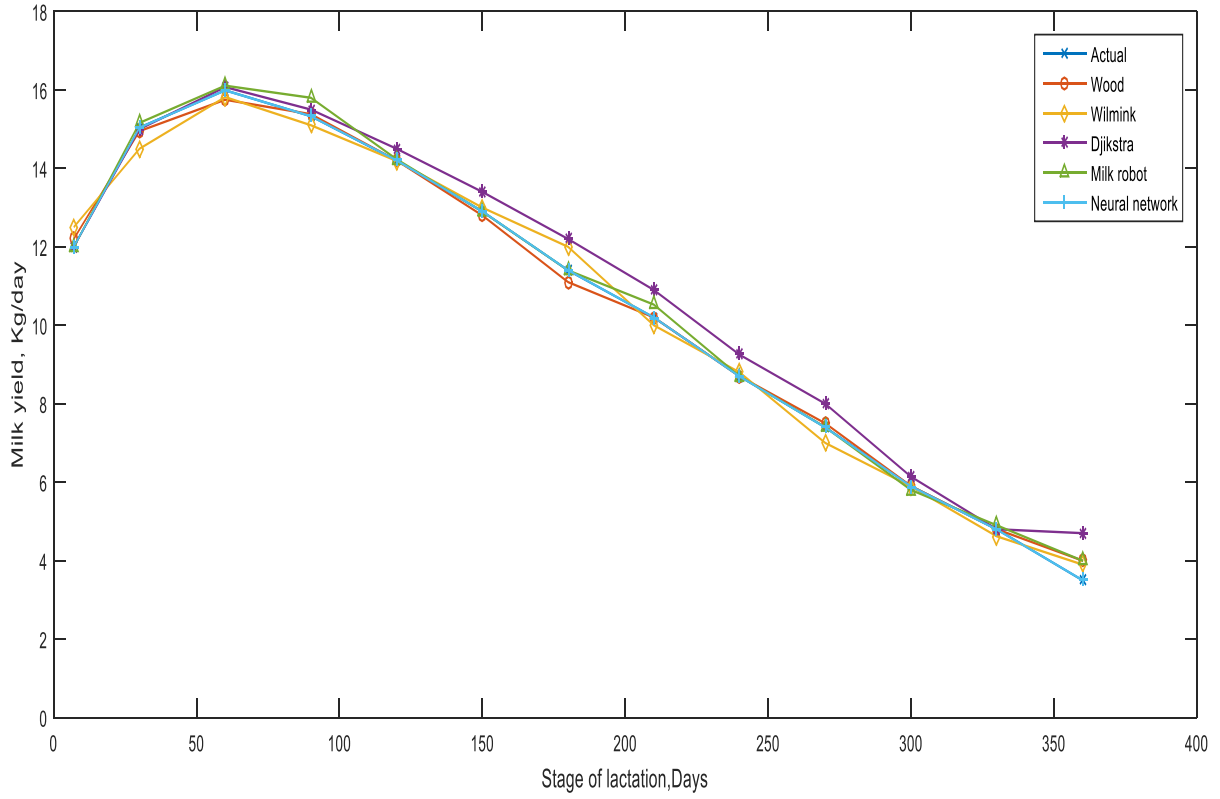


Figure 4.5: Lactation curves estimated for Holstein Friesian cows in Integrated Dairies Limited in Plateau State

Dijkstra had a perfect accuracy for predicting observed yield at day 60 while it was recorded in MB at 180 and 300 days in milk. NN had perfect estimations at 30, 60, 120, 150, 300, 330 and 360 days but over predicted the observed yield at day 270 and under predicted at 180 through 240 days in lactation.

4.10.1 Estimate of yield characteristics using different lactation models in Sebore farm in Adamawa State

The results of yield characteristics for average lactation curve fitted to sample data are shown in Table 4.38. In Holstein Friesian cows, Wilmink perfectly predicted the observed yield for initial milk production but was over-predicted by the remaining computational models. All the models under predicted the peak time. The MB and NN perfectly predicted the observed yield in the last day of milk production but Wood and Djisktra underestimated it by 28.6 % and 14.3 %. Wilmink over predicted by 8.6 %. The NN and Djisktra over predicted the observed total yield by 0.1 % increment while Wood under predicted by 0.2 % decrement. At days 60 and 240, Wood model accurately predicted the observed milk yield but over predicted it at 90 and 120 to 210 days, respectively and underestimated it at days 30 and 270 to 360 days in milk (Figure 4.7). The observed milk yield was perfectly estimated by Wilmink model at 7, 30, 210, 240, 300 and 330 days in milk but was underestimated at 60, 150, 180 and 270 days, respectively. Djisktra overestimated the observed milk yield at days 7 and 360, respectively and underestimated it in all the remaining days in lactation with no perfect estimation. MilkBot perfectly estimated on 30th day but underestimated at day 60 while it overestimated in all the test days in lactation. NN under predicted the observed yield on days 7 and 60 while the remaining test days perfectly predicted the observed yield.

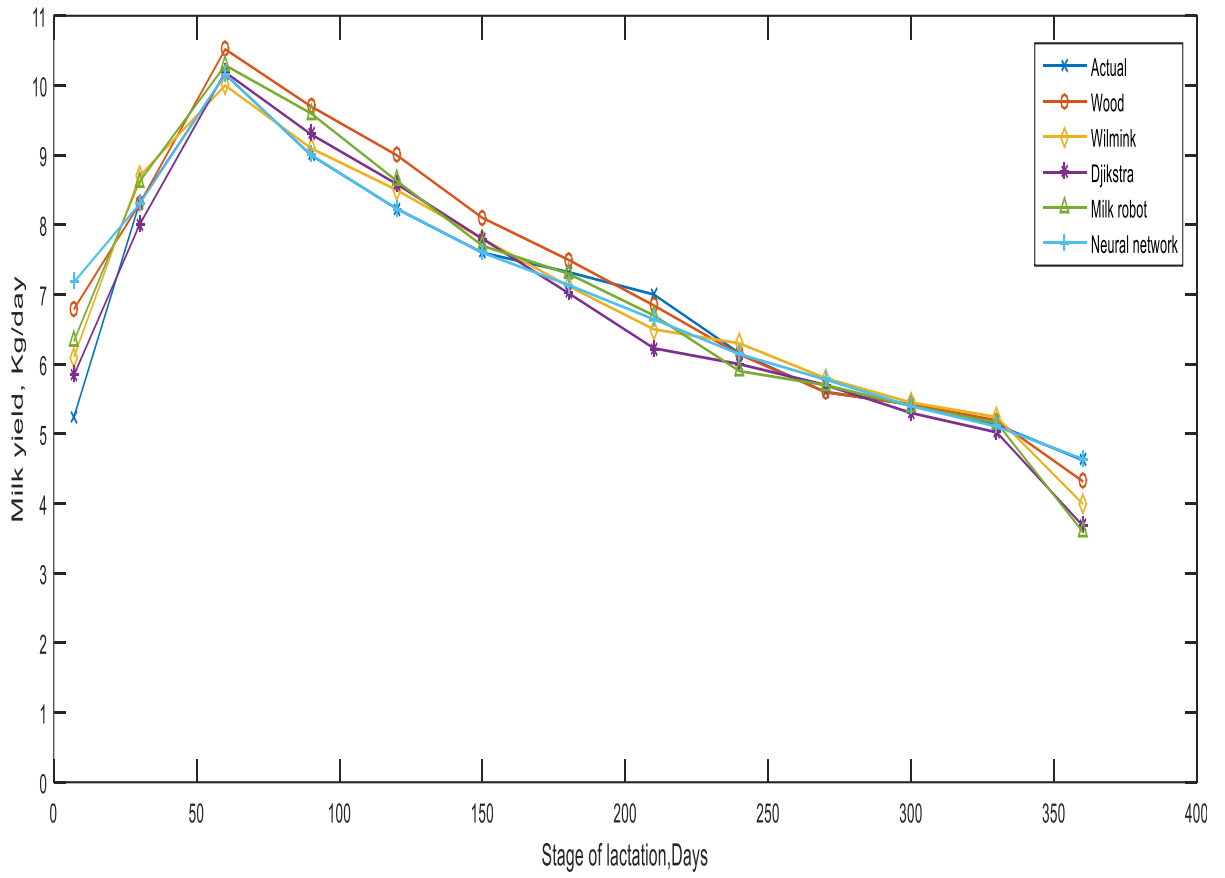


Figure 4.6: Lactation curve estimated for FriesianxBunaji cows in Integrated Dairies Limited in Plateau State

Dijkstra model perfectly predicted the observed yield but was over-predicted by the Wood, MilkBot and NN models excepting Wilmink at the initial yield of milk production in Jersey cows. Wood, Wilmink and Dijkstra over-predicted peak yield while MilkBot and NN underpredicted it. All the models under-predicted peak time. Wood and MB perfectly fitted the observed yield in the last day of milk production. In Figure 4.8, Wood model accurately predicted the observed milk yield at 30, 150, 180, 300 and 360, days but under-predicted at 240 and 270 days, respectively. Wilmink had perfect predictions for observed milk yield at 30 and 60 days but under predicted the actual milk yield at day 7 and over-predicted the actual milk yield at the remaining test days. Dijkstra perfectly predicted the observed milk yield at 7, 240, 270 and 300 days in milk yield but under-predicted at 30, 330 and 360 days of milk production and over predicted at 60 through 180 test days. The MB accurately modelled the observed yield at 120, 330 and 360 but under predicted at 30 and 60 days in milk while it was over predicted at 7, 90, 150, 180, 210, 240, 270 and 300 days of milk production. NN intelligently predicted the observed yield at 150, 180, 210, 330 and 360 days in milk but over-predicted at 7, 90 and 120 test days while it under-predicted at 30, 60, 240, 270 and 300 days in milk production.

All the computational models over-predicted the observed yield at the initial stage of milk production in Brown Swiss cows. Also, the models perfectly predicted the observed yield at peak production excepting Dijkstra and MB models which were over predicted while in peak time, the observed yield was under predicted by the models. Wilmink perfectly predicted total and last yield but under-predicted Wood, Dijkstra and MilkBot while NN over-predicted it.

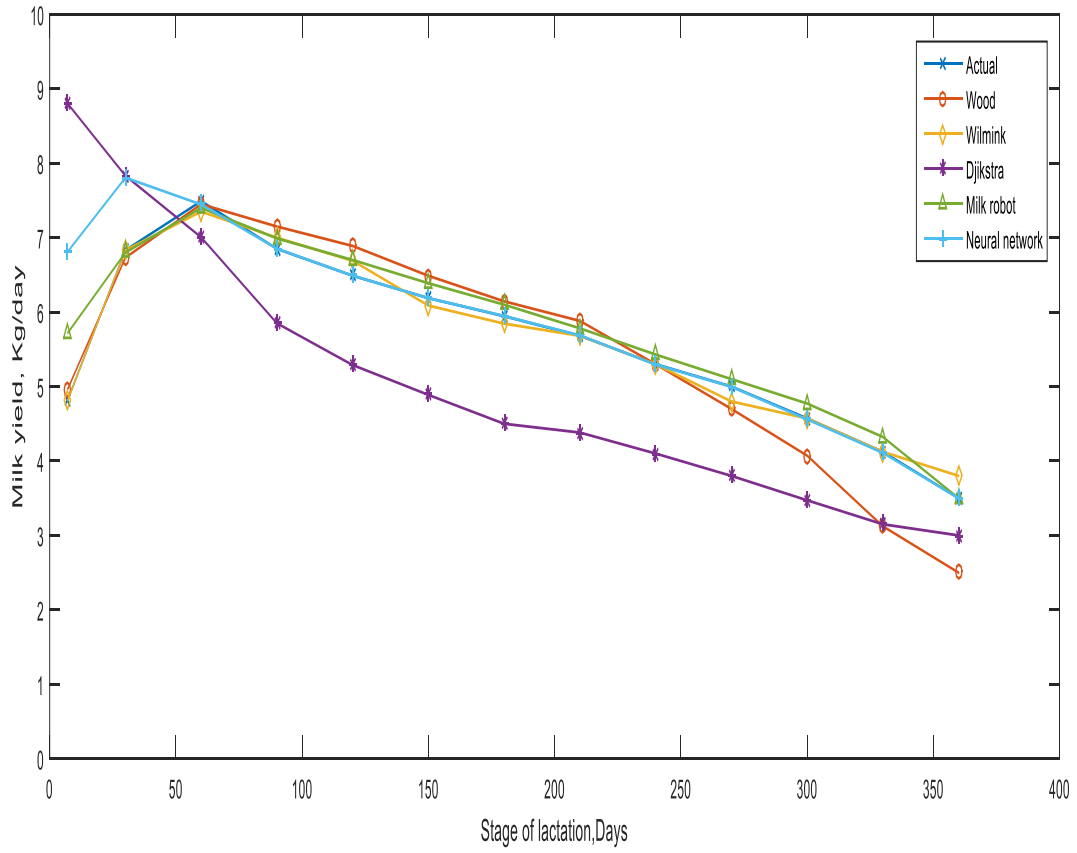


Figure 4.7: Lactation curves estimated for Holstein Friesian cows in Sebore farm in Adamawa State

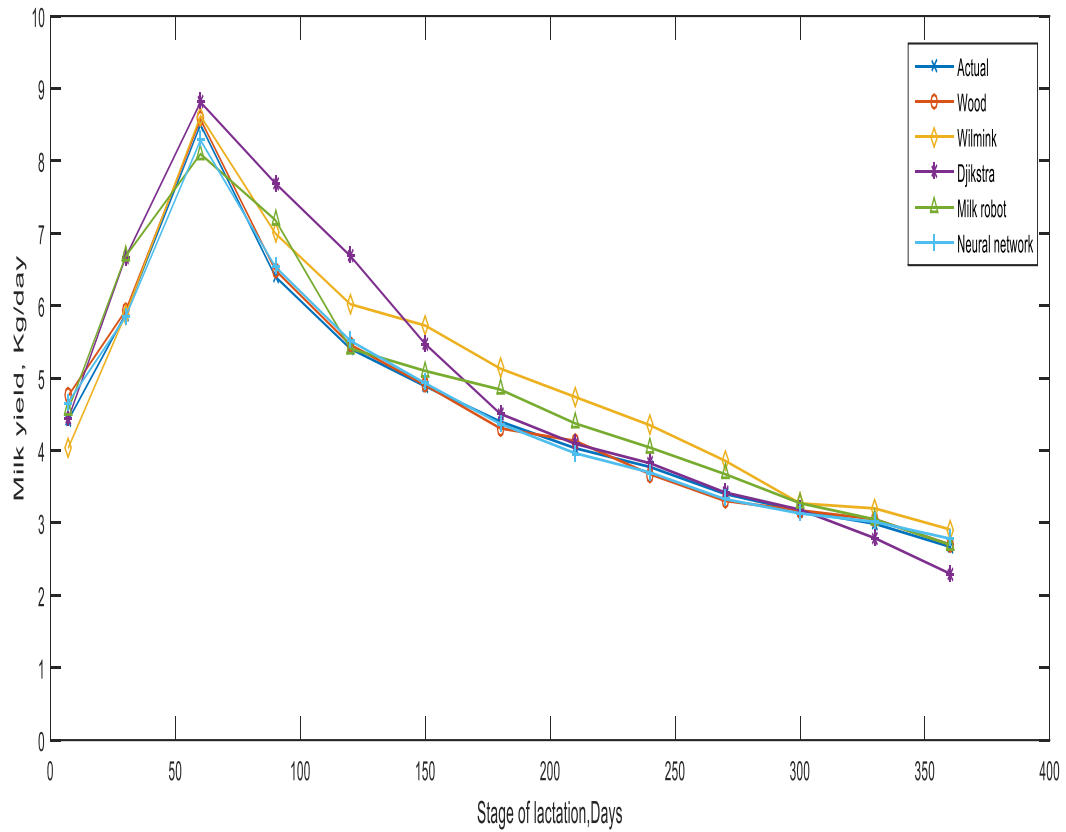


Figure 4.8: Lactation curves estimated for Jersey cows in Sebare farm in Adamawa State

A close visualization at the curve in Figure 4.9 showed that Wood model perfectly predicted the observed yield at 60 days but under-predicted at 300 days and over-predicted at the remaining test days. Wilmink model perfectly predicted the observed yield at 60, 150, 300 and 330 days but under-predicted at day 90, 120, 180 and 360 days while the remaining test days were over predicted. Djisktra perfectly predicted at 90 and 330 days but over-predicted at 7, 30 and 60 days while the remaining test days were under-predicted. The MB perfectly predicted the observed yield at 120th day but were under-predicted at days 270, 300, 330 and 360 days while the remaining test days was over estimated it. The NN intelligently predicted the observed yield at 30, 60, 90, 180 and 330 days but under-predicted at days 120 and 150, respectively.

