# GENETIC EVALUATION OF TRYPANOTOLERANT N`DAMA CATTLE UNDER AN OPEN NUCLEUS BREEDING PROGRAMME IN THE GAMBIA

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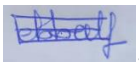
## DECLARATION AND RECOMMENDATION

**Declaration**

This thesis is my original work and has not been presented in this university or any other for the award of a degree.

Signature: ……  ……. Date: 26th October 2024……..

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## DEDICATION

This work is dedicated to my beloved wife, Kumba Ceesay, my son, Muhammed Lamin Nyabally, my daughter, Maimuna Nyabally, and my guardians, Sheriff Muhammed Lamin Hydara and Halimatou Hydara.

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## ABSTRACT

The N'Dama cattle breed is adapted to survive in tsetse-infested areas and to thrive on poor-quality feeds in West Africa. Despite the importance of the N'Dama cattle in the Gambia, genetic parameters such as heritability estimates, genetic correlations and response to selection for traits in the breeding goal have not been estimated. Therefore, this study aimed to estimate genetic parameters and correlations between growth traits and packed cell volume (PCV), test day milk yield, early growth and fertility traits, and to explore the use of principal component analysis (PCA) to predict multiple trait response to selection for alternative selection indexes of the traits in the breeding goal for N'Dama cattle in the Gambia. Genetic parameters were estimated from univariate and bivariate analyses using the Bayesian procedure implemented in Gibbs sampling in the GIBBS1F90 software. The heritability estimates for body weight at birth, 12 months, 16 months, 24 months, 36 months and 50 months were estimated as 0.30±0.04, 0.51±0.06, 0.47±0.05, 0.39±0.05, 0.36±0.05, 0.22±0.07, 0.31±0.06 and 0.31±0.06, respectively. The respective heritability estimates for PCV were 0.15±0.01, 0.10±0.01, 0.09±0.01, 0.12±0.01, and 0.14±0.3. Genetic correlations between body weight and PCV range from negative and low (-0.14±0.02) to positive and medium (0.59±0.02). The highest genetic correlations were reported for WT18 and PCV18 (0.59±0.02). Direct heritability estimates for BW, WWT, Pre-ADG, Post-ADG, AFC and CI were 0.44±0.04, 0.48±0.03, 0.42±0.03, 0.38±0.03, 0.39±0.01 and 0.14±0.01, respectively, while maternal heritability estimates for BW, WWT and ADG were 0.13±0.03, 0.00±0.00, and 0.19±0.01, respectively. Test-day milk yield had high and positive genetic correlations with early growth traits and CI, ranging from 0.51 to 0.88. The correlation between CI and AFC was 0.80±0.03. CI had negative correlations with early growth traits (-0.01±0.04 to -0.97±0.02). The first three principal components (PC) were associated with eigenvalues greater than 1 and cumulatively explained 70% of the total variation. The expected genetic progress for $MY_{100}$, pre-ADG, post-ADG, and PCV were positive for the three PCIs as well as CSI. The expected genetic progress for $MY_{100}$, pre-ADG, post-ADG, and PCV for all SIs ranged from 1.76kg to 4.05kg, 0.01kg to 1.71kg, 0.00 kg to 0.90kg, 0.11% to 0.55%, respectively. CI and AFC reduced by -0.57 to -1.56 months and -0.23 to -1.60 months, respectively. SIPC1 resulted in favourable responses in $MY_{100}$, CI, AFC, pre-weaning and post-weaning growth rates and PCV and also had the highest overall response. Genetic improvement of pre-ADG, Post-ADG and TDMY in the N'Dama cattle breeding programme is expected to result in precocious AFC and increased CI. Therefore, a multiple trait selection index based on the first principal component (SIPC1) would lead to favourable genetic response in all breeding goal traits.

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| | |
|---|---|
| AAT | African Animal Trypanosomiasis |
| ADG | Average Daily Gain |
| AG | Additive Genetic |
| AFC | Age at First Calving |
| BLUP | Best Linear Unbiased Prediction |
| CBPP | Contagious Bovine Pleuro Pneumonia |
| CI | Calving Interval |
| CSI | Conventional Selection Index |
| DIM | Days in Milk |
| DLS | Department of Livestock Services of The Gambia |
| FAO | Food and Agriculture Organization of the United Nations |
| ILCA | International Livestock Centre for Africa |
| ITC | International Trypanotolerant Centre |
| NLS | National Livestock Census The Gambia |
| NARS | National Agricultural Research System |
| ONBS | Open Nucleus Breeding Scheme |
| PCA | Principal Component Analysis |
| PCS | Principal Component Score |
| PCV | Packed Cell Volume |
| PE | Permanent Environment |
| RRC | Random Regression Coefficient |
| SEBV | Standardized Estimated Breeding Value |
| SSC | Standardized Score Coefficient |
| TDMY | Test Day Milk Yield |
| UNEP | United Nations Environmental Programme |
| WALIC | West African Livestock Innovation Centre |
| WWT | Weaning Weight |

# CHAPTER ONE
# INTRODUCTION

## 1.1 Background Information

Livestock must possess both resistance and tolerance to infectious diseases to mitigate the potential harm that infections may cause to animal health and productivity. Disease tolerance is the capacity to lessen the influence of infections on host function without necessarily decreasing pathogen load (Martins *et al.,* 2019). In contrast, host resistance is the capacity to limit pathogen reproduction in its widest definition (Doeschl-Wilson *et al.,* 2021). Because of this special quality, disease tolerance is positioned as an interesting alternative breeding goal trait for livestock production, offering a way to improve animal populations' resistance to infections without directly impacting the dynamics of evolving pathogen resistance. Since disease tolerance emphasizes the host's capacity to withstand the consequences of infection rather than the pathogens' complete elimination, it presents a fresh and potentially long-lasting solution to the problems associated with infectious diseases in the context of livestock production (Shourian & Qureshi, 2019).

The N`Dama cattle breed (*Bos taurus*) is endemic in the Gambia and remains a valuable breed due to its adaptive traits such as trypanotolerance, drought tolerance, and good traction ability. A country that lies within the tsetse belt of the African region and practices mixed production farming systems, N`Dama cattle is the most widely used breed by farmers due to its tolerance to trypanosomiasis disease (Olaniyan *et al.,* 2021, Olaniyan, 2015). Furthermore, this multi-disease-resistant N`Dama cattle has been recommended for low-input traditional African farming systems in areas where trypanosomiasis, ticks, and tick-borne diseases are constraints to livestock production (Janssen-Tapken, 2009). Having been recognized for its adaptive qualities and importance to many households, attempts have been made to improve its productivity. These attempts focused on designing a breeding programme for its genetic improvement. In 1994 a genetic improvement programme was designed and implemented at the International Trypanotolerance Centre (ITC) now the West African Livestock Innovation Centre (WALIC) in The Gambia. The objective of this programme was to genetically improve the production of milk and meat of the N'Dama cattle breed to meet the current and future market demands without loss of its adaptive traits. The programme operates as an open nucleus breeding scheme comprising a well-recorded herd of about 400 breeding females in the nucleus at any given time (Bosso *et al.,* 2009). A genetic evaluation procedure and strategies for the dissemination of improved genetic material in the population were put in place (Ouédraogo *et al.,* 2021). While the breeding programme has been evaluated, the genetic progress realized so

far has been limited. Genetic evaluation of breeding programmes is important as it helps monitor genetic gains achieved in breeding programmes over time for informed decision-making.

## 1.2 Statement of the Problem

Despite the significant contribution of the N'Dama breed towards beef and milk production, the overall performance of the breed within the breeding programme has not been well evaluated. Numerous studies have evaluated the breed's performance and estimated genetic parameters for growth traits, reporting high heritability estimates and strong genetic correlations among these traits. However, there is a lack of heritability estimates for other breeding objective traits such as milk yield and their genetic correlation with trypanotolerance as measured using packed cell volume (PCV). This limits the evaluation of the overall success of the N'Dama cattle breeding programme in relation to the original aim of improving growth and milk yield in the presence of natural trypanosome infection.

## 1.3 Overall Objective

The overall objective of this study was to estimate heritability, genetic correlations, and the development of an optimal multiple trait selection index to predict response to selection for growth, milk yield, trypanotolerance, and fertility traits of N'Dama cattle in an open nucleus breeding programme in the Gambia.

### 1.3.1 Specific Objectives

i. To estimate heritability and genetic correlation between growth rates and packed cell volume (PCV) along the growth curve of N`Dama cattle in The Gambia.
ii. To estimate genetic correlations between test day milk yield, early growth and fertility traits of the N'Dama cattle in The Gambia.
iii. To predict multiple trait response to selection of alternative selection indexes for growth, milk yield, trypanotolerance, and fertility traits for N'Dama cattle in the Gambia.

### 1.3.2 Research Questions

i. What are the heritability estimates and genetic correlations between body weight and trypanotolerance (PCV) along the growth curve of N'Dama cattle in The Gambia?
ii. What are the genetic correlations between test day milk yields, early growth, and fertility traits for N'Dama cattle in The Gambia?

iii. What are the predicted multiple trait responses to selection of alternative selection indexes for growth, milk yield, trypanotolerance, and fertility traits in N'Dama cattle in the Gambia?

### 1.4 Justification

Estimating heritability for growth traits, milk yield, packed cell volume (PCV), and fertility and their genetic correlations provided a basis for determining the extent to which the traits can be improved through selection. For body weight and PCVs, the magnitude of heritability estimates along the growth curve enabled the determination of the age at which selection should be carried out to accelerate the rate of gain and avoid lengthening of generation interval. The genetic correlations between the traits enabled the identification of the traits to develop a weighted multiple-trait selection index to ensure a balanced genetic improvement in the traits of interest. The use of principal component analysis (PCA) to develop a weighted multiple trait selection index provided an objective strategy to weigh the traits in the breeding goal and the optimization of genetic response.

# CHAPTER TWO
# LITERATURE REVIEW

## 2.1 A Description of the N`Dama Cattle Breed

The N'Dama cattle have short, fine-boned legs that are compact and well-muscled in the neck and back, straight from the withers to the tail head (Mwai *et al.,* 2015). The dewlap and umbilical folds are well developed; the typical coat colour is fawn with darker extremities and a lighter underside; common solid colours are light (Plate 2.1) to dark fawn, grey, and dun; the average horn size is about 60 cm; the horns typically curve upward and outward or have a lyre-shape; and occasionally, there are individuals with polls, especially in Sierra Leone and Guinea (Fasae *et al.,* 2010). The breed has a broad and strong head and is of medium size, standing 100 cm at the shoulder for cows and 120 cm for bulls. Plate 2.1 presents a picture of the N`Dama cattle breed.

**Plate 2.1:** Picture of selected N'Dama cattle breeding bulls for dissemination in the Gambia
**Source:** Secka *et al.* (2022)

### 2.1.1 N`Dama Cattle Origin and Distribution

The N'Dama also known as Boenca, Boyenca, and Fouta, is a humpless breed of longhorn *Bos taurus* cattle (Udeh, 2021). Until recently, it was believed that the Humpless (*Bos taurus*) and Hametic Longhorn cattle breeds descended from the earliest domesticated populations of the animal in the region's "Fertile Crescent," most likely in Asia around 9000 BC (Fasae *et al.,* 2010). These cattle were the first to be introduced to Africa from Asia by

nomadic tribes, and they have since migrated to the west and south of Egypt. The Sahara, which stretches from southern Libya and north-western Niger to southern Egypt, is thought to have been an African centre of domestication, according to a unique theory based on archaeological findings (Grigson *et al.,* 2000).

Additional genetic studies have shown that separate domestication may have occurred in Africa because of the current humpless cattle groups' extreme genetic divergence from related European cattle populations (Bradley *et al.,* 2000). The genetic evidence, which showed a tiny but exogenous genetic effect of non-African origin from Europe and/or the Near East in the breeds of north and north-eastern Africa as well as localized areas of southern Africa, supports this assertion. Additionally, the modest genetic introgression of Asian zebu cattle (*Bos indicus*) had an impact on these African taurine cattle. There are now strong genetic and historical indications that these African taurine cattle breeds were domesticated in Africa (Hanotte *et al.,* 2002; Stock & Gifford-Gonzalez, 2013). There are two breeds of humpless longhorn cattle: the N'Dama and the Kuri, both of which have somewhat different morphologies (Mwai *et al.,* 2015).

The Fouta Djallon plateau in Guinea is thought to have been the original home of N'Dama cattle, which are now widespread throughout coastal West and Central Africa, particularly in tsetse fly-infested areas like Senegal, The Gambia, Guinea-Bissau, Guinea, Sierra Leone, Cote d'Ivoire, western Mali, Ghana, Togo, Nigeria, Cameroon, Central African Republic, Gabon, Congo (Brazzaville), and Democratic Republic of Congo (formerly Zaire) (DAGRIS, 2007; Ozoje, 2018).

### 2.1.2 Peculiarity of the N`Dama Breed

The N'Dama cattle breed is renowned for its natural resistance to helminths (Bahta *et al.,* 2023), resistance to dermatophylosis, heart-water, anaplasmosis, and babesiosis (Murray *et al.,* 1991) as well as its tolerance to trypanosomiasis (Agyemang, 2005; Murray *et al.,* 1991). In comparison to other breeds, they are more resistant to heat, drought, and a lack of feed because of their physiological adaption to adverse climatic conditions. The breed has notable resistance to tick-borne infections as well (Haikukutu, 2018) but not to Rinderpest. The breed also adapts well to challenging humid and arid tropical regions. N'Dama cattle are typically raised in substandard habitats with traditional management practices; in these conditions, their capacity for survival and productivity are crucial. Compared to other African beef breeds, they are more productive and respond well to better management, better pastures, and lower trypanosomiasis risk (Ravel *et al.,* 2015).

### 2.1.3 Status of the N'Dama Breed in Africa

The population of N'Dama cattle has been estimated at 6,618,713 heads spread both in West and Central African countries. A private company called Compagne J. Van Lanckeic, which has over 40,000 pure N'Dama cattle, has been working to improve large-scale herds of this breed in Zaire for the past 65 years (Fasae *et al.,* 2010). This breed mature weight has increased by 30 to 50 kg without compromising its adaptation abilities. In Guinea, commercial herds are also kept, and large herds are raised solely for meat under ranching conditions (Molina-Flores *et al.,* 2020). Since 1955, the breed has been developed and crossed with Jersey in Côte d'Ivoire; it has also been crossed with the Sokoto Gudali in Ghana; and, following its arrival in 1923, it has been crossed with the West African Shorthorn in Togo. Some N'Dama were transferred from Senegal to the Virgin Islands in 1986, where they were crossed with Red Poll to create the Senepol breed (Wilson, 2018).

## 2.2 The Main Breeds of Cattle and Their Characteristics

Africa with its rapidly increasing human population is faced with the challenge of satisfying a dramatic increase in demand for livestock products, particularly milk and meat (Yitbarek & Berhane, 2014). In 1963 the annual loss in meat production alone was estimated at US $5 billion (Agyemang, 1997). Losses such as in milk and manure production and attractive power could be prevented, and the benefit from livestock and mixed agricultural development in tsetse-infested Africa could amount to US $50 billion annually, and with the paucity of reliable data, even this figure could be an underestimate (Agyemang, 2005; Murray *et al.,* 1991). It has been estimated that about 37% of the continent, 11 million $km^2$ involving 40 countries is infested with tsetse (Denbarga *et al.,* 2012), and that approximately 65% of this area (7 million $km^2$) could be used for livestock or mixed agricultural development without stress to the environment if trypanosomiasis was controlled (Marta *et al.,* 2016).

Trypanosomiasis is argued to be the single most important constraint to animal agriculture in the sub-humid and non-forested portions of the humid zone of Africa. The disease has both direct and indirect economic impacts on livestock production (Bosso, 2006; Mekonnen *et al.,* 2017). The direct impacts are associated with losses in milk and meat production as well as mortality and morbidity (Agyemang *et al.,* 1997; Dumesa & Demessie, 2015). The indirect impact is related to the opportunity cost of land and other resources currently not used for livestock production owing to the presence of tsetse flies.

Trypanosomiasis control relies on trypanocidal drugs, vector control, and trypanotolerant livestock farming (Agyemang, 2005; Yaro *et al.,* 2016). Each of these options

suffers shortcomings. Resistance in trypanosomes to the available trypanocides is constant and, in some areas, increasing threat. Drugs are not readily available and their purchase consumes valuable foreign exchange. Considerable advances have been made in recent years developing new insecticides and melliods for their application and with trap and target technology for vector control (Chitanga *et al.,* 2011; Torr & Vale, 2015). Undoubtedly, these approaches hold great promise. However, they require continuous commitment, and when control programmes are relaxed the tsetse fly vectors recolonize previously cleared areas very rapidly (Agyemang, 1997). In the case of trypanotolerant breeds of cattle, availability is limited and they amount to only 17% of the total cattle population in the affected areas (Agyemang, 1997). Improvement and wider dissemination of trypanotolerant animals are needed if the genetic approach to control is to have a greater impact in the foreseeable future (Agyemang, 2005).

Although the trypanotolerance of N`Dama has long been recognized, and indeed experimental studies comparing N`Dama and zebu breeds have confirmed these assertions (Ilori *et al.,* 2019), these breeds represent only 6% of the cattle production in Africa. It has been postulated that the small number of these animals in Africa, despite their unique ability to withstand trypanosomiasis and possibly other parasitic infections too (Dicko *et al.,* 2015), is due in part to the widely held belief that they are not productive because of their relatively small size. This belief was disputed and shown to be incorrect following a survey conducted by the International Livestock Centre for Africa (ILCA), the Food and Agriculture Organisation (FAO), and the United Nations Environmental Programme (UNEP) of trypanotolerant livestock in 18 western and central African countries (Rege & Lipner, 1992). The study compared the productivity of different breeds based on body weight, calving rate, and mortality, and found that in the areas where tsetse fly risk was low, the productivity of N`Dama and West African shorthorn cattle was only marginally below that of zebu (Voh *et al.,* 2004). A similar comparison in areas of medium to high tsetse challenge was not possible because only trypanotolerant livestock was present.

### 2.2.1 Situation of N`Dama Cattle Genetic Resources in The Gambia

The vast majority (98%) of The Gambia's (286, 220 heads) cattle are categorized as being of the N'Dama breed. Zebus, "Gobras," (crosses of N'Dama and Zebu cattle), and crossbred N'Dama cattle with Jersey, Holstein-Friesian, and other European breeds make up the remaining 2% (Table 2.1) of the total cattle population. The National Livestock Census 2017 data revealed that 286, 220 (97.7%) of the 292, 837 head total of cattle are of the N'Dama breed (Bahta *et al.,* 2023). In contrast, Zebu/Gobra and other breeds make up about 1.4% of

the population (i.e. 4,083 heads). Draught cattle (35,209 heads) make up 12% of the total cattle population and provide the majority of agriculture activities with the draught power needs in The Gambia (Bahta *et al.,* 2023).

**Table 2.1:** Cattle numbers by breed and region in the Gambia

| Region | Cattle Breeds | | | Draught Cattle | | Total |
|---|---|---|---|---|---|---|
| | N'Dama | Zebu | Other | N'Dama | Zebu | |
| KMC | 5 | 0 | 0 | 0 | 0 | 5 |
| WCR | 33111 | 447 | 190 | 3778 | 117 | 37643 |
| LRR | 23640 | 994 | 2 | 1628 | 107 | 26371 |
| NBR | 52165 | 773 | 7 | 10812 | 726 | 64483 |
| CRR/N | 38753 | 405 | 11 | 4644 | 728 | 44541 |
| CRR/S | 34869 | 252 | 2 | 8299 | 789 | 44211 |
| URR | 71002 | 885 | 115 | 3514 | 67 | 75211 |
| Gambia | 253545 | 3756 | 327 | 32675 | 2534 | 292837 |
| (%) | 86.6 | 1.3 | 0.1 | 11.1 | 0.9 | 100 |

Kanifing Municipal Council (KMC), West Coast Region (WCR), Lower River Region (LRR), North Bank Region (NBR), Northern Central River Region (CRR/N), Southern Central River Region (CRR/S) and Upper River Region (URR).

**Source**: Bahta *et al.* (2023)

### 2.2.2 N'Dama Cattle Productive and Reproductive Performance

The Gambia is home to roughly 300,000 cattle and a comparable number of small ruminants (Agyemang *et al.,* 1997). In the sub-region, The Gambia is the nation with the highest concentration of N'Dama cattle managed by small-holder farmers. These cattle are also exposed to a variety of tsetse threat areas across the nation. Numerous authors have emphasized the significance of the N'Dama in areas where tsetse flies are an extremely serious problem. It is amazing how they manage to nurture a calf to maturity while dealing with severe trypanosome infection and tsetse disease, all while providing milk and revenue for their families (Agyemang *et al.,* 1997; Bosso *et al.,* 2009).

There is a wide range of information on the number of milking animals and the volume of milk produced. According to FAO data, The Gambia had approximately 54,000 lactating cattle in total, which generated 75,869 tons of milk in 2018 (Table 2.2). In contrast, data from the 2016 national livestock census show that there are 44,385 lactating N'Dama cows in the

nation, and they produce 20.3 million litres of milk annually, worth GMD1.02 million, of which 52% is consumed at home and the balance is sold (Bahta *et al.*, 2022; Loum, 2019). However, FAO data seem to assume a higher level of productivity (3.8 litres of milk per cow per day compared to the 1.5 litres used in the census data) compared to the documented level in literature (Jaitner *et al.*, 2003). This is even though the number of milking cows during the census may have been lower due to the death and sale of animals during the 2012-2013 Contagious Bovine Pleuro Pneumonia (CBPP) outbreak. Using FAO statistics for the number of milking cows and assuming an average milk yield of 1.5 litres per cow per day, as was the case during the census (Rich *et al.*, 2020).

**Table 2.2:** Number of milking cows and quantity of milk produced in the Gambia

| Year | Milk animals | Annual growth rate | Milk quantity produced | Annual growth rate |
|---|---|---|---|---|
| 2010 | 50,871 | | 70,586 | |
| 2011 | 53,500 | 5.2 | 74,250 | 5.19 |
| 2012 | 54,000 | 0.9 | 74,956 | 0.95 |
| 2013 | 54,000 | 0.0 | 74,968 | 0.02 |
| 2014 | 55,792 | 3.3 | 77,625 | 3.54 |
| 2015 | 57,503 | 3.1 | 80,051 | 3.13 |
| 2016 | 53,642 | -6.7 | 74,598 | -6.81 |
| 2017 | 54,175 | 1.0 | 75,356 | 1.02 |
| 2018 | 54,534 | 0.7 | 75,869 | 0.68 |

**Source:** FAOSTAT, 2019

Beef conformation is a trademark of N'Dama cattle. In two locations with high and low trypanosomiasis risk, the average birth weight was 19 and 22 kg, respectively (Yunus, 2016), while the average body weight of cows in the two areas was 296 and 331 kg. The average adult weights for males and females are 250 - 270 kg and 320 - 360 kg, respectively. The meat has a really good flavour and lean, and the dressing ratio is about 50%. (Pesonen, 2020). Although partial milking is often practised in the traditional herds of West Africa, the N'Dama is a multipurpose breed with a relatively low milk yield (Rege, 2001). In these conditions, the yield of milk for human use (milk offtake) is often estimated at 70 - 100 kg per cow per year, with Mali reporting a greater output of 178 kg/year (Bessong, 2016). The estimated whole lactation production is between 500 and 600 kg (Rege, 2001). The ox is a useful animal for traction. Heifers typically give calves down at 48 months of age (Table 2.3), and there is an average 20-

month gap between calves under the conventional system. The heifers calve at 35 to 42 months under ranching circumstances including grazing, salt licking, mineral supplementation, and dipping (Agyemang, 1997; Bayemi *et al.,* 2005).

**Table 2.3:** Reproductive performance of village N`Dama cattle

| **Parameters** | **Value** |
|---|---|
| Age at first calving | 3.5 - 4 years |
| Average calving rate | 47 to 52% |
| Calving interval | 23 to 25 months |
| Number of calving per cow | 5 |
| Age at first slaughter for bulls | 3 – 4 years |
| Weight at slaughter (bulls) | 300 kg |
| Weight at slaughter (cows) | 250 kg |
| Mean live weight of dry female cows | 225kg (s.d 29) |
| Mean live weight of lactating cows | 207kg (s.d 27.8) |

**Source:** Santoze and Gicheha (2019)

Land preparation, crop cultivation, and agricultural transportation all involve the use of draught oxen. The fields where grain and fruit trees are grown are fertilized with cow manure and the droppings of small ruminants. Following harvest, farmers collect and store some crop residues, primarily groundnut hay, for feeding oxen while leaving other residues on the field for cattle to graze (Powell *et al.,* 2004).

### 2.2.3 N'Dama Cattle Management Systems in The Gambia

There are two management systems under which N'Dama cattle are kept. Firstly, the owners of the herd, who are primarily of the Mandinka ethnic group, do not have daily control over the management of their cattle, and the herdsmen, who are primarily of the Fula ethnic group, manage the herds in exchange for milk as full or partial payment (Jaitner *et al.,* 2003), these herds are milked twice daily. In the second management system, the typical members of the Fula ethnic group manage their herds. The herds owned and managed by the same Fula people are milked either once or twice daily for domestic consumption. Different regions of

the country employ both once-daily and twice-daily milking systems. The owners live in family compounds and maintain their livestock in herds with those of other owners (Rowlings *et al.,* 1995). In addition, there could be a few oxen in each compound. During the rainy season, the oxen remain in the compounds, but after harvesting during the dry season, they are herded with the other cattle.

All herds are individually attached to pegs during the night in wide fields close to homesteads. After milking, cattle are let out in the morning to graze on shared fields. To prevent the devastation of farmed crops during the rainy season, which lasts from June to October, they are herded collectively. Around the tethering places, calves are let to graze (Agyemang, 1997). Animals typically roam freely throughout the dry season (November to May) and after the crops have been harvested without the assistance of a herdsman. In the late evening, some animals may return to the tethering grounds, while others may choose to stay away. The calf is attached tight to the mother while being milked by hand after being given a brief opportunity to commence milk let-down during each milking. The calf is then let go to finish the last of the milk. The milker decides when to wean the calves, and the procedure can take a few days or even a few weeks (Agyemang *et al.,* 1997).

The frequency of herd transfers varies depending on various factors, including the physical state of the ground, the number of fields that need to be fertilized by manure, and the herdsman's labour force. The average herd size ranges from 20 - 200 animals. There are typically more than two bulls running within any herd at any given time, and breeding is unrestricted. Where grazing is permitted on communal pastures, males may mate with females from other herds (Agyemang, 2005). Few animals are taken for slaughter or sale, and when they are, it's either during difficult financial times or happy family occasions. There are typically many aged cows retained, and cows are rarely slaughtered.

### 2.3 N`Dama Cattle Breeding Programme

Sub-Saharan Africa has a sizable population of indigenous cattle, which are comprised of 150 native breeds and 30 exotic and commercial hybrids that have been imported (Stock & Gifford-Gonzalez, 2013). According to DAD-IS FAO, (2019), there are 23 exotic and 63 local cattle breeds in West Africa (Ouedraogo *et al.,* 2021). Native breeds are a special source of genetic resources for the ongoing enhancement of livestock productivity in Africa and worldwide since they have long since evolved to the conditions of the local environment (Mwai *et al.,* 2015). However, the majority of these breeds exhibit low output, which may be due to a failure to fully utilize their genetic potential as well as inadequate management, nutrition, and

healthcare (Omer, 2022). As a result, it is necessary to import dairy products to supply the expanding demand for items made from cattle, such as milk, in many different nations.

Various breeding techniques and regulations have been implemented to enhance cattle productivity in West Africa. Like several other developing nations, West African countries have predominantly adopted centralized breeding programmes, which are primarily government-run with minimal involvement from farmers (Haile *et al.,* 2020). However, only a small number of cattle breeding initiatives in sub-Saharan Africa have been successful (Rewe *et al.,* 2009). Previous research looked into cattle breeding programmes used in the region with trypanotolerant N'Dama cattle in Senegal, Mali, and the Gambia (Bosso *et al.,* 2009; Camara *et al.,* 2020; Jaitner *et al.,* 2003). Other breeding plans incorporating those breeds and others have also been carried out; however, they have undergone less thorough analysis (Ouedraogo *et al.,* 2021).

### 2.3.1 Structure of Breeding Programmes

Different models have been attempted for within-breed development programmes, such as sire rotation or loan schemes, community-based programmes (Peacock *et al.,* 2011; Wurzinger *et al.,* 2011), and nucleus-based programmes administered by the public sector or connected to multipliers at the community-level (Haile *et al.,* 2013).

In smallholder herds, nucleus-based programmes lessen the need for community collaboration and intensive recording, which might be useful in some situations. The best places to establish community-based breeding programmes are in communal grazing areas, where livestock owners already manage their animals jointly (Gizaw *et al.,* 2014). Other community-level collective initiatives, like cooperative service procurement (for veterinarians, feeding, and marketing), may be possible in these circumstances. The success of programmes that use community-based strategies depends on properly taking into account farmers' breeding objectives, infrastructure, participation, and ownership (Wurzinger *et al.,* 2011). Farmers' needs, opinions, decisions, and active participation must be taken into consideration throughout the entire programme development process. Therefore, for the design and execution of such programmes, a thorough understanding of the local knowledge and practices of communities in animal management is of the utmost importance. Indigenous knowledge is strongly tied to survival and sustenance, and it serves as a foundation for local-level decisions about the management of natural resources, food security, the health of people and animals, education, and a variety of other community-based endeavours (Haile *et al.,* 2013).

We frequently refer to the "design of a breeding programme," implying that breeding programs can be distinguished by a certain structure. The pyramid population is the conventional hierarchical model in this case, and the nucleus is made up of herds that typically produce their own male and female replacements or draw members from other nucleus herds (Bondoc & Smith, 1993; Janssen-Tapken, 2009). With an open nucleus breeding scheme, the nucleus may import chosen dams from the base population, unlike the pyramid scheme, which has a small group of breeding animals that are improved (the "elite breeders" in the nucleus) and underlying levels of a multiplier and a commercial tier (Van der Werf, 2000). The males in the base (commercial) population come from the nucleus. Figure 2.1 presents a three-tier open nucleus breeding scheme. A multiplier group that takes sires from the nucleus and then produces sires for the base herds may be an additional tier (Bondoc & Smith, 1993).

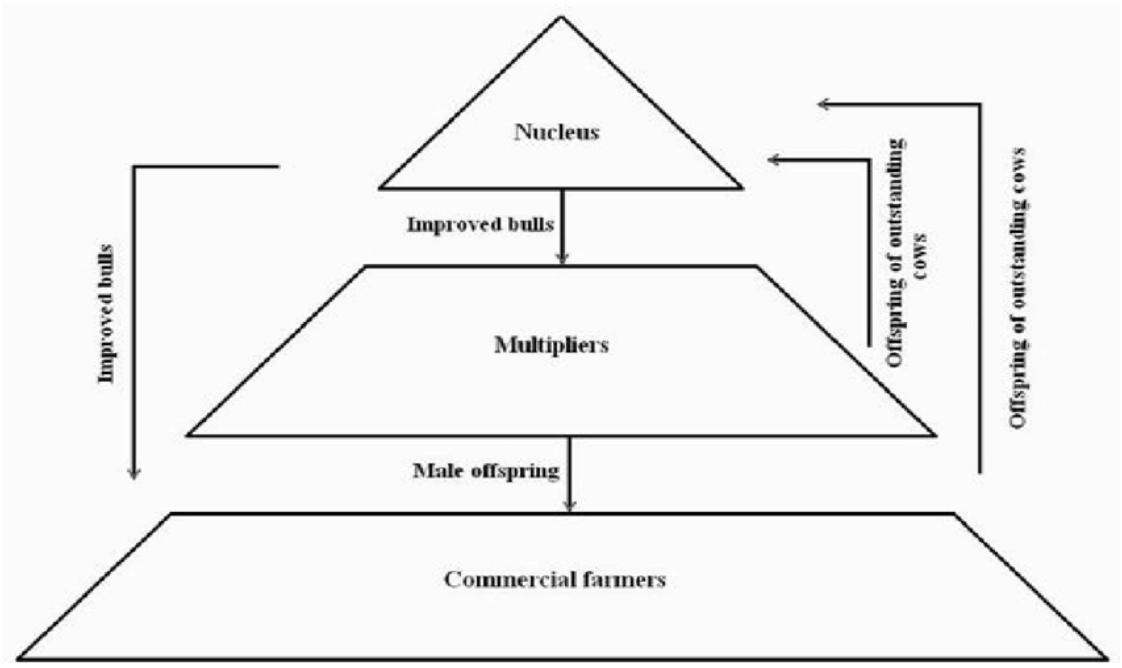


**Figure 2.1:** An open nucleus breeding scheme
**Source**: Dempfle and Jaitner (2000)

The pyramid breeding scheme uses breeding bulls exclusively to transfer genetic gain from the nucleus to the multiplier and commercial herds. Pedigree and performance recording and selection are used in the nucleus herds to generate genetic gain through selection (Bondoc & Smith, 1993). The commercial and multiplier groups may not participate in selection; instead, passively receive genes from the nucleus and then develop over time. Although the

nucleus' genetic mean is slightly higher than that of the lower tiers, in theory, the pace of improvement is equivalent (Visscher, 2000).

***Closed nucleus breeding programme***: This breeding programme entails a one-way flow of genes from elite populations (the nucleus) to commercial herds or populations (Ilatsia *et al.,* 2011; Rege *et al.,* 2011; Sagwa *et al.,* 2019a). This suggests that the nucleus prevents the entry of foreign genetic material. Therefore, only the genetically superior candidates are sold to the multiplier or commercial tiers for breeding, while the remainder are kept in the nucleus as replacement stock (Wahinya, 2014). Closed-nucleus breeding programmes outperform open-nucleus breeding schemes in terms of profitability but fall short in genetic gain (Ilatsia *et al.,* 2011; Rewe *et al.,* 2011). Their higher profitability may be attributed to the commercial herds' lack of documentation, which lowers production costs. The high incidence of inbreeding caused by the quick loss of genetic variation in confined populations could be the cause of the low genetic gain (Cock *et al.,* 2009).

***Open nucleus breeding programme***: Although the structure of this breeding programme is similar to that of closed nucleus breeding programmes, it allows genetic material to flow from the lower tiers to the nucleus. To facilitate breeding, the top candidates from the lower tiers are administered into the nucleus (Barasa, 2020). The dominant females are mostly delivered into the nucleus. Mendelian sampling, which can produce high-performing animals in the lower tiers even though they are daughters of nucleus-born candidates, has been attributed to introducing females from the lower tiers to the nucleus. Due to their strong responsiveness to selection, open nucleus breeding programmes using reproductive technologies including artificial insemination, multiple ovulation, and embryo transfer have been suggested for developing countries (Mezgebe-Weldeslassie, 2018). It has been shown that this programme has a reduced inbreeding rate and offers roughly 10% greater genetic gain than closed systems (Gandini *et al.,* 2014).

### 2.4 N'Dama Cattle Genetic Improvement Programme in The Gambia

The first stage in genetic improvement is the development of a breeding objective, which specifies the direction of selection and the genetic value of performance attributes (Aby *et al.,* 2012). It involves identifying the breeding production and marketing systems, identifying sources of income and expenditure, determining the biological traits that influence revenues and costs, and deriving economic values for each trait in the breeding goal.

In general, substantial research has been done on the advantages and disadvantages of constructing breeding programmes for developing countries (Rege, 2001). The issue of developing significant animal breeding programmes for a specific objective is still difficult. In keeping with this, not many studies have been done on the ideal designs for these breeding programmes. Through studies comparing several indices concerning predicted genetic progress and expected profit, the N'Dama cattle breeding system is being optimized at ITC (Bosso *et al.,* 2009). Genetic determinants and biological constraints, which together determine the potential rates of genetic advancement, determine the type of breeding programmes to be employed for the best genetic improvement (Bosso, 2006). Genetic and economic parameters have been computed to use in the genetic evaluation of the N'Dama cattle development programme (Bosso *et al.,* 2007). Since the N'Dama cattle breed is employed in low-input production systems, it is imperative to analyse alternatives to encourage the scheme's gradual development and, if necessary, expand the recording of alternative attributes.

In 1994, a genetic improvement programme was established at the International Trypanotolerance Centre (ITC), which is now known as the West African Livestock Innovation Centre (WALIC). The objective of this programme was to genetically improve the N'Dama cattle breed for maximum output in terms of milk and meat (Bosso *et al.,* 2009). This gave researchers the chance to assess the productivity and reproductive abilities of Gambian N'Dama cattle. The ability of N`Dama to resist trypanosome infection has been recognised, and allowing the use of trypanotolerant stock to contribute to food security has been considered one of the major methods by which sustainable animal production can be developed in tsetse-infested regions. Open Nucleus Breeding Systems (ONBS) have been recommended in developing countries (Bosso *et al.,* 2007). Reports show that among the improvement programmes implemented, few are well-designed, and are facing the bottlenecks, of long-term sustainability and involvement of local farmers (Bosso *et al.,* 2007; Kosgey *et al.,* 2007).

### 2.4.1 N'Dama Cattle Breeding Scheme in the Gambia

The N'Dama cattle are extensively dispersed throughout western Africa and are raised in low-input systems characterized by intermittent extreme feed scarcity, the presence of trypanosomiasis and tick-borne illnesses, and low labour costs (Dempfle & Jaitner, 2000). To spread the genetics of the adapted N'Dama cattle across western Africa, the International Trypanotolerance Centre (ITC) launched the N'Dama pure-breeding initiative in 1995. The breeding programme is run by the ITC now the West African Livestock Innovation Centre (WALIC) and was created as a multi-objective (meat, milk, and disease resistance) three-tier

open-nucleus system (Bosso *et al.,* 2009). The three stages of the breeding system that were designed and implemented are the nucleus, multipliers, and commercial tiers. In the nucleus, where the genetic gain is generated, sire selection is the primary activity. All animals are raised under a very high tsetse challenge for three years following weaning. There are around six breeding Bulls and 400 adult females in the breeding stock at any given time, for a total of 1000 - 1200 animals (Bosso, 2006). The breeding bulls and the breeding females with their nursing calves are found at Keneba. The young animals are transferred to Bansang after weaning at the age of 10 - 12 months. Females' movement to the lower levels is largely disregarded due to their low reproductive potential. Selected sires descend from the nucleus through the multipliers i.e. the village herds while based on milk yield evaluations, farmer herds may be selected upward and moved to the nucleus (Secka *et al.,* 2022).

***The breeding strategy, scheme, and objectives*:** The programme started in 1995 at the International Trypanotolerance Centre now WALIC (Bosso *et al.,* 2009; Camara *et al.,* 2020). The strategy follows that of an open nucleus breeding scheme (ONBS), with selection based on individual performance and the performance of relatives. It involves a three-tier scheme including the nucleus (ITC), multipliers, and commercial farmers. Figure 2.2 represents the geographical location of ITC's research stations in the Gambia.

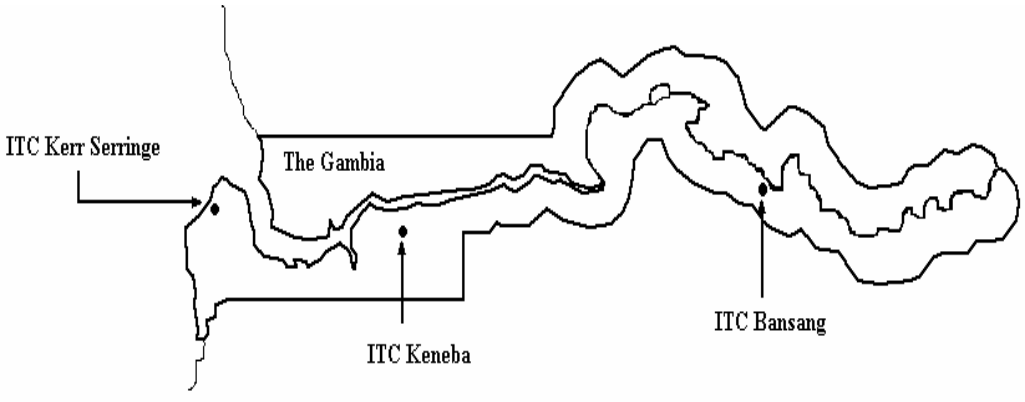


**Figure 2.2**: Geographical location of ITC's research stations in the Gambia
**Source**: Agyemang *et al.* (1997)

Selection units in one area with moderate tsetse fly prevalence (Keneba) and one area with high tsetse prevalence (Bansang). Favourable conditions at the Keneba selection unit led to good birth and weaning rates. Trypanotolerance and adaptation were tested in Bansang. The following two activities can be distinguished: (1) generation of genetic progress, and (2) dissemination of genetic progress (van Arendonk, 2011; van Arendonk & Bijma, 2003). The

aim was to improve the welfare of the livestock owners and their families through better performance and increased livestock productivity (Bosso, 2006).

The programme was funded by the Bundesministerium für Wirtschaftliche Zusammenarbeit (BMZ) of Germany from 1994 to 1998, by the FAO until the year 2000, by the European Union through the project "Programme de Concertation de Recherche-Développement de l´Elevage en Afrique de l´Ouest (PROCORDEL)" (Livestock Research-Development Concertation Programme in West Africa) until 2008, and since then by the African Development Bank and FAO through PROGEBE (Bosso *et al.,* 2003; Camara *et al.,* 2020). The breeding objectives of increasing meat and milk production without compromising cattle adaptation and disease resistance were defined in a participatory way with farmers and implemented (Dempfle & Jaitner, 2000; Jaitner *et al.,* 2003).

***Selection process:*** Animals in the improvement programme are maintained under a low input management system (Agyemang, 2005; Agyemang *et al.,* 1991), and since 2008, a complex selection index has been used that includes the growth performance of young bulls and their relatives. At Keneba, calves were selected based on their daily gain from 0 - 12 months. After weaning, selected calves were transferred to Bansang a high tsetse challenge area for performance testing, where the best bulls were selected using an index that took into account their daily gain from 15 - 36 months and the milk productivity (0-100 day milk yields of all lactations) of their dams (Bosso *et al.,* 2007).

The station located at Keneba maintains the breeding herd of six sires and 400 cows at any given time. Each year, approximately 400 cows are mated to produce 100 male and 100 female calves. These calves are maintained at Keneba until weaning after which 95 males and 90 females are moved to Bansang. At any one time, approximately 230 males and 225 female weaners are present at Bansang. At the end of the testing period (at 36 months of age), 84 male and 80 female animals are available for selection. Two best bulls are selected out of the 84 candidates each year to replace the breeding males. From the 80 female selection candidates, 75 are selected and mated after which 55 best females are retained based on their first lactation performance to replace the females in the breeding unit. The second-best bulls (around 10) were designated and sent to the multiplication tier for reproduction, while non-selected bulls were sold to butchers. Selection was carried out in a participatory way by staff from the National Agricultural Research System (NARS) and by farmers (Bosso *et al.,* 2007).

The purpose of animal breeding is not to improve an individual animal but to improve a population, therefore realising such a goal requires an accurate calculation of the genetic

parameters of the animals being improved (Corr, 2009). Genetic monitoring using an animal model, the Best Linear Unbiased Prediction (BLUP) methodology used to estimate breeding values to optimize the selection, showed an annual genetic gain of 0.40 kg and heritability of 0.48 for body weight at 12 months and 0.28 for weight at 36 months (Ouedraogo *et al.*, 2021).

***Dissemination of genetic progress:*** The breeding programme is now well established, the recording scheme is ongoing and most importantly the genetic progress realised from the nucleus has been disseminated to farmers through the establishment of multiplier herds (Secka *et al.*, 2022). The multiplier tier plays a major role in disseminating the genetic progress of a nucleus breeding programme; the multiplier herds receive the second-best males and to a much lesser extent females from the nucleus, use these males for a specified period, and sell offspring of these breeding bulls to other farmers. In such a way they multiply and disseminate the genetic progress made in the nucleus (Bosso *et al.*, 2009).

Multipliers are village-based herds that have been selected to receive improved breeding bulls from the ITC nucleus breeding herds with the view to producing offspring from these stocks for sale as breeding stock to other farmers (commercial farmers). Multipliers are crucial components of the pure breeding scheme, the efficiency of the dissemination of the genetic progress made on stations and the success of the pure breeding programme depends on the sound selection and management of multiplier herds so that they can fulfil their role (Corr, 2009).

***Challenges of the breeding programme:*** Although the aim is to eventually have the government and farmers take over the programme, it is still in its early stages and dependent on donor funding. Right now, it is challenging to predict its outcome (N'Guetta Bosso, personal communication). The initiative has the potential for success given the approach used, which includes farmer participation, choice of local breeds, selection under low-input circumstances, and no free incentives for the farmers (Haile *et al.*, 2019).

### 2.4.2 Derivation of Selection Index Weights

Selection in cattle breeding programmes aims to simultaneously improve multiple traits (Marques *et al.*, 2012; Sagwa *et al.*, 2019a). The derivation of the weighting factors associated with each trait is empirical due to the difficulty of coming up with a precise value. To overcome this challenge, principal component analysis (PCA) has been suggested in order to make selection more balanced and effective (Amaya *et al.*, 2021; Tramonte *et al.*, 2019; Viana *et al.*,

2020). The principal component technique reduces the originally correlated set of variables (traits) into a smaller set of uncorrelated traits while maintaining most of the original variability explained by the first two to three principal components (Kirkpatrick & Meyer, 2004). Principal components work by standardizing estimated breeding values viz:

$$z_i = (x_i - \bar{x}_i)/s_i \quad (1)$$

where $z_i$=standardized breeding value of the i[th] trait; $x_i$ = EBV of animal i, $\bar{x}_i$ =mean EBV; $s_i$ =standard deviation of EBVs of trait *i*. The standardized EBVs are then subjected to Principal Component analysis (PCA) to reduce the information contained in EBVs for traits in the breeding objective of a breeding programme. The output of this analysis is a new set of uncorrelated variables which retain most of the original variability. The PCA achieves this by identifying hidden patterns in dataset, reducing the dimensionality of the dataset through removal of noise and redundancy and identification of highly correlated variables (Kirkpatrick & Meyer, 2004).