In Simmental cows, NN perfectly predicted the observed yield at the onset of milk production while the remaining models overestimated it excepting the Wilmink model. Wood and NN models accurately estimated the observed yield at peak production while Wilmink and Djisktra under estimated it and was over-predicted by MilkBot model. Wilmink, Djisktra and NN model perfectly predicted the peak time while Wood model under-estimated it was over-estimated by MilkBot model. Djisktra and NN had perfect predictions for the observed yield while Wilmink under-estimated and it was over-estimated by MilkBot model. Wood and Djisktra model accurately estimated the observed yield at the last day of milk production. In Figure 4.10, Wood model accurately predicted the observed yield at 60 and 270 days while it was under-predicted at 120 through 240 days and over predicted at 7, 30, 90, 300, 330 and 360 days in milk. Wilmink perfectly predicted at day 300 but under predicted at 30, 270 and 330 days while the remaining

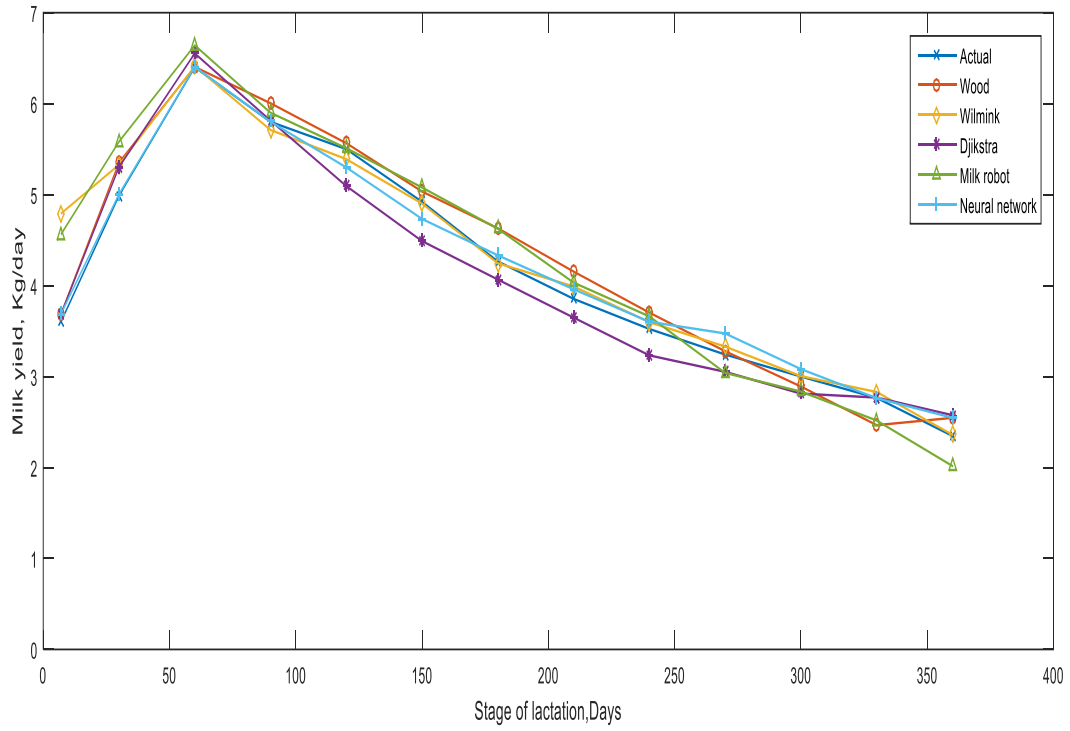


Figure 4.9: Lactation curves estimated for Brownswiss dairy cows in Sebore farm in Adamawa State

test days were over predicted. Djisktra accurately predicted at day 300 but over predicted at 7, 30, 300 and 360 days while the remaining test days were under-predicted. The MB perfectly predicted at 270 and 330 days while the remaining test days were all over-predicted.

The NN over-predicted at 90 days and under-predicted at 30 and 150 days while the remaining test days were perfectly predicted.

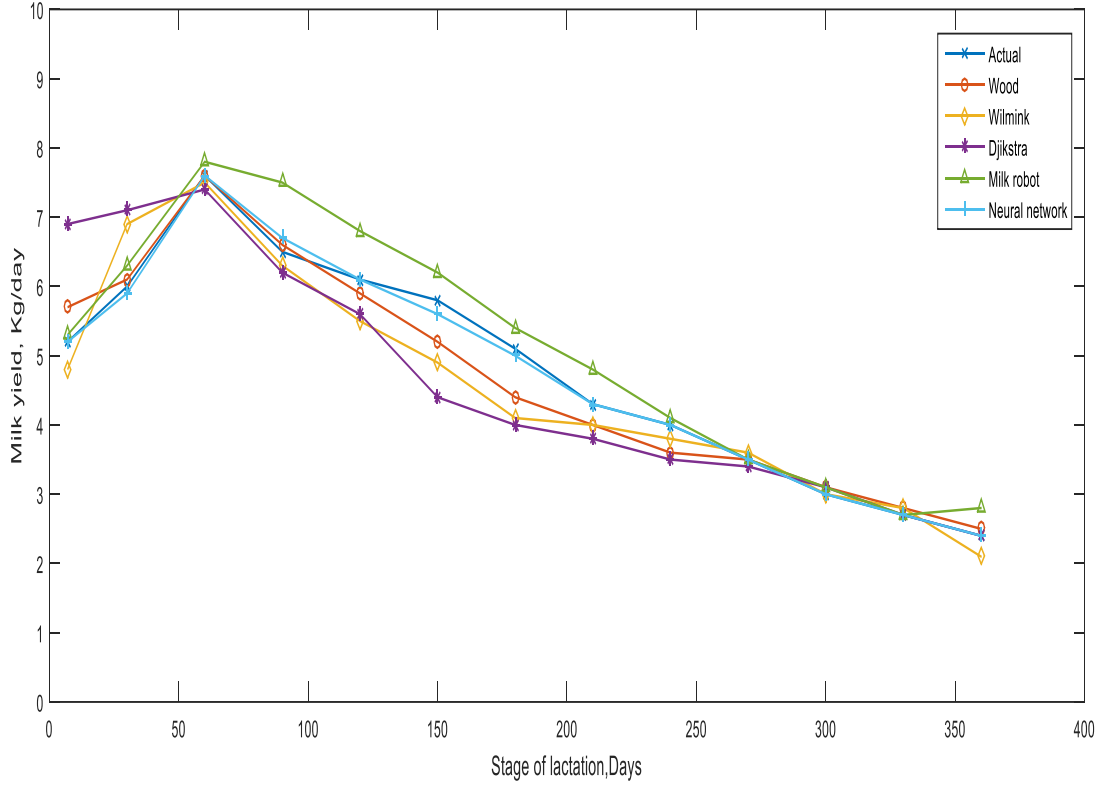


Figure 4.10: Lactation curves estimated for Simmental cows in Sebore farm in Adamawa State

Table 4.38: Milk yield characteristics of the computational lactation curve models in Sebores farm in Adamawa State for multi-genotypes cows

Genotype and Herd/Trait	Observed	W	d	Wk	d	Dsa	d	MB	d	NN	d
Holstein Friesian											
Initial yield (kg)	4.8	5.0	+0.2	4.8	00	8.8	+4.0	5.7	+0.9	6.8	+2.0
Peak yield (kg)	7.5	7.5	00	7.4	-0.1	7.0	-0.5	7.4	-0.1	7.4	-0.1
Peak time (days)	60.5	60	-0.5	60	-0.5	58.9	-1.6	60	-0.5	60.4	-0.1
Last day yield (kg)	3.5	2.5	-1.0	3.8	+0.3	3.0	-0.5	3.5	00	3.5	00
Total yield (kg)	2348	2344	+4.0	2347	+1.0	2350	-2.0	2348	00	2351	+3.0
Jersey											
Initial yield (kg)	5.4	5.8	+0.3	5.0	-0.4	5.4	00	5.6	+0.1	5.7	+0.2
Peak yield (kg)	8.5	8.6	+0.1	8.6	+0.1	8.8	+0.3	8.1	-0.4	8.3	-0.2
Peak time (days)	62.5	60	-2.5	62	-0.5	60.6	-1.9	60	-2.5	62	-0.5
Last day yield (kg)	2.7	2.7	00	2.9	+0.2	2.3	-0.4	2.7	00	2.8	+0.1
Total yield (kg)	2060	2060	00	2065	+5.0	2054	-6.0	2060	00	2064	+4.0
Brown Swiss											
Initial yield (kg)	3.6	3.7	+0.1	4.8	+1.2	3.7	+0.1	4.6	+1.0	3.7	+0.1
Peak yield (kg)	6.4	6.4	00	6.4	00	6.6	+0.2	6.6	+0.2	6.4	00
Peak time (days)	67	63	-04	61	-06	60	-07	60	-07	60	-07
Last day yield (kg)	2.3	2.5	+0.2	2.4	+0.1	2.6	+0.3	2.0	-0.3	2.5	+0.2
Total yield (kg)	1710	1706	-4.0	1710	00	1709	-1.0	1701	-9.0	1714	+4.0
Simmental											
Initial yield (kg)	5.2	5.7	+0.5	4.8	-0.4	6.9	+1.7	5.3	+0.1	5.2	00
Peak yield (kg)	7.6	7.6	00	7.5	-0.1	7.4	-0.2	7.8	+0.2	7.6	00
Peak time (days)	60	58	-02	60	00	60	00	61	+01	60	00
Last day yield (kg)	2.4	2.5	+0.1	2.1	-0.3	2.4	00	2.8	+0.4	2.4	00
Total yield (kg)	2242	2242	00	2244	+2.0	2242	00	2243	+1.0	2243	+1.0

d-deviation; Under-prediction of the observed yield by model; +=increment in deviation; -=decrement in deviation.
W-Wood; Wk-Wilmink; Dsa-Dijkstra; MB-Milkbot; NN-Neural network

4.10.2 The parameters and goodness of fit measurements of all lactation curve models under the influence of genotype x environment interactions

4.10.2.1 The parameters and goodness of fit measurements of all lactation curve models in Shonga Dairy Holdings in Kwara State

Tables 4.39 a and b depicts the estimates for curve parameters by different model prototypes in Kwara State for different genetic groups of cows. The accuracy of reconstructing the lactation curves among the models in Holstein Friesian cow in Kwara State for Wood, Wilmink, Djisktra, MilkBot and Neural Network was 85, 62, 86, 88 and 88 %, respectively. Amongst the five models, the MilkBot had the best accuracy for reconstructing the lactation curves (Adj R^2 =88 %; BIC=0.20 and RSD=27.15) and the worst accuracy (Adj R^2 =62 %) was recorded in the Wilmink model. The worst accuracy observed in the Wilmink model was due to convergence failure which could be attributed to over parameterisation of the function relative to the information in the data.

In FriesianxBunaji cow, all the models were efficient (Adj R^2 = 75 - 97 %; RSD=0.15-0.63; BIC=10.40-148.93) in fitting the lactation curves with the exception of Djisktra model (Adj R^2 =62 %; RSD=0.64; BIC=32.24) which was less efficient. Accuracy of prediction was higher in Neural network (Adj R^2 =97 %) compared to Wood (Adj R^2 =89 %), Wilmink (Adj R^2 =92 %), MilkBot (Adj R^2 =95 %) and (Adj R^2 =96 %). Persistency of milk yield ranged from 4.24 in Wood to 6.30 in MilkBot model. In Jersey cows, all the computational models were efficient in reconstructing the lactation curves (Adj R^2 =80 % - 92 %). Neural Network was robust and had best predictive capability for estimating the efficiency of lactation curves. In JerseyxBunaji cows, amongst the five computational models, the Neural Network (97 %) had the best accuracy for modelling milk yield over trajectory of time while Djisktra model was least in ranking (75 %).

Table 4.39a: Estimates for curve parameters by different models for different genetic groups of cows in Shonga Dairy Holdings in Kwara State

Parameters	Empirical		Mechanistic		Intelligence
	Wood	Wilmink	Djisktra	MilkBot	Neural network
Holstein Friesian					
$a \pm s_a^-$	7.96±2.105	7.64±2.008	7.75±2.191	8.13±2.470	8.00±3.329
$b \pm s_b^-$	0.13±0.004	-0.01±0.001	0.03±0.001	0.03±0.001	0.01±0.001
$c \pm s_c^-$	0.02±0.001	-3.21±0.217	4.72±1.159	-3.19±0.906	4.29±2.317
$d \pm S_d^-$			0.01±0.002	0.10±0.004	
Adj R ²	0.85	0.62	0.86	0.88	0.88
RSD	0.47	0.52	0.55	0.20	0.45
BIC	33.93	35.36	36.04	37.15	30.28
S	4.42	4.75	4.72	4.08	6.05
FriesianxBunaji					
$a \pm s_a^-$	7.39±3.018	7.70±2.854	7.05±1.210	8.66±5.241	7.61±3.103
$b \pm s_b^-$	0.21±0.022	-0.03±0.008	0.01±0.001	0.08±0.003	0.06±0.004
$c \pm s_c^-$	0.03±0.001	-4.18±2.350	5.58±2.173	1.53±0.812	5.53±2.328
$d \pm S_d^-$			0.01±0.001	0.11±0.02	
Adj R ²	0.89	0.92	0.62	0.95	0.96
RSD	0.63	0.50	0.64	0.41	0.15
BIC	31.85	25.82	32.24	20.66	10.4
S	4.24	4.59	5.58	6.30	4.25

S-persistence; BIC-Bayesian Information criterion; Adj R²-Adjusted coefficient of determination; RSD-Residual standard deviation; $a \pm s_a^-$ -scaling factor with its standard error; $b \pm s_b^-$ -inclining slope to peak production; $c \pm s_c^-$ - declining slope after peak production; $d \pm S_d^-$ -decay rate

Table 4.39b: Estimates of curve parameters of different models in different genetic groups of cows in Shonga Dairy Holdings in Kwara State

Parameter	Wood	Wilmink	Djisktra	MilkBot	Neural network
Jersey					
$a \pm s_a^-$	9.20±0.103	8.93±0.101	8.61±0.004	8.63±0.051	8.77±0.156
$b \pm s_b^-$	0.08±0.003	0.02±0.004	0.01±0.002	0.01±0.003	-0.01±0.002
$c \pm s_c^-$	0.01±0.005	-2.34±0.328	-5.85±1.116	1.77±0.227	1.24±0.947
$d \pm S_d^-$			0.03±0.01	0.14±0.01	
Adj R ²	0.90	0.88	0.80	0.89	0.92
RSD	0.78	0.83	0.84	0.81	0.77
BIC	36.93	38.94	36.16	38.15	37.15
S	4.97	5.26	5.85	4.95	5.04
JerseyxBunaji					
$a \pm s_a^-$	6.8±0.03	7.6±3.92	5.7±0.02	5.8±0.04	5.9±0.08
$b \pm s_b^-$	0.2±0.02	0.02±0.001	0.1±0.02	0.1±0.002	0.1±0.02
$c \pm s_c^-$	0.02±0.001	-1.9 ±0.007	4.8±1.60	4.9±1.59	4.9±1.48
$d \pm S_d^-$			0.02±0.01	0.13±0.03	
Adj R ²	0.89	0.85	0.75	0.80	0.97
RSD	0.39	0.49	0.64	0.56	0.15
BIC	27.70	90.97	141.80	148.93	10.4
S	4.69	4.90	4.80	5.33	6.44

S-persistence; BIC-Bayesian Information criterion; NE-Not estimable; Adj R²-Adjusted coefficient of determination; RSD-Residual standard deviation; $a \pm s_a^-$ -scaling factor with its standard error; $b \pm s_b^-$ -inclining slope to peak production; $c \pm s_c^-$ - declining slope after peak production; $d \pm S_d^-$ -decay rate

4.10.2.2 The parameters and goodness of fit measurements of all lactation curve models in Integrated Dairies Limited in Plateau State

The results of fitting the five mathematical models in fitting the lactation curve for 305dFCM data are summarized in Table 4.40. In Holstein Friesian cows, all the five models were best suited to predict milk yield. Neural Network model was the best model for explaining properties of milk yield (Adj R^2 =98 %; RSD=0.32; BIC=47.11). The highest persistency value was recorded in Djisktra model (4.77) which implies that character of Djisktra model were flatter than Wood, Wilmink, Djisktra and Neural Network in this study. Wood, Wilmink, Djisktra and MilkBot models had adjusted coefficient of determination of 93 %, 98 %, 92 % and 92 %, respectively with residual standard deviation of 1.18, 0.34, 1.23 and 1.32. The highest efficiency of Neural Network models could be linked to high rate of generalization by learning at a faster rate and minimizing the deviations between the actual and predicted yield in a low search space.

In FriesianxBunaji cows, all the models had the highest efficiency in reconstructing the lactation curves ((Adj R^2 =74-80 %; RSD=0.43-0.55; BIC=37.91-42.66). Neural Network had the most efficient predictive capability. Wood, Wilmink, Djisktra and MilkBot models had adjusted coefficient of determination of 78 %, 74 %, 74 % and 76 %, respectively with residual standard deviation of 0.55, 0.51, 0.50 and 0.54. The Bayesian information criterion was highest in Wood model (42.66) while the least value was observed in Neural Network (37.91). Persistency of the model was flatter in Wilmink (6.27) than Wood, Wilmink, MilkBot and Neural Network models.

Table 4.40: Estimates of curve parameters of different models for different genetic groups of cows in Integrated Dairies Limited in Plateau State

Parameters	Empirical		Mechanistic		Intelligence
	Wood	Wilink	Djisktra	MilkBot	Neural network
Holstein Friesian					
$a \pm s_a^-$	12.01±5.322	14.40±6.001	14.29±6.169	14.55±5.983	14.38±5.902
$b \pm s_b^-$	0.48±0.016	0.05±0.002	0.01±0.004	0.04±0.002	0.06±0.003
$c \pm s_c^-$	0.10±0.005	0.01±0.002	4.23±1.827	0.02±0.004	0.02±0.001
$d \pm S_d^-$			0.02±0.001	0.20±0.08	
Adj R ²	0.93	0.98	0.92	0.92	0.98
RSD	1.18	0.34	1.23	1.32	0.32
BIC	48.09	48.07	49.22	50.88	47.11
S	3.40	4.00	4.23	3.47	4.77
FriesianxBunaji					
$a \pm s_a^-$	9.12±5.121	7.93±3.246	7.80±3.307	8.08±4.001	8.51±4.086
$b \pm s_b^-$	0.19±0.014	0.09±0.031	0.06±0.003	0.01±0.008	0.01±0.005
$c \pm s_c^-$	0.04±0.023	-5.64±2.892	6.27±2.001	0.62±0.005	0.06±0.014
$d \pm S_d^-$			0.05±0.001	0.01±0.002	
Adj R ²	0.78	0.74	0.74	0.76	0.80
RSD	0.55	0.51	0.50	0.54	0.43
BIC	42.66	42.57	42.54	42.63	37.91
S	3.82	5.90	6.27	4.99	5.40

S-persistency; BIC-Bayesian Information criterion; NE-Not estimable; Adj R²-Adjusted coefficient of determination; RSD-Residual standard deviation; $a \pm s_a^-$ -scaling factor with its standard error; $b \pm s_b^-$ -inclining slope to peak production; $c \pm s_c^-$ - declining slope after peak production; $d \pm S_d^-$ -decay rate

4.10.2.3 *The parameters and goodness of fit measurements of all lactation curve models in Sebore farm in Adamawa State*

Table 4.41 a and b shows the parameters and goodness of fit measurements of lactation curve model among different genotypes of dairy cows. In Holstein Friesian cows, the accuracy of reconstructing the lactation curves among the models in Holstein Friesian cows for Wood, Wilmink, Djisktra, MilkBot and Neural Network was 84, 79, 56, 98 and 90 %, respectively. Amongst the five models, the MilkBot had the best accuracy for reconstructing the lactation curves (Adj R^2 =98 %; RSD=0.02 and BIC=6.40) and the least accuracy (Adj R^2 =56 %) was recorded in the Djisktra model. The persistency of the models range from 4.42 in Wood model to 6.05 in Neural Network model.