### 2.4.5 Construction of Selection Index

Conventionally, selection indexes for multiple trait breeding goals are constructed by weighting each trait in the goal by an economic weight (Sagwa *et al.,* 2019b) defined as the marginal change in profitability if the trait in question is improved by a unit while holding the change in other traits constant. Weighting factors have also been developed by weighting a trait by the reciprocal of its standard deviation, such that the Index becomes:

$$Index = \sum_{i=1}^{n} b_i X_i \quad (2)$$

where $X_i$ is the EBV of the $i^{th}$ trait in the goal; $b_i$=weighting factor calculated as $b = \frac{1}{\sigma_p}$ (Amaya *et al.,* 2021).

When using PCA a multiple trait selection index ($ICP_k$) can be constructed as:

$$ICP_K = \sum_{i=1}^{I} eig_i x EBV_{ik} \quad (3)$$

where $eig_i$ is the eigenvector of the $i_{th}$ trait and $EBV_{ik}$ is the estimated breeding value for the $i^{th}$ trait.

Alternatively, the standardized EBVs (SEBV) are weighted by respective standardized score coefficients (SSC) calculated as (Buzanskas *et al.,* 2012):

$$SSC_{ij} = \frac{eigenvector_{ij}}{\sqrt{eigenvalue_j}} \quad (4)$$

such that the principal component scores become:

$$PCS_{ji} = \sum_{i=1}^{m} SSC_{ij}\, SEBV_{il} \quad (5)$$

# CHAPTER THREE

# HERITABILITY AND GENETIC CORRELATIONS BETWEEN BODY WEIGHT AND PACKED CELL VOLUME ALONG THE GROWTH CURVE OF N'DAMA CATTLE IN THE GAMBIA


## Abstract

For the N'Dama cattle maternal genetic effects are not accounted for in evaluation of early growth traits or the association between growth and trypanotolerance (PCV). Therefore, this study aimed to estimate genetic co-variance components and parameters and the genetic correlation between body weight and packed cell volume (PCV) along the growth curve of N'Dama cattle in the Gambia. A total of 5,173, 3,130, 2,488, 2,422, 2,442, 1,471, 1,934, and 1,452 bodyweight records for birth weight (BW) weight at 7 months (WT7), 12 months (WT12), 16 months (WT16), 18 months (WT18), 24 months (WT24), 36 months (WT36) and 50 months (WT50) and 1,782, 1,800, 1,844, 1,608, and 1,459 records for packed cell volume (PCV) at 12 months (PCV12) 18 months (PCV18), 24 months (PCV24), 36 months (PCV36), and 50 months (PCV50) respectively, were used for analysis. The effect of fixed factors and least square means were estimated using a general linear model of statistical analysis system (SAS, 2016) fitting herd-year-season of birth and sex as fixed effects and age of dam at calving as a linear covariate. Variance-covariance components were estimated by fitting a univariate and multivariate animal model using the GIBBSF90 algorithm of the BLUPF90 package. The heritability estimates for growth were 0.30±0.04, 0.51±0.06, 0.47±0.05, 0.39±0.05, 0.36±0.05, 0.22±0.07, 0.31±0.06 and 0.31±0.06 for BW, WT7, WT12, WT16, WT18, WT24, WT36, and WT50 while the respective heritability estimates for PCV12, PCV18, PCV24, PCV36, and PCV50 were 0.15±0.01, 0.10±0.01, 0.09±0.01, 0.12±0.01, and 0.14±0.3. Genetic correlations between body weight and PCV range from negative and low (-0.14±0.02) to positive and medium (0.59±0.02). The respective phenotypic correlations between PCV at different ages were generally low ranging from 0.06±0.01 to 0.22±0.01. The highest phenotypic correlations were found between PCV50 and PCV36 (0.22±0.01). The highest genetic correlations were reported for WT18 and PCV18 (0.59±0.02). The results indicate low phenotypic correlations between body weight and PCV at different ages. Body weight at 18 months and PCV18 had the highest heritability estimate and, therefore could be used as selection criteria for body weight and trypanotolerance, respectively.

## 3.1 Introduction

Cattle become infected with trypanosomosis through the bite of tsetse flies harbouring the pathogenic protozoa (Welburn *et al.,* 2016). The disease is caused by *trypanosoma congolense, trypanosoma vivax,* and *trypanosoma brucei brucei* (Batista *et al.,* 2011; Yaro *et al.,* 2016), with *T. congolense* being the most common cause of the disease in the region (Naessens, 2006). The disease, referred to as African Animal Trypanosomiasis (AAT) causes anaemia, pyrexia, weight loss, abortions, reduced milk yield, and eventually death in the absence of treatment (Eisler *et al.,* 2004; Giorgani *et al.,* 2016; Shaw *et al.,* 2014) and is a major constraint to livestock production in sub-Saharan countries. African Animal Trypanosomosis is among the top ten diseases of economic importance in sub-Saharan Africa (Thornton *et al.,* 2002), causing an estimated loss of US$ 5 billion (Giordani *et al.,* 2016) due to lack of effective control methods. However, a systematic review and meta-analysis studies with focus on field-based AAT infection conducted in the Gambia revealed a slight decrease (Olaniyan *et al.,* 2021).

Current techniques employed to control AAT include vector control and chemotherapy (Traoré *et al.,* 2018). The control of the tsetse flies is limited due to the need to use insecticides over extensive areas, which is expensive and has adverse environmental effects while the use of trypanocidal drugs is costly and the drugs are usually not readily available (Chitanga *et al.,* 2011; Torr & Vale, 2015). Resistance of the parasites to the drugs has also been reported (Delespaux *et al.,* 2008). The parasite can evade the host immune system through antigen variation by periodically changing its variant surface glycoprotein coat (Michel-Todó *et al.,* 2020; Yaro *et al.,* 2016).

A promising approach to control AAT is to use trypanotolerant breeds that are domiciled in the sub-Saharan region (Naessens *et al.,* 2002). These breeds can produce meat and milk in the low input conditions prevalent in most of the West African countries and contribute significantly to the livelihoods of resource-limited households (Olaniyan, 2015). Under the natural trypanosome challenge, animals that are tolerant to the disease can survive, reproduce, and gain weight without trypanocidal treatment (Stein *et al.,* 2011). This display of phenotypic superiority is of utmost importance because it provides an opportunity to improve the trait under the prevailing production circumstances. Optimization of cattle production requires the development of cattle genotypes that combine trypanotolerance with high growth rates. Utilization of animals tolerant to AAT is also a way of enhancing sustainable control of AAT (Hanotte *et al.,* 2010; Degneh *et al.,* 2021). To achieve this, trypanotolerant breeds have been used to cross with susceptible populations to enhance trypanotolerance (Maichomo *et al.,*

2005; Ogbu *et al.,* 2023; Orenge *et al.,* 2012). The trypanotolerant breeds and genotypes are known to have a strong immune response against parasite antigens and cytokine synthesis which is lethal to Trypanosoma proliferation (Abenga *et al.,* 2005; Yoshihara *et al.,* 2007).

The N'Dama cattle are adapted to survive on poor-quality feed resources and thrive in tsetse-infested areas with a high risk of trypanosome infection in western Africa (Traoré *et al.,* 2018). Several studies on the growth performance of the N'Dama cattle (Bosso *et al.,* 2009; Camara *et al.,* 2020) and other trypanotolerant breeds (Mekonen *et al.,* 2019) under tsetse challenge have shown that growth traits have medium to high heritability estimates. As such, the trait can be improved through selection. Heritability estimates of traits related to trypanotolerance such as packed cell volume (PCV) and parasitemia have been reported to range from 0.08 to 0.54 (Fukasawa *et al.,* 2002; Rowlands *et al.,* 1995). However, estimates of heritability for PCV and genetic correlation with growth traits for the N'Dama cattle are lacking, despite the breed being widely acclaimed to be trypanotolerant (Traoré *et al.,* 2016). Such correlations provide evidence of indirect response to selection in correlated traits and guide the development of a balanced breeding objective (Zhang *et al.,* 2024). If growth and disease tolerance have an unfavourable genetic correlation, indirect response harms the other trait, if a balanced selection index is not used (Carvalho *et al.,* 2019). Therefore, estimates of heritability and genetic correlations between disease tolerance and growth traits are crucial population parameters to determine which of the targeted traits promise the best results in a multiple-trait breeding objective. As a result, this study aimed to estimate heritability and genetic correlations between body weight and PCV along the growth curve of N'Dama cattle in the Gambia.

## 3.2 Materials and Methods

### 3.2.1 The Environment and Production System

N'Dama cattle breed is reared under a low-input system of animal husbandry and is a source of draught power and animal protein in the form of milk and meat as well as manure and cash income (Olaniyan, 2015). The environment under which the breed is reared is characterized by moderate to high tsetse fly infestation, (Bosso *et al.,* 2009). Each night, the animals are tethered individually, and during the day, the International Trypanotolerance Centre's (ITC) herders accompany them to grazing fields away from the station. While feeding practices differ between Keneba and Bansang, animals typically engage in communal grazing, which involves grazing over a large area daily from 9:00 to 16:00h without supplementation. Calves spend a considerable amount of time with their dams. The animals typically lose weight

during the dry season, which runs from November to June, as a result of the poor quality and quantity of feed. Between the end of the dry season and the start of the wet season (May - October), the animals suffer from severe feed shortages (Bosso *et al.*, 2009). Animals feed on grass during the wet season in Keneba, which has a medium tsetse challenge. In the village fields, crop wastes take over following the harvest in the early dry season. Animals graze over vast areas of burned bush during the late dry season, feeding on fruits and forage. The grazing patterns are different and feed shortage is not as noticeable in Bansang as it is in Keneba due to the significant tsetse issue. Animal feed resources are available most of the year, with a slight decrease during the beginning of the rainy season. Typically, grass regrowth happens towards the end of the rainy season and just before the start of the dry season (Bosso *et al.,* 2009).

### 3.2.2 Breeding Programme of the N'Dama Cattle

Genetic improvement of the N'Dama cattle in the Gambia is carried out under an open nucleus breeding programme composed of a nucleus, multiplier, and commercial tiers. In the nucleus, where the genetic gain is generated, sire selection is the primary activity. All animals are raised under a high tsetse challenge for three years following weaning. The favourable conditions and the moderate tsetse fly prevalence at the Keneba selection unit led to good birth and weaning rates. The breeding bulls and the breeding females with their nursing calves are reared in Keneba. The young animals are transferred to Bansang after weaning at ages 10 - 12 months for trypanotolerance and adaptation testing. Females' movement to the lower levels is largely disregarded due to their low reproductive rate since natural mating is practiced. Selected sires descend from the nucleus through the multipliers i.e. the village herds while based on milk yield evaluations, farmer herds may be selected upward and moved to the nucleus (Secka *et al.,* 2022). The role of the nucleus tier is to generate genetic progress and disseminate the same to multiplier herds (Van Arendonk, 2011). The goal of multipliers herds is to produce progeny from these stocks that can be sold as breeding stock to other farmers. These herds are village-based and have been chosen to get better breeding stock (bulls) from the nucleus breeding herds. Multipliers are essential to the pure breeding strategy; their proper selection and management are essential to their ability to perform their function, as well as the effectiveness of the programme in terms of disseminating the genetic advances accomplished on-station to village-based commercial herds.

### 3.2.3 Data Collection and Processing

Production data related to growth performance and PCV were obtained from the central database of the West African Livestock Innovation Centre (WALIC) breeding scheme in The Gambia. This database is a centre for important data, providing a comprehensive view of the livestock's genetic development and general health under the WALIC breeding scheme. To examine the complexities of performance levels and obtain a more detailed understanding of the effectiveness of the breeding programme, a targeted performance evaluation study was carried out, specifically in the nucleus tier. The nucleus tier is the centre of genetic improvement. A detailed analysis was carried out within this evaluation system, focusing on growth performance traits and packed cell volume. Blood samples were collected from the animals at the time of weighing and preserved on ice in the ITC laboratory where packed cell volume was determined based on a microhaematocrit centrifuge (Hawksey, UK). The assessment aimed at identifying animals exhibiting desirable growth traits and good overall health about trypanotolerance. Through comprehensive analysis of these traits, the breeding programme aimed to identify and select animals that show resilience and adaptation in a wide range of environmental situations, in addition to their ability to contribute to enhanced productivity.

### 3.2.4 Evaluation of the Effect of Fixed Factors

Performance records of body weight traits (BW) and packed cell volume (PCV) were analyzed (Table 3.1) to determine the fixed effects to be included in the subsequent genetic analyses.

The model used for the analysis of variance of fixed effects was as follows:

$$\boldsymbol{y_{ijklm} = \mu + Sex_i + HYS_j + P_k + age_l + e_{ijklm}} \quad \textbf{(6)}$$

where $y_{ijklm}$=the i$^{th}$ observation; $\mu$=overall mean $Sex_i$=i$^{th}$ sex (i=1,2); $HYS_j$=j$^{th}$ herd-year-season of birth class (j=1, …, 152); $P_k$=k$^{th}$ parity class (k=1, …, 6; $age_l$=linear covariate of age of dam at calving (l=43.4 months to 98.2 months) and $e_{ijklm}$=residual associated with each observation.

**Table 3.1:** Number of records (N) and descriptive statistics for growth and disease tolerance (PCV) traits for N'Dama cattle in the Gambia

| Trait | | N | Mean | SD | CV |
|---|---|---|---|---|---|
| Growth | BW, kg | 8,889 | 15.5 | 3.9 | 25.1 |
| | W7, kg | 3,130 | 51.8 | 11.9 | 22.9 |
| | WT12, kg | 2,488 | 75.1 | 18.5 | 24.7 |
| | WT18, kg | 2,442 | 95.3 | 25.0 | 25.0 |
| | WT24, kg | 1,471 | 123.8 | 22.7 | 22.7 |
| | WT36, kg | 1,934 | 149.9 | 32.0 | 32.0 |
| | WT50, kg | 1,452 | 190.4 | 25.9 | 25.9 |
| Disease tolerance | PCV12, % | 1,782 | 23.8 | 4.0 | 16.8 |
| | PCV18, % | 1,800 | 23.6 | 3.7 | 15.5 |
| | PCV24, % | 1,844 | 23.4 | 3.8 | 16.2 |
| | PCV36, % | 1,608 | 23.6 | 3.5 | 15.0 |
| | PCV50, % | 1,459 | 23.1 | 3.5 | 15.3 |

birth weight (BW), weight at 12 months (WT12), weight at 18 months (WT18), weight at 24 months (WT24), weight at 36 months (WT36), and weight at 50 months (WT50), packed cell volume at 12 months (PCV12), packed cell volume at 18 months (PCV18), packed cell volume at 24 months (PCV24), packed cell volume at 36 months (PCV36), and packed cell volume at 50 months (PCV50)

### 3.2.5 Estimation of Variance-covariance Components and Genetic Parameters for Growth and Disease Tolerance Traits

A univariate animal model was fitted using the BLUPF90 package (Misztal *et al.*, 2018) to estimate variance components and to obtain solutions for fixed and random effects relevant to each trait. For analysis of monthly body weights up to 50 months, the age of the dam at calving was fitted as a covariate. In addition to the direct additive genetic effects, maternal genetic, residual variance, direct heritability, and maternal heritability effects on the traits studied were tested by fitting them as additional random effects. In matrix notation, the full model was:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Za} + \mathbf{Mmg} + \mathbf{Wpe} + \mathbf{e} \quad \textbf{(7)}$$

where y is a vector of observations; $\beta$ is a vector of fixed effects; **a**, **mg**, and **pe** are vectors of random direct genetic, maternal genetic, and permanent maternal environmental effects,

respectively; **e** is a vector of random residual effects. **X**, **Z**, **M,** and **W** are incidence matrices relating $\boldsymbol{\beta}$, **a**, and **mg**, and **pe**, respectively, to **y**. The assumptions of the model were:

$$\boldsymbol{E} = \begin{bmatrix} \boldsymbol{y} \\ \boldsymbol{a} \\ \boldsymbol{m} \\ \boldsymbol{c} \\ \boldsymbol{e} \end{bmatrix} = \begin{bmatrix} \boldsymbol{Xb} \\ \boldsymbol{0} \\ \boldsymbol{0} \\ \boldsymbol{0} \\ \boldsymbol{0} \end{bmatrix}; \boldsymbol{V} \begin{bmatrix} \boldsymbol{a} \\ \boldsymbol{m} \\ \boldsymbol{c} \\ \boldsymbol{e} \end{bmatrix} = \begin{bmatrix} \boldsymbol{G} \otimes \boldsymbol{A} & \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{I_d} \otimes \boldsymbol{\sigma_c^2} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{I_n} \otimes \boldsymbol{R} \end{bmatrix} \quad (8)$$

where **G**=matrix of genetic covariance between direct and maternal effects; **A**=numerator relationship matrix; $\boldsymbol{\sigma_c^2}$=maternal permanent environmental variance; $\boldsymbol{I_d}$=identity matrix of order equal to the number of dams; $\boldsymbol{I_n}$=identity matrix of order equal to a number of records; **R**=residual (co)variance matrix. The matrix **G** had the following structure:

$$G = \begin{bmatrix} \sigma_a^2 & \sigma_{a,mg} \\ \sigma_{a,mg} & \sigma_{mg}^2 \end{bmatrix}, \quad (9)$$

where $\sigma_a^2$=variance of additive genetic effects; $\sigma_m^2$=maternal genetic effects; $\sigma_{am}$=covariance between direct and maternal genetic effects. The variances were var(a)=A$\sigma_a^2$; var(mg)= A$\sigma_{\mathrm{mg}}^2$ var(pe) $\mathrm{I_d}\sigma_{\mathrm{pe}}^2$; var(e) = $\mathrm{I_{nb}}\sigma_{\mathrm{e}}^2$ and cov(a, mg)= A$\sigma_{\mathrm{a,}}^2$ mg; where A is the additive genetic relationship matrix; Id and In are identity matrices of the number of dams (d) and the total number of observations (n); $\sigma_{\mathrm{a}}^2$ is the direct additive genetic variance; $\sigma_{\mathrm{mg}}^2$ is the maternal genetic variance; is the covariance between direct and maternal genetic effects; $\sigma_{\mathrm{pe}}^2$ is the variance of maternal permanent environment; and $\sigma_{\mathrm{e}}^2$ is the residual variance. The inclusion of maternal genetic effect influences was only shown to be relevant for birth weight and weight at 7 months and was irrelevant for the remaining growth traits and PCV traits. The inclusion of maternal permanent environmental effects for the above traits in the study did not apply to the current dataset.

### 3.2.6 Estimation of Genetic Correlations

An unequal design multiple trait animal model was fitted to model the data and estimate covariance components and genetic correlations between the traits as follows:

$$\mathbf{y}_i = \mathbf{X}_i\boldsymbol{\beta}_i + \mathbf{Z}_i\mathbf{a}_i + \mathbf{e}_i \quad \textbf{(10)}$$

where $\mathbf{y}_i$=vector of observations for trait i; $\mathbf{X}_i$ and $\mathbf{Z}_i$=known incidence matrices associated with a vector of fixed effects $\boldsymbol{\beta}_i$ and random effects associated with direct genetic effects for each trait; $\mathbf{e}_i$=vector of random residuals for trait *i*. assumptions of the analyses were:

$$E(y)=Xb,\ E(a)=E(e)=E(mg)=0 \quad \textbf{(11)}$$

and

$$\boldsymbol{V(a) = \sigma_a^2 \otimes A = G_0},$$
$$\boldsymbol{V(e) = I\sigma_e^2 = R_0 \otimes I = R},$$
$$\text{Cov(a,e)=0}$$

where ⊗=Kronecker product; $\mathbf{G_0}$=genetic variance-covariance matrix; $\mathbf{R_0}$=residual variance-covariance matrix; **A**=Additive genetic relationship matrix; **I**=identity matrix; **V(e)**=residual variance.

Genetic and non-genetic parameters (phenotypic, direct genetic and residual variances and heritability estimates) were estimated using the GIBBSF90 algorithm of the BLUPF90 package (Mistzal *et al.,* 2018). A uniform distribution for all the location parameters and variance components was assumed. A total of 300,000 Gibbs samples with a burn-in of 50,000 were used with every 50$^{th}$ sample retained for further analyses using POSTGIBBSF90

### 3.2.7 Testing for the Significance of the Genetic Correlations

The magnitude of genetic correlations was tested against unity using the likelihood ratio test of Robert *et al.* (1995). The likelihood of the model fitting a correlation of unity was maximized subject to this constraint. The likelihood of the full model i.e. without this constraint was also obtained. The difference in twice the log-likelihood was used to test the result with a chi-square statistic with one degree of freedom. Phenotypic and genetic covariance, and correlations among the traits were estimated through univariate and multivariate analyses.

### 3.3 Results

The least-square means for growth and disease tolerance (PCV) are presented in Table 3.2. The mean growth weights were shown to increase with age ranging from 16.93±0.04 kg, for birth weight (BW) to 190.37±0.68 kg, for weight at 50 months. The Least square means for PCV at different ages were significantly different (P<0.05), and declined over time from a high of 24.56±0.18 at 12 months of age to 23.18±0.19 at 50 months.

Estimates of heritability for body weight from univariate analysis ranged from 0.30±0.04 for BW to 0.51±0.06 for WT7. The direct-maternal genetic correlation for BW and WT7 were 0.11±0.02 and 0.20±0.04, respectively. The heritability estimates for PCV range from 0.09±0.01 for PCV24 to 0.15±0.01 for PCV12 (Table 3.2).

**Table 3.2:** Least square means, estimates of additive ($\boldsymbol{\sigma_a^2}$), maternal genetic ($\boldsymbol{\sigma_m^2}$) variances, direct ($\boldsymbol{h_a^2}$ ) and maternal ($\boldsymbol{h_m^2}$ ) heritability estimates of growth and disease tolerance traits in the N'Dama cattle from univariate analysis.

| Trait | | Lsmean | $\sigma_a^2$ | $\sigma_e^2$ | $\sigma_m^2$ | $h_a^2$ | $h_m^2$ |
|---|---|---|---|---|---|---|---|
| Growth | BW, kg | 16.93±0.04 | 1.70 | 3.34 | 0.63 | 0.30±0.04 | 0.11±0.02 |
| | W7, kg | 51.76±0.21 | 66.19 | 37.95 | 25.64 | 0.51±0.06 | 0.20±0.04 |
| | WT12, | 75.08±0.37 | 114.15 | 128.72 | | 0.47±0.05 | |
| | WT18, | 95.58±0.52 | 132.78 | 236.05 | | 0.36±0.05 | |
| | WT24, | 123.80±0.52 | 59.06 | 209.39 | | 0.22±0.07 | |
| | WT36, | 149.90±0.73 | 148.84 | 331.29 | | 0.31±0.06 | |
| | WT50, | 190.37±0.68 | 168.03 | 374.00 | | 0.31±0.06 | |
| Disease | PCV12, | 24.56±0.18[a] | 0.72 | 4.02 | | 0.15±0.01 | |
| | PCV18, | 24.09±0.16[b] | 0.49 | 4.62 | | 0.10±0.01 | |
| | PCV24, | 23.71±0.15[c] | 0.49 | 4.89 | | 0.09±0.01 | |
| | PCV36, | 23.81±0.16[c] | 0.62 | 4.37 | | 0.12±0.01 | |
| | PCV50, | 23.18±0.19[d] | 0.48 | 2.94 | | 0.14±0.03 | |

birth weight (BW), weight at 12 months (WT12), weight at 18 months (WT18), weight at 24 months (WT24), weight at 36 months (WT36), and weight at 50 months (WT50), packed cell volume at 12 months (PCV12), packed cell volume at 18 months (PCV18), packed cell volume at 24 months (PCV24), packed cell volume at 36 months (PCV36), and packed cell volume at 50 months (PCV50)

Heritability estimates for body weight from multi-variate analyses ranged from 0.31 for BW to 0.46±0.01 for WT12. The trait with the next highest heritability was WT18 (0.44±0.01). The heritability estimate for PCV was highest at 12 months of age at 0.17±0.01 and declined to 0.13±0.01 at 18 months before increasing to 0.18±0.01 at 50 months of age (Table 3.3). The genetic correlations between PCV at different ages were medium and ranged from 0.56±0.01 between PCV12 and PCV18 to 0.54±0.01 between PCV18 and PCV50. In general, genetic correlations were high for body weights that were close together and decayed as the distance between the measurements increased. Phenotypic correlations between PCV at different ages were generally low, ranging from 0.06±0.01 to 0.22±0.01, and tended to increase as the distance between the measurements increased. The highest phenotypic correlation of 0.22±0.01

was found between PCV50 and PCV36 while the lowest (0.06±0.01) was between PCV50 and PCV12. The genetic correlations between body weight and PCV range from negative and low (-0.14±0.03) to positive and medium (0.59±0.01) and decayed with the age of an animal implying that the selection against. The highest genetic correlations were reported for WT18 and PCV18 (0.59±0.01) followed by WT24 and PCV18 (0.55±0.02). The phenotypic correlations between body weights and PCV at different ages were low ranging from -0.09±0.01 to 0.33±0.01 between PCV50 and WT12, and PCV18 and WT18, respectively.

**Table 3.3:** Genetic (above diagonal), phenotypic correlations (below diagonal) between PCV and body weight and heritability estimates (along diagonal) at different ages in N'Dama cattle

| | Body weight | | | | | | Packed cell volume | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | BW | WT12 | WT18 | WT24 | WT36 | WT50 | PCV12 | PCV18 | PCV24 | PCV36 | PCV50 |
| BW | **0.31±0.07** | 0.22±0.01 | -0.07±0.01 | -0.20±0.01 | -0.12±0.02 | -0.10±0.02 | | | | | |
| WT12 | 0.06±0.02 | **0.46±0.01** | 0.97±0.01 | 0.90±0.01 | 0.82±0.01 | 0.73±0.01 | 0.44±0.01 | 0.46±0.02 | 0.11±0.02 | 0.13±0.01 | -0.14±0.03 |
| WT18 | -0.02±0.02 | 0.83±0.01 | **0.44±0.01** | 0.96±0.01 | 0.89±0.01 | 0.80±0.01 | 0.40±0.01 | 0.59±0.01 | 0.21±0.01 | 0.14±0.01 | -0.07±0.03 |
| WT24 | -0.05±0.02 | 0.76±0.01 | 0.86±0.01 | **0.42±0.01** | 0.93±0.01 | 0.85±0.01 | 0.32±0.02 | 0.55±0.02 | 0.36±0.02 | 0.17±0.02 | 0.01±0.02 |
| WT36 | -0.03±0.01 | 0.69±0.01 | 0.78±0.01 | 0.82±0.01 | **0.33±0.01** | 0.95±0.01 | 0.18±0.02 | 0.51±0.01 | 0.24±0.02 | 0.33±0.02 | 0.07±0.02 |
| WT50 | -0.02±0.02 | 0.57±0.01 | 0.66±0.01 | 0.70±0.01 | 0.77±0.01 | **0.34±0.01** | 0.08±0.03 | 0.45±0.02 | 0.19±0.01 | 0.34±0.01 | 0.21±0.02 |
| PCV12 | | 0.26±0.01 | 0.24±0.01 | 0.20±0.01 | 0.11±0.01 | 0.05±0.02 | **0.17±0.01** | 0.56±0.02 | 0.50±0.08 | 0.45±0.04 | 0.16±0.04 |
| PCV18 | | 0.24±0.01 | 0.33±0.01 | 0.31±0.01 | 0.27±0.01 | 0.23±0.01 | 0.21±0.01 | **0.13±0.01** | 0.52±0.01 | 0.50±0.03 | 0.54±0.05 |
| PCV24 | | 0.06±0.01 | 0.12±0.01 | 0.21±0.01 | 0.14±0.01 | 0.14±0.01 | 0.20±0.03 | 0.19±0.01 | **0.16±0.01** | 0.52±0.01 | 0.40±0.02 |
| PCV36 | | 0.07±0.01 | 0.09±0.01 | 0.10±0.01 | 0.20±0.01 | 0.20±0.01 | 0.19±0.01 | 0.19±0.01 | 0.21±0.01 | **0.16±0.01** | 0.42±0.02 |
| PCV50 | | -0.09±0.01 | -0.05±0.02 | 0.00±0.01 | 0.04±0.01 | 0.04±0.01 | 0.06±0.01 | 0.20±0.01 | 0.16±0.01 | 0.22±0.01 | **0.18±0.02** |

birth weight (BW), weight at 12 months (WT12), weight at 18 months (WT18), weight at 24 months (WT24), weight at 36 months (WT36), and weight at 50 months (WT50), packed cell volume at 12 months (PCV12), packed cell volume at 18 months (PCV18), packed cell volume at 24 months (PCV24), packed cell volume at 36 months (PCV36), and packed cell volume at 50 months (PCV50)

### 3.4 Discussion

Trypanosome infection in cattle leads to anaemia followed by loss of appetite and consequently weight loss, low milk yield, infertility and eventually death (Berthier *et al.,* 2015; Dagnachew *et al.,* 2015; Leta *et al.,* 2016). The decline in PCV with age in the current study is similar to the trend reported by van Wyk *et al.* (2012) in indigenous cattle. A number of studies have reported a strong association of infection risk with age (Attree *et al.,* 2024; Brooks-Pollock *et al.,* 2013) possibly due to general loss of condition as the animals' age. Trypanotolerant breeds can survive, reproduce and remain productive under natural trypanosome challenge (Dayo *et al.,* 2010; Knap & Doeschl-Wilson, 2020; Yaro *et al.,* 2011) whereas other trypano-susceptible breeds succumb to the disease (Berthier *et al.,* 2015). The Utilisation of trypanotolerant breeds of animals is beneficial in regions such as sub-Saharan Africa where trypanosomosis is prevalent. Many trypanotolerant breeds are indigenous to specific regions. Their utilization helps preserve genetic diversity and supports the continued existence of breeds adapted to local environmental conditions. The heritability estimates of between 0.31±001 to 0.46±0.01 reported in the present study for the N'Dama cattle suggest the potential to improve body weight through selection within the trypanosome environment. The N'Dama cattle were able to maintain their haematological parameters within acceptable normal levels, highlighting the importance of the breed in tsetse and trypanosomiasis control strategies (Ganyo *et al.,* 2018). The evolution of body weight under the natural trypanosome challenge is the most economically important trait (Kristjanson *et al.,* 1999).

In the present study, WT12 had the highest heritability estimate (0.46±0.01) and could be used as a selection criterion for body weight under the trypanosome challenge, while WT18 had the next highest heritability estimate of 0.44±0.01. Heritability estimates for the traits studied showed to decrease with age. This result is contrary in magnitude and trend to those reported by Koetz Junior *et al.* (2019), which revealed heritability estimates for the traits increasing with age on genetic parameter studies for Nellore cattle in Brazil. This can be attributed to the contrasting environmental conditions in which the cattle were raised, which significantly influence the expression of traits and their heritability estimates. The Nellore cattle were raised in pastures with mineral supplementation and water ad-libitum, while the N'Dama cattle in the Gambia were kept in an environment resembling village herd settings without supplementation. The genetic correlation between body weights at different ages was high (0.73±0.01 to 0.97±0.01). A similar trend was observed for the genetic correlation measured at similar ages ranging from 0.25±0.04 to 0.97±0.11 between body weight and body measurements on Brahman cattle research across Thailand (Kamprasert *et al.,* 2019).

The highest genetic correlations for body weight at different ages were reported for WT12 and WT18 (0.97±0.01), and the second highest was recorded between WT18 and WT24 (0.96±0.01), followed by WT36 and WT50 (0.95±0.01). This implies that animals that were selected for high body weight in the early stage of the animal's life from 12 months would also be heavy at maturity and any other age. The study also reported a genetic correlation of 0.22±0.01 between birth weight and WT12. It has been shown that beef cattle have low birth weight as an adaptation against dystocia, but the calves can grow fast after birth due to the good mothering ability of their dams. The heritability of PCV at all ages was lower than the estimates of 0.08±0.01 to 0.54±0.11 reported for Japanese shorthorn calves under natural challenge of Japanese theileriosis (Fukasawa *et al.,* 2002) but similar to 0.19±0.20 reported by Janssen-Tapken *et al.* (2007) under natural trypanosome challenge. The heritability estimates for PCV show the existence of additive genetic variation which can be used as the basis of selection and identify the extent of anaemia as an indicator of an animal's susceptibility or resistance to trypanosomosis infection. Due to the evidence of existing genetic variability, selection for resistance to trypanosomosis would be efficient.

Estimates of the genetic correlation of body weight with PCV are important because although the N'Dama cattle can tolerate moderate levels of trypanosome infection, they are small-bodied and hence unsuited for draft purposes. The results highlight the potential benefits of improving the body size of N'Dama cattle without compromising their ability to withstand trypanosomosis. These improvements can increase meat and milk yield and enhance crop production through manure and draught power. The present study showed that genetic correlations between growth traits and PCV range from negative and low (-0.14±0.03) to positive and medium (0.59±0.01) and decayed with the age of the animal. Gathura *et al.* (2020) reported that disease-resistance traits had low and negative genetic correlations with body weight and growth traits in cattle. Oliveira *et al.* (2018) also found a negative genetic correlation (-0.63) between body weight and PCV in sheep. The results of the present study concur with these results. While a negative correlation implies a trade-off between growth and PCV, a positive correlation indicates a moderately favourable relationship between growth traits and PCV. The strength of these correlations suggests that genetic factors influencing growth traits are also associated with higher PCV values and vice versa. This means that growth trait improvements are likely accompanied by increases in PCV due to shared genetic influences. Considering that measures of PCV had low to medium genetic correlations with body weight at different ages, it is possible to develop an index of selection to ensure that genetic improvement in body weight is achieved without compromising disease tolerance.

However, it is important to note that low PCV is not only caused by trypanosomosis but also by poor nutrition, tick-borne diseases and helminthosis (Moti *et al.,* 2013). Therefore, selection in the N'Dama cattle should be based on a weighted selection index to ensure meat and milk production and draft power are improved without compromising the breed's disease tolerance.

The main objective of the N'Dama cattle breeding programme in tsetse-infested areas is to optimize meat and milk production as well as trypanotolerance (Bosso *et al.,* 2009; Ouédraogo *et al.,* 2021; Traoré *et al.,* 2017), it is important to note that the genetic correlations between the traits are expected to evolve (Gathura, 2021). In the present study, the genetic correlation between PCV at different ages of 0.16±0.02 to 0.56±0.05 indicates a favourable correlated response to PCV at any age due to selection for PCV. Selection for PCV at 12 months would lead to the highest genetic response in this trait since it had the highest heritability estimate (0.17) and also had medium genetic correlations with all the other measures of this trait. Genetic correlations between body weight at different ages ranged from -0.07 to 0.96. These genetic correlations indicate that the additive genetic covariance matrix for multiple breeding objectives evolves. In a simulation study, Gathura (2021) demonstrated that genetic correlations among the breeding objective traits can decline by up to 120%. Similar results were reported by Careau *et al*. (2015) where genetic and heritability estimates decreased over generations because of selection. These changes in the nature and magnitude of additive genetic correlations in multiple trait breeding objectives can affect the efficacy of selection (Walsh & Blows, 2009) because the response to selection in a given trait is obtained after adjusting for trait correlations, and the additive genetic variance-covariance matrix of all the traits (Lande, 1979). These findings suggest that through selective breeding, it's possible to enhance the natural ability of the N'Dama cattle to tolerate and resist trypanosomosis. This information is important for designing strategies to improve livestock health and productivity in regions where trypanosomosis is a concern.

### 3.5 Conclusion

Heritability estimates were moderate for growth traits and low for PCV. Body weights showed high genetic correlations across ages, while PCV correlations were moderate. Correlations between body weight and PCV ranged from low and negative to medium and positive. WT12 had strong genetic ties with body weight at different ages, and PCV18 showed moderate correlations with other PCV measures. Therefore, WT18 and PCV18, with high heritability and genetic correlations, could be effective selection criteria for body weight and trypanotolerance in multi-trait breeding.

# CHAPTER FOUR

# GENETIC PARAMETERS AND CORRELATIONS BETWEEN TEST DAY MILK YIELD, EARLY GROWTH AND FERTILITY TRAITS OF N'DAMA CATTLE IN THE GAMBIA


## Abstract

Genetic selection of N'Dama cattle in challenging environments is crucial for enhancing locally adapted breeds. In cattle, growth traits have medium to high heritability and genetic correlations. However, heritability estimates for milk yield and fertility traits, and their relationship with growth traits for the N'Dama cattle are still lacking. Therefore, this study aimed to estimate genetic parameters for test day milk yield, early growth, and fertility traits of N'Dama cattle in the Gambia. A total of 10,418, 1,878, 3,691, 2,320, and 1,557 records of test day milk yield (TDMY), age at first calving (AFC), Calving interval (CI) and early growth rates of (Birth weight (BW), weaning weight (WWT), average daily gain from birth to weaning (pre-ADG)) and from 15 months to 36 months (Post-ADG) were used to estimate genetic parameters. A random regression Legendre polynomial animal model was fitted to TDMY data to obtain random regression coefficients for the average population, additive genetic, and permanent environment curves. Genetic parameters for BW, ADG, WWT, AFC, and CI were estimated via univariate and bivariate analyses using the Bayesian procedure implemented in Gibbs sampling in the GIBBS1F90 software. A total of 300,000 Gibbs samples with a burn-in of 50,000 were used with every $50^{th}$ sample retained for further analyses using POSTGIBBSF90 to obtain posterior distribution statistics. Direct heritability estimates for BW, WWT, Pre-ADG, Post-ADG, AFC and CI were 0.44±0.04, 0.48±0.03, 0.42±0.03, 0.38±0.03, 0.39±0.01 and 0.14±0.01, respectively, while maternal heritability estimates for BW, WWT, and Pre-ADG were 0.13±0.03, 0.00±0.00, and 0.19±0.01, respectively. The correlation between direct and maternal genetic effects was negatively high and medium for BW, WWT and ADG, respectively. Genetic correlations between daily milk were positive and medium (0.39) to high (0.94). Genetic correlations between AFC and average TDMY and early growth traits were negative, ranging from -0.26 to -0.66 except for correlation with BW (0.06). Test day milk yield had high and positive genetic correlations with early growth traits, CI and AFC ranging from 0.51 to 0.88. However, CI had negative and favourable genetic correlations with early growth traits (-0.01±0.04 to -0.97±0.02). The results of the present study suggest that weaning weight could be used as an indicator trait to select for improve test day milk yield, fertility and growth traits due to favourable high and positive genetic correlations.

## 4.1 Introduction

The N'Dama cattle are endemic to West Africa, where they are reared under arid and semi-arid conditions in tsetse-infested areas (Traoré *et al.,* 2017). The breed has developed resistance to trypanosomosis and can therefore survive, reproduce, and perform under the prevailing challenging production circumstances (Ganyo *et al.,* 2018; Olaniyan *et al.,* 2021; Yaro *et al.,* 2016). The breed and its crosses with other cattle breeds are utilized for meat and milk production, provision of draft power, and socio-cultural purposes (Camara *et al.,* 2020; Traoré *et al.,* 2017). Trypanotolerant breeds, therefore, are a sustainable strategy to complement efforts to combat the tsetse and trypanosomosis challenge (Degneh *et al.,* 2021; Hanotte *et al.,* 2010) and to safeguard the livelihoods of the cattle keepers (Ouédraogo *et al.,* 2021). Such breeds include the N'Dama in West Africa (Ganyo *et al.,* 2018), the Orma Boran and the horn in Eastern Africa (Maichomo *et al.,* 2005; Orenge *et al.,* 2012), and the Sheko breed in Ethiopia (Aleme & Megistu, 2023) and their crosses with other cattle breeds (Orenge *et al.,* 2012).

Genetic selection of the N'Dama cattle in challenging environments is central to improving the performance of locally adapted cattle breeds. To achieve this objective, breeding programmes have been implemented in different countries in West Africa (Camara *et al.,* 2020; Ouédraogo *et al.,* 2021; Traoré *et al.,* 2017). The breeding objective for the improvement programmes is to improve milk yield and body weight without losing trypanotolerance and adaptive traits (Jaitner *et al.,* 2003). Several studies have been carried out to evaluate performance and estimate genetic parameters for growth traits (Bosso *et al.,* 2009; Ohagenyi *et al.,* 2023). These studies reported high heritability estimates (0.39 to 0.62) and genetic correlations among growth traits (0.82). However, heritability estimates for milk yield and fertility traits and their association with growth traits in the N'Dama cattle have not been estimated.

Knowledge of the genetic correlations among the breeding objective traits is important because the additive genetic covariance matrix for multiple breeding objectives evolves over time due to selection (Gathura *et al.,* 2020). Gathura (2021) demonstrated that genetic correlations among the breeding objective traits can decline by up to 120%. Heritability estimates also decrease over generations because of selection (Careau *et al*., 2015). These changes in the nature and magnitude of additive genetic correlations in multiple trait breeding objectives can affect the efficacy of selection (Walsh & Blows, 2009). This is because response to selection in a given trait is obtained after adjusting for trait correlations, and the additive genetic variance-covariance matrix of all the traits (Lande, 1979). This suggests that selective

breeding can enhance or alter traits not included in a breeding programme's selection criteria or breeding goal favourably or unfavourably. This study aimed to estimate genetic parameters for test day milk yield, early growth and fertility traits in N'Dama cattle in the nucleus tier of the breeding programme in the Gambia.

## 4.2 Materials and Methods

A total of 10,418, 1,878, 3,691 and 2,320 records of test day milk yield (TDMY), age at first calving (AFC), Calving interval (CI), early growth traits (Birth weight (BW), weaning weight (WWT) and average daily gain from birth to weaning (ADG)) were obtained from the central database of the breeding scheme of the West African Livestock Innovation Centre (WALIC) in The Gambia. For the N'Dama cattle, weaning occurs at 12 months to 14 months of age (Bosso *et al.*, 2007). This database is a centre for important data, providing a comprehensive view of the livestock's genetic development and general health under the WALIC breeding scheme.

### 4.2.1 The Environment and Production System

N'Dama cattle are reared under a low-input system characterized by moderate to high tsetse fly infestations (Bosso *et al.*, 2003). The animals are grazed on communal fields on natural pastures without supplementation and tethered individually at night. The animals suffer severe feed shortages during the dry season which runs from November to June (Bosso *et al.*, 2009). The animals are also fed on crop residue following the harvest in the early dry season. In the late dry season, animals graze over vast areas of burned bush, feeding on fruits and forage. Typically, grass regrowth happens towards the end of the rainy season and just before the start of the dry season (Bosso *et al.*, 2009). Calves spend a considerable amount of time with their dams until weaning when they are about 12 months old.

### 4.2.2 Data Analysis

A random regression Legendre polynomial animal model was fitted to TDMY data to obtain random regression coefficients for the average population, additive genetic, and permanent environment curves. The random regression equation, fitting a first-order sub-model to fit fixed and fourth and fourth-order for genetic and permanent environment effects was:

$$y_{ijkl} = HTD_i + AC_j + \sum_{m=0}^{2} \beta_{jm} X_m(t) + \sum_{m=0}^{4} \alpha_{km} \varphi_{a,m}(t) + \sum_{m=0}^{4} \gamma_{km} \varphi_{p,m}(t) + e_{ijkl} \quad \textbf{(12)}$$

where $y_{ikl}$is the *l*th TD milk yield of cow k; $HTD_i$ is the fixed effect of herd-year-test-day of recording *i*; $AC_j$ is fixed effect of $j^{th}$ age at calving class;$\beta_{jm}$is the $m^{th}$ fixed regression coefficient describing the average population curve; $X_m\ (t)$is the $m^{th}$ covariate evaluated at DIM *t*; $\alpha_{km}$ and $\gamma_{km}$ are the $m^{th}$ random regression coefficients (RRC) associated with daily additive genetic (AG) and permanent environmental (PE) variances for animal *k*, respectively; $\varphi_{a,m}\ (t)$and $\varphi_{p,m}\ (t)$ are the $m^{th}$ covariates depending on days in milk, *t*; and $e_{ijkl}$ is the error term, assumed to be independently distributed and constant throughout a lactation. The residual error is assumed to be homogeneous within the test day. The results on the choice of order to fit and whether the residual error was homogenous or heterogeneous were determined in a separate analysis.

### 4.2.3 Estimation of Genetic Parameters for Early Growth and Fertility Traits

A univariate animal model was fitted to BW, ADG, WWT and AFC performance records to estimate genetic and phenotypic parameters. For CI, a univariate repeatability model was fitted due to the repeated records for this trait. For early growth traits, the model included maternal genetic, maternal permanent environment and covariance between direct genetic and maternal genetic effects and was:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Za} + \mathbf{Mmg} + \mathbf{Wpe} + \mathbf{e} \quad (13)$$

where **y** is a vector of observations; $\boldsymbol{\beta}$ is a vector of fixed effects (herd-year-month of birth, sex of calf, and parity); **a**, **mg**, and **pe** are vectors of random direct genetic, maternal genetic and permanent maternal environmental effects, respectively; e is a vector of random residual effects. **X**, **Z**, **M** and **W** are incidence matrices relating $\boldsymbol{\beta}$, **a**, **m**, and **pe**, respectively, to **y**.