In Jersey cows, all the models were good predictors of milk yield. NN recorded the best predictive capabilities which ranked first, followed by Wood and MilkBot while Wilmink was the least predictor. Persistency ranged from 2.46 in Djisktra to 4.05 in NN models.

In Brown Swiss cows (Table 4.41b), all the models were efficient in estimating milk yield at different test days. Wilmink ranked first (Adj R^2 =92 % and BIC=16.20); the second in rank was MB (Adj R^2 =89 % and BIC=21.59); third in rank was Wood (Adj R^2 =88 % and BIC=23.11), fourth in rank was Djisktra (Adj R^2 =84 % and BIC=26.64) while the least in ranking was NN (Adj R^2 =80 % and BIC=20.67). The residual standard deviation was lowest in Wilmink (0.06) and highest in MB (0.39).

Lastly, in Simmental cows, Neural network model had the best accuracy (Adj R^2 = 86 %) for estimating milk yield while MilkBot models had a poor fit (62 %) with large noise (0.65).

Table 4.41a: Estimates of curve parameters of different models for Holstein Friesian and Jersey cows in Sebore farm in Adamawa State

Parameters	Empirical		Mechanistic		Intelligence
	Wood	Wilmink	Dijkstra	MilkBot	Neural network
Holstein Friesian					
$a \pm s_a^-$	7.38±2.024	6.08±2.178	9.69±2.680	6.42±2.308	7.42±2.292
$b \pm s_b^-$	0.04±0.002	0.08±0.003	-0.06±0.002	0.06±0.003	0.04±0.002
$c \pm s_c^-$	0.01±0.001	0.36±0.022	4.42±2.100	-4.15±1.034	-1.70±0.445
$d \pm S_d^-$			0.03±0.02	0.17±0.05	
Adj R ²	0.84	0.79	0.56	0.98	0.90
RSD	0.18	0.33	0.07	0.02	0.05
BIC	22.05	29.36	9.47	6.40	8.00
S	4.79	5.20	4.42	4.08	6.48
Jersey					
$a \pm s_a^-$	8.32±3.054	6.77±2.330	7.19±3.259	6.95±1.854	7.23±2.309
$b \pm s_b^-$	0.16±0.006	0.02±0.001	0.06±0.004	0.07±0.004	0.01±0.001
$c \pm s_c^-$	0.05±0.003	0.05±0.004	-2.46±1.281	1.30±0.080	2.47±1.006
$d \pm S_d^-$			0.03±0.01	0.28±0.07	
Adj R ²	0.82	0.79	0.81	0.82	0.87
RSD	0.70	0.73	0.68	0.56	0.32
BIC	39.22	35.58	39.03	36.25	17.54
S	3.48	4.01	2.46	2.48	4.05

S-persistence; BIC-Bayesian Information criterion; NE-Not estimable; Adj R²-Adjusted coefficient of determination; RSD-Residual standard deviation; $a \pm s_a^-$ -scaling factor with its standard error; $b \pm s_b^-$ -inclining slope to peak production; $c \pm s_c^-$ -declining slope after peak production; $d \pm S_d^-$ -decay rate

Table 4.41b: Estimates of curve parameters by different models for different genetic groups of cows in Sebore farm in Adamawa State

Parameters	Wood	Wilmink	Dijkstra	MilkBot	Neural network
Brown Swiss					
$a \pm s_a^-$	7.22±4.000	6.46±2.319	7.74±2.566	6.54±2.168	6.25±2.001
$b \pm s_b^-$	0.08±0.002	0.06±0.003	0.03±0.002	0.03±0.002	0.01±0.002
$c \pm s_c^-$	0.02±0.006	-1.79±0.192	2.07±1.106	0.06±0.002	3.59±1.224
$d \pm S_d^-$			0.02±0.002	0.03±0.01	
Adj R ²	0.88	0.92	0.84	0.89	0.80
RSD	0.38	0.06	0.20	0.39	0.11
BIC	23.11	16.20	26.64	21.59	20.67
S	4.22	4.19	2.07	5.01	4.80
Simmental					
$a \pm s_a^-$	5.92	5.57	5.20	5.56	4.90
$b \pm s_b^-$	0.18	0.01	0.05	0.02	0.05
$c \pm s_c^-$	0.04	2.32	2.27	2.32	3.59
$d \pm S_d^-$			0.01±0.001	0.01±0.006	
Adj R ²	0.83	0.80	0.73	0.62	0.86
RSD	0.16	0.18	0.53	0.65	0.69
BIC	30.34	21.52	35.51	0.20	31.35
S	4.80	4.63	2.27	4.62	3.97

S-persistence; BIC-Bayesian Information criterion; NE-Not estimable; Adj R²-Adjusted coefficient of determination; RSD-Residual standard deviation; $a \pm s_a^-$ -scaling factor with its standard error; $b \pm s_b^-$ -inclining slope to peak production; $c \pm s_c^-$ - declining slope after peak production; $d \pm S_d^-$ -decay rate

4.11 Fitting models to milk yield in different genotypes of cows

4.11.1 Final candidate model for milk prediction over a 305 day full lactation cycle in

Shonga Dairy Holdings in Kwara State

Table 4.42 shows the MLR, NN and GFA models prediction of 305d FCM milk yield from milk production characteristics and conformation traits over a full cycle (305d) of lactation of genotype and environment interactions. All the models were good predictors of FCM305d yield. The NN model had the highest coefficient of determination and therefore ranked first (Adj $R^2 = 0.99, 0.99, 0.99$ and 0.96); the second in rank was MLR (Adj $R^2 = 0.96, 0.98, 0.98$ and 0.94) and third in rank was GFA (Adj $R^2 = 0.87, 0.98, 0.95$ and 0.90) model for Holstein Friesian, FriesianxBunaji, Jersey and JerseyxBunaji in Kwara climatic gradients. The RMSE of the NN prediction (2, 4, 1 and 9 %) was lower than that of the MLR (8, 6, 7 and 13 %) and GFA (20, 7, 11 and 14 %), indicating the presence of larger residual errors in the MLR and GFA forecasts. Neural Network had the best adequacy for model selection than MLR and GFA in prediction of FCM305d yield. The BD, FCM100, FY and PY were traits that featured in the prediction equation of Friesian and FriesianxBunaji cows. The RP and FCM100 were the major predictors of FCM305d yield using different models (MLR, NN and GFA) in Jersey purebred dairy cows while RP, FCM100 and FY were the markers that predicted FCM305d efficiently in JerseyxBunaji cows. It was observed that the accuracy of the prediction method was consistently higher in NN than MLR and GFA studied albeit with different precision across the four genotypes of cows in Kwara State.

Table 4.42: Prediction equation for FCM305d from milk and conformation traits using different models in Shonga Dairy Holdings in Kwara State

Genotype and Herd	Model	Equation	Adj R ²	RMSE	BIC
Holstein Friesian	MLR	FCM305=-323.7+7.22BD-0.16FCM100+22.00FY+1.72PY	0.96	0.08	1024.18
	NN	FCM305=1125.36+0.26BD-0.01FCM100+0.44FY+0.48PY	0.99	0.02	988.34
	GFA	FCM305=1681.58+3.48BD-1.58FCM100+11.23FY+44.61PY	0.87	0.20	1360.09
FRxBJ	MLR	FCM305=26.83+1.18BD-2.38FCM100+79.78FY+1.43PY	0.98	0.06	1000.01
	NN	FCM305=868.43+0.01BD+0.08FCM100-2.08FY-0.05PY	0.99	0.04	990.06
	GFA	FCM305=36.08-12.77BD-0.22FCM100+21.99FY+15.92PY	0.98	0.07	1000.26
Jersey	MLR	FCM305=1722.5-13.70RP-0.33FCM100	0.98	0.07	1000.20
	NN	FCM305=1341.3+0.38RP+0.02FCM100	0.99	0.01	980.71
	GFA	FCM305=1246.5-62.8RP-66.2FCM100	0.95	0.11	1205.09
JxBJ	MLR	FCM305=1062.1-15.22RP-1.45FCM100-0.08FY	0.94	0.13	1232.43
	NN	FCM305=2628.6+10.18RP+0.17FCM100-8.24FY	0.96	0.09	1530.07
	GFA	FCM305=988.44-35.2RP-1.80FCM100-11.06FY	0.90	0.14	1298.22

FCM305-Fatcorrectedmilk for 305day; JXBJ-JerseyxBunaji; FRXBJ-FriesianxBunaji; JxBJ-JerseyxBunaji; NN-Artificial neural network; MLR-Multiple linear regression and GFA-Genetic algorithm function approximation; BD-Bodydepth; FY-Fat yield; PY-Protein yield; Adj R²-Adjusted coefficient of determination, Bayesian information criterion; d=day; RMSE-Root mean square error

4.11.2 Final candidate model for milk prediction over a 305 day full cycle in Integrated

Dairies Limited in Plateau State

Table 4.43 shows the model equation, adjusted coefficient of determination, root mean square error and Bayesian information criterion in predicting FCM305d in Plateau State. Neural network model outclassed MLR and GFA in predicting FCM305d yield with lower RMSE and BIC for Plateau State in Holstein Friesian and FriesianxBunaji. The MLR was more accurate than the GFA with over 9 % increment of the FCM305d yield prediction. The MLR and NN were more sensitive in Holstein Friesian dairy cows than FriesianxBunaji in modelling FCM305d yield. The FY and TL were the observed traits that predicted FCM305d in all the models accurately for FriesianxBunaji in Plateau State. It was observed that the accuracy of the prediction method was consistently higher in NN than MLR and GFA studied albeit with different precision across the two genotypes of dairy cows in Plateau State.

4.11.3 Final candidate model for 305 day milk prediction in Sebore farm in Adamawa State

Multiple linear and nonlinear regression equations derived from milk yield characteristics and conformation traits measurement were modelled for standardized 305 full lactation cycle (Table 4.44). The NN and MLR had the best accuracy of prediction with 99 % of all the FCM305d yield in a full lactation cycle with low noise (0.02 and 0.03) and minimum tears (961.06 and 983.41), respectively in Holstein Friesian breed. The NN was best in Jersey and Brown Swiss cows while in Simmental all the models were very efficient and similar in their efficiency of prediction (Adj $R^2=99\%$) with varying goodness of fit (0.04 and 983.80, 0.03 and 984.12 and 0.05 and 983.68) in MLR, NN and GFA, respectively.

Table 4.43: Prediction equation for FCM305d from milk components and conformation traits using different models in Integrated Dairies Limited in Plateau State

Genotype and Herd	Models	Equation	Adj R ²	RMSE	BIC
Holstein Friesian	MLR	FCM305=1012.4+3.76ST-0.24FCM100+23.53FY+0.66PY-3.18UC-0.44BWT	0.98	0.06	1020.22
	NN	FCM305=3844.4-0.02ST+0.02BD +0.01FCM100+0.009FY+0.009PY -0.003UC-0.003BWT	0.99	0.01	960.42
	GFA	FCM305=348.7+6.82ST-8.93BD-0.13FCM100+20.3FY+1.28PY-9.39UC-1.18BWT	0.87	0.14	1290.50
FRxBJ	MLR	FCM305d=1512.8+21.1FY-50.9TL	0.96	0.05	1022.36
	NN	FCM305d=868.4 -2.08FY-0.17TL	0.98	0.03	1018.41
	GFA	FCM305d=1515.9-21.1FY-51.4TL	0.96	0.07	985.55

FCM305-Fatcorrectedmilk for 305day; FRXBJ-FriesianxBunaji; JXBJ-JerseyXBunaji; NN-Artificial neural network; MLR-Multiple linear regression and GFA-Genetic algorithm function approximation; BWT-Bodyweight; ST-stature; UC-Udder clearance; FCM100-Fat corrected milk at 100 day; BD-Bodydepth; FY-Fat yield; PY-Protein yield; Adj R²-Adjusted coefficient of determination; Bayesian information criterion; d=day, RMSE-Root mean square error.

It was observed that the accuracy of prediction method was consistently higher in NN than MLR and GFA studied albeit with different precision across the four genotypes of dairy cows excepting Simmental cows with similar coefficient of determination across the models in Adamawa State.

4.11.4 Final candidate model for pooled prediction of milk yield

Table 4.45 presents the 305dFCM yield equation pooled for all genotypes for the different models. Prediction equation of 305dFCM within models showed high adjusted R^2 values ranging from 0.995 in the MLR to 0.997 in the NN and GFA, respectively. The BCS, HG, FCM100, FY, PY and RUW were traits that featured in the overall prediction equation for MLR. In the NN with R^2 value of 0.997 consisted of RUW, BCS, HG, FCM100, FY and PY as predictors for 305dFCM while RP, FY, UC and RUH were observed in the GFA with R^2 value of 0.997. It was observed that accuracy of the prediction method was best in GFA with three predictor variables as compared to NN and MLR with six predictors.

Table 4.44: Prediction equation for FCM305d from milk and conformation traits using different model in Sebare farm in Adamawa State

Genotype and Herd	Model	Equation	Adj R ²	RMSE	BIC
Holstein Friesian	MLR	FCM305d=3048.5-26.1RP-3.23BD+24.1FY+3.1UC-21.5RUH	0.99	0.03	983.41
	NN	FCM305d=806.9-0.14RP+0.06FY+0.01UC-0.07RUH	0.99	0.02	961.06
	GFA	FCM305d=1036.1-98.3RP+22FY+15.92UC-0.07RUH	0.98	0.05	997.28
Jersey	MLR	FCM305d=-1059.93-26.78BCS-16.20HG+10.07UC	0.96	0.08	1050.82
	NN	FCM305d= 868.4-2.08FY+0.17TL	0.98	0.05	990.01
	GFA	FCM305d= 1515.9+21.1FY-51.4TL	0.96	0.10	1100.08
Brownswiss	MLR	FCM305d=1291.8-0.37FCM100+24.9FY	0.98	0.06	988.57
	NN	FCM305d=1208.8+0.0002RP+0.02FCM100+0.04FY	0.99	0.02	985.50
	GFA	FCM305d=-1008.92+0.05FCM100+22.05FY	0.97	0.08	993.84
Simmental	MLR	FCM305d=1241.3-0.29FCM100+23.2FY	0.99	0.04	983.80
	NN	FCM305d=1428.2-0.002FCM100+0.06FY	0.99	0.03	984.12
	GFA	FCM305d=1283.1-0.04FCM100-11.03FY	0.99	0.05	983.68

FCM305-Fatcorrectedmilk for 305day; NN-Artificial neural network; MLR-Multiple linear regression and GFA-Genetic algorithm function approximation; FCM100-Fatcorrectedmilk for 100day milk yield; FY-Fat yield; TL-Teat length; UC-Udder clearance; RP-Rump; BD-Body depth; BCS-Body condition score, RUH-Rear udder height; HG-Heart girth; Adj R²-Adjusted coefficient of determination; Bayesian information criterion; d=day; RMSE-Root mean square error

4.11.5 Genetic architecture, specification and statistic information of the neural network modelling of FCM305dMY

Table 4.46 shows the architecture of Neural Network for FCM305dMY. The effect of the architecture for FCM305dMY was generally small. Multilayer feedforward network was the best ($R^2=0.99$) model with architecture of 6-2-1 hidden layers and efficient learning rate of 88% using 100000 epoch while Bayesian regulatory neural network had the weakest structure for dissecting the architecture (1-2-2-1) of FCM305dMY. The GRNI using particle swarm algorithm revealed an architecture of 1-8-1 with an efficiency of 90 % under a minimal computation cost with less bias of 5 %. It was observed that the accuracy for dissecting the architecture of FCM305dMY using computational method was best in Multiple Layer Perceptron with Back propagation algorithm.

Table 4.45: Prediction equation for FCM305d from milk and conformation traits using different models pooled for all genotypes

Model	Equation	Adj R ²	RMSE	BIC
MLR	FCM305d=1425.49-7.83BCS-1.09HG-0.04FCM100+24.0FY+0.94PY-15.0RUW	0.995	36.77	7497.88
NN	FCM305d=-2848.99+0.03RUW+0.26BCS+0.01HG-0.002FCM100-0.008FY-0.0007PY	0.997	30.14	2424.69
GFA	FCM305d=1036.1-98.3RP+22FY+15.92UC-0.07RUH	0.997	30.07	1997.28

FCM305d-Fatcorrectedmilk for 305day; NN-Artificial neural network; MLR-Multiple linear regression and GFA-Genetic algorithm function approximation; Adj R²-Adjusted coefficient of determination; Bayesian information criterion FCM100-Fatcorrectedmilk for 100day milk yield; FY-Fat yield; TL-Teat length; UC-Udder clearance; RP-Rump; BD-Body depth; RMSE-Root mean square error

Table 4.46: Network architecture, specification and statistic information for modelling FCM305dMY of cows

Architecture	Structure	Algorithm	Learning rate	Transfer function	MAD	Epochx10 ³	RMSE	R ²	Bias
6-2-1	MLP	BP	0.88	Sigmoid	0.11	10	0.01	0.99	0.02
1-2-2-1	Bayesian	Monte carlo	0.40	MCMC	0.26	4	0.58	0.43	0.03
1-14-1	RBF	SVM	0.53	GA	0.24	16	0.06	0.61	0.11
1-8-1	GRNI	Particle swarm	0.72	MAS	0.15	7	0.01	0.90	0.05

GRNI-Genetic regulatory network inference; GA-Genetic algorithm; MAS-Multi agent system, GA-Genetic algorithm; SVM-support vector machines; BP-Back propagation, RMSE-Root mean square error, R²-coefficient of determination, MAD-Mean absolute deviation; d= day; RMSE-Root mean square error

CHAPTER FIVE

DISCUSSION

5.1 Variation in Measures of Efficiency of Milk Production Traits in Genotypes of Cows in Different Environments

Enhancing milk production remains a key objective of dairy cattle breeding systems worldwide. However, environmental variations often influence the performance of traits under selection, leading to different genotypes excelling in different environments. In this study, the average 305-day fat-corrected milk yield (305dFCM) was 2496.4 kg, which surpasses the 2015 kg reported by Ngongoni et al. (2006) for cows in Zimbabwe but falls short of the 3408–8645 kg reported by USDA-NASS (2016) in the United States and other studies in Turkey, Sri Lanka, and Pakistan (Katok and Yanar, 2012; Kollalpitaya *et al.*, 2012; Usman *et al.*, 2012). These differences likely stem from variations in breeding practices, feeding, climate, altitude, herd size, production levels, and management strategies across countries. Additionally, discrepancies in breeding objectives between the countries of origin and production environments could contribute to inconsistencies in the performance of elite bulls for milk production.

The 305-day milk yield per cow per day (305MY/cow/day) observed in this study was 7.2 kg, lower than the 8.9 kg reported by Ángel Ríos-Utrera (2013) under subtropical conditions and the 9.43–10.25 kg/day range reported by Mureja *et al.*, (2002). These differences are likely attributable to variations in herd size, management systems, and breed characteristics. Similarly, the fat yield (FY) and protein yield (PY) of 63.3 kg and 58.7 kg, respectively, were lower than estimates from European countries (Eurostat, 2016) and medium- to high-producing dairy cows in the Czech Republic, where FY and PY values ranged from 237.3 to 346.8 kg (Jóźwik *et al.*, 2012). This disparity may be attributed to significant changes in milk composition driven by

advances in feeding, breeding, and cattle management over recent decades. The higher fat yield compared to protein yield aligns with observations that dietary changes affect milk fat more prominently (Jerkins and McGuire, 2006).

The study further revealed that purebred Holstein and Jersey cows outperformed crossbreeds in fat and protein yields, contradicting findings by VanRaden and Sanders (2003), where Brown Swiss by Holstein (BH) crosses matched Holsteins for protein yield, and JerseyxHolstein (JH) and BH crosses exceeded Holsteins in fat yield. Heins *et al.*, (2008a) also reported no differences in fat production between JH crosses and Holsteins.

The total solids (TS) content of 12.5% in this study was comparable to 13% reported in Ethiopia (Anyalem *et al.*, 2008) and similar to values for Brown Swiss in Kirsehir (11.93%, Dogan *et al.*, 2002), Swiss breeds (13%, Lindmark *et al.*, 2003), and Khartoum dairy cattle (12.62%, Ahmed and El-Zubeir, 2007). These similarities suggest that breed, feeding, genetics, environment, and milking practices significantly influence milk composition and quality.

The mean lactation length (LL) of 344.9 days observed in this study was influenced by milk yield, with cows producing less than 3 kg/day removed from milking. This LL exceeded the 327.5 days reported by Mureja *et al.*, (2002) and Demeke *et al.*, (2000) but was shorter than the 362–366.5 days reported by Million *et al.*, (2003) and Usman *et al.* (2012) for Holstein Friesians. It was also higher than the 302 days reported for Jersey cows in the hot and humid conditions of Kwara State, Nigeria (Adebayo and Oseni, 2016).

The 4.8 kg FCM/kg body weight (FCM/kgW) recorded in this study was lower than the 6.66 kg and 7.01 kg reported for Friesian and Jersey cows, respectively (Rao and Nagarceukar, 1979), but higher than the 2.72 kg observed for Red Sokoto goats in Nigeria (Akpa *et al.*, 2001). It was,

however, lower than the 34.4 kg and 8.5 kg reported for Saanen and Sudanese Nubian goats, respectively (Gall, 1996).

The lower FCM/kg MW observed in Nigerian dairy cows likely indicates a higher metabolic body size, resulting in increased energy requirements for maintenance relative to the FCM produced. The net energy efficiency (NEE) of 42.4% recorded in this study surpasses the 30.1% reported for Zebu cattle in Nigeria by Ibeawuchi (1993). This suggests that 42.4% of the total digestible nutrient (TDN) energy consumed, excluding maintenance, was converted into milk. Genetic variation among the cow groups for NEE was evident, contrasting with Veerkamp and Emmans (1995), who reported difficulty in detecting genetic differences in net efficiency. Nevertheless, genetic differences likely influence how cows allocate energy for production and tissue maintenance. Supporting this, Veerkamp (1998) suggested that field data reveal genetic variability in energy partitioning between tissue recovery and milk production. Key traits for improving feed utilization through genetic selection include feed intake capacity, energy requirements for production and maintenance, body condition changes, and energy partitioning among these components.

Heins et al. (2008b), however, reported no significant differences in NEE between crossbred and purebred Holsteins. The dairy merit (DM) of 61.8% in this study exceeds the values of 19.6% and 19.4% reported for Friesian and Jersey cows (Rao and Nagerceukar, 1979) and the 5.98% observed for Zebu cattle in Nigeria (Ibeawuchi, 1993). The superior NEE of Holstein Friesian, FriesianxBunaji, and Jersey cows—up to 8% higher than JerseyxBunaji, Brown Swiss, and Simmental cows—is attributed to factors such as greater feed intake capacity, larger gastrointestinal capacity, and higher digestive efficiency. These differences may also relate to

variations in mastication rate during grazing and distinct rumen microbial populations (Beecher *et al.*, 2014).

The DM observed indicates that 61.8% of the TDN consumed was converted to milk energy, including maintenance energy, with 1g TDN equating to 4 calories. Feed efficiency, defined as the energy required for milk production relative to energy consumed, aligns with Heins *et al.* (2008b), who found no difference in feed efficiency between crossbred and pure Holsteins. Schwager-Suter *et al.* (2001) reported higher feed efficiency in crossbred cows compared to pure Holsteins, defined as the energy content in milk relative to net energy intake. This study supports these findings, with significant differences in feed efficiency observed across genetic groups.

Genotype-environment interactions play a crucial role in cattle breeding in tropical regions. Cattle from temperate climates often perform differently when raised in tropical conditions (Javed *et al.*, 2002a). In Kwara State, Jersey cattle demonstrated significantly higher 305-day fat-corrected milk (FCM) yields compared to other genetic groups. However, the average 305-day FCM yield in this study was lower than the annual milk production of Holstein (7441 kg), Ayrshire (6072 kg), Guernsey (5570 kg), and Jersey (5187 kg) in South Africa (NMRIS, 2012). These higher yields in South Africa reflect greater genetic adaptability for milk production driven by selection for milk volume. This suggests that the other breeds in the study were more sensitive to heat stress, as productivity in high-temperature environments depends on balancing metabolic heat production with heat dissipation. Consequently, heat stress was found to impair milk production (Ominski *et al.*, 2002).

The results of this study differ notably from those of Fayeye *et al.* (2013), who worked with similar populations of dairy cows. These discrepancies may stem from differences in sample size, statistical methods, or variations in herds and pedigree information. Among the genetic

groups, Holstein Friesian cows excelled in part-period (100-day FCM) milk yield, likely due to their genetic selection for high milk production and significant gene flow across countries (Kadzere et al., 2001). However, the average daily milk yield of 7.2 ± 0.31 kg per cow was lower than the parental average of 9.4 ± 1.3 liters per day, indicating a decline in production efficiency in the new environment.

Jersey cows showed a higher propensity for fat yield compared to other genotypes, though their performance was still lower than reported European estimates (Eurostat, 2016). This highlights the reduced productive efficiency of dairy cattle under high-temperature conditions. Given that Jerseys are traditionally known for milk quality over quantity, their superiority in fat yield over Holstein Friesians in this study appears justified.

Milk efficiency traits were strongly influenced by genotype, with Jersey cows outperforming other breeds in most efficiency traits except for dairy merit, which was similar to Holstein Friesians. Crossbred populations exhibited superior FCM per kilogram of body weight. These genotype effects align with findings from other researchers studying diverse dairy cattle groups. The study underscores the importance of providing a cooler environment to optimize dairy efficiency. The observed similarities in efficiency between Holstein Friesian and Jersey cows suggest comparable potential for milk production, although Holsteins tend to consume more feed and produce less milk under heat stress. This reduced efficiency makes Holsteins less suitable for dairy production in Kwara State compared to Jerseys.

In Plateau State, Holstein Friesian cows exhibited significantly better performance in milk production and efficiency traits compared to Friesian x Bunaji crossbreds. This suggests that the mountainous climate of the region enables these cows to adapt better, minimizing heat stress and allowing for optimal milk production. The superiority of purebred Holsteins over Holstein x

Bunaji crossbreeds for these traits aligns with the general expectations in genetic improvement studies. Similar findings were reported by Mukasa (2008) and Ojedapo *et al.*, (2004), who observed higher productivity in Holstein cows compared to crossbreeds in Plateau State.

The average 305-day fat-corrected milk (FCM) yield of 4996.8 kg recorded in this study exceeds the 2678 kg reported by Million and Tadelle (2003) in Ethiopia, the 3678.09 kg reported by Mukasa (2008), and the 4457.72 kg reported by Ojedapo *et al.* (2004) in Nigeria. However, it is lower than the 8600 kg average for Holstein cows in more favorable conditions (World Holstein Friesian Federation, 2006). While the study's average 305-day yield surpasses the 9.43 kg/day recorded by Million and Tadelle (2003) in Ethiopia, it falls short of recent estimates for fat and protein yields from developed countries such as the USA and Canada (World Holstein Friesian Federation, 2006). The overall 305-day yield per lactation in developed nations averages 40 kg/day per cow, significantly higher than in developing regions (Ranawana, 2008).

In Adamawa State, characterized by high temperatures and a dry climate, the observed mean 305-day FCM yield was lower than the 5519 kg reported by Kollalpitiya *et al.*, (2012) in Sri Lanka, the 2772.76 kg recorded by Sattar *et al.*, (2005) in India, the 5152 kg reported by Jairath *et al.*, (1995) in Canada, and the 5905 kg reported by Ajili *et al.*, (2007) in Tunisia. These lower yields reflect poor adaptation of Holstein cows to hot climates, reduced dry matter intake, and less-than-ideal management practices in the study area. However, Holstein cows in the Sebore herd showed superior performance for milk production and efficiency traits, likely due to the use of shade and fan systems that mitigated heat stress. This approach allowed the cows to allocate more energy toward milk production rather than maintenance.

The mean daily 305-day FCM yield in this study was also lower than the average daily milk production of Holstein heifers (22.12 kg), Brown Swiss cows (18.99 kg), and Simmental cows

(19.41 kg) reported by Yvette and Haja (2005) in Switzerland. The six milk efficiency traits assessed in this study revealed significant differences in energy-efficiency profiles across genotypes, highlighting the variation in biological efficiency driven by genetic selection and management practices. These efficiency profiles were consistent with findings for Holstein Friesian cows throughout lactation (Prendiville et al., 2011).

High-yielding cows were shown to be more profitable due to their superior ability to convert feed energy into milk. Heavier, high-producing cows were particularly advantageous as they allocated less energy to maintenance and more to milk production. This observation aligns with the findings of Friggens and Newbold (2007), who demonstrated the importance of genetically driven nutrient partitioning in enhancing dairy cattle efficiency.

Variations in milk production and efficiency traits across locations can be attributed to differences in climatic factors such as temperature, humidity, wind speed, local aspect effects, and altitude, as well as management practices in the herds across the three locations. According to Waheed and Khan (2011), feeding and management practices accounted for 27–37% of the differences observed in milk production and efficiency traits among herds.

The substantial genotype-by-environment (G×E) interactions observed for these traits indicate shifts in the ranking of genotypes depending on the environment. In this study, some genotypes achieved their highest performance in specific regions, while others excelled in different environments better suited to their genetic potential. This phenomenon underscores the effect of G×E interactions, as described by Falconer and Mackay (1996), where the phenotypic superiority of one genotype in a given environment may not hold in another, highlighting the environment-specific nature of genetic expression.

5.2 Variation in Bodyweight and Udder Conformation in Genotypes of Cows in Different Environments

Conformation traits are essential for dairy producers as they enhance both milk production efficiency and the aesthetic appeal of cows over their productive lifespan. Consequently, these traits are routinely recorded in modern dairy cattle breeds. In the hot climate of Kwara State, genotype significantly influenced traits such as body weight, body depth, heart girth, and rear udder depth. Crossbreds of Holstein Friesian and Jersey showed superior performance compared to other crossbreds, likely due to hybrid vigor. Additionally, Friesian × Bunaji crosses outperformed Jersey × Bunaji crosses, which may be attributed to the larger body size of Holstein cows compared to the smaller stature of Jersey cows. The observed mean body weight and heart girth of 517.3 kg and 201.7 cm exceeded the values reported for Holstein cattle in developed countries by Ozkaya and Bozkurt (2009). Purebred Holstein Friesian and Jersey cows had larger udders than their crossbred counterparts, but crossbreds showed reduced rear udder attachment height, potentially leading to weaker attachment and higher susceptibility to mastitis or culling. This reduction may be more influenced by dam effects than sire breed effects, as dams of crossbreds had lower rear udder heights compared to purebred dams. Holstein Friesians, being a larger breed, exhibited greater body depth than Jersey cows, which are designed to have a smaller frame. The high variability observed in traits like teat length reflects differences in adaptation to machine milking.

In Plateau State's mountainous climate, milk production traits such as conformation are valuable indicators of productivity, longevity, and reproductive capacity. Optimal conformation traits are associated with higher productivity and extended lifespan (Chirinos et al., 2007; Meszaros et al., 2008). In this study, genotype significantly affected body condition score, body depth, heart girth, and udder clearance, aligning with previous research (Gwaza et al., 2007). The observed

low to moderate coefficient of variation suggests room for genetic improvement. Holstein Friesian × Bunaji crossbreds were superior in traits like body weight and udder clearance, emphasizing the role of hybrid vigor. However, the lack of significant effects for some traits could be due to the high proportion of Holstein genes in the crossbreds. In Adamawa State's hot climate, genotype significantly influenced body weight, chest width, body depth, rump, heart girth, and udder traits. Holstein Friesian, Simmental, and Brown Swiss breeds performed better in body weight due to their larger frame compared to Jersey cows. The mean body weight of 585.4 kg for Holstein Friesian cows in Adamawa was within the range reported by Jessica *et al.*, (2015), though slightly lower values in other genetic groups likely reflect heat stress. Body condition scores (BCS) averaged 3.1, exceeding values reported in Argentina, suggesting adequate energy balance under the local feeding systems. Teat length and central ligament strength in this study matched or exceeded values from other regions, indicating favorable adaptation to local conditions and milking systems. Across tropical Nigeria, genotype had significant effects ($P < 0.05$) on traits such as body weight, body depth, heart girth, udder clearance, and rear udder dimensions. Variability in traits like BCS, stature, and udder conformation highlights opportunities for genetic selection. Environmental factors such as temperature, humidity, altitude, and management practices contributed to differences among ecological zones. Traits like body weight, BCS, and udder clearance should be prioritized in genetic improvement programs to enhance the functionality and productivity of dairy cattle in Nigeria. The observed hybrid vigor in crossbreds underscores their potential for inclusion in breeding strategies.

5.3 Variations in Reproductive Traits in Genotypes of Cows in Different Environments

This study identified breed-related differences in reproductive performance among various cow genetic groups in Kwara State, where high environmental temperature and humidity prevail due to the farm's proximity to River Niger tributaries. The study observed an average age at first calving (AFC) of 1134.9 ± 18.91 days (37.83 months), which was shorter than the AFC values reported in Sri Lanka and Ethiopia for dairy cattle by Chandrasiri *et al.*, (2007), Weerasinghe *et al.*, (2008), Tassew and Seifu (2009), Fekadu *et al.*, (2011), and Tadesse *et al.*, (2010). However, it exceeded the AFC values reported for Sri Lankan and Tunisian Holstein-Friesian cows by Kollalpitiya *et al.*, (2012) and Ajili *et al.*, (2007). Murdi and Tripathi (1990) and Govindaiah *et al.*, (1998) reported lower AFCs for Jersey cows in India, while Rahumathullah *et al.*, (1994) found higher values for Jersey and Therparker cows. Variations in AFC across studies may reflect differences in breeding practices, climate, and statistical methods. The extended AFC observed in pure Jersey and JerseyxBunaji crossbreds might be attributed to delayed attainment of sufficient body weight for mating, as natural mating predominated in these herds.

The average number of services per conception (NSC) was 2.4 ± 0.03 , differing from the 1.81 ± 1 reported by Tadesse *et al.*, (2010) for Friesian cattle in Ethiopia and the 2.0 for Holstein Friesian cattle in Nigeria (Ngodigha *et al.*, 2009). However, it was lower than the 2.5 reported for Holstein Friesian cows in Iran (Ansari-Lari *et al.*, 2010) and higher than the 1.6 for crossbred cows in Ethiopia (Lobago *et al.*, 2007). These discrepancies are likely due to varying management practices, with heat detection and timely insemination influencing the NSC (Yifat *et al.*, 2009). The present findings suggest relatively efficient insemination practices in the herds during the study.