The assumptions for the models where applicable were: E(**y**)=**X**$\boldsymbol{\beta}$; E(**a**)=0; E(**mg**)=0; E(**pe**)=0; and E(**e**)=0.

The variances were var(**a**)=**A**$\sigma_a^2$; var(**mg**)= **A**$\sigma_{\mathrm{mg}}^2$, var(**pe**) $\mathbf{I}_{\mathrm{d}}\sigma_{\mathrm{pe}}^2$; var(**e**) = $\mathbf{I}_{\mathrm{nb}}\sigma_{\mathrm{e}}^2$ and cov(**a**,**mg**)= **A**$\sigma_{\mathrm{a,mg}}$

where **A** is the additive genetic relationship matrix; $\mathbf{I}_{\mathrm{d}}$ and $\mathbf{I}_{\mathrm{n}}$ are identity matrices of the number of dams (d) and total number of observations (n); $\sigma_{\mathrm{a}}^2$ is the direct additive genetic variance; $\sigma_{\mathrm{mg}}^2$ is the maternal genetic variance;  is the covariance between direct and maternal genetic effects; $\sigma_{\mathrm{pe}}^2$ is the variance of maternal permanent environment; and $\sigma_{\mathrm{e}}^2$ is the residual variance.

### 4.2.4 Genetic Correlation between Early Growth, Test Day Milk Yield and Fertility Traits

#### 4.2.4.1 Estimation of Variances and Covariances

A series of bivariate animal models were fitted using the BLUPF90 package (Aguilar *et al.*, 2018) to estimate the covariance between growth and fertility traits. The variances obtained from the univariate analyses were as starting values for multivariate analyses. The model in matrix notation was:

$$\boldsymbol{y_i = X_i b_i + Z_{1i} a_i + Z_{2i} m_i + W_i pe_i + e_i} \quad \textbf{(14)}$$

with

$$\begin{pmatrix} \boldsymbol{y_1} \\ \boldsymbol{y_2} \end{pmatrix} = \begin{pmatrix} \boldsymbol{X_1} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{X_2} \end{pmatrix} \begin{pmatrix} \boldsymbol{b_1} \\ \boldsymbol{b_2} \end{pmatrix} + \begin{pmatrix} \boldsymbol{Z_{11}} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{Z_{12}} \end{pmatrix} \begin{pmatrix} \boldsymbol{a_1} \\ \boldsymbol{a_2} \end{pmatrix} + \begin{pmatrix} 0 & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{Z_{22}} \end{pmatrix} \begin{pmatrix} 0 \\ \boldsymbol{p_2} \end{pmatrix} + \begin{pmatrix} \boldsymbol{e_1} \\ \boldsymbol{e_2} \end{pmatrix}$$

where $\mathbf{y_i}$ is the vector of observations for a trait i; $\mathbf{b_i}$=vector of fixed effects for trait i=1, 2; $\mathbf{a_i}$=vector of random animal genetic effects for trait i; $X_i$, $\mathbf{Z_1}$ and $\mathbf{Z_2}$ are known incidence matrices associated with vectors of fixed effects, $b_i$, random animal genetic effects, $a_i$, permanent environmental effects $\boldsymbol{p_i}$, respectively; $\mathbf{e_i}$ is the vector of residual effects for trait *i*. The assumptions of the model were:

$$\boldsymbol{E} = \begin{bmatrix} \boldsymbol{y} \\ \boldsymbol{a} \\ \boldsymbol{m} \\ \boldsymbol{c} \\ \boldsymbol{e} \end{bmatrix} = \begin{bmatrix} \boldsymbol{Xb} \\ \boldsymbol{0} \\ \boldsymbol{0} \\ \boldsymbol{0} \\ \boldsymbol{0} \end{bmatrix}; \boldsymbol{V} \begin{bmatrix} \boldsymbol{a} \\ \boldsymbol{pe} \\ \boldsymbol{e} \end{bmatrix} = \begin{bmatrix} \boldsymbol{G} \otimes \boldsymbol{A} & \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{I_d} \otimes \boldsymbol{\sigma^2_{pe}} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{I_n} \otimes \boldsymbol{R} \end{bmatrix} \quad \textbf{(15)}$$

where **G**=matrix of genetic covariances between the two traits; **A**=numerator relationship matrix; $\boldsymbol{\sigma^2_{pe}}$=permanent environmental variance; $\boldsymbol{I_d}$=identity matrix of order equal to number of animals; $\boldsymbol{I_n}$=identity matrix of order equal to number of records; **R**=residual (co)variance matrix. The matrix **G** had the following structure:

$$G = \begin{bmatrix} \sigma^2_{a_1} & \sigma_{a_1 a_2} & \sigma_{a_1 a_3} & \sigma_{a_1 a_4} & \sigma_{a_1 a_{f1}} \\ \sigma_{a_2 a_{m1}} & \sigma^2_{a_2} & \sigma_{a_2 a_3} & \sigma_{a_2 a_4} & \sigma_{a_2 a_{f1}} \\ \sigma_{a_3 a_1} & \sigma_{a_3 a_2} & \sigma^2_{a_3} & \sigma_{a_3 a_4} & \sigma_{a_3 a_{f1}} \\ \sigma_{a_4 a_1} & \sigma_{a_4 a_2} & \sigma_{a_4 a_3} & \sigma^2_{a_4} & \sigma_{a_4 a_{f1}} \\ \sigma_{a_{f1} a_1} & \sigma_{a_{f1} a_2} & \sigma_{a_{f1} a_3} & \sigma_{a_{f1} a_4} & \sigma^2_{a_{f1}} \end{bmatrix}, \quad (16)$$

$$P = \begin{bmatrix} \sigma^2_{p_{e1}} & \sigma_{p_{e1} p_{e2}} & \sigma_{p_{e1} p_{e3}} & \sigma_{p_{e1} p_{e4}} & \sigma_{p_{e1} p_{f1}} \\ \sigma_{p_{e2} p_{e1}} & \sigma^2_{p_{e2}} & \sigma_{p_{e2} p_{e3}} & \sigma_{p_{e2} p_{e4}} & \sigma_{p_{e2} p_{f1}} \\ \sigma_{p_{m3} p_{m1}} & \sigma_{p_{m3} p_{m2}} & \sigma^2_{p_{m2}} & \sigma_{p_{m3} p_{m4}} & \sigma_{p_{m3} p_{f1}} \\ \sigma_{p_{m4} p_{m1}} & \sigma_{p_{m4} p_{m2}} & \sigma_{p_{m4} p_{m3}} & \sigma^2_{p_{m2}} & \sigma_{p_{m4} p_{f1}} \\ \sigma_{p_{f1} p_{m1}} & \sigma_{p_{f1} p_{m2}} & \sigma_{p_{f1} p_{m3}} & \sigma_{p_{f1} p_{m4}} & \sigma^2_{p_{f1}} \end{bmatrix}$$

where $\sigma^2_{ai}$=additive genetic random regression coefficients; $\sigma_{a_i a_j}$=covariance between additive genetic random regression coefficients;$\sigma^2_{p_{ei}}$=permanent environment random regression coefficients; $\sigma_{p_{ei}p_{ej}}$=covariance between permanent environment random regression coefficients; $\sigma^2_{a_{f1}}$=additive genetic variance for single record trait; $\sigma^2_{pe_{f1}}$=permanent environment variance.

$\mathbf{R}=\mathbf{I}\otimes\mathbf{R_o}$ is the residual covariance matrix for

$$\mathbf{R_o}=\begin{bmatrix}\sigma^2_{e_{11}} & 0\\ 0 & \sigma^2_{e_{22}}\end{bmatrix} \quad (17)$$

where $\sigma^2_{e_{ii}}$is the residual variance for trait i=1,2

#### 4.2.4.2 Estimation of Heritability and Genetic and Phenotypic Correlations

Co-variance components were estimated from univariate and bivariate analyses using the Bayesian procedure implemented in Gibbs sampling in the GIBBS1F90 software (Aguilar *et al.,* 2018). A uniform distribution for all the location parameters and variance components was assumed. A total of 300,000 Gibbs samples with a burn-in of 50,000 were used with every 50$^{th}$ sample retained for further analyses using POSTGIBBSF90 (Aguilar *et al.,* 2018) to obtain posterior distribution statistics. The estimated posterior variances and covariances were used to obtain heritability estimates and genetic and phenotypic correlations among the traits. Estimates of heritability were obtained from co-variances obtained from univariate analyses while genetic and phenotypic correlations were calculated using co-variances from bivariate analyses. The additive genetic variance for TDMY for a day *t* was calculated as:

$$\hat{\boldsymbol{\sigma}}^{\mathbf{2}}_{\boldsymbol{t}} = \boldsymbol{\Phi}'_{\boldsymbol{r}}(\boldsymbol{DIM_t})\boldsymbol{G}\boldsymbol{\Phi_r}(\boldsymbol{DIM_t}) \quad \textbf{(18)}$$

where **G** is the variance-covariance matrix of AG random regression coefficients for TDMY. Heritability estimates for at any day $DIM_t$ along the lactation curve were calculated as:

$$\hat{\boldsymbol{r}}^{\mathbf{2}}_{\boldsymbol{g}}(\boldsymbol{DIM_t}) = \frac{\boldsymbol{\Phi}'_{\boldsymbol{r}}(\boldsymbol{DIM_t})\boldsymbol{G}_{\boldsymbol{m,f}}\mathbf{1}}{\sqrt{\hat{\boldsymbol{\sigma}}^{\mathbf{2}}_{\boldsymbol{am}}(\boldsymbol{DIM_t})\hat{\boldsymbol{\sigma}}^{\mathbf{2}}_{\boldsymbol{af}}}} \quad \textbf{(19)}$$

where 1 is a vector of ones and $\boldsymbol{G_{m,f}}$=random regression coefficients of the AG covariance between TDMY and fertility; $\hat{\sigma}^2_{af}$=additive genetic variance of the fertility trait.

### 4.3 Results

Means, standard deviation, and coefficient of variation for test day milk yield, early growth, and fertility traits are presented in Table 4.1. The mean BW, WWT, Pre-ADG, Post-ADG, AFC, CI, and TDMY, and the associated standard deviations were 17.36±2.96kg,

83.06±18.85kg, 0.16±0.04 kg/day, 0.10±0.04kg/day, 45.46±7.06 months, 23.3±6.65 months, 1.19±0.52 kg, respectively. The coefficient of variation for birth weight and AFC were low (<20%), while that for WWT, Pre-ADG, and CI were medium, ranging from 22.7% to 28.5%, while those for TDMY and Post-ADG were high (>30%).

**Table 4.1:** Means, standard error of the mean (SEM) and coefficient of variation for test day milk yield, early growth and fertility traits

| Trait | Mean | SD | CV, % |
|---|---|---|---|
| Birth weight, kg | 17.36 | 2.96 | 17.7 |
| Weaning weight, kg | 83.06 | 18.85 | 22.7 |
| Pre-weaning average daily gain, kg/day | 0.16 | 0.04 | 27.4 |
| Post-weaning average daily gain, kg/day | 0.10 | 0.04 | 39.6 |
| Test day milk yield, kg | 1.19 | 0.52 | 43.7 |
| Age at first calving, months | 45.46 | 7.06 | 15.5 |
| Calving interval, months | 23.3 | 6.65 | 28.5 |

The lactation curve for N'Dama showed that daily milk yield peaked around days in milk (DIM) 42 and declined steadily towards the end of the curve presented in Figure 4.1.

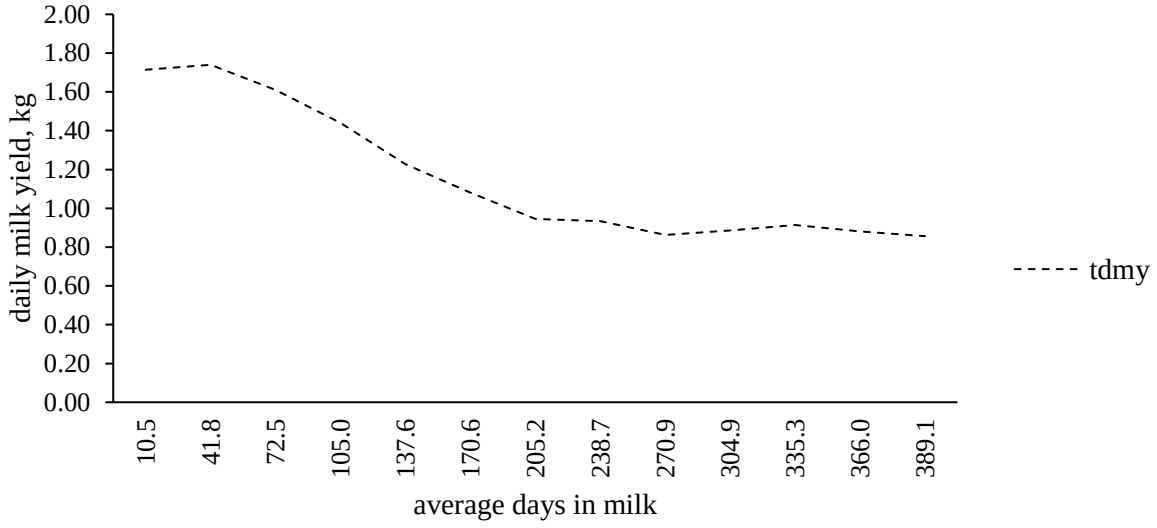


**Figure 2.1:** Lactation curve showing daily milk yield

**Heritability Estimates**

Heritability estimates for TDMY for selected days along the lactation curve are shown in Table 4.2. The estimated average daily heritability estimate was 0.39. Daily heritability estimates ranged from 0.07 at the beginning of lactation to 0.44 at DIM 245, before declining steadily towards the end of lactation.

Genetic correlations among daily milk yield between DIM 5 to DIM 185 (0.39 to 0.93) and DIM 305 to DIM 425 (0.85 to 0.94) were medium to high and positive. However, those between daily milk yields in early lactation and those in late lactation were medium to high and negative, ranging from -0.14 to -0.83, except for the correlation between daily yield in DIM 35 and DIM 185 of -0.03. Phenotypic correlations followed the same pattern as the genetic correlations but were lower in magnitude.

**Table 4.2:** Estimates of heritability (on diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations between test day milk yield for selected days in milk (DIM)

| DIM | 5 | 35 | 65 | 125 | 185 | 245 | 305 | 365 | 395 | 425 |
|---|---|---|---|---|---|---|---|---|---|---|
| 5 | **0.07** | 0.39 | 0.48 | 0.70 | 0.63 | 0.47 | 0.03 | 0.40 | -0.73 | -0.83 |
| 35 | 0.59 | **0.17** | 0.93 | 0.44 | -0.03 | -0.31 | -0.61 | -0.68 | -0.53 | -0.33 |
| 65 | 0.06 | 0.72 | **0.21** | 0.73 | 0.33 | 0.04 | -0.32 | -0.53 | -0.56 | -0.48 |
| 125 | 0.10 | 0.29 | 0.75 | **0.27** | 0.89 | 0.71 | 0.31 | -0.14 | -0.55 | -0.71 |
| 185 | 0.20 | 0.04 | 0.44 | 0.91 | **0.39** | 0.95 | 0.66 | 0.19 | -0.34 | -0.63 |
| 245 | 0.18 | -0.09 | 0.28 | 0.80 | 0.96 | **0.44** | 0.85 | 0.45 | -0.08 | -0.42 |
| 305 | -0.11 | -0.18 | 0.19 | 0.55 | 0.69 | 0.83 | **0.36** | 0.85 | 0.46 | 0.11 |
| 365 | -0.37 | -0.18 | 0.14 | 0.25 | 0.30 | 0.48 | 0.88 | **0.30** | 0.85 | 0.61 |
| 395 | -0.52 | -0.14 | 0.08 | -0.05 | -0.09 | 0.08 | 0.61 | 0.91 | **0.31** | 0.94 |
| 425 | -0.59 | -0.09 | 0.06 | -0.23 | -0.32 | -0.18 | 0.38 | 0.77 | 0.96 | **0.36** |

Direct heritability estimates for BW, WWT, Pre-ADG, Post-ADG, AFC and CI were 0.44±0.04, 0.48±0.03, 0.42±0.03, 0.38±0.03, 0.39±0.01 and 0.14±0.01, respectively (Table 4.3). While maternal heritability estimates for BW, WWT and Pre-ADG were 0.13±0.03, 0.00±0.00 and 0.19±0.01, respectively. The ratio of maternal permanent environment to phenotypic variance for BW, WWT, and Pre-ADG were 0.12±0.01, 0.08±0.02 and 0.06±0.02, respectively. The correlation between direct genetic and maternal genetic effects were -0.70±0.06, -0.87±0.03 and -0.47±0.03 for BW, WWT and Pre-ADG, respectively (Table 4.3).

**Table 4.3:** Variance components and parameter estimates for early growth and reproductive traits from univariate analysis

| Trait | Early growth | | | | Fertility | |
|---|---|---|---|---|---|---|
| Effect | BW | WWT | Pre-ADG | Post-ADG | AFC | CI |
| $\sigma_a^2$ | 3.45 | 102.94 | 0.57x10$^{-3}$ | 0.59 x10$^{-3}$ | 87.81 | 3937.9 |
| $\sigma_{mg}^2$ | 1.09 | 0.73 | 0.27x10$^{-3}$ | - | - | - |
| $\sigma_{a,mg}$ | -1.30 | -7.51 | -0.19x10$^{-3}$ | - | - | - |
| $\sigma_{mpe}^2$ | 0.91 | 17.73 | 0.08x10$^{-3}$ | - | - | - |
| $\sigma_{pe}^2$ | - | - | - | - | - | 1157.9 |
| $\sigma_e^2$ | 2.34 | 93.4 | 0.50x10$^{-3}$ | 0.97 x10$^{-3}$ | 138.24 | 22857 |
| $h_d^2$ | 0.44±0.04 | 0.48±0.03 | 0.42±0.03 | 0.38±0.03 | 0.39±0.01 | 0.14±01 |
| $h_m^2$ | 0.13±0.03 | 0.00±0.00 | 0.19±0.01 | - | - | - |
| $pe^2$ | 0.12±0.01 | 0.08±0.02 | 0.06±0.02 | - | - | 0.04±01 |
| $r_{a,mg}$ | -0.70±0.06 | -0.87±0.03 | -0.47±0.03 | - | - | - |

$\sigma_a^2$=additive variance; $\sigma_{mg}^2$=maternal genetic variance; $\sigma_{a,mg}$=covariance between direct and maternal genetic effects;$\sigma_{mpe}^2$=maternal permanent environmental effect; $\sigma_{mpe}^2$=permanent environment; $\sigma_e^2$=residual variance; $h_d^2$=direct heritability; $h_m^2$=maternal heritability; BW=birth weight; WWT=weaning weight; Pre-ADG=average daily gain from birth to weaning (12 months); Post-ADG=average daily gain from weaning to 36 months; AFC=age at first calving; CI=calving interval

Genetic and phenotypic correlations between growth, and fertility are presented in Table 4.4. The correlation between calving interval and age at first calving was high and positive (0.80±0.03).

**Table 4.4:** Genetic and phenotypic correlations between growth and fertility traits and their posterior standard deviations

| Trait | BW | WWT | Pre-ADG | Post-ADG | AFC | CI |
|---|---|---|---|---|---|---|
| BW | | 0.60±0.05 | 0.25±0.01 | 0.51±0.02 | 0.06±0.02 | -0.01±0.12 |
| WWT | 0.30±0.02 | | 0.99±0.01 | 0.88±0.03 | -0.26±0.02 | -0.21±0.03 |
| Pre-ADG | 0.11±0.01 | 0.97±0.01 | | 0.52±0.02 | -0.27±0.02 | -0.97±0.02 |
| Post-ADG | 0.04±0.02 | 0.69±0.01 | 0.41±0.01 | | -0.66±0.01 | 0.57±0.03 |
| AFC | 0.02±0.01 | -0.10±0.01 | -0.11±0.01 | -0.14±0.02 | | 0.80±0.03 |
| CI | 0.01±0.03 | -0.03±0.01 | -0.05±0.01 | -0.32±0.01 | 0.66±0.02 | |

BW=birth weight; WWT=weaning weight; Pre-ADG=average daily gain from birth to weaning (12 months); Post-ADG=average daily gain from weaning (36 months); AFC=age at first calving; CI=calving interval

However, CI was negatively correlated with early growth traits (-0.01±0.04 to -0.97±0.02). Genetic correlations between AFC and growth traits were mostly negative, ranging from -0.26 to -0.66 except for correlation with BW which was 0.06. Post-ADG had high and positive genetic correlations with other growth traits and calving intervals, ranging from 0.51 to 0.88 (Table 4.4).

Genetic correlations between TDMY, growth and fertility traits are presented in Table 4.5. The correlations between TDMY, BW and WWT were all positive for all DIM and ranged from low (0.04) to high (0.84) and peaked mid-lactation for BW and mid-to-late lactation for WWT. The genetic correlations between TDMY and Pre-and Post-ADG followed the same pattern as those with BW. Genetic correlations between TDMY and AFC were negative in early lactation (DIM 5 to DIM 125) and from DIM 305 to the end of lactation. Calving interval had low to high (0.12 to 0.66) positive genetic correlations with TDMY.