The mean days open (DO) of 185.4 ± 1.56 was comparable to values reported by Heins *et al.* (2008a) but was 20 days shorter than for purebred Jersey cows. This aligns with trends observed by Dechow *et al.*, (2007) and Heins *et al.*, (2008a), where crossbreds exhibited fewer days open than purebreds. Lower DO in crossbreds has been associated with better health and reduced lameness (Anderson *et al.*, 2007; Heins *et al.*, 2006c). The study recorded a low overall calving rate of $47.3 \pm 0.48\%$, consistent with the 41.08% reported on communal grazing in South Africa (Bembridge and Tapson, 1993). However, purebred Jersey cows in the herd had longer DO, which contradicted Heins *et al.*, (2006c), who reported longer herd survivability for crossbreds.

In the cooler climate of Jos, the AFC of 1020.9 ± 12.59 days (34 months) was higher than the 30.25 months reported by Mukasa (2008) and 30.9 months at VOM (Ojedapo *et al.*, 2004) but lower than the 44-month AFC typical for *Bos indicus* cattle. The observed variation may be attributed to differences in sample size and management systems, with traditional systems resulting in slower maturation compared to commercial farms.

The mean NSC of 2.8 ± 0.03 exceeded values reported for various regions of Ethiopia (Shiferaw *et al.*, 2003; Yifat *et al.*, 2009; Haile-Mariam *et al.*, 2003) and for indigenous cows (Ali *et al.*, 2006). The higher NSC observed may be influenced by the retrospective nature of the data. The mean DO of 143.6 ± 0.29 days was longer than reported values for Holstein Friesian cows in Ethiopia, Turkey, Tanzania, Tunisia, and Sri Lanka but exceeded the optimal 60–90 days recommended by Berry *et al.*, (2003), likely due to negative energy balance delaying ovarian activity in modern dairy cows.

The mean calving interval (CI) was 687.9 ± 1.31 days, longer than values reported by Fekadu *et al.*, (2011) and Ansari-Lari *et al.*, (2010), possibly reflecting differences in environmental conditions, management practices, and estrous detection efficiency. The calving rate of $49.3 \pm$

0.13% exceeded Ethiopia's national average (27.06%; Desalegn, 2008) but was lower than rates reported for crossbred cows in Sweden (Heins *et al.*, 2007) and California dairies (Heins *et al.*, 2012).

The herd life (HL) of 66.7 ± 0.45 months was consistent with values reported for Jersey crosses with Boran and Horro breeds (Gebreegziabher and Mulugeta, 2006) but lower than the recommended HL of 9.35 years for dairy cattle (Enyew *et al.*, 2000). Shorter HL suggests involuntary culling due to repeated breeding issues. In Adamawa State, the AFC was 1261.6 ± 2.46 days (42.05 months), with longer AFC values noted in other studies for Deoni, Ongole, and East African Shorthorn Zebu cattle, influenced by nutrition and management. Overall, these findings highlight the impact of breed, management, and environmental conditions on reproductive performance across different cattle populations.

5.4 Estimates of Genetic Parameters for Milk Production Traits in Multi-Genotypes Cows in Different Environments

In Kwara State, all the milk production traits (100 dMY, MYCD, protein yield and lactation length) are correlated with 305-day fat-corrected milk yield except fat yield for Holstein Friesian cows. Similar effects of the milk production traits on 305-day fat-corrected milk yield have been reported by some researchers for dairy cattle (Beavers and Van Doormaal, 2014; Hinde *et al.*, 2014). This illustrates the opportunities to change the protein content in milk, extend the lactation length, and increase part-period milk yield (100 dMY) and milk yield per cow per day through genetic selection and optimal feeding and management practices. However, less is known about the possibilities of changing the protein composition in milk by selection and feeding. Heritability estimates indicate that genetic variation for 305 days fat corrected milk yield and milk production traits are present and, therefore, selective breeding to alter

composition is possible except for lactation length. The low heritability for lactation length might be due to the high negative impact of heat stress on Holstein Friesian cows, which may be under less genetic control. Heritability for fat-corrected milk yield, protein and fat yield are generally in line with the moderate to high estimates reported by the previous studies (Kadarmideen *et al.*, 2000; Mulder *et al.*, 2004). Genetic correlations showed that an increase in 305-day fat corrected milk yield implies an increase in 100 dMY, MYCD, protein yield and lactation length while decreasing fat yield. It is likely that selection in dairy cattle over the past decades has improved milk production traits but resulted also in less fat yield. This result agrees with Ibeawuchi (1987) who reported that there is an inverse relationship between milk yield and butterfat content of milk. This had been confirmed by Ahamefule *et al.*, (2003).

Low to high heritability estimates recorded for fat-corrected 305 days milk yield and milk production traits in FriesianxBunaji cows agree with the report in the literature (Misztal *et al.*, 1992). Misztal *et al.* (1992) obtained much lower heritability estimates than those in the present study of 0.53, 0.21, and 0.19, respectively for yields of milk, fat, and protein. The high estimates were thought to have been due to use of inclusion of genetic levels of unknown parents in the analysis. Visscher and Thompson (1992), with British cows, also reported higher heritability estimates for yields of milk and fat of 0.39 and 0.36, respectively. The heritability estimates for yield traits are slightly lower than those in the current literature (Short and Lawlor, 1992; Miglior *et al.*, 1995), possibly as a result of comparatively higher residual variance. The high repeatability estimates obtained in this study suggest that milk yield and milk production traits are weakly influenced by temporary environmental factors. Moderate to high estimates of repeatability indicate that milk production performance on any occasion is of use in predicting later performance. Genetic correlations were largest between fat-corrected 305-day milk yield

and fat yield (-0.54) in this study. However, estimates from different studies are not directly comparable, mainly because of differences in data sets, models, and the number of traits analysed. Van der Werf and de Boer (1989) reported a smaller genetic correlation for protein and fat which was similar to the one found in this study.

Moderate to high heritability for fat-corrected 305 days milk yield and milk production in Jersey purebred cattle were similar to other findings that used various methods of estimation in cattle breeds (Campos *et al.*, 1994; Jairath *et al.*, 1995; Roman *et al.*, 1999). The genetic correlation was very high between milk yield and fat yield (0.86). The genetic correlation between fat and protein yields, which directly conditions the possibilities for preferential or exclusive improvement of one or both traits, was low (0.19). Thus, any possible evolution arising from any preferential improvement is increased when selecting for either of them. Genetic correlations between milk and milk production traits were positive and in the range of those reported in the literature for dairy cattle (Boichard and Bonaiti, 1987; Welper and Freeman, 1992). The positive genetic correlation observed between milk yield and the milk production traits indicates that selection for fat-corrected 305 days milk yield is expected to increase milk composition.

Moderate to high heritability estimates were observed for 305dFCM yield, MYCD and protein yield in JerseyxBunaji cows. In dairy cattle, De Paula *et al.* (2008) reported the same trend for the genetic correlations between milk yield and milk components. The genetic correlation estimates between fat yield and protein were moderately high and positive. Similar results were obtained by Tonhati *et al.*, (2000) (0.50) and Rosati and Van Vleck (2002) (0.31). Therefore, selection for higher fat yield in milk would also increase protein yield. Differences in the genetic variability of breed, in the methodology applied to estimate the (co)variance components and also in the production system (management and environment) probably explain the divergence

between the results obtained in the present study and those reported in the literature (Tonhati *et al.*, 2000; Rosati and Van Vleck, 2002). Moderate to high repeatability estimate for 305dFCM yield, MYCD, fat yield and protein yield implies that traits could be of significant use in predicting later performance. The highest genetic correlation observed between MYCD and lactation length implies that selection for MYCD is expected to extend the lactation length.

In Plateau State, moderate heritability estimates (34 %) recorded for 305dFCM yield in Holstein cows agree with some reports in literature. Interbull (2015) reported heritability estimates for milk yield to be 0.25 to 0.40 for Holstein, Brown Swiss, Jersey and Guernsey cows in the national genetic evaluation system which varies with herd variance. High heritability estimates for 100dMY is a buildup of more additive genetic variance. High heritability estimates for fat yield (41%) were similar to the 40 % reported for Brown Swiss and Jersey cows and higher than the range of 0.25 to 0.35 reported for Holstein according to Interbull (2015). A protein yield of 20 % was lower than the range of 30 to 40 % in the National genetic evaluation for countries under the Interbull scheme (Interbull, 2015). The low estimate of heritability is a reflection of more non-additive genetic variance and variance due to the common environment in lactation length. Moderate to high repeatability for milk and milk production traits, suggests that a single measurement per lactation would be sufficient for each trait (Serrano *et al.*, 2002). Positive and moderate to high genetic correlations between 305dFCM and 100dMY, MYCD, fat and protein yield indicate favourable relationship amongst the traits except for LL which had an antagonistic correlation with 305dFCM yield.

FriesianxBunaji had low heritability estimates for 305dFCM yield and MYCD of 18 and 14 % which was lower than the value of 29 % reported by Mukasa (2008). The estimates of the present study are comparable with the report made by Lobo *et al.*, (2000) for tropical dairy animals.

However, it is larger than the estimate made for Friesian cattle (0.119) in Kenya (Rege, 1991). Some researchers (Moya *et al.*, 1985; Roman *et al.*, 2000) on the other hand reported a similar heritability for fat yield. Estimates of heritability for protein yield were 20 %. This estimate is moderately lower than some of the available estimates elsewhere (Moya *et al.*, 1985; Roman *et al.*, 2000) but higher than the average of literature reports for tropical dairy cattle (Lobo *et al.*, 2000). Moderate to high values for repeatability estimates are within the reported range for dairy cattle (Roman *et al.*, 2000). However, lower repeatability for MYCD suggests that genetic parameters for this trait were affected by the large errors correlated with MYCD due to incomplete lactations. Large and significant genetic correlations between 305dFCM with 100dMY, MYCD, fat and protein yield agree well with the report in the literature for Holstein crossbred cows (Misra and Joshi, 2004; Lobo *et al.*, 2000).

In Adamawa State, moderate to high heritability reported for 305dFCM, MYCD, fat yield and lactation length in Jersey purebred cows agree with some reports in the literature (Interbull, 2015; Lobo *et al.*, 2000; Misra and Joshi, 2004). Low repeatability estimates for 100dMY imply the influence of large non-additive genetic variance on the part period milk production. The moderate to high genetic correlations between 305dFCM and 100dMY and MYCD except in the lactation length where the correlation was antagonistic is an indication of pleiotropic effect indicating that the same set of genes are responsible for the milk production.

Moderate heritability estimates for 305 days fat corrected milk yield and milk production traits except 100dMY and fat yield were higher than the findings of Espinoza *et al.* (2007) for milk yield in the range of 0.14-0.17 in Brown Swiss. Repeatability estimates for milk production traits were lower and higher than some of the estimates in the literature for Brown Swiss (Ilatsia *et al.*, 2007; Ojango and Pollott, 2001). The highest repeatability was obtained by lactation length, thus

it may be sufficiently reliable to use lactation length for early selection in Brown Swiss cows. The genetic correlation between 100dMY and 305-day fat-corrected milk yield was high and significant which implies that early milk production could be used to predict later milk production.

Moderate heritability estimates of 25 and 21%; 6 and 19 %; 22 and 24 %; 33 and 20 % for 305dFCM, fat yield, MYCD and protein yield in Holstein Friesian and Simmental cows are within the moderate to high range for dairy cattle in the National Genetic Evaluation (Interbull, 2015). Heritability estimates in the Iranian Holsteins population ranged from 0.13 to 0.26, from 0.1 to 0.17, and from 0.15 to 0.21 for milk, fat and protein yields, respectively, in the first three lactations by REML procedure. Respective estimates obtained in the same study using Bayesian analysis ranged from 0.19 to 0.29, 0.17 to 0.21 and 0.2 to 0.25 for milk, fat and protein yields, respectively.

Low to high repeatability estimates might be due to difficulties encountered by daughters of superior sires to express their genetic potential under harsh climatic conditions and limited feed resources (Hammami *et al.*, 2008). Moderate to high genetic correlation of milk production traits with 305dFCM excepting LL (antagonistic) in Holstein cows implies that traits are essentially controlled by the same set of genes. High and positive genetic correlations between 305dFCM and milk production traits agree with the report of Hammami *et al.* (2008) for dairy cows. Low and positive genetic correlations between 305dFCM and milk production traits agree with some reports in the literature (Ben Gara *et al.*, 2006; Hammami *et al.*, 2009a).

5.5 Genetic Parameters for Conformation Traits and 305d FCM Yields in Multi-Genotypes cows in different Environments

In Holstein Friesian cows, high heritability estimates for 305dFCM (44 %) in Holstein cows in Nigeria would allow breeders to select better cows for milk yield based on individual selection. This value was within the moderate to high range reported for 305d heritability estimates used by the majority of countries in their genetic evaluations (Interbull, 2012). The heritability estimates of the conformation traits which varied between 0.06 (stature) to 0.41(bodyweight) were within the range reported in several publications for the Holstein breed (Němcová *et al.*, 2011; Pérez-Cabal *et al.*, 2006; Tsuruta *et al.*, 2005). The low to high h^2 estimates for the body and udder conformation traits implied that traits were governed by additive and non-additive gene action and it may or may not take a longer time to yield progress from selection. The estimated heritability for BCS was low (7 %) which is in agreement with other sources, which showed that BCS was the least heritable in Holstein cows at the beginning of lactation, and the most heritable in mid to late lactation (Koenen *et al.*, 2001; Berry *et al.*, 2003b; Dechow *et al.*, 2004).

The low repeatability for BCS, chest ligament and stature implied greater variability within the lactation length. This might be because Holstein cows increased the extent and duration of the negative energy balance to achieve greater milk production (Dechow *et al.*, 2002; Butchereit *et al.*, 2011). Low repeatability for rear udder height might be partly attributed to the difficulty in taking accurate measurements of a soft tissue (udder) which might have contributed to the greater variability.

The positive and significant genetic correlation between 305-day fat-corrected milk yield with some selected body and udder conformation traits (CL, HG, HG, RUH, BCS, and BW) implied that taller, deeper, wider and longer cows in a positive energy balance with a longer teat length would produce more milk. This agreed with the genetic estimates by Dechow *et al.* (2003) and

Dal Zotto *et al.* (2007) in Holstein cows. High and negative correlated estimates observed between 305-day fat-corrected milk yield and udder clearance indicate that under proper conditions Holstein cows with high breeding value for 305dFCM yield would yield a decreasing trend in these correlated traits as long as variation is still high for such traits. The highest genetic relatedness between HG and UC (0.99) implied that an increase in heart girth in Holstein cows can be achieved through selection for deeper udder clearance.

The heritability estimates (35 %) obtained for Jersey cows were within the range of 30-35 % under low and high input production systems (Heins *et al.*, 2011; Morek-Kopéc and Zarnecki, 2012) but higher than the 30 % reported by Ojango and Pollot (2001). Heritability estimates of conformation traits with a range of 2-72 % were either less than (Heins *et al.*, 2008; Roche *et al.*, 2009; Interbull, 2012) or comparable to other reported estimates (Nawaz *et al.*, 1993; Campos *et al.*, 1994). Moderate to high repeatability estimates for 305dFCM, BCS, CL, CW, BD, HG, RUH and RUW implicated that low variability exists within lactations; implying that all the measurements taken on the body conformation traits were closely related to the bone structure of the cows. The antagonistic genetic correlation between 305dFCM and TL suggests that correlated responses from selection on milk yield would result in smaller teat length probably due to the prolonged effect of milking. This was in contrast to the report of Němcová *et al.* (2007) who showed that the highest values for milk yield occurred at the higher TL. Positive and significant genetic correlation between 305dFCM and some conformation traits that cows with sound conformation traits can give good milk. Vukasinovic *et al.* (2002) found significant and positive genetic correlations between milk production and the evaluation of the udder traits (r ranged from 0.38 to 0.66). The high and significant residual correlations between 305dFCM and

udder conformation traits excepting teat length implied that cows with larger and stronger udder attachment had a higher propensity for milk yield.

In FriesianxBunaji cows, the heritability of 30 % was similar to the estimates reported by several researchers (Kadarmideen, 2004; Berry *et al.*, 2005; Alphonsus, 2008). This shows that 70 % of the variations in the fat-corrected milk yield could be attributed to management and environmental factors (Wattiaux, 2002). Heritability estimates for conformation traits ranged from 16-42 % which was lower than the range of 19-58 % reported by Alphonsus (2008) in FriesianxBunaji cows at National Animal Production Research Institute, Shika, Nigeria. Differences in estimates obtained may be linked to the management and the estimation method used for the computation of the variance component for genetic parameters (REML vs EMS). A high repeatability estimate for 305 fat-corrected milk yield and all the conformation traits signified that a single measurement per lactation would be sufficient for each trait (Serrano *et al.*, 2002). The antagonistic genetic relationship between 305dFCM and CW, rump and udder clearance implied that genetic selection for 305dFCM would cause a reduction in the stability of the cows. Thus, selection for 305dFCM should be done with caution so as not to increase the risk of involuntary culling. Positive genetic correlation between 305dFCM yield and conformation traits implied that an increase in 305dFCM would cause a corresponding increase in conformation traits under selection.

In JerseyxBunaji cows, the heritability estimate was 39 % which was lower than the estimates reported by several works (Singh and Gurnani, 2004; Nehra *et al.*, 2005). The moderate heritability value suggested that sufficient additive genetic variation is required and thus the scope for genetic improvement through a selection of Indigenous and crossbred populations to

increase milk yield. Low (2 %) to high (51 %) repeatability estimates are more than the estimates reported (Demeke *et al.*, 2004; Haile *et al.*, 2009) for crossbred cows.

The positive genetic correlation between 305dFCM yield and conformation traits is an indication that traits were influenced by the same set of genes. The antagonistic environmental correlations between 305dFCM yield and BCS have also been reported by many authors (Berry *et al.*, 2005). Positive and moderate environmental correlations between 305dFCM yield and BW implied that an increase in 305dFCM yield would cause a corresponding increase in the BW of dairy cows. Antagonistic correlations between 305dFCM yield and udder conformation traits (RUH, RUW and udder clearance) were in contrast to the observation of Kuczaj (2003) who reported a positive correlation. Negative correlations of udder conformation traits with 305dFCM yield had been indicated to have serious health implications on the udder (Tsuruta *et al.*, 2004; MacNeil and Mott, 2006).

In Brown Swiss cows, moderate heritability estimates obtained were lower than the 37 % reported by Galip *et al.* (2004) in Turkey. This implied that improvement of milk yield via individual selection will be possible. The low to high heritability estimates for conformation traits implied that traits were under the influence of additive and non-additive gene action. High repeatability estimates for all the quantitative traits signify less variability within the body and udder conformations of the cows. Since the linear measurements were taken on mature milking cows, it is presumed that the bone structure of mature cows may not change significantly within lactation. This might be attributed to physiological changes that may occur during lactation, indicating that high genetic merit for BCS is correlated with less severe negative energy balance (Dechow *et al.*, 2002). The antagonistic genetic correlations between 305dFCM yield and CW have also been reported by many authors (Veerkamp *et al.*, 2001; Berry *et al.*, 2005; Atkins *et*

al., 2008). This showed that genetic selection for 305dFCM yield alone would reduce the chest width. The positive and moderate correlations between 305dFCM yield and RUH implied that an increase in udder length would lead to a major increase in 305dFCM milk volume.

Lastly, moderate heritability estimates of 21 % were lower than 49 % reported by Vlada *et al.*, (2011) in Simmental cows from Serbia. However, it was lower when compared to the results reported by Costa *et al.*, (2000) but significantly higher than the results established by Silvestre *et al.*, (2005). The heritability values were relatively moderate which can be explained to some extent through moderate variation within the group of daughters of one bull-sire and between groups of bulls. Heritability estimates range of 6 % in rump and 59 % in teat length was higher than the values used in the October national evaluation of breeding values for classified conformation traits (Center za strokovno delo, 2011). In this study, better estimates of heritability were obtained using continuous linear body measurement rather than the scale classification system.

The low repeatability estimates obtained in this study suggested that rump was strongly influenced by temporary environmental factors. The antagonistic genetic relationship between 305dFCM yield and rump implied that genetic improvement of milk volume would lead to an extremely sloped rump. Cows with extreme slope to the rump sometimes also have undesirable set to the hock or are awkward in their hind leg movement which might lead to a high risk of calving difficulty and reduced longevity. The positive genetic correlation between 305dFCM yield and the other body and udder conformation traits could be due to pleiotropic effects. The negative correlation between 305dFCM yield with BW, ST and RUH was an indication that selection to increase 305dFCM yield would lead to a decreased body size and length of udder in Simmental cows.

5.6 Genetic Parameter of Reproductive Traits and 305d FCM Yields in Multi-Genotypes Cows in Different Environments

The heritability estimates for the reproductive indices computed for Holstein Friesian varied between 0.02 (CI) and 0.27 (HL) in Kwara State. The heritability of the calving interval reported here was close to 0.022 reported by Kadarmideen *et al.*, (2003), but slightly lower than 0.032 reported by Pryce *et al.* (1997). However, Dong and Van Vleck (1988), Campos *et al.* (1994), Ertugrul *et al.* (2002) and Ulutaş *et al.* (2004) reported higher heritability estimates for CI than the ones in this study, which ranged from 0.07 to 0.16. Low h^2 estimates for fertility traits would indicate that a major part of the variation in these characteristics was environmental and selection might contribute little improvement. The estimated heritability for DO was small (0.10), however, these results were higher than the heritability estimates of DO from field data (0.037) using similar editing criteria and repeatability animal model (Van Raden, 2004). In contrast, was lower than the 48 % heritability estimate for DO from another experimental farm using a repeatability animal model (Gonzales-Recio and Alenda, 2005). It was not surprising to get a higher value of heritability estimates from this study because data were trained to minimize the effect of environmental factors (e.g. management, feeding, health care). The calving rate estimate of 0.05 was slightly higher than h^2 of 0.01 for CR in the USA (Kuhn *et al.*, 2008) and 0.02 reported in the Interbull evaluation for France. The heritability of direct genetic effect for AFC was 0.24. It was higher than 0.19 ± 0.00 by Hadi *et al.*, (2011) for Iranian Holstein; 0.21 ± 0.03 by Oyama *et al.*, (2002) for Wagyu cattle. However, it was lower than 0.404 ± 0.069 (Deb *et al.*, 2008) and 0.53 ± 0.116 (Gebeyehu, 2014) for Holstein cows. Heritability estimate for NSC (0.08) is within the range of the average weighed heritability estimate reported by Lobo *et al.*, (2000) and higher than the report of Aggeb and Hayes (2000). Moderate heritability estimates of herd life were obtained in this study, which was higher than most reports in the literature. This

implied that cows in Nigeria were not under intense selection for milk yield which tend to reduce the stress for milk production and enhance longevity in the herd.

Amirpour Najafabadi *et al.* (2016) reported heritability estimates of 0.074 and 0.18 based on a logarithmic scale and original scale, respectively in Slovakia Holstein cows. Caraviello *et al.* (2004) reported heritability estimates for herd life ranging from 0.05 to 0.13. The low heritability estimate for total lifetime performance traits suggest that direct selection for herd life holds little promise for enhancing the lifetime performance of cows, because of slow response to selection (Jairath *et al.*, 1994). Those results could be the consequence of the data validation procedure which produced a more reliable data set and confirmed the hypothesis of Pryce *et al.*, (1998) that higher estimates might be expected from more accurate data sets. Repeatability estimates in this study are within the range reported in the literature (Kadarmirdeen *et al.*, 2001; Ojango and Pollot, 2001; Campos *et al.*, 2004). Moderately unfavorable r_g between 305d FCM yield with AFC and DO was observed in this study. Biologically, this indicates unfavorable pleiotropic effects of genes which implied that selection for 305d FCM yield would lead to a decline in fertility traits (longer age at first calving and days open). This supports the earliest findings that selection for milk yield alone is expected to lead to a decline in fertility traits (Pryce *et al.*, 1997; 1998; Lindhe and Philipsson, 1998).

The high genetic correlation between NSC and CR is an indication that NSC can be used to influence CR in selection studies. Positive, moderate, and significant correlation between NSC and 305dFCM yield could indicate that high-producing cows might require more inseminations to conceive. Low heritability estimates for fertility traits were within the low range reported by Mukasa (2008) in HolsteinxBunaji cows. Moderate repeatability estimates observed in AFC suggest the possibility of selecting cows based on first lactation yield because such results are

reliable indicators of the future performance of the cows. Moderate, positive, genetic correlations between 305dFCM yield with CR and HL were in contrast with the report of Abe *et al.* (2009) who observed a negative trend. The positive trend in this study might be linked to the heterotic effect of the crossbred cows but the estimates were not quantified in this study. Significant and positive correlations exhibited by 305dFCM yield and HL imply that cows with higher milk volume will stay longer in the herd.

In Jersey purebred cows, low heritability and repeatability estimates for all the fertility traits were consistent with those reported in other studies (Baco *et al.*, 1998; Ojango and Pollot, 2001). Despite the differences in data, cattle populations and estimation procedures used. The low heritability estimates were due to low additive genetic variance attributable to long term natural selection in the breed and it implies that little genetic improvement would be expected from selection for such traits. The effect of large environmental variance on the phenotypic variance also led to low heritability. Poor heat detection and insemination techniques are important contributors to increased phenotypic variance of these traits (Dechow *et al.*, 2004). The AFC, CR and HL had positive and significant genetic correlations with 305 d FCM which indicate that selection studies to improve milk volume will lead to increase in calving rate and herd life but with a longer AFC due to pleiotropic effect. Positive environmental correlation between 305 d FCM with NSC and HL suggests that both traits are affected in part by the same environmental factors.

In JerseyxBunaji cows, similar trend of low heritability and repeatability estimates were observed as seen in Jersey cows. Such similarity could be linked to the high proportion of Jersey gene in the crossbred cows. Antagonistic genetic correlation between 305d FCM and all the reproductive traits excepting AFC in this study implied that genetic improvement for increase

milk yield would lead to favorable decrease in NSC, DO and CI but unfavourable extension of AFC and reduction in calving rate and herd life. Moderate and significant phenotypic correlation between 305 d FCM yield and CI has been reported by some authors (Rege, 1991; Ojango and Pollot, 2001).

In Plateau State, moderate heritability obtained for AFC in Holstein Friesian (23 %) was higher than the 0.19 ± 0.00 by Hadi *et al.*, (2011) for Iranian Holstein. However, it was lower than 0.404 ± 0.069 (Deb *et al.*, 2008) and 0.53 ± 0.116 (Gebeyehu, 2014) for Holstein cows. The low heritability estimates for NSC, DO CI, CR and HL agreed with the reports in the literatures (Hadi *et al.*, 2011; Yosef, 2006; Demeke *et al.*, 2004). Heritability estimates for CI (9 %) in this study was higher than the 0.04 ± 0.00 by Hadi *et al.* (2011) for Iranian Holstein; 0.08 ± 0.05 by Yosef (2006) for Holstein breed and 0.08 ± 0.03 by Demeke *et al.* (2004). The direct heritability for DO was 0.14 which was higher than 0.01 ± 0.03 reported by Almaz (2012) in dairy cattle. Heritability estimates for DO, CR and HL (0.01-0.18) in this study were higher than the estimates reported in the literature for tropical cattle (Lobo *et al.*, 2000; Almaz 2012). High repeatability estimates of AFC, NSC, DO and HL implied lower variability within the lactations. The genetic correlation between 305 d FCM yield with DO and CI agreed with the report of Berry *et al.*, (2003a) who used a random regression model to estimate the genetic correlation between milk yield and fertility traits but contrasted the findings of König *et al.* (2008) in Germany who found genetic correlations of -0.31 in Holstein cows. High and moderate environmental correlations between 305 d FCM yield with CI and AFC suggest that traits were affected by the same environmental factors.

The heritability and repeatability estimates for fertility traits in FRXBJ cows were generally low except AFC and DO. The genetic parameter estimates in this study generally confirmed the

literature data that fertility traits had heritability (Biffani *et al.*, 2005; Jamrozik *et al.*, 2005), although some differences do exist between traits related to period traits which were seen in AFC and DO, respectively. In the literature, a substantial variation in heritabilities for AFC is found. For example, 0.04 for Japanese Black in Hiroshima (Oyama *et al.*, 1996), 0.075 for Boran (Haile-Mariam and Kassa-Mersha, 1994), 0.109 for Japanese Black (Uchida, 2001) and 0.38 for Holstein-Friesian (Ojango and Pollott, 2001) were reported. An antagonistic relationship between 305 d FCM yield and HL with CR has been confirmed from previous studies reporting an unfavorable genetic correlation between yield and fertility traits (Abe *et al.*, 2009; Hagiya *et al.*, 2009). Positive and moderate environmental correlations between 305 d FCM with DO, CR and HL implied that improvement of milk volume in selection studies would lead to unfavorable longer day open and favorable CR and HL, respectively.

In Adamawa State, low to moderate heritabilities and repeatabilities estimates for all the fertility traits is an indication that selection to increase milk yield would reduce reproductive performance and this could affect culling rates and reduce the genetic gain from primary traits (Haile-Mariam *et al.*, 2003). The genetic relationship between 305 d FCM with AFC, CI, DO and herd life indicated that a reduction in AFC, CI, DO and herd life could be used to influence 305 d FCM yield in selection studies. The highest genetic correlations between CI and AFC agreed with the findings of Oyama *et al.* (2004) and Goyache *et al.*, (2005). The varying magnitudes and directions for the genetic and environmental correlations observed between fertility traits were supported by the findings of several authors who worked on dairy cattle (Wasike *et al.*, 2009; Hadi *et al.*, 2011).

The heritability obtained for Jersey cows (0.11) was similar to those reported by Ghiasi *et al.* (2011), Restrepo *et al.* (2008) and Demeke *et al.* (2004). However, this estimate was lower than

those obtained by Ríos-Ultrera *et al.* (2010a) and Estrada-León *et al.* (2008) in dairy cattle. As for DO, the heritability estimate obtained in this study was 0.18; this was consistent with the results reported by Pantelic *et al.* (2011) and Ghiasi *et al.* (2011). In contrast, some authors reported very low heritability values (Estrada-León *et al.*, 2008; M'hamdi *et al.*, 2010; Ríos-Ultrera *et al.*, 2010a). The heritability estimate for NSC in Jersey cows (0.24) was larger than that reported by Demeke *et al.* (2004). The heritability for CR obtained in this study for Jersey cows was 0.08, which was higher when compared with the findings of 0.049 reported by Abe *et al.*, (2009), 0.052 by Tsuruta *et al.* (2009) but lower than 0.147 by Haile-Mariam *et al.* (2003) for Jersey cows. All these results indicated that reproductive traits are lowly heritable, below 0.10 according to most authors, which implied that they are notably affected by the environment and that the selection of superior individuals would be very slow. Repeatability estimates for fertility traits were higher than some reports in the literature (Ojango and Pollott, 2001; Kadarmideen *et al.*, 2000; Biffani *et al.*, 2005) except AFC (0.05) which was lower than some findings in the literature (Biffani *et al.*, 2005; Jamrozik *et al.*, 2005). The genetic correlations between herd life and calving interval were large which might be due to the pleiotropic effect. The antagonistic relationship between 305 d FCM with CI and DO implies that intense selection for milk volume will lead to improvement in fertility traits.

In Brown Swiss cows, heritability and repeatability estimates in this study were higher than the estimates obtained by Ángel *et al.* (2010) for Brown Swiss cows in Mexico. The low heritability implies that genetics have negligible contribution to variation in the trait and management practices might influence improvement in the trait more than selection. Genetic improvement in milk volume would shorten herd life and calving intervals of the cows but extend the AFC, DO and NSC. This trend has been reported in the literature by several authors (Campos *et al.*, 2004;

Ojango and Pollott, 2001; Heins *et al.*, 2008). Positive genetic correlations between 305 d FCM and fertility traits implied that an increase in milk yield would extend the age at first calvings, extend the calving interval increase the number of semen doses for insemination, and increase the rate of calving. Negative genetic correlations between 305 d FCM and fertility traits (DO and herd life) implied that an increase in milk volume would reduce the day open before conception and herd life.

In Simmental cows, heritability and repeatability estimates were low except CI. This agrees with the report of low and high estimates in the literature. Dearborn *et al.* (1973) reported low heritability and repeatability estimates for reproductive traits of cows indicating that the major part of variations were due to non-genetic (environment) factors and that rapid response could be expected only by improving environmental conditions such as feeding regime and management system (Ulutas and Sezer, 2009). Phillips (2006) reported that reproductive traits usually have a heritability and repeatability greater than 0.10 which agreed with the 0.23 observed for CI in this study. Results of heritability and repeatability of fertility traits obtained in our research were higher compared with coefficients for the same traits published by Panić and Vidović (2006); and lower compared to research results of Petrović *et al.* (1999) and Kapš and Špehar (2004); and by heritability estimates determined in a Turkish population of Simmental cows by Ulek and Tekun (2006). Positive, negative genetic and environmental correlations between 305 d FCM yield and fertility traits in Simmental cows have been reported by several authors (Petrović *et al.*, 1999; Kapš and Špehar, 2004).

5.7 Predicted Breeding Value Estimation for 305 d FCM and some selected Reproductive traits

The predicted breeding value showed a large variation for the milk production in the first and pooled lactations. The highest genetic levels with the highest accuracy of Holstein cows in

Plateau State for both first and pooled lactations as compared to genotypes in different environments in Nigeria indicated a major genetic improvement. This might be due to the use of imported semen from the sires having better breeding values for milk yield. Large variations in sire ranking for 305 d FCM yield across the environment could be linked to the negative effect of environments on the genetic expression of economic traits in tropical countries where the ambient temperature often rises to 45°C in summer months (Javed *et al.*, 2002b). Genotype x Environment interaction (G x E) is potentially extremely important in cattle breeding in the tropics. The animals of temperate regions maintained in tropical conditions cannot behave similarly in both environments (Javed *et al.*, 2002b). The deteriorating trend in Jersey cows for 305-day milk yield in this study has been reported in the literature (Javed *et al.*, 2002b; Kaya *et al.*, 2003)

However, a deteriorating genetic trend has been observed in Jersey cows in Pakistan which might be due to the use of semen from the sires produced from the same herd (Javed *et al.*, 2003). It was also reported that breeding values estimated according to 305-day milk yield and test-day milk yield indicated only minor changes in the sire and cow rankings (Swalve, 1995; Kaya *et al.*, 2003). This was in contrast with the findings in this study as there was a major change in sire rankings. Accuracy of breeding value was low to moderate in this study (0.10-0.50: Lund *et al.*, 2010; Interbull, 2012). This is because a cow on average only has relatively few lactations and offspring which limits the amount of information available for estimating genetic merit in this study. The accuracies obtained in this study (0.10-0.90; first lactation and 0.10-0.80; pooled lactations) for reproductive traits may be overestimated, compared with the accuracies obtained in national evaluation centers, as it is likely that most national evaluation centers use economic values instead of optimal weights. Unfavorable breeding values for

reproductive traits observed in this study have been reported in the literature (Abdallah and McDaniel, 2000; El-Shalmani, 2011) for traits of dairy cattle.