**Table 4.5:** Genetic and phenotypic correlations between TDMY, growth and fertility traits for selected days in milk (DIM)

| DIM | BW | WWT | Pre-ADG | Post-ADG | AFC | CI |
|---|---|---|---|---|---|---|
| 5 | 0.33 | 0.67 | 0.39 | 0.37 | -0.81 | 0.12 |
| 35 | 0.45 | 0.64 | 0.41 | 0.36 | -0.90 | 0.19 |
| 65 | 0.57 | 0.58 | 0.45 | 0.29 | -0.94 | 0.35 |
| 125 | 0.72 | 0.61 | 0.71 | 0.21 | -0.52 | 0.48 |
| 185 | 0.25 | 0.72 | 0.70 | 0.24 | -0.31 | 0.60 |
| 245 | 0.04 | 0.77 | 0.53 | 0.04 | -0.18 | 0.65 |
| 305 | 0.14 | 0.84 | 0.45 | 0.25 | -0.21 | 0.51 |
| 365 | 0.36 | 0.63 | 0.22 | 0.37 | -0.53 | 0.52 |
| 395 | 0.40 | 0.41 | 0.08 | 0.35 | -0.58 | 0.66 |
| 425 | 0.40 | 0.23 | 0.03 | 0.30 | -0.59 | 0.65 |

BW=birth weight; WWT=weaning weight; Pre-ADG=average daily gain from birth to weaning (12 months); Post-ADG=average daily gain from weaning to 36 months; AFC=age at first calving; CI=calving interval

## 4.4 Discussion

Birth weight in the N'Dama cattle of 17.36±2.96 kg was within the range of 17.5±0.10 to 19.4±0.56kg reported for the breed in West Africa (Agyemang *et al.,* 1991). The consistent birth weight (BW) and weaning weight (WW) of N'Dama cattle over several decades, as indicated by the research findings, suggest a stable but potentially stagnant breeding programme. Similarly, this estimate was lower than 20.41±0.23kg for Sahiwal (Wakchaure & Meena, 2010) in India. Elsewhere, Brunes *et al.* (2023) found a birth weight of 34.1 kg of Nellore cattle in Brazil. The average weaning weight of 83.06kg was below 158.94 kg of Nguni cattle in South Africa (Nesengani *et al.,* 2018). Other studies which reported higher weaning weights include Collins-Lusweti (2000) which reported 135.6kg. The Nellore cattle of Brazil were reported to have a weaning weight of 203.67kg. For these studies, weaning was done around 7 months of age, while for the N'Dama this occurred at about 12 months of age (Camara *et al.,* 2020). The observed differences in weaning weight between N'Dama and other breeds emphasise the role of environmental factors, management practices, and breed differences in shaping growth and improvement curves. While environmental constraints and management limitations may contribute to suboptimal growth in N'Dama cattle, the persistence of these differences over time suggests that genetic factors may also play a significant role.

The average daily milk yield of 1.2±1.1 kg was lower than that of 5.52 kg/day reported for Nguni cattle in South Africa (Nesengani *et al.,* 2018). Other higher daily estimates of 3.6 kg/day and 4.9kg/day were reported for Hereford and Wokalups cattle (Meyer *et al.,* 1994). Maiwashe *et al.* (2013) reported a daily milk yield s of 8.50kg for Bonsmara cattle. The differences in milk yield observed among different cattle breeds and studies are likely the results of a combination of genetic, environmental, management, nutritional and methodological factors. Daily heritability estimates for milk yield in the present study were similar in magnitude and trend to 0.37 to 0.48 reported for dairy cattle in Thailand (Bauban *et al.,* 2020). Nesengani *et al.* (2018) reported a value of 0.22±0.24 for Nguni cattle, while Ilatsia *et al.* (2007) reported heritability estimates ranging from 0.28 to 0.52 across different parities in Sahiwal cattle in Kenya. Whereas the genetic and phenotypic correlations between TDMY across the lactation ranged from -0.83 to 0.95 in the present study, Ilatsia *et al.* (2007) reported high and positive correlations (0.50 to 1.00). The negative correlations between TDMY in early and late lactation in the N'Dama imply that a different set of genes influences daily milk yields in these stages. Therefore, a weighted selection index should be implemented to ensure sustainable genetic improvement of daily milk yield across lactation.

Heritability estimates for BW and WWT of 0.44±0.04 and 0.48±0.03, respectively reported in the present study were within the range of 0.22±0.02 to 0.51±0.03 reported for Hanwoo cattle in Japan (Lopez *et al.,* 2020) and 0.47 for Nguni cattle in South Africa (Nesengani *et al.,* 2018). Maternal heritability estimates were within the range (0.12 to 0.17) reported in the same study. Similar ranges of direct and maternal heritability estimates (0.21 to 0.68 and 0.12 to 0.17, respectively) were reported for Nguni cattle in Zimbabwe (Assana & Masacheb, 2012). Lower estimates of direct (0.39±0.06 and 0.31±0.04) and maternal (0.06±0.03 and 0.07±0.03) heritability have been reported for BW and WWT, respectively (Brunes *et al.,* 2024). Other studies which reported low direct and maternal heritability estimates for weaning weight include Boligon *et al.* (2010) and Chud *et al.* (2014). Pre-weaning daily gain in the N'Dama cattle in the present study had a heritability estimate of 0.19±0.01 which was lower than 023±0.02 for Nellore cattle in Brazil (Brunes *et al.,* 2024). Other studies which reported lower maternal heritability estimates in the range of 0.03 to 0.11 include Kluska *et al.* (2018), Caetano *et al.* (2013) and Kamei *et al.* (2017). The larger proportion of direct genetic variance relative to environmental variance and differences in selection pressure in different populations could explain the higher magnitude of direct heritability estimates for BW and WWT. Birth weight is the first trait to be measured. It plays the role of an economic indicator in beef cattle (Utsunomiya *et al.,* 2013) because it has a positive and favourable genetic correlation with subsequent weight including mature weight (MacNeil, 2005; Meyer, 1995). It is also inversely associated with calving ease (Hohnholz *et al.,* 2019; Hwang *et al.,* 2008). Choi *et al.* (2005) reported lower direct (0.10) and maternal (0.27) heritability estimates for Hanwoo calves. The differences in the direct and maternal heritability estimates could be attributed to differences in breeds and model and method analysis for the different studies.

Estimates of direct genetic and maternal genetic correlation for BW, WWT, Post-ADG (-0.47 to -0.87) are within the range of values reported for Nguni cattle of -0.57 to -0.71 (Nesengani *et al.,* 2018; Norris *et al.,* 2004). Other studies reported values of -0.57 and -0.17 for Hereford and Wokalups cattle (Meyer *et al.,* 1994), -0.42 for Gudali cattle (Ndofor-Foleng *et al.,* 2012) and -0.18 for crossbred cattle (Splan *et al.,* 2002). The strong and negative direct genetic and maternal genetic correlation indicate the genetic antagonism between the two effects (Norris *et al.,* 2004; Van Niekerk *et al.,* 2004) and the effect of maternal genes in the offspring would be reduced if selection is solely based on direct genetic breeding values. The values suggest maternal genetic effects should be considered when developing a selection index involving early growth traits.

The heritability estimate of calving interval (CI) in N'Dama cattle, at 0.14±0.01, unveils an understanding of the genetic control of reproductive traits in this indigenous breed. This estimate falls within the range of 0.13 to 0.16 reported for Hanwoo cows (Shin *et al.,* 2021), suggesting similar genetic influences on calving interval across these breeds. However, this estimate surpasses that of Sahiwal cattle (0.03) reared in semi-arid Kenya (Ilatsia *et al.,* 2007) and 0.11 for Nguni cattle in South Africa (Ngayo, 2017), underscoring potential breed-specific variations in the heritability of reproductive traits. Age at first calving in the N'Dama cattle is higher than the estimates of 24.1 months reported for Hanwoo cattle (Shin *et al.,* 2021). Other studies have reported lower values in the range of 24.7 months (Shin *et al.,* 2021), 25.1 months (Lopez *et al.,* 2020) and 33.14 months (Brunes *et al.,* 2024). The AFC of N'Dama cattle is higher than for most beef breeds of 28 months to 34 months (Lopez *et al.,* 2020). Wakchaure and Meena (2010) reported an AFC of 1078.09±21.12 days for Sahiwal cattle. The heritability estimate for AFC of 0.39 was similar to that of Nguni cattle of 0.36 (Ngayo, 2017). This value was higher than the 0.21 to 0.24 reported for early and late AFC in the Nellore cattle (Brunes *et al.,* 2024). Studies that reported lower values for AFC (0.21 to 0.37) are Bonamy *et al.* (2019), Kluska *et al*. (2018) and Buzanskas *et al.* (2017). The differences in the heritability estimates for AFC could arise due to differences in management decisions regarding the age at which heifers are bred (Heise *et al.,* 2018) as well as the history of a selection of the populations. The moderate heritability for AFC in the N'Dama cattle indicates that this trait can respond to selection, since earlier AFC results in longer stability and productivity of beef cows (Claus *et al.,* 2017).

For fertility traits, a notable positive correlation between age at first calving (AFC) and calving interval (CI) of 0.81 was observed. This correlation was higher than that reported for Czech Holstein cattle 0.29 (Brzáková *et al.,* 2019), indicating a strong relationship between these reproductive parameters. Conversely, genetic correlations between early growth traits and AFC ranged from 0.06 to -0.27 (Brunes *et al.,* 2024), differing from those found in Nellore cattle (-0.33 to -0.62), suggesting breed-specific variations in growth-reproduction relationships. Lopez *et al.* (2020) highlighted genetic correlations of 0.33±0.06 between AFC and birth weight (BW), and 0.04±0.07 with weaning weight (WWT), while Shin *et al.* (2021) found a strong negative correlation of -0.71 between AFC and BW in Hanwoo cows. Other studies which reported low genetic correlations between AFC and WWT include -0.02 in Brown Swiss (Segura-Correa *et al.,* 2012), and 0.10 in Nellore (Perreira *et al.,* 2001). Higher genetic correlations with BW (0.77) were reported for Fogera cattle (Bekele *et al.,* 2017). These findings underscore the intricate balance between growth and reproductive performance in

different breeds. The lower phenotypic correlations could be due to the interaction between additive genetic and environmental factors. When precocious sexual maturity is desired, Pre-ADG could be used as a selection criterion, as selection for faster growth rates would lead to a lowering of age at first calving. This is important because when body weight is the principal focus of selection (Camara *et al.,* 2020), heavier animals tend to be late maturing (Pereira *et al.,* 2017; Snelling *et al.,* 2021; Terry *et al.,* 2020) and increased incidences of dystocia (Hohnholz *et al.,* 2019).

The positive genetic correlations between TDMY and CI in early to mid-lactation align with similar findings for fertility traits (day's open, calving interval) of 0.22 to 0.79 in tropical smallholder dairy farms (Bauban *et al.,* 2015) and sub-tropical environments (Ali *et al.,* 2019). However, this positive correlation signifies a potential trade-off, as selection for increased milk yield may prolong calving intervals, leading to economic implications such as higher culling rates and reduced lifetime productivity (Musingi *et al.,* 2021; Sung *et al.,* 2016). The N'Dama cattle are reared under harsh environmental conditions under tsetse challenge (Camara *et al.,* 2020). As such heat stress due to the arid conditions under which the animals are raised can lower conception rates in cattle (Wolfenson & Roth, 2019). Poor herd management can also lead to poor fertility (Martinez-Castillero *et al.,* 2020). Additionally, indigenous cattle in the tropics are associated with delayed postpartum resumption of ovarian activity, leading to long calving intervals (Murillo-Medina *et al.,* 2009). This is because of the effect of sucking and loss of body condition pre-calving (Díaz, *et al.,* 2018). In contrast, the mainly negative genetic correlations of -0.21 to -0.94 between TDMY and AFC are consistent with previous studies (Canaza-Cayo *et al.,* 2018; Muir *et al.,* 2004) and higher but similar in sign to -0.04 reported for Brazilian Holstein cows (Stefan *et al.,* 2020). This negative correlation suggests that selection for earlier age at first calving would result in higher milk yield, offering potential benefits in terms of lifetime productivity and management efficiency.

The medium to high and positive genetic correlation of 0.4 to 0.84 between TDMY and growth traits indicates a strong relationship between milk production and calf growth. These findings diverge from the result of -0.71 reported in Nguni cattle (Nesengani *et al.,* 2018), highlighting breed-specific variations in milk yield-growth associations. Discrepancies in genetic correlations across studies may stem from differences in data collection methods and analytical models, emphasizing the need for standardized approaches in genetic evaluations. Beef and dairy cattle farmers select for improved ease of calving combined with fast postnatal growth, leading to significant increases in post-weaning weight and a moderate decrease in birth weight (de Negreiros *et al.,* 2024; Kuehn & Thalman, 2017; Saad *et al.,* 2020). Reduction

of birth weight is important because it is directly related to dystocia which can lead to loss of offspring, increased cases of calf morbidity related to hypoxia and or poor calf passive immunity, resulting in reduced profits (Arnott *et al.*, 2012). Other undesirable consequences to watch out for include older age at first calving and lengthened calving intervals (Berry & Evans, 2014). Therefore, whereas growth traits had a favourable genetic correlation with TDMY in N'Dama cattle, it is of interest to ensure that the medium to high genetic correlations between TDMY and birth weight do not lead to a rapid increase in birth weight. Bennett *et al.* (2021) reported that calves born of heifers with better calving ease had better survival to weaning. Hence, while the N'Dama cattle breeding goal is to improve body weight and milk yield, the multiple trait selection index should reduce birth weight as a proxy for calving ease.

### 4.5 Conclusion

The results of the present study suggest that weaning weight could be an alternative selection criterion to improve test-day milk yield. Given that the genetic correlations between TDMY and AFC were negative, selecting for higher milk yield, directly or indirectly would result in a favourable response in AFC. The positive genetic correlations between TDMY, CI and BW call for a trade-off to ensure that increased milk yield does not lead to longer calving intervals and heavier calves at birth which can cause dystocia.

# CHAPTER FIVE

# SELECTION INDEXES USING PRINCIPAL COMPONENT ANALYSIS FOR GROWTH RATES, MILK YIELD, TRYPANOTOLERANCE AND FERTILITY TRAITS OF N'DAMA CATTLE IN THE GAMBIA


## Abstract

N'Dama cattle is a breed indigenous to West Africa and well-known for their ability to thrive in challenging environmental conditions and diseases, particularly trypanosomiasis. However, the effectiveness of selection for breeding objective traits has not been evaluated. This study aimed to explore the use of principal component analysis (PCA) to predict response to selection based on multiple trait selection indexes. Estimated breeding values (EBVs) of 6938 animals for birthweight, pre-weaning daily gain (Pre-ADG), post-weaning daily gain (Post-ADG), and cumulative milk yield in the first 100 days of lactation ($MY_{100}$) and packed cell volume (PCV), calving interval (CI) and age at first calving (AFC) were standardized to mean of zero and variance of 1. Selection indexes (SI) were constructed using principal components (PC) with eigenvalues greater than 1 and their expected response to selection compared to a conventional selection index (CSI) constructed by weighting the EBVs of each trait by the reciprocal of the phenotypic standard deviation. The PCA analyses were performed using the FactorMineR library of the R-Project software. The first three principal components were associated with eigenvalues greater than 1 and cumulatively explained >70% of the total variation. The standardized score coefficients or weighting factors of the first 3 PCs associated with EBVs for $MY_{100}$, Pre-ADG, Post-ADG, PCV, CI and AFC ranged from 0.12 to 0.50, -0.62 to 0.41, -0.32 to 0.43, 0.12 to 0.50, -0.81 to -0.03, and -0.42 to 0.48, respectively. All six traits evaluated for the N'Dama cattle exhibited medium to high correlation with either PC1, PC2, or PC3. The expected genetic progress for $MY_{100}$, pre-ADG, post-ADG, and PCV were positive for the three PCIs as well as CSI. The expected genetic progress for $MY_{100}$, pre-ADG, post-ADG, and PCV for all SIs ranged from 1.76kg to 4.05kg, 0.01kg to 1.71kg, 0.00 kg to 0.90kg, 0.11% to 0.55%, respectively. All SIs resulted in reductions in CI and AFC ranging from -0.57 to 1.56 and -0.23 to -1.60, respectively. The selection index based on PC1 resulted in high and favourable expected response in all traits as well as the highest overall response and is therefore recommended for genetic improvement of the multiple trait breeding objective of the N'Dama cattle in the Gambia. Due to the superiority of the PCA approach over CSI, has presented a practical approach to selection in breeding programmes due to its objective derivation of weighting factors for EBVs of the traits.

## 5.1 Introduction

The N'Dama cattle genetic improvement programme was initiated in 1994 to improve production performance without compromising adaptation and disease resistance (trypanotolerance) under low input, tsetse-infested production systems (Camara *et al.,* 2020). The selection criteria for animals included average daily gain from birth to 12 months in a controlled environment at Keneba and average daily gain from 15 to 36 months in the actual low input environment at Bansang and first 100-day milk yield of multiple lactations (Bosso *et al.,* 2007). This aimed to ensure that trypanotolerance and adaptation to the prevailing harsh environmental conditions were not compromised in the quest to increase growth and milk yield (Traoré *et al.,* 2016).

Heritability estimates for growth traits recorded in the N'Dama cattle improvement programme have medium to high heritability estimates ranging from 0.28 to 0.48 and a high and favourable genetic correlation of 0.69 (Bosso *et al.,* 2003). These genetic parameters imply selection would result in genetic improvement of growth-related traits. Bosso *et al.* (2007) reported positive genetic trends for weight at birth, yearling, and 3 years of age in the N'Dama cattle in the Gambia. Genetic improvement and utilization of the trypanotolerant N'Dama cattle (Ganyo *et al.,* 2018) has the potential to reduce the demand and consequently lower the cost of trypanocidal drugs to control trypanosomosis and other diseases by up to 50% (Bosso *et al.,* 2007) while delivering heavier animals at maturity to farmers. Body weight has positive and favourable (Amaya *et al.,* 2021) and negative and unfavourable genetic correlations with milk yield and fertility and disease tolerance and feed efficiency traits, respectively. Whereas it is expected that heavier cows produce more milk yield, fertility and disease resistance would deteriorate (Brito *et al.,* 2021). However, genetic parameters and response to selection for milk yield, trypanotolerance, and fertility traits for the N'Dama cattle are lacking.

Most breeding programmes select for multiple traits based on a weighted selection index (Marques *et al.,* 2012; Viana *et al.,* 2020). The assignment of the weighting factors is empirical, because of the challenges of deriving precise values. To overcome this challenge, principal component analysis (PCA) can be used to create selection indexes based on a linear combination of standardized estimated breeding values of breeding goal traits in beef cattle (Boligon *et al.,* 2016; Buzanskas *et al.,* 2013). This technique reduces a set of originally correlated variables into a smaller set of uncorrelated variables by removing repeated information while retaining most of the original variability in the original variance-covariance (Boligon *et al.,* 2016; Kirkpatrick & Meyer, 2004). This enables the simultaneous selection of traits of interest (Vargas *et al.,* 2018). Principal component analysis has therefore been applied

in studying the relationship between estimated breeding values for traits in White leghorn (Savegnago *et al.*, 2011), dual-purpose buffaloes (Agudelo-Gómez *et al.*, 2015), Nellore cattle (Viana *et al.*, 2020), Egyptian buffaloes (Salem *et al.*, 2021) and Guzera cattle (Tramonte *et al.*, 2019). This study therefore aimed to explore the use of PCA to develop and compare selection indexes that include growth, milk, reproductive and disease tolerance traits in N'Dama cattle in the Gambia.

## 5.2 Materials and Methods

### 5.2.1 Data Collection

Estimated breeding values of 6938 animals for pre-weaning daily gain, post-weaning daily gain, age at first calving, calving interval, packed cell volume and cumulative first lactation milk yield at 100 days in milk were obtained from a previous genetic evaluation of the N'Dama cattle breeding programme. The animals were managed in natural pasture conditions. In addition, the animals were fed on crop residues following the harvest season.

### 5.2.2 Data Analysis

#### 5.2.2.1 Test Day Milk Yield

An additive genetic random regression coefficient for test day milk yield was obtained using a second-order polynomial for the fixed population curve and a fourth-order polynomial for the additive animal genetic and permanent environmental effects were used to calculate estimated breeding values for each animal. The Legendre polynomial coefficients were evaluated at day *t*. In matrix notation, $\hat{\alpha}_i$and $Z_t$ were:

$$\hat{\alpha}_i = \begin{bmatrix} \hat{\alpha}_{i0} \\ \hat{\alpha}_{i1} \\ \hat{\alpha}_{i2} \\ \hat{\alpha}_{i3} \end{bmatrix}, \qquad Z_t \begin{bmatrix} \emptyset_{0t} \\ \emptyset_{1t} \\ \emptyset_{2t} \\ \emptyset_{3t} \end{bmatrix} \tag{20}$$

The EBV of animal ***i*** for day ***t*** was calculated as:

$$\boldsymbol{EBV_{it} = \acute{Z}_t \hat{\alpha}_i = \sum_{j=1}^{k_a - 1} \alpha_{ij} \emptyset_j (DIM)_t} \tag{21}$$

Therefore, the EBV of the animal *i* for the first 100 days was obtained as the summation of daily EBVs from day 5 to day 100as:

$$EBV_{it} = \sum_{t=5}^{DIM} \hat{\alpha}_{0i}\emptyset_{0t} + \hat{\alpha}_{i1}\emptyset_{1t} + + \hat{\alpha}_{i2}\emptyset_{2t} + \hat{\alpha}_{i3}\emptyset_{3t} = \left( \sum_{t=5}^{T} \emptyset_{0t} \sum_{t=5}^{T} \emptyset_{1t} \sum_{t=5}^{T} \emptyset_{2t} \sum_{t=5}^{T} \emptyset_{3t} \right) \hat{\alpha}_i$$

$$= Z_{c_{TMY}} \hat{\alpha}_i$$

where $Z_{c_{nMY}}$ is a vector of Legendre polynomial coefficients summed over the first 100 days (Bosso *et al.*, 2009). The corresponding summations of Legendre polynomials for each trait in the current study were:

$$Z_{c_{100MY}} = [67.88 \ -92.75 \ 69.25 \ -24.04]$$

The EBVs for the traits were obtained from the analysis in Chapter Four.

#### 5.2.2.2 Principal Component Analysis and Estimation of Index Weights

The EBVs were standardized to a zero mean and unit variance as before PCA to avoid inconsistent solutions due to differences in the scales of measurement and magnitude of the variable as:

$$\boldsymbol{z_i = (x_i - \bar{x}_i)/s_i} \quad \textbf{(22)}$$

where $z_i$=standardized breeding value of the i[th] trait; $x_i$, $\bar{x}_{i,}$ and $s_i$ correspond to the EBV of animal I, mean EBV, and standard deviation of EBVs of trait *i*. The standardized EBVs were subjected to Principal Component analysis (PCA) to reduce the information contained in EBVs for breeding objective traits for the N'Dama cattle breeding programme (pre-weaning daily gain, post-weaning daily gain, cumulative milk yield for the first 100 days). Fertility traits (calving interval and age at first calving) and packed cell volume (PCV) were included in the analysis to evaluate whether the breeding programme achieved its original objective i.e. to improve performance without compromising adaptability and disease resistance (Camara *et al.*, 2020). The PCA analyses were performed using the FactoMineR library (Lee *et al.*, 2018) of the R-Project software (R Core Time, 2020). Selection indexes (SI) were constructed using principal components (PC) with eigenvalues greater than 1. The PCs and the standardized estimated breeding values (SEBVs) were used as Principal component scores which was the sum of the SEBVs for each trait weighted by the respective standardized score coefficient (SSC) (Buzanskas *et al.*, 2013) as:

$$\boldsymbol{SSC_{ij} = \frac{Eigenvector_{ij}}{\sqrt{Eigenvalue_j}}} \quad \textbf{(23)}$$

where $SSC_{ij}$ is the standardized score coefficient for the standardized estimated breeding value (SEBV) of the i[th] trait in the j[th] PC. The selection index or principal component score (PCS) for a selection candidate for a given trait was computed as the summation of the products of the animal's EBV and the corresponding SSC and was calculated as:

$$\boldsymbol{PCS_{jl} = \sum_{i=1}^{m} SSC_{ij} * SEBV_{il}} \quad \textbf{(24)}$$

where $PCS_{jl}$=principal component score for the $l^{th}$ animal in the $j^{th}$ principal component; $SSC_{ij}$= is the standardized score coefficient for the standardized estimated breeding value (SEBV) of the i$^{th}$ trait in the j$^{th}$ PC; and $SEBV_{il}$=standardized estimated breeding value of the $i^{th}$ trait for the $l^{th}$ animal.