5.8 Inbreeding Depression for Milk Production and Reproduction Traits in First and Pooled Lactations in Breed x Environment Interaction

Milk production traits

The average inbreeding effects for all the lactations was higher in Wright method of estimation than it was in the best linear unbiased estimates under different genotype x environment interactions. Thus, Wright method is more uncertain than best linear unbiased estimates in breeding schemes using progeny testing for inbreeding estimation. Holstein and Jersey cows had the highest severity of inbreeding in both methods of estimation (Thompson *et al.*, 2000). This could be linked to high rate in movement of Holstein and Jersey genes between countries, low effective population size and focus on similar breeding objectives. However, the losses per lactation for milk production traits caused by inbreeding estimated in this study (-350.2 kg vs -381.4 kg; Holstein Plateau, -220.1 kg vs -225.5 kg; Holstein Adamawa, -419.6 kg vs -422.1 kg; Jersey Kwara, -102.9kg vs -107.7 kg; Jersey Adamawa, -50.3 kg vs -53.1 kg; Brown Swiss; -89.3 kg vs -100 kg; Simmental Adamawa) in both methods of estimation were higher than values cited in the North American literature (-29.6 to -19.7 kg) (Miglior *et al.*, 1995; Wiggans *et al.*, 1995; Smith *et al.*, 1998). An explanation could be that the scale of inbreeding depression is not a constant value, but is relative to the mean production and management strategies in different dairy herds.

In consequence, in less productive populations such as the Brown Swiss and Simmental compared with Holsteins, one would also expect less severity of inbreeding depression. A notable exception in this study is that a fitness advantage was observed for Holstein cows in Plateau which extended lactation length in both methods of estimation by 5 days. This is in the

same direction as the study of Lori (1997) who reported a positive effect of inbreeding on age at first calving in Holstein cattle in Virginia Polytechnic Institute and University in the United States of America. This could be linked to the additive effect of high genetic merit bulls on lactation length in this study.

Reproductive traits

There were very few differences in both methods of estimation across the genotype x environment interactions for all the reproductive traits. This agreed with the report of Lori (1997) who indicated slight differences in fixed and mixed model analysis in estimating inbreeding depression for reproductive traits in dairy cattle, though a large negative effect was observed in this study. This could be linked to malapropism or mismatching of pedigree information in the herd record, improper monitoring of breeding records to minimize the effect of inbreeding and lack of use of semen of bulls with high genetic ranking. Inbreeding had a significant negative effect when it was fitted for the reproductive traits with a few exceptions in this study between genotype x environment interactions. This inbreeding depression on fertility could explain the higher risk of culling for cows as reported by Sewalem *et al.* (2006), as well as the lower economic indices values for inbred cows (Croquet *et al.*, 2006). The consistent negative effect of inbreeding on reproductive performance in dairy cattle has been reported in the literature (Adamec *et al.*, 2006; Croquet *et al.*, 2006; Sewalem *et al.*, 2006). These negative effects of inbreeding indicate that there were still deleterious recessive alleles segregating in this population which reduced individual survival and reproductive output. The positive effect of inbreeding on NSC in Holstein cows in Plateau State, CI in Holstein cows reared in Adamawa State, NSC in Jersey cows in Kwara State, AFC and CI in Simmental cows in Adamawa State

was an indication that inbreeding has not been purged out in the populations of dairy cattle reared in Nigeria.

5.9 Genotype and Environment Effect on the Predicted Estimate of Lactation Yield Characteristics

In Kwara State, the estimated lactation initial yield was 6.5 kg which ascended to a peak yield (PY) of 8.7 kg at PT (62.66 days) with LDY and TY of 3.2 and 2503.3 kg in the lifetime lactation period. Similar results were found in other breeds such as Iranian Holsteins (Torshizi *et al.*, 2011) whereas, another study (Ural and Koskan, 2014) found different results for Holstein-Friesian cows. PY and PT in this study were lower than the estimated lactation peak yield (PY; 9.11 kg) at PT (70.77 days) during the lactation period of Dhofari cows in Iran as reported by Salim and Salim (2014). Conflicting results could be attributed to breed, management, environment, and ecological zones (Orman and Ertugrul, 1999). The low to high coefficient of variation could be a response to different environmental stressors and genetic factors.

In Plateau State, the mean lactation peak yield was lower than the range reported by several authors in temperate countries (16 kg; Olori *et al.*, 1997; Swalve and Guo, 1999; Garcia and Holmes, 2001). However, the mean peak yield (10.2 ± 0.96 kg) for HolsteinxBunaji cows in the present study was less by 12.30 ± 0.16 kg and 12.15 ± 0.82 kg in HF crossbred dairy cows maintained under farmers' management system as reported by Kumar *et al.*, (2014) in India and Ethiopia, respectively but similar to the 10.6 ± 0.41 kg in HolsteinxBunaji cows in Nigeria (Alphonsus *et al.*, 2014). The observed peak time (PT) of 65.0 days was higher than the 40-45 days in multi-breed cattle populations and 26 days in Friesian-Bunaji crossbred cows in Nigeria (Akpa *et al.*, 2006). Time to peak milk production also fell within the range of 3-9 weeks reported in the literature (Jenness, 1985; Bheekhee *et al.*, 2002). The total milk yield averaging

4551.3±268.7 kg in this study was similar to the 4457.72±330.41 kg reported by Ojedapo *et al.*, (2004) and higher than 3687.096±104.673 kg by Mukasa (2008) for the same herd. The variation observed in this study was due to the larger sample size and choice of statistical methods used during analysis. The mean total yield for the crossbred (3751.3±292.0 kg) exceeded the 1988±118.1 kg reported for FriesianxBunaji cows at Shika (Malau-Aduli *et al.*, 1996) and 1189.00±130.86 liters for the FriesianxBunaji cows in Integrated Dairies Limited (Ojedapo *et al.*, 2004). The benefit of genetic improvement of purebred sire and dams for milk production has no doubt been reflected in the total milk yield as compared to the crossbred cows which explains the high coefficient of variation in this study.

In Adamawa State, the mean initial yield, peak yield, peak time, last day yield and total milk yield of 4.8±0.38 kg, 7.5±0.55 kg, 2.7±0.17 kg and 2051.3±268.7 kg were lower than the PY; 15.6 kg and TY; 3074 kg reported by Lopez-Villalobos *et al.*, (2005). Peak time was within the normal range of 60-90 days in our study (Olori *et al.*, 1997). Several studies (Olori *et al.*, 1997; Swalve and Guo, 1999; Garcia and Holmes, 2001) have shown the differences between the scaling factors correlated with yield at the beginning of lactation, inclining and declining slopes after the peak yield, total lactation yield and last day yield.

A desirable lactation model should be parsimonious, capable of depicting the production pattern and flexible enough to account for the influence of environmental factors affecting the curve shape without compromising accuracy (Pollott and Gootwine, 2000). All five models were persistent and possess these attributes with high efficiency to model the lactation curve with minimum error in FriesianxBunaji cows in Kwara State. The outstanding efficiency of MilkBot models both in terms of accuracy of fits and distribution of residuals in the construction of data imitating the biological process of lactation curve for FriesianxBunaji cows in Kwara State ($R^2 =$

88 %; RSD= 0.20) and Adamawa ($R^2 = 98$ %; RSD= 0.12) further validates the results of other authors (Cole *et al.*, 2012; Hostens *et al.*, 2012; Charlier *et al.*, (2012). Hostens *et al.*, (2012) used the DairySight fitting engine successfully in fitting individual lactations from monthly test data and they showed that MilkBot predictions are usually more accurate with high-efficiency predictions. The slight differences in the accuracy of the models in this study were mainly due to variations in the positions of the peaks and rate of decline (persistence). The MilkBot model is derived from abstract suppositions about the growth of udder capacity which permits inference about the shape of the lactation curve directly from parameter values. This suggests that the use of this model may be sufficient to study factors affecting lactation curves in Holstein cows (Hostens *et al.*, 2012). Persistence of the lactation curve for Holstein in Kwara and Adamawa States ranged from 4.12- 6.05 and 4.00-6.48 among the models which were similar to 6.11 - 6.36 reported by Gloria *et al.*, (2012) in crossbred Holstein Zebu cows. However, persistence is difficult to interpret because it lacks a biological unit of measure. An increased value indicates increased lactation persistence and ability to maintain milk stability after peak (Capuco *et al.*, 2003). Poor generalization of the Djisktra model in Adamawa was due to the atypical shape of the lactation which overestimated the actual yield at a decreasing rate in day 7 which implied that there was a constant rate of decrease from the initial to the last day yield. Since this model lacked convergence, it only applies to the declining phase of the milk yield curve and, therefore not useful for describing the whole lactation or estimating the optimum peak yield although it provides relevant measures of persistence. Tozer and Huffaker (1999) studying lactations of Australian Holstein cows, perceived the presence of some atypical curves.

Numerous studies have reported the highest efficiency and persistence of lactation curves using Neural Network (NN) models for various cattle genotypes under specific climatic conditions.

These genotypes include FriesianxBunaji, Jersey, and JerseyxBunaji cows in Kwara State; Holstein Friesian and FriesianxBunaji in Plateau State; and Jersey and Simmental cows in Adamawa State. These findings align with the results of earlier research (Schaeffer *et al.*, 2000; Jensen, 2001; Ferreira *et al.*, 2002). For example, Grzesiak *et al.* (2003) achieved an R^2 of 0.93 and RMSE values of 9.84% and 9.05%, while Sharma *et al.* (2007) reported a prediction accuracy of 92.03% with their NN model compared to 91.38% using multiple linear regression (MLR). Similarly, Dongre *et al.* (2012) documented NN prediction accuracies of 86.08% in dairy cattle.

Pre-processing techniques, such as data standardization and normalization, have been shown to enhance the learning efficiency of NNs, resulting in superior predictive performance compared to empirical and mechanistic models (Stein, 1993). Structuring input data effectively allows for improved NN training by orthogonalizing and classifying input vectors, which enhances interpolation accuracy and predictive ability.

For Brown Swiss cows, the Wilmink model demonstrated high predictive efficiency ($R^2=92\%$) in previous studies (Olori *et al.*, 1999; Schaeffer *et al.*, 2000). In this study, the postpartum peak day was set at 60 days, with Olori *et al.*, (1999) estimating a k value of 0.61 for UK Holstein-Friesians and Catillo *et al.* (2002) using a k value of 0.70 for average lactation curves in Italian river buffaloes. Furthermore, the strong predictive performance of the Wood and MilkBot models in Kwara and Adamawa States underscores their widespread application in dairy cattle management software (Wood, 1967; Ehrlich, 2011; Hostens *et al.*, 2012).

5.10 Model Fitting of FCM305dMY in Different Genotype x Environment Interactions in Dairy Cattle

The observed high adequacy of NN as the best model for predicting fat corrected 305 day milk yield using part period milk production (FCM100), milk components and conformation traits within genotype x environment interactions was consistent with the report of several authors (Schaeffer *et al.*, 2000; Jensen, 2001; Ferreira *et al.*, 2002). Sanzogni and Kerr (2001) compared qualitative properties of MLR and two different models of NN. The MLR model, depending on the region, was characterised by R^2 values ranging from 78 to 86 %. A classical NN showed lower R^2 values (0.74–0.82), while that with polynomial post-processing demonstrated higher values of R^2 (0.80–0.90), which was still lower than the range of 0.96 – 0.99 (NN) reported in this study. The NN models applied in the studies were of better predictive properties, mainly due to larger and more comprehensive datasets and more independent variables used for NN design. MLR proposed by other authors for predicting the first lactation milk yield demonstrated moderate ($R^2 = 0.64$; Pan *et al.*, 1997), or low R^2 values ($R^2 = 0.36$; Shive-Kumar *et al.*, 1995). Olori *et al.* (1999) analysed standard models for predicting some parameters of cow milk performance in a small herd. They obtained a very high R^2 (0.94 to 0.99) for the peak yield, whereas for the overall lactation yield, the coefficients were much lower: $R^2 = 0.66$. When the data were pooled within genotype x environmental interactions in Nigeria, all the models were excellent predictors of 305-day fat-corrected milk yield and the Genetic function algorithm was the best with three predictor variables and the lowest variance of estimation (RMSE and BIC). Perz and Sobek (1999) suggested, however, that the lowest variance of estimation error, rather than coefficient R^2 , should be taken into account as a criterion of the model performance. Linear regression models are simple in design and parameter interpretation. More simple models are less sensitive to fluctuations that appear in data; however, they do not fully reflect the real course

of lactation. This speaks for a wider testing of the models in practice (Perz and Sobek, 1999). On the other hand, predictions based on GFA and NNs as demonstrated in this study, do deviate from a classical MLR model either by their quality parameters or their predictive properties. New, additional data require a new statistical model, whereas a genetic function algorithm and neural network can undergo additional training.

The network architecture was optimized by selecting the best number of hidden layers and nodes per layer. Several models were analyzed with varying number of hidden layers and nodes per layer ranging from 1 to 20. Multilayer perceptrons (MLP; 6-2-1) with one hidden layer were shown to model the fat-corrected 305-day lactation milk yield resulting in the best accuracy. It has been demonstrated that at most, two hidden layers are sufficient to solve any problem accurately (Haykin, 2009). The best architectures in this study was closer to the best fitness for the three models which varied from [7-4-1] to [4-2-1] when test day records were used in dissecting the architectures of first lactation 305 day milk yield (Njubi *et al.*, 2010).

CHAPTER SIX

SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

6.1 Summary

A multilocational study was undertaken to investigate the milk yield, conformation and fertility traits among the multi-genotype cows in Nigeria.

The data from the study came from six different genotypes (Holstein Friesian, FriesianxBunaji, Jersey, JerseyxBunaji, Brown Swiss and Simmental) of cows in three different commercial farms (Shonga; Kwara State, West Africa Milk Company Integrated Dairies Limited; Plateau State and Sebore Farm; Adamawa State) in Nigeria.

Phenotypic data were collected from 2000 to 2015 in Plateau and Adamawa States while it was collected from 2008 to 2015 in Kwara State.

Quantitative and qualitative traits measured in this study included 305 days fat corrected milk yield, 305 milk yield per cow per day, 100 days fat corrected milk, fat yield, protein yield, and lactation length. Six milk production efficiency indices (FCM Kg W, FCM Kg MW, FCM/day/kgW, FCM/day/kgMW, net energy efficiency and dairy merit), four lactation traits (initial yield, IY; peak yield, PY; peak day, PD; last day yield, LDY), seven body traits (Bodyweight, BW; Body condition scores, BCS; stature, ST; chest width, CW; body depth, BD; heart girth, HG; rump width, RW), five udder traits (chest ligament, CL; rear udder height, RUH; rear udder width, RUW; udder clearance, UC; teat length, TL) and six fertility traits (age at first calving, AFC; calving interval, CI; day open, DO; number of services per conception, NSC; calving rate, CR; herd life, HL).

The interaction effects of genotype, breed improvement and year of calvings were also evaluated for fertility traits.

Multi-trait animal models were used to estimate the (co)variance components based on the average information restricted maximum likelihood method (AIREML) using R 3.0.3 software. The R 3.0.3 statistical software was used for basic descriptives and regression analyses while MATLAB (2015) was used for the computational modeling of the data.

The average milk production characteristics were 2496.4 kg, 7.2 kg/day, 1549.2 kg, 63.3 kg, 58.7 kg, 12.5 g/100g, 344.9 days, 4.8 kg FCM kg W, 22.7 kg FCM kg MW, 0.02 kg dayFCM kg W, 0.07 kg day FCM MW, 42.4 % and 61.8 % for 305-day fat corrected milk yield, 305milk yield per cows per day, 100-day fat corrected milk, fat yield, protein yield, lactation length, FCM Kg W, FCM Kg MW, FCM/day/kgW, FCM/day/kgMW, net energy efficiency and dairy merit, respectively.

Jersey cows had optimal performance with higher milk yield and components in Shonga Dairy Holdings which was significantly above other genetic groups while Holstein cows had strong dairy strength for milk volume and components in Integrated Dairy Limited; Plateau and Sebare; farm in Adamawa States.

Body and udder conformation traits in the populations of cows studied were 517.3 kg, 3.3, 4.3 cm, 23.1cm, 210.5 cm, 150 cm, 13.09 cm, 201.7 cm, 42.6 cm, 35.7 cm, 13.9 cm and 5.06 cm for bodyweight, body condition score, chest ligament, chest width, body depth, stature, rump, heart girth, udder clearance, rear udder height, rear udder width and teat length, respectively.

Fertility results indicated an important advantage of the interactions between genotype, breed improvement and year of calvings.

It was evident that the udder of the purebred cows (Holstein Friesian, Jersey, Brown Swiss and Simmental) were too deep to milk conveniently or to avoid injury and mastitis. Special attention must be paid to udder depth and teat placement in choosing Holstein Friesian, Jersey, Brown Swiss and Simmental for crossbreeding programs.

The 305 days corrected milk yield and milk components were moderate to highly heritable and repeatable across the six genetic groups in the three locations except for lactation length which had low to moderate heritability and repeatability estimates. However, heritability and repeatability estimates for conformation traits were low to high while low to moderate estimates were obtained for fertility traits.

Holstein Friesian cows in Kwara and Plateau States for age at first calvings, FriesianxBunaji cows in Plateau State for age at first calvings and calving intervals and Jersey cows in Adamawa State for number of services per conception had a moderate heritability and repeatability which indicate that these traits can be improved genetically through selection.

Genotypic and environmental correlations amongst 305 days fat corrected milk yield, milk components, conformation and reproductive traits varied widely in magnitude and direction.

Holstein Friesian cows in Plateau and Adamawa States and Jersey cows in Adamawa and Kwara States in first lactation had moderate to high accuracy for estimating the true breeding value with higher genetic gains in fat corrected 305 days milk yield while Holstein Friesian and Brown Swiss showed high genetic merit for extending the lactation length and reducing the days open in the first and pooled lactations.

Best linear unbiased estimation and Wright method of estimating inbreeding depression at 1% increase in inbreeding were similar for both milk and fertility traits; though the severity of

inbreeding depression was greater in 305 days fat corrected milk yield, especially in Jersey cows in Kwara State and Holstein Friesian cows in Plateau State.

The average yield characteristics in the three production environments (Kwara, Plateau and Adamawa States) were 6.5 kg, 8.7 kg, 62.6 kg, 3.2 kg and 2503.3 kg; 8.6 kg, 13.1 kg, 62.7 kg, 4.2 kg and 4551.3 kg; 4.8 kg, 7.5 kg, 62.4 kg, 2.7 kg and 2051 kg, respectively for initial yield, peak yield, peak time, last day yield and total yield.

All the lactation models (Wood, Wilmink, Djisktra, MilkBot, and Neural Network) had the best accuracy in reconstructing the ascending, peak and descending phases of lactation across the genetic groups in different climatic gradients except the Wilmink model having atypical curves in FriesianxBunaji (62 %) cows in Kwara State and Djisktra model for Holstein Friesian (56 %) cows in Adamawa State.

Neural Network models consistently had the best accuracy in predicting 305-day fat-corrected milk yield across the genotypes within different climatic gradients. However, the Genetic function algorithm was best for the overall prediction ($FCM_{305d}=1036.1-98.3RP+22FY+15.92UC-0.07RUH$; Adj $R^2=0.997$; RMSE=30.07; BIC=1997.28) with the least predictor variables (rump, udder clearance, fat yield and rear udder height).

6.2 Conclusion

The following conclusions are drawn from this study:

1. The most efficient and economical model for predicting fat corrected 305-day milk yield was the Genetic Function Algorithm ($FCM_{305d}=1036.1-98.3RP+22FY+15.92UC-0.07RUH$; Adj $R^2=0.997$; RMSE=30.07; BIC=1997.28) in Nigeria dairy herd. Artificial Neural Network model had the best prediction accuracy across varying environments.

The best neural network architecture for modeling 305 day fat corrected milk yield in developing milk calculator was 6-2-1 hidden nodes in the multilayer perceptron using back propagation algorithm with 88 % learning rate and 2 % bias.

2. Holstein Friesian cows showed the strongest dairy merit for milk production in Plateau and Adamawa States while in Kwara State, Jersey cows were the best. Multi-genotype cows showed a good variation for milk, conformation and fertility traits thus these traits can be used as candidate markers for selection to develop direct lines for this trait and other correlated traits.
3. Moderate to high heritability ($h^2 = 21$ to 44 %) for 305 day fat corrected milk yield suggests that milk yield can be changed at a rapid rate by selection.
4. The repeatability estimate for 305 day fat corrected milk yield is moderate to high ($W^2 = 27$ to 61 %) and can be employed early in lactation to select cows with potentials for higher milk yield.
5. The genetic relationship between 305 days fat corrected milk yield, milk components, conformation and fertility traits in multi-genotype cows were less than unity indicated that milk components, conformation and fertility traits could be used to enhance the accuracy of genetic evaluation for milk yield.
6. The moderate to high accuracy (30-50 %) for estimated breeding value for milk yield in Holstein Friesian cows in Plateau and Adamawa States and Jersey cows in Adamawa and Kwara States in the first lactation suggests that selection for milk yield in first lactation will be more efficient.

7. Inbreeding effect showed high severity in Holstein Friesian cows in Plateau State (BLUE -350.2kg and Wright -381.4kg) and Jersey cows (BLUE -419.6kg and Wright -422.1kg) in Kwara State suggest that inbreeding has reached levels that are detrimental to milk production.
8. The pattern of lactation was parsimonious and adequately reconstructed by all the models (Adj $R^2 = 0.74-0.98$) across environments except Wilmink (Adj $R^2=0.62$) for FriesianxBunaji cows in Kwara States and Djisktra (Adj $R^2=0.56$) for Holstein Friesian cows in Adamawa State with atypical lactation curves. MilkBot model was best in Holstein Friesian cows in Adamawa and Kwara States while Wilmink model had the best predictive capability for Brown Swiss cows in Adamawa State.

6.3 Recommendation

1. The use of Jersey breed in Kwara State and Holstein Friesian breed in Plateau and Adamawa States is recommended as the best option for dairy production in these agro ecological zones. The outstanding performance of Holstein cows for dairy merit ($66.9\pm 0.78\%$) in Nigeria make them suitable candidate for genetic improvement of our local cattle genetic resources for milk yield. However, economic research would be needed to observe on the long-run which is the most profitable breed for each agro-ecological zones.
2. Direct selection for 305 days fat corrected milk yield could lead to genetic progress, which could be relatively fast due to the moderate to high heritability. Traits related to milk production, fertility and conformation in this study should be included in breeding programmes of dairy cattle in Nigeria, in order to maximize improvement of breeding goal involving traits related to income and costs.

3. It is also recommended that Neural Network models will be appropriate in describing the milk production pattern and prediction of 305 day fat corrected milk yield under different climatic gradients in Nigeria. Genetic function algorithm promises to be a veritable and added tool for milk yield prediction under a large scale evaluation.

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APPENDICES

Appendix



Plate I: Holstein cows in Integrated Dairies Limited, Plateau State



Plate II: Holstein and Jersey cows in the milking parlour in Shonga Dairy Holdings, Kwara State



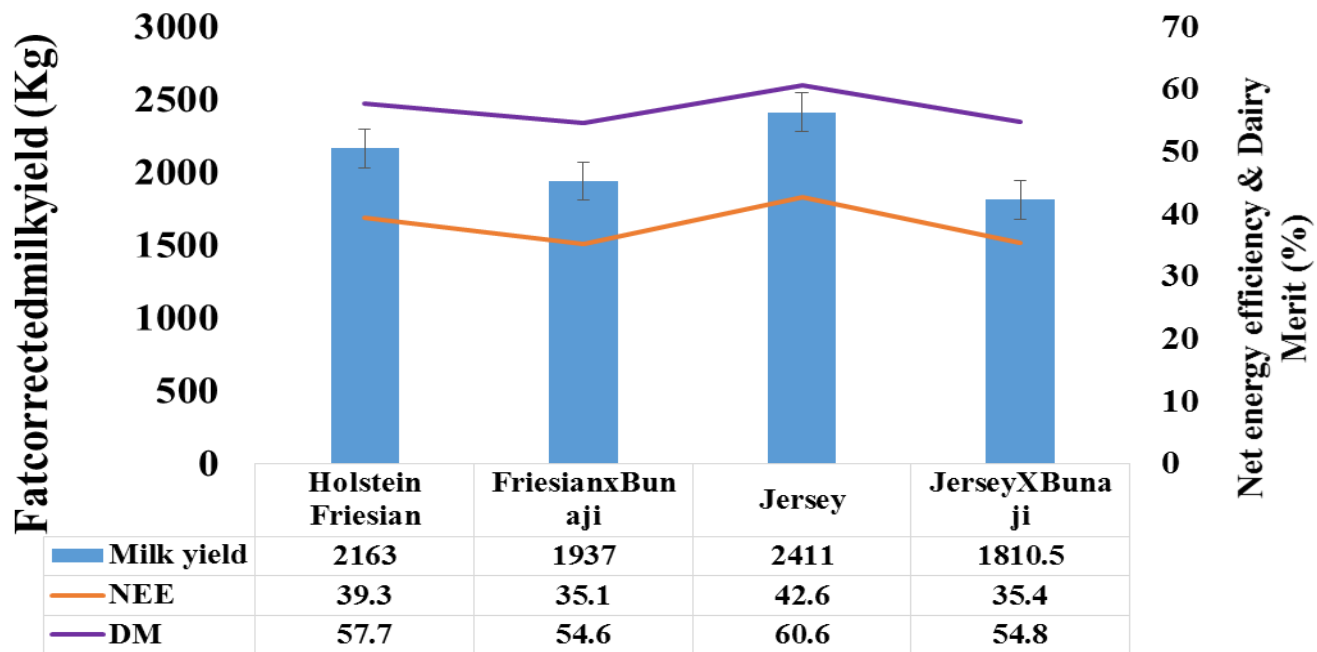
Plate III: Simmental cows in the Freestall in Sebore Farm Adamawa State



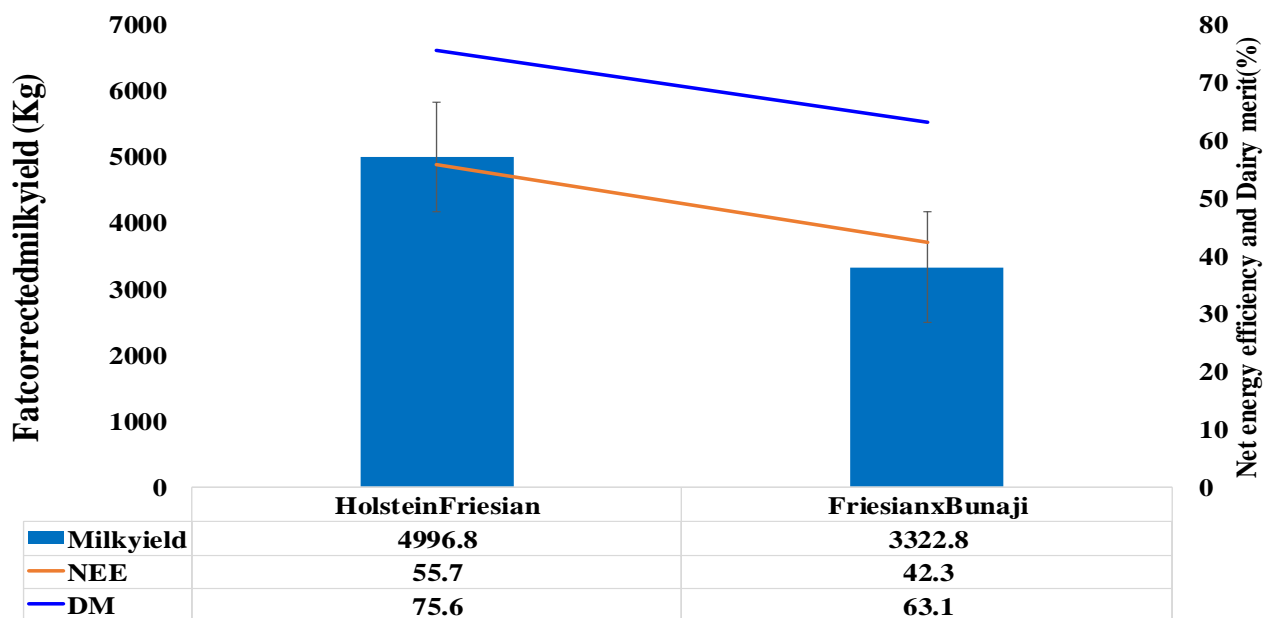
Plate IV: Holstein cows in the Freestall in Sebore Farm Adamawa State



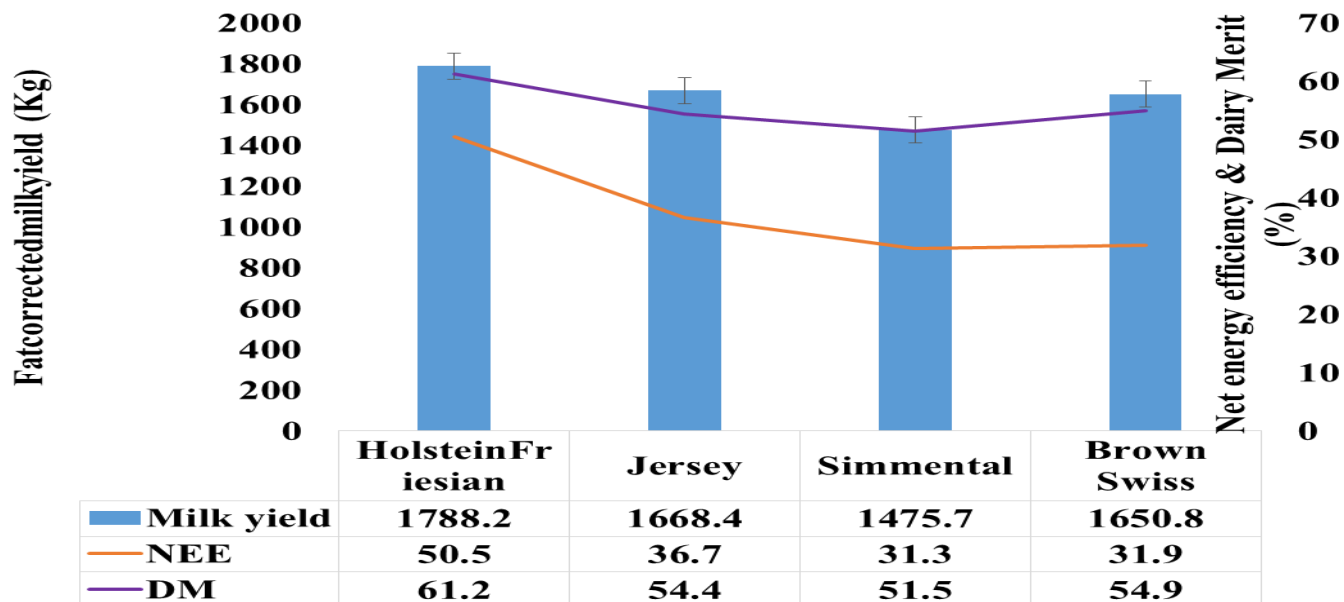
Plate V: Brown Swiss cows in the Freestall in Sebore Farm Adamawa State



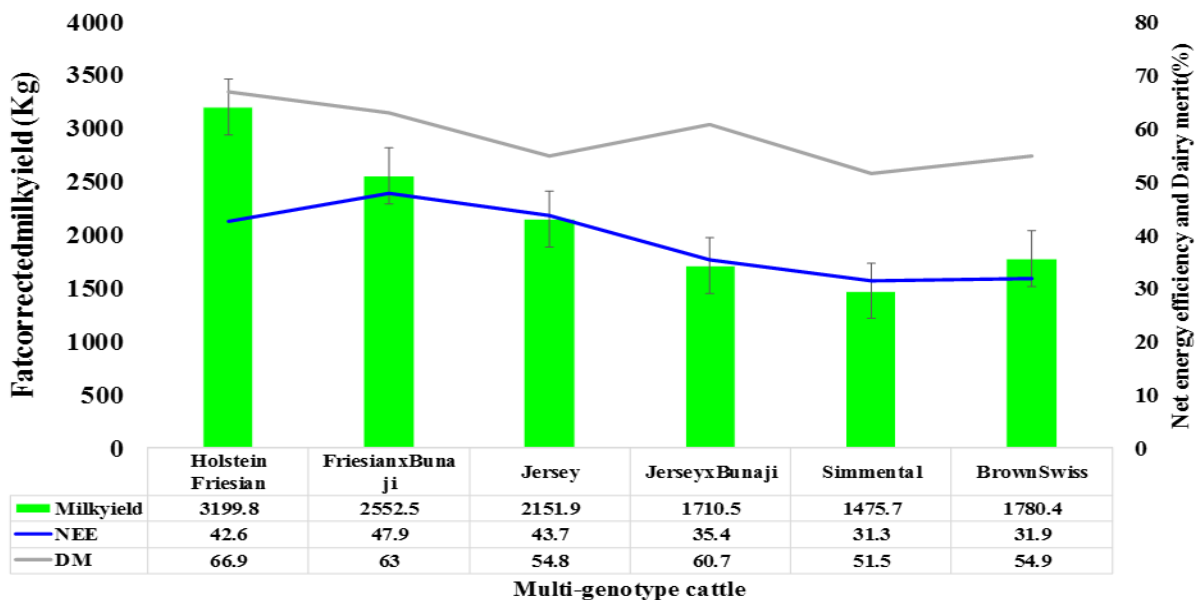
Appendix I: Multi-genotype cows in Kwara-State



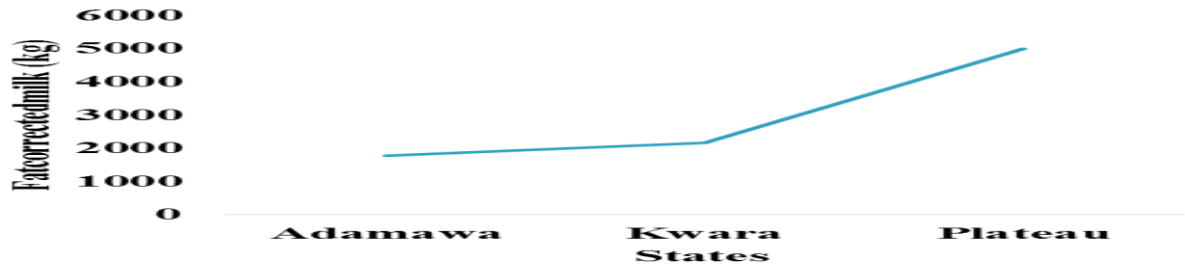
Appendix II: Multi-genotype cows in Plateau State



Appendix III: Multi-genotype cows in Adamawa-State



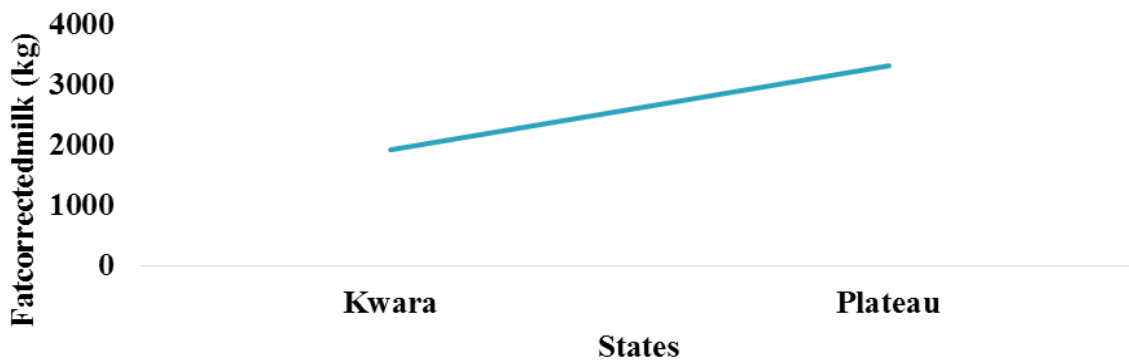
Appendix IV: Multi-genotype cows in Adamawa-State



Appendix V: Genotype x Environment interactions for fatcorrected milkyield in HolsteinFriesian cows



Appendix VI: Genotype x Environment interactions for fatcorrected milkyield in Jersey cows



Appendix VII: Genotype x Environment interactions for fatcorrected milkyield in FriesianxBunaji cows