The expected genetic progress obtained from the principal component index methodology was compared to that obtained from a conventional selection index (CSI) (Hazel, 1943). The CSI was calculated as:

$$\boldsymbol{CSI = b_{MY100}X_{MY100} + b_{Pre\_aADG}X_{Pre\_aADG} + b_{Post\_ADG}X_{Post\_ADG} + + b_{CI}X_{CI} + b_{AFC}X_{AFC} + b_{PCV}X_{PCV}} \quad \textbf{(25)}$$

where X and b are EBV and weight for each trait. The weighting factor, b, was calculated as:

$$\boldsymbol{b = \frac{1}{\sigma_P}} \quad \textbf{(26)}$$

where $\sigma_P$ is the phenotypic standard deviation of the trait (Falconer & MacKay, 1996).

### 5.2.3 Expected Genetic Progress

The expected genetic progress for each index was computed by selecting the top 94% of females and the top 2% of males (Bosso *et al.*, 2007) based on the ranking outcome of each index. Three indexes were considered: $SI_{PC1}$, $SI_{PC2}$, and $SI_{PC3}$, constructed using the first, second, and third principal components, respectively, and CSI constructed using weighing factors.

## 5.3 Results

The Pearson's correlations between EBVs for the six traits studied in the N'Dama cattle in the Gambia are presented in Table 5.1. $MY_{100}$ showed significant positive correlations (P<0.05)

**Table 5.1:** Pearson correlations between estimated breeding values for breeding objective traits in N'Dama cattle in the Gambia

| Trait | $MY_{100}$ | Pre_ADG | Post_ADG | CI | AFC | PCV |
|---|---|---|---|---|---|---|
| $MY_{100}$ | | 0.011 | 0.093*** | -0.113*** | 0.162*** | 0.025* |
| Pre-ADG | | | 0.032** | 0.126*** | 0.013 | -0.067*** |
| Post-ADG | | | | -0.185*** | 0.076*** | 0.085*** |
| CI | | | | | -0.044*** | -0.033** |
| AFC | | | | | | -0.016 |

$MY_{100}$= milk yield at 100 days of all lactation; Pre_ADG= pre-weaning average daily gain; Post_ADG= post-weaning average daily gain; CI= calving interval; AFC= age at first calving; PCV= packed cell volume

with Post-ADG (0.093), AFC (0.162), and PCV (0.025). However, $MY_{100}$ had a significant negative correlation with CI (-0.113). Pre-ADG had significant ($P<0.05$) and positive correlations with Post-ADG (0.032), AFC (0.013), and CI (0.126). Packed cell volume (PCV) was favourably correlated with $MY_{100}$ (0.025), CI (-0.033), and Post-ADG (0.085) and unfavourably correlated with Pre-ADG (-0.067).

The first three principal components were associated with eigenvalues greater than 1 and cumulatively explained 70% of the total variation (Table 5.2). Therefore, three PCs were used to describe the variation in estimated breeding values for the studied traits. The first PC explained 27.7% of the total variation and had positive coefficients for all traits except calving interval (Table 5.2). The second principal component accounted for 22.7% of the total variation and had positive coefficients for Post-ADG, and PCV and negative coefficients for $MY_{100,}$ Pre-ADG, CI, and AFC. While explaining 20% of the total variation, the third principal component had positive coefficients for $MY_{100}$, and AFC. Eigenvectors of the first three PCs are also presented in Table 5.2.

**Table 5.2:** Eigenvectors of the 3 principal components for first 100-days milk yield ($MY_{100}$), pre-weaning daily gain (Pre_ADG), post-weaning daily gain (Post_ADG), calving interval (CI), age at first calving (AFC) and packed cell volume (PCV) in N'Dama cattle

| | | PC1 | PC2 | PC3 |
|---|---|---|---|---|
| Trait | $MY_{100}$ | 0.48 | -0.34 | 0.16 |
| | Pre-ADG | -0.15 | -0.62 | -0.60 |
| | Post-ADG | 0.52 | 0.01 | -0.48 |
| | CI | -0.54 | -0.29 | -0.17 |
| | AFC | 0.38 | -0.48 | 0.28 |
| | PCV | 0.22 | 0.43 | -0.53 |
| Eigenvalue | | 1.36 | 1.12 | 1.01 |
| Variance, % | | 27.68 | 22.66 | 20.55 |
| Cumulative variance, % | | 27.68 | 50.34 | 70.89 |

The eigenvectors for $MY_{100}$ ranged from -0.34 for PC2 to 0.48 for PC1. Pre-ADG and CI had positive eigenvectors for all PCs, while PCV and Post-ADG had positive eigenvectors for the first two PCs (Table 5.2). From the Table above, the trait with the highest positive eigenvector for PC1 was Post-ADG (0.52) followed by ($MY_{100}$) while CI had the least (-0.54). The traits with the least eigenvector for PC2 were Pre-ADG (-0.62), AFC (-0.48) and MY100 (-0.34) while PCV had the highest positive eigenvector (0.43). However, Pre-ADG (-0.60) and PCV (-0.53) had the lowest eigenvectors for PC3 while AFC had the highest (0.28).

All six traits evaluated for the N'Dama cattle exhibited medium to high correlation with either PC1, PC2, or PC3 (Table 5.3), emphasizing the importance of measuring and evaluating the traits in the N'Dama cattle breeding programme, except Post-ADG (PC2). The results in Table 5.3 indicate that EBVs for $MY_{100}$ and Post_ADG were favourably correlated to PC1 (0.56 and 0.60, respectively), while those favourably related to Pre-ADG and AFC were correlated to PC2 (0.66 and 0.51, respectively). The traits favourably correlated to PC3 were Pre_ADG (0.59) and PCV (0.53). The calving interval was correlated to PC2 (0.30).

**Table 5.3:** Linear correlation coefficients between standardized estimated breeding values and the first three principal components for first 100-days milk yield ($MY_{100}$), pre-weaning daily gain (Pre_ADG), post-weaning daily gain (Post_ADG), calving interval (CI), age at first calving (AFC) and packed cell volume (PCV) in N'Dama cattle

| Trait | PC1 | PC2 | PC3 |
|---|---|---|---|
| $MY_{100}$ | 0.56 | 0.36 | -0.16 |
| Pre_ADG | -0.18 | 0.66 | 0.59 |
| Post_ADG | 0.60 | -0.01 | 0.48 |
| CI | -0.63 | 0.30 | 0.17 |
| AFC | 0.44 | 0.51 | -0.28 |
| PCV | 0.25 | -0.45 | 0.53 |

PC1, PC2 and PC3 are the first, second and third principal components, respectively

The standardized score coefficients or weighting factors associated with EBVs for $MY_{100}$, Post-ADG, PCV, CI, and AFC for PC1 and PC3 were medium to high (Table 5.4). This means that these traits would have a faster response to selection compared to the other evaluated traits. This approach presents a practical approach to selection in breeding programmes because the

definition of weighting factors for EBVs of traits is a major difficulty in multiple trait breeding objectives.

**Table 5.4:** Standardized principal score coefficients for standardized estimated breeding values for breeding objective traits of N'Dama cattle in the Gambia

| | PC1 | PC2 | PC3 |
|---|---|---|---|
| $MY_{100}$ | 0.49 | 0.12 | 0.50 |
| Pre-ADG | 0.41 | -0.05 | -0.62 |
| Post-ADG | 0.46 | 0.31 | -0.32 |
| CI | -0.03 | -0.81 | -0.17 |
| AFC | 0.48 | -0.42 | 0.31 |
| PCV | 0.49 | 0.12 | 0.50 |

$MY_{100}$= milk yield at 100 days of all lactation; Pre-ADG= pre-weaning average daily gain; Post-ADG= post-weaning average daily gain; CI= calving interval; AFC= age at first calving; PCV= packed cell volume

The multiple trait selection indexes constructed based on the first three PCs were:

$$SI_{PC1} = 0.49MY_{100} + 0.41Pre\_ADG + 0.46Post\_ADG - 0.03CI + 0.48AFC + 0.49PCV$$

$$SI_{PC2} = 0.12MY_{100} - 0.05Pre\_ADG + 0.31Post\_ADG - 0.81CI - 0.42AFC + 0.12PCV$$

$$SI_{PC3} = 0.50MY_{100} - 0.62Pre\_ADG - 0.32Post\_ADG - 0.17CI + 0.31AFC + 0.50PCV$$

and

$$CSI = b_{MY100}X_{MY100} + b_{Pre\_aADG}X_{Pre\_aADG} + b_{Post\_ADG}X_{Post\_ADG} + +b_{CI}X_{CI} + b_{AFC}X_{AFC} + b_{PCV}X_{PCV}$$ for the conventional selection index

The expected genetic responses for the six traits for the first three PCs and CSI are presented in Table 5.5. The expected genetic progress for $MY_{100}$, Pre_ADG, Post_ADG, and PCV were positive for the three PCIs as well as CSI. The expected progress for $MY_{100}$ ranged from 1.76 kg with a selection index based on CSI and PC3 to 4.05 kg based on PC1 (SIPC1). All the selection indexes resulted in reductions in CI and AFC ranging from -0.57 to -1.56 and -0.23 to -1.60, respectively. Packed cell volume showed the highest response of 0.55 based on SIPC3, while the lowest response of 0.11 was predicted by SIPC1. An index of all traits resulted

in positive responses for SIPC1 and SIPC3 of 4.08 and 2.42, respectively. SIPC2 and CSI resulted in negative genetic responses of -4.47 and -1.55, respectively (Table 5.5).

**Table 5.5:** Predicted genetic response using different selection indexes in N'Dama cattle

| Trait | SIPC1 | SIPC2 | SIPC3 | CSI |
|---|---|---|---|---|
| $MY_{100}$, kg | 4.05 | 3.05 | 1.76 | 1.76 |
| Pre_ADG, kg/day | 0.01 | 0.04 | 0.04 | 1.71 |
| Post_ADG, kg/day | 0.02 | 0.00 | 0.02 | 0.90 |
| CI, months | -1.56 | -0.94 | -0.64 | -0.57 |
| AFC, months | -0.88 | -1.60 | -0.84 | -0.23 |
| PCV, % | 0.11 | 0.25 | 0.55 | 0.27 |
| Index Response | 4.08 | -4.47 | 2.42 | -1.55 |

$MY_{100}$= milk yield at 100 days of all lactation; Pre_ADG= pre-weaning average daily gain; Post_ADG= post-weaning average daily gain; CI= calving interval; AFC= age at first calving; PCV= packed cell volume; SIPC1, SIPC2, SIPC3 are selection indexes constructed using eigenvalues of the first tree principal components; CSI= conventional selection index

### 5.4 Discussion

Results for the N'Dama cattle in the present study imply that increasing the AFC could lead to an improvement in the cumulative milk yield in the first 100 days of lactation. Conversely, improving the milk yield in the first 100 days of lactation could increase AFC. This indicates a trade-off between these two traits, where enhancing one could potentially have an inverse effect on the other. Contrary to the positive genetic correlation of 0.162 found in the present study, Amaya *et al.* (2021), Ayalew *et al.* (2017) and Makgahlela *et al.* (2007) reported negative correlations ranging from -0.19 to -0.44. Selecting for increased pre-and post-ADG would lead to longer AFC. Amaya *et al.* (2021), and Chin-Colli *et al.* (2016) reported a negative genetic correlation between AFC and body weight of -0.33 and -0.34, respectively. The negative genetic correlation of -0.04 between AFC and CI indicates that selecting a reduction in AFC would lead to an increase in CI. This means that improving one of these traits through selection is likely to have a negative effect on the other. These results are similar to those reported for Simmental cattle in Colombia by Amaya *et al.* (2021) where a negative correlation (-0.17) implied an inverse relationship in terms of selection outcome.

In this study, the first three principal components were associated with eigenvalues greater than 1 and cumulatively explained 70% of the total variation. Therefore, three PCs were

sufficient to explain the variation in estimated breeding values for the studied traits. The results of this study agree with the study by Boligon *et al.* (2016) and Vargas *et al.* (2018) in which the first three PCs were able to explain most of the additive genetic variation of different traits in Nellore cattle. In contrast, Tramonte *et al.* (2019) and Viana *et al.* (2020) reported that the first two PCs explained 68.2% and 96% of additive genetic variation for growth traits in Guzera and Nellore cattle, respectively. The proportion of total variation explained by the first three PCs in the present study was within the range of 65.75% (Agudelo-Gómez *et al.,* 2015), 79.06% (Boligon *et al.,* 2016) and 78% (Amaya *et al.,* 2021) reported for milk, growth and fertility traits in various beef cattle populations. In all studies using PCA to study variation in additive genetic variation, the Kaiser criterion which states that the PCs with eigenvalues greater than 1 were responsible for most variation was used (Boligon *et al.,* 2016; Tramonte *et al.,* 2019). This demonstrates that PCA is effective in the simplification of the complexity of data, as when dealing with a multiple trait breeding objective, while still being able to retain most of the original trends and patterns in the data (Macciotta *et al.,* 2015).

Based on PCAs, Viana *et al.* (2020) recommended that a multiple trait selection index comprising growth and visual scores was most appropriate for Nellore cattle. According to Marques *et al.* (2012), the traits to include in the selection index are those that maximize the correlation between the index and the breeding or selection objective. Other studies that have proposed the use of principal component analysis in the development of selection indices include Buzanskas *et al.* (2013), Boligon *et al.* (2016) and Tramonte *et al.* (2019). In the present study, the standardized score coefficients (SSC) or weighting factors associated with EBVs for $MY_{100,}$ Post-ADG, PCV, CI, and AFC were high. This means that these traits would have a faster response to selection compared to the other evaluated traits. This approach presents a practical approach to selection in breeding programmes because the definition of weighting factors for EBVs of traits is a major difficulty in multiple trait breeding objectives. Based on the predicted response to selection, this study recommends the construction of a genetic selection index based on PC1, since the eigenvectors of this PC and principal score coefficients (PSC) associated with the evaluated traits were favourable for the genetic improvement of the traits. Selection on PC2 is not favourable for the N'Dama cattle as it would lead to a reduction of PCV, which is contrary to the breeding objective of improving performance while maintaining resistance to trypanosomosis (Camara *et al.,* 2020). While selection for PC3 would lead to faster pre-weaning and post-weaning growth rates and enhanced disease resistance, animals would have longer intervals between Calvings. Amaya *et al.* (2021) recommended the use of PC1 for selection in Colombian Simmental cattle since it had a high positive correlation

with cumulative milk yield in the first 100 days, implying that animals with the highest values for PC1 would have the highest milk yield (Pinto *et al.*, 2006). Other studies that recommended the use of PC1 for the construction of selection indexes in cattle include Viana *et al.* (2020) and Lopes *et al.* (2016). These studies considered the correlation between the studied traits and the principal components as well as the principal score coefficients and eigenvectors to identify traits that can have the greatest genetic response in a breeding programme (Boligon *et al.*, 2013; Tramonte *et al.*, 2019).

The index based on PC1 (SIPC1) was the best to increase $MY_{100}$ and led to the highest and second highest reductions in CI and AFC and also had the highest overall response. SIPC1 also led to favourable responses in pre-weaning and post-weaning growth rates. Amaya *et al.* (2021) reported that SIPC2 was the best index to increase 305-day milk yield, will small expected genetic progress in the first lactation CI. Selection based on SIPC1 would therefore lead to desirable changes in all traits in the breeding objective of N'Dama cattle. Calving interval is especially important since although it is lowly heritable, its economic impact on beef production is up to 3 - 4 times of milk and beef production traits (growth and carcass traits) (Brumatti *et al.*, 2002; Eler *et al.*, 2014). SIPCI2 resulted in the highest response in AFC and the second highest response in CI, $MY_{100}$ and pre-weaning daily gain, but the worst in post-weaning daily gain and overall response. Amaya *et al.* (2021) and McManus *et al.* (2011) argued that a favourable response in CI does not always mean a reduction in milk yield, but rather an improvement in the efficiency of the production system. According to the production and breeding goal of N'Dama cattle (Bosso *et al.*, 2007; Traoré *et al.*, 2016), SIPC3 would be the best in improving tolerance to trypanosomosis while improving $MY_{100}$, growth, and fertility. Amaya *et al.* (2021) found that SIPC1 was the best index to improve the productive goals of Colombian dual-purpose Simmental cattle of simultaneously increasing beef production and milk production traits. When using PCA, it is important to identify the expected response to the selection of individual goal traits as well as the overall index response. A similar conclusion was made by Sölkner *et al.* (2000) for Austrian Simmental cattle where selection indexes that simultaneously considered beef and milk production yielded greater genetic progress than those that considered the traits singly.

### 5.5 Conclusion

The selection index principal component (SIPC1) resulted in the highest favourable response in $MY_{100}$ and led to the highest and second highest reductions in CI and AFC and also had the highest overall response. SIPC1 also led to favourable responses in pre-weaning and

post-weaning growth rates and PCV. SIPC3 was intermediate in terms of expected genetic responses in $MY_{100,}$ pre- and post-weaning growth rates and AFC and CI, but led to the highest response in PCV. This study has demonstrated that it is possible to build a multiple selection index based on principal component analysis that can be used to accelerate the rate of gain in the breeding goal of the N'Dama cattle.

# CHAPTER SIX
# GENERAL DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS

## 6.1 Aim of the Study

N'Dama cattle are an indigenous breed of cattle reared in West Africa and are well-known for their trypanotolerance and the ability to thrive in challenging environmental conditions. The breed is utilized under such conditions for the production of milk, meat, and draft power among other uses. Techniques used in the control of African Animal Trypanosomosis (AAT) are vector control and chemotherapy (Traoré *et al.,* 2017). Vector is limited due to the vastness of the areas needing the use of insecticides, which becomes an expensive undertaking often resulting in adverse environmental effects coupled with the high cost of trypanocidal drugs which are usually not readily available (Chitanga *et al.,* 2011; Torr & Vale, 2015). Oftentimes, the parasites develop resistance to the drugs (Delespaux *et al.,* 2008) by evading the host immune system through antigen variation by periodically changing its variant surface glycoprotein coat (Michel-Todó *et al.,* 2020; Yaro *et al.,* 2016). Utilization of trypanotolerant breeds that are adapted to sub-Saharan regions (Naessens *et al.,* 2002) is a viable and sustainable alternative to combating AAT. The breeds display the ability to survive, reproduce, and remain productive under trypanosome challenge (Stein *et al.,* 2011). This expressed heritability provides an avenue to improve the performance traits under the prevailing conditions. However, the extent of genetic variation for growth, milk yield, fertility, and disease tolerance traits and their correlations in the N'Dama cattle have not been estimated. The expected response to selection for the breeding goal traits and its implications on other traits of economic importance has not been evaluated.

This thesis aimed at contributing to increased productivity of the N'Dama cattle in the Gambia through the estimation of the genetic parameters and correlation between growth, fertility, milk yield and disease resistance traits and the construction of selection indexes to predict response to selection. The research questions that were addressed include: i) what are the heritability estimates and genetic correlations between body weight and trypanotolerance (PCV) along the growth curve of N'Dama cattle in the Gambia? ii) what are the Genetic correlations between test day milk yield, early growth, and fertility traits for N'Dama cattle in the Gambia? iii) what are the predicted multiple trait responses to selection of alternative selection indexes for growth, milk yield, trypanotolerance, and fertility traits in N'Dama cattle in the Gambia? These questions were derived from the following specific objectives which include: i) to estimate heritability and genetic correlations between growth rates and

trypanotolerance (PCV) along the growth curve of N'Dama cattle in the Gambia, ii) to estimate genetic correlations between test day milk yield, early growth, and fertility traits of N'Dama cattle in the Gambia, iii) to predict multiple trait response to selection of alternative selection indexes for growth, milk yield, trypanotolerance, and fertility traits for N'Dama cattle in the Gambia.

### 6.2 Study Methodology

This study used a total of 5,173, 3,130, 2,488, 2,422, 2,442, 1,471, 1,934, and 1,452 bodyweight records for birth weight (BW) weight at 7 months (WT7), 12 months (WT12), 16 months (WT16), 18 months (WT18), 24 months (WT24), 36 months (WT36) and 50 months (WT50) and 1,782, 1,800, 1,844, 1,608, and 1,459 records for packed cell volume (PCV) at 12 months (PCV12) 18 months (PCV18), 24 months (PCV24), 36 months (PCV36), and 50 months (PCV50) respectively. A total of 10,418 test-day records from the first parity were used to obtain genetic parameters for test-day milk yield

For objectives 1 and 2, variance-covariance components, genetic parameters for growth, fertility, milk yield and trypanotolerance (PCV) were estimated by fitting a univariate animal model via the GIBBSF90 algorithm implemented in the BLUPF90 package (Aguilar *et al.,* 2018). The genetic correlations between the traits were obtained by fitting a multivariate animal model using the same software. For each set of analyses, a total of 300,000 Gibbs samples with a burn-in of 50,000 were used with every 50th sample retained for further analyses using POSTGIBBSF90 (Aguilar *et al.,* 2018) to obtain posterior distribution statistics. The estimated posterior variances and covariances were used to obtain heritability estimates and genetic and phenotypic correlations among the traits. Estimates of heritability were obtained from co-variances obtained from univariate analyses while genetic and phenotypic correlations were calculated using co-variances from bivariate analyses. For test-day milk yield, a second-order and a fourth-order Legendre polynomial was for the fixed, animal genetic and permanent environmental curves to compute random regression coefficients.

For the third objective, principal component analysis was used to construct selection indexes. The procedure used estimated breeding values for pre-weaning daily gain (Pre-ADG), post-weaning daily gain (Post-ADG), cumulative milk yield in the first 100 days of lactation ($MY_{100}$) and packed cell volume (PCV), calving interval (CI) and age at first calving (AFC) standardised to mean of zero and variance of 1. Selection indexes (SI) were constructed using principal components (PC) with eigenvalues greater than 1 and their expected response to selection compared to a conventional selection index (CSI). The CSI was constructed by

weighting the EBV of each trait by the reciprocal of the phenotypic standard deviation. The PCA analyses were performed using the FactoMineR library of the R-Project software.

### 6.3 Genetic Improvement of Production Traits in Tsetse-infested Areas

Large areas of sub-Saharan Africa are not used for cattle production because of the challenge of trypanosomosis which is transmitted by tsetse flies with about 11 million km2 in 40 countries infested with the vector. It is for this reason that the N'Dama cattle genetic improvement programme in the Gambia was initiated to improve growth and milk yield while retaining the breed's ability to tolerate the disease in harsh environmental conditions. The N'Dama is a breed of cattle indigenous to the West African region where it is highly preferred for meat and milk production (Camara *et al.,* 2020). The breed possesses crucial attributes including heat tolerance, adaptation to harsh environments, and the ability to survive on poor-quality feeds (Traoré *et al.,* 2016). Most importantly, the breed has the innate ability to thrive in tsetse-infested areas where there is a high risk of animal trypanosomiasis infection. These qualities are necessary to achieve sustainable livestock production under the low input conditions prevalent in most of the West African countries where animals have an integral role. For these reasons, the N`Dama cattle breed is the most widely reared by cattle keepers within the mixed crop-livestock production farming systems in The Gambia (Olaniyan *et al.,* 2021; Olaniyan, 2015). Apart from resistance to trypanosomosis, the breed is tolerant to heat and has good draught power and the ability to thrive on low-quality feeds. The establishment of the genetic improvement program in 1994 at the then International Trypanotolerance Centre (ITC) (now WALIC) in The Gambia aimed to improve milk production and meat of the N'Dama cattle breed for current and future needs without compromising the breed's adaptive traits (Camara *et al.,* 2020). The programme operates as an open nucleus breeding scheme comprising a well-recorded herd of about 400 breeding females (Bosso *et al.,* 2009). The selection criteria for choosing superior animals were growth rate from birth to 12 months in a controlled environment at Keneba and growth rate from 15 months and 36 months in the actual low input environment at Bansang as well as first 100-day milk yield of multiple lactations (Bosso *et al.,* 2007).

### 6.4 Growth Traits

To understand the genetic basis of growth traits, this thesis evaluates genetic variation and parameters for body weight measurements along the growth curve. The heritability estimates for body weight at various ages along the growth curve were medium ranging from

0.31±0.06 to 0.47±0.05. The genetic correlations among body weights were high in the region of 0.73±0.01 to 0.96±0.01. The heritability estimates for average daily gain from birth to 12 months and from 15 months to 36 months were 0.42±0.02 and 0.38±0.03, respectively. The evolution of body weight under the natural trypanosome challenge is the most economically important trait (Kristjanson *et al.,* 1999). The present study demonstrated that among the body weight measures considered, WT12 had the highest heritability estimate (0.46±0.01) followed by WT18 (0.44±0.01). Heritability estimates provide evidence that a trait can be improved through selection (Koetz Junior *et al.,* 2019). The high genetic correlation between body weights at different ages was high (0.73±0.01 to 0.97±0.01) suggesting that any body weight among those studied can be used as a selection criterion and would lead to improvement of body weight along the growth curve (Kamprasert *et al.,* 2019). The results of this study indicate that animals can be selected for high body weight in the early stage of the animal's life from 12 months and would also be heavy at maturity and any other age. It has been shown that beef cattle have low birth weight as an adaptation against dystocia, but the calves can grow fast after birth due to the good mothering ability of their dams. The heritability estimates for growth traits obtained for the N'Dama cattle indicate that selection would result in improved growth and body weight at various ages. Indeed, studies have shown that local farmers prefer the N'Dama over other breeds and genotypes when it comes to consideration of resistance to diseases and traction (Traoré *et al.,* 2016). Whereas improvement in body weight for the N'Dama cattle is desirable in terms of availing heavy animals at the point of sale and for draft power, it is expected that there will be a related increase in feed intake (Majoya *et al.,* 2022). For this reason, most breeding programmes are shifting from focusing on growth-related traits only to incorporating feed efficiency traits (Hozáková *et al.,* 2020; Matos *et al.,* 2021; Pryce *et al.,* 2014). Therefore, the economic efficiency of beef production has to be considered (Hozáková *et al.,* 2020) and calls for strategies that lead to efficient utilization of natural pastures (Rojas-Downing *et al.,* 2017). Body weight is negatively genetically correlated with measures of feed efficiency such as the Kleiber Index and relative growth rate (de Figuiredo *et al.,* 2019; Majoya *et al.,* 2022). Thus, while selecting for faster growth rates leading to heavier body weight in the N'Dama cattle, consideration should be made for the scarcity of feed resources under natural grazing systems where the breed is reared.

### 6.5 Disease Resistance (Trypanotolerance)

In cattle, African Animal trypanosomosis is transmitted when cattle are bitten by tsetse flies carrying pathogenic protozoa (Welburn *et al.,* 2016). The disease-causing pathogens

include *trypanosoma congolense*, *trypanosoma vivax*, and *trypanosoma brucei brucei* (Batista *et al.,* 2011; Yaro *et al.,* 2016), with *T. congolense* being the main cause of the disease in sub-Saharan Africa (Naessens, 2006). The most common method in the prevention and control of trypanosomosis centres on reduction of the contact between cattle and vectors. These include tsetse fly control, the use of a trypanocidal drug and cattle breeds that tolerate the disease (Achenef & Bekele, 2013; Bouyer *et al.,* 2015). The first two methods though effective to some extent, are limited by high cost, expansiveness of the areas infested by tsetse flies, unavailability of trypanocidal drugs and development of drug resistance by the parasites (Chitanga *et al.,* 2011; Michel-Todó *et al.,* 2020; Torr & Vale, 2015; Yaro *et al.,* 2016). Breeds that display Trypanotolerance thrive under natural trypanosome challenge, reproducing and remaining productive under such conditions (Dayo *et al.,* 2010; Knap & Doeschl-Wilson, 2020; Yaro *et al.,* 2011) in contrast to trypano-susceptible breeds which succumb to the disease challenge (Berthier *et al.,* 2015). The Utilization of trypanotolerant breeds such as the N'Dama (Camara *et al.,* 2020), Sheko (Bayou *et al.,* 2015) and Orma Boran (Orenge *et al.,* 2012) among others is therefore beneficial in production systems and regions with a high prevalence of trypanosomosis. Their utilization also helps to conserve the genetic diversity of such breeds. The N'Dama cattle have been found to maintain their haematological parameters within acceptable normal levels, highlighting the importance of the breed in tsetse and trypanosomiasis control strategies (Ganyo *et al.,* 2018). The breed is preferred because of its ability to resist diseases, especially trypanosomosis (Traoré *et al.,* 2016). Packed cell volume is a reliable indicator of AAT barring other anaemia-causing infections (Aksoy *et al.,* 2008; Van Wyk *et al.,* 2013) and has higher sensitivity and specificity compared to other parasitological diagnoses (Marcotty *et al.,* 2008). The present study found heritability estimates for PCV in the range of 0.13±0.01 to 0.18±0.01. The low to medium estimates of heritability indicate that disease resistance to trypanosomosis can be enhanced through the selection of PCV as a proxy. This attribute is important because trypanosome infection causes animals to be anaemic accompanied by loss of appetite leading to loss of weight and reduced milk yield, poor fertility and finally death (Berthier *et al.,* 2015; Dagnachew *et al.,* 2015; Leta *et al.,* 2016). The heritability estimates for PCV show the existence of additive genetic variation which can be used as the basis of selection and identify the extent of anaemia as an indicator of an animal's susceptibility or resistance to trypanosomosis infection. Due to the evidence of the existing genetic variability, selection for resistance to trypanosomosis would be efficient. The heritability estimates for PCV at various ages in the N'Dama cattle which are consistent with estimates reported for other breeds in sub-Saharan Africa (Rowlands *et al.,* 1995) and Asia

(Fukasawa *et al.,* 2002) mean that the N'Dama cattle have evolved in the presence of the trypanosome parasites and therefore provide a strategic alternative to the control of trypanosomosis. The present study reported favourable genetic correlations between PCV at different ages ranging from low (0.16±0.02) to high (0.56±0.05). As such, the use of any measure of PCV would result in a favourable correlated response at any age. PCV at 12 months had the highest heritability estimate (0.15±0.01) and also had medium genetic correlations with all the other measures of this trait and therefore is recommended for use as the selection criterion to improve resistance to trypanosomosis.

### 6.6 Fertility Traits

Whereas the N'Dama cattle breeding programme was designed to improve growth rates and milk production in the first 100 days of lactation (Camara *et al.,* 2020), fertility plays a crucial role in the efficiency of cattle enterprises (Johnston, 2014; Krupová *et al.,* 2020). Age at first calving and calving intervals are the most studied traits in cattle because their data is easily and routinely recorded in most production systems. An early age at first calving increases the productive rate and decreases the replacement rate in cattle herds (López-Paredes *et al.,* 2018). In cattle, a calving interval of 365 days is desired with the focus being on reducing the non-productive periods since the calving interval is directly associated with the number of calves born annually (López-Paredes *et al.,* 2018) and in the lifetime of a cow.

The N'Dama cattle had a mean AFC of 65.46±0.39 months, which is longer than estimates of 24.1 months to 34 months reported for most cattle breeds (Lopez *et al.,* 2020; Shin *et al.,* 2021). This calls for the need to develop strategies to reduce the age at first calving. Age at first calving is a complex trait which includes the rate at which animals grow to puberty, the heifer's ability to conceive, carry the pregnancy to term and give birth to the calf (López-Paredes *et al.,* 2018). Age at first calving for the N'Dama cattle was medium (0.39±0.01) and higher than estimates reported for most cattle breeds which ranged from 0.1 (Lopez *et al.,* 2020) to 0.28 (Ulhôa *et al.,* 2016). Therefore, the late age at first calving for the N'Dama cattle could be improved through selection. However, changes in management and improvement in environmental factors could also contribute to the shortening of age at first calving. The calving interval for the N'Dama cattle of 23.3±0.11 months was higher than intervals reported for most cattle breeds (Brzáková *et al.,* 2019; López-Paredes *et al.,* 2018) of below 17 months. When this is viewed together with the reported heritability estimate of 0.14±0.01, there is potential to improve the calving interval in the N'Dama cattle population. This is especially important because N'Dama cattle are raised under harsh environmental conditions (Traoré *et al.,* 2016).

The breeding objective of the N'Dama cattle breeding programme should be reviewed to include fertility traits since a later age at first calving and longer calving interval are associated with decreased lifetime productivity in cattle (Cammack *et al.,* 2009; Gutiérrez *et al.,* 2002).

## 6.7 Genetic correlations between breeding objective traits of N'Dama cattle in the Gambia

The N'Dama cattle breeding programme aims to improve meat and milk production under the natural trypanosome challenge (Bosso *et al.,* 2009; Traoré *et al.,* 2018; Ouédraogo *et al.,* 2021). Therefore, the selection goal is to improve the growth rate from birth to 12 months and from 15 months to 36 months as well as cumulative milk yield in the first 100 days of lactation over multiple locations (Bosso *et al.,* 2007). The present study reported medium to high genetic correlations between TDMY and BW (0.51±0.02), WWT (0.88±0.03), and ADG (0.52±0.02). The results differed from -0.71±0.4 between milk yield and weaning weight for Nguni cattle (Nesengani *et al.,* 2018). The results for N'Dama cattle imply that weaning weight could be used as a selection criterion to improve TDMY along the lactation curve. The genetic correlations between birth weight and weaning weight (0.60±0.05) and between birth weight and average daily gain (0.25±0.01) were favourable and therefore the use of weaning weight as a selection criterion which also had a high direct heritability estimate (0.48±0.03) would not compromise average daily gain. The favourable genetic correlation between weaning weight and birth weight implies that birth weight would increase concomitantly due to selection for weaning weight. In cattle birth weight is used as a predictor of difficulty in giving birth or dystocia, perinatal calf mortality (Hohnholz *et al.,* 2019) and longer calving intervals (Hwang *et al.,* 2008; Lopez *et al.,* 2020). Therefore, while the results of the present study indicate that weaning weight can be used to indirectly select for TDMY, care has to be taken to ensure that an increase in birth weight does not lead to dystocia, perinatal calf mortality or prolonged calving intervals.

## 6.8 Implications of Trypanotolerance and Fertility Traits

Whereas the primary focus of the N'Dama breeding programme is to improve body weight and milk yield under natural trypanosome challenge (Ouédraogo *et al.,* 2021), it is important to consider other traits that have a significant economic effect on cattle enterprises. It is a well-established fact that prolonged age at first calving and prolonged calving intervals have a negative impact on the efficacy of production and lifetime production and productivity in cattle enterprises ((Johnston, 2014; Krupová *et al.,* 2020). Similarly, although selection for

the breeding goal traits in the N'Dama cattle breeding programme is carried out under natural trypanosome, aiming to increase milk yield and body weight may comprise disease resistance (Schneider *et al.,* 2023). The present study found a positive genetic correlation between test day milk yield (TDMY) and CI which implies the need for a trade-off, since selection for increased milk yield would result in prolonged calving intervals which is associated with reduced lifetime productivity and higher culling rates (Musingi *et al.,* 2021; Sung *et al.,* 2016) leading to significant losses. The N'Dama cattle are reared under harsh environmental conditions under tsetse challenge (Camara *et al.,* 2020). Other than genetics, sub-optimal management can contribute to poor fertility (Martinez-Castillero *et al.,* 2020). Indigenous cattle in the tropics are also associated with delayed postpartum resumption of ovarian activity, leading to longer calving intervals (Murillo-Medina *et al.,* 2009). This is because of the effect of suckling and loss of body condition pre-calving (Diaz *et al.,* 2018). The negative genetic correlation between TDMY and AFC (-0.66±0.01) was favourable since selecting for increased TDMY would shorten AFC (Stefan *et al.,* 2020), leading to increased lifetime productivity and herd management efficiency.

Resistance to trypanosomosis, indicated by PCV, is an important attribute of the N'Dama cattle with the prevailing production conditions (Ouédraogo *et al.,* 2021). Though the breeding goal aims to improve body weight and milk yield under the natural trypanosome challenge, there is a need to ensure that resultant superior animals are not immune-compromised. Previous studies have reported that disease-resistance traits are unfavourably genetically correlated with growth traits (Gathura *et al.,* 2020; Oliveira *et al.,* 2018). For N'Dama cattle, the genetic correlations between growth traits and PCV reported by the present study (-0.14±0.03 to 0.59±0.01), imply an indirect response ranging from a trade-off between growth and PCV (for negative correlations) to a favourable direct response in PCV (for positive correlations). The unfavourable genetic correlations occurred at the later stages of the growth curve (50 months of age). Therefore, it can be generally argued that the genetic factors responsible for growth traits are also largely associated with higher PCV. It is however important to acknowledge that PCV is not solely indicative of infection by trypanosomosis but can also imply poor nutrition, tick-borne diseases and helminthosis (Moti *et al.,* 2013).

### 6.9 Selection Indexes for Improvement of Growth Rates, Milk Yield, Trypanotolerance and Fertility Traits in N'Dama Cattle

The results of the present study call for the need to simultaneously select multiple traits using a weighted selection index as has been suggested by other studies (Marques *et al.,* 2012;

Viana *et al.,* 2020). However, the derivation and assignment of weighting factors are problematic because of the empirical nature of the process. This study found that this challenge can be overcome by the use of principal component analysis (PCA) to create selection indexes based on a linear combination of standardized estimated breeding values of breeding goal traits for N'Dama cattle (Boligon *et al.,* 2016; Buzanskas *et al.,* 2013). The process involved the reduction of originally correlated variables into a smaller set of uncorrelated variables by taking away repeated information while retaining most of the original variability in the original variance-covariances (Boligon *et al.,* 2016; Kirkpatrick & Meyer, 2004). This enables the simultaneous selection of traits of interest (Vargas *et al.,* 2018). The present study therefore found that the first three principal components were associated with eigenvalues >1 and cumulatively explained 70% of the total variation in the EBVs of the breeding goal traits. The first three Principal components were used to create multiple trait selection indexes and their expected response compared to a conventional selection index. The multiple trait selection indexes resulted in an overall positive response and favourable response in all the traits in the index. The conventional selection index resulted in a favourable expected response in all the traits in the index but had a negative overall response. This study has therefore shown that principal components (PC) can be used to develop a selection index using the first principal component for the N'Dama cattle breeding programme using the first principal component. Other livestock populations in which Principal component analysis has been applied include White leghorn (Savegnago *et al.*, 2011), dual-purpose buffaloes (Agudelo-Gómez *et al.*, 2016), Nellore cattle (Viana *et al.,* 2020), Egyptian buffaloes (Salem *et al.,* 2021) and Guzera cattle (Tramonte *et al.,* 2019).

### 6.10 Conclusions

i. Body weight and PCV in N'Dama cattle had low to medium heritability estimates and can be improved through selection. However, genetic correlations in the first 24 months were unfavourable but subsequently, body weight could be used as a selection criterion for trypanotolerance.
ii. Genetic improvement of pre-weaning, post-weaning growth rates and TDMY in the N'Dama cattle breeding programme will result in precocious age at first calving and lengthening of calving intervals.
iii. A multiple trait selection index based on the first principal component (SIPC1) resulted in favourable responses in $MY_{100}$, CI, AFC, pre-weaning and post-weaning growth rates, and PCV and also had the highest overall response.

### 6.11 Recommendations

i. Simultaneous improvement of body weight and PCV should consider the genetic correlations between the two trait categories in the first 24 months of age.

ii. Genetic improvement of the N'Dama cattle should be based on a weighted multiple trait index that includes pre- and post-weaning growth rate and TDMY in addition to calving interval and BW to avoid longer calving intervals and heavier calves at birth.

iii. Principal Component Analysis can be used to construct a multiple-trait selection index to accelerate the rate of gain in the breeding goal of the N'Dama cattle.

### 6.12 Areas for Further Research

Further research is required to evaluate whether genotype by environment interaction exists between the nucleus and commercial herds for growth, disease tolerance, fertility traits, and survival traits.

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## APPENDICES

### Appendix A. NACOSTI Permit

License No: **NACOSTI/P/24/33476**

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NATIONAL COMMISSION FOR SCIENCE,TECHNOLOGY & INNOVATION

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**RESEARCH LICENSE**

This is to Certify that Mr.. Kebba Nyabally of Egerton University, has been licensed to conduct research as per the provision of the Science, Technology and Innovation Act, 2013 (Rev. 2014) in Baringo on the topic: Genetic and Economic Evaluation of Trypanotolerant N'Dama Cattle under Open Nucleus Breeding Program in the Gambia for the period ending : 09/March/2025.

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**Appendix B: Research Ethics Clearance**

EU/RE/DIR/009

*Approval No: EUISERC/APP/305/2024*


**EGERTON UNIVERSITY**

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**EGERTON UNIVERSITY INSTITUTIONAL SCIENTIFIC AND ETHICS REVIEW COMMITTEE**

**EU/RE/DIR/009**
***Approval No. EUISERC/APP/305/2024*** ***20th February 2024***


Kebba Nyabally,
Egerton University,
Dept. Animal Science,
PO Box 536-20115, Riverside Hostels
Egerton, Njoro
Telephone: (+254) 0757492277
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Dear Kebba,

**RE: ETHICAL APPROVAL: GENETIC AND ECONOMIC EVALUATION OF TRYPANOTOLERANT N'DAMA CATTLE UNDER THE OPEN NUCLEUS BREEDING PROGRAM IN THE GAMBIA**

This is to inform you that the ***Egerton University Institutional Scientific and Ethics Review Committee*** has reviewed and approved your above research proposal. Your application approval number is ***EUISERC/APP/305/2024.*** The approval period is ***20th February 2024 – 21st February, 2025***

This approval is subject to compliance with the following requirements;

i. Only approved documents including (informed consents, study instruments, MTA) will be used.
ii. You are required to adhere to the Institutional Experimental Animals Use and Care policy.
iii. All changes including (amendments, deviations, and violations) are submitted for review and approval by ***Egerton University Institutional Scientific and Ethics Review Committee***.
iv. Death and life-threatening problems and serious adverse events or unexpected adverse events whether related or unrelated to the study must be reported to ***Egerton University Institutional Scientific and Ethics Review Committee*** within 72 hours of notification
v. Any changes, anticipated or otherwise that may increase the risks or affect safety or welfare of study participants and others or affect the integrity of the research must be reported to ***Egerton University Institutional Scientific and Ethics Review Committee*** within 72 hours.

vi. Clearance for Material Transfer of biological specimens must be obtained from relevant institutions.

vii. Submission of a request for renewal of approval at least 60 days prior to expiry of the approval period. Attach a comprehensive progress report to support the renewal.

viii. Submission of an executive summary report within 90 days upon completion of the study to ***Egerton University Institutional Scientific and Ethics Review Committee***.

Prior to commencing your study, you will be expected to obtain a research license from National Commission for Science, Technology and Innovation (NACOSTI) https://oris.nacosti.go.ke and also obtain other clearances needed.

Yours sincerely.

EGERTON UNIVERSITY RESEARCH ETHICS Date. 20/02/2024

Prof. Raphael M. Ngure

**CHAIRMAN, EGERTON UNIVERSITY INSTITUTIONAL SCIENTIFIC AND ETHICS REVIEW CTTEE**

*RMN/BK/*

## Appendix C. Research Outputs

Bayesian Procedure Implemented in Gibbs Sampling in the GIBBS1F90 software

Variable A: Bodyweight post-Gibbs

******** Monte Carlo Error by Time Series ********

| Pos. | eff1 | eff2 | trt1 | trt2 | MCE | Mean | HPD Interval (95%) | | Effective sample size | Median | Mode | Independent chain size |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 4 | 4 | 1 | 1 | 0.69220E-01 | 0.98818 | 0.71920 | 1.2570 | 5.4 | 0.98350 | 1.0930 | 396 |
| 2 | 4 | 4 | 1 | 2 | 0.14261 | 2.6330 | 1.4470 | 3.6920 | 16.1 | 2.6700 | 2.5938 | 212 |
| 3 | 4 | 4 | 1 | 3 | 0.13762 | 3.7386 | 2.0960 | 5.3640 | 37.3 | 3.7650 | 3.5044 | 80 |
| 4 | 4 | 4 | 1 | 4 | 0.35676 | -1.7726 | -4.4060 | 0.67450 | 13.9 | -1.7880 | -2.1270 | 418 |
| 5 | 4 | 4 | 1 | 5 | 0.29221 | -5.1798 | -8.0040 | -2.5660 | 23.8 | -5.1660 | -5.9984 | 144 |
| 6 | 4 | 4 | 1 | 6 | 0.57399 | -3.9776 | -7.8240 | -0.98660 | 9.7 | -3.7390 | -3.3296 | 426 |
| 7 | 4 | 4 | 1 | 7 | 0.63560 | -2.7111 | -6.0400 | 0.28210 | 7.3 | -2.5520 | -2.2549 | 390 |
| 8 | 4 | 4 | 2 | 2 | 1.6352 | 90.829 | 83.090 | 98.530 | 6.2 | 90.800 | 90.366 | 634 |
| 9 | 4 | 4 | 2 | 3 | 0.99382 | 159.50 | 148.90 | 170.50 | 32.2 | 159.40 | 160.40 | 222 |
| 10 | 4 | 4 | 2 | 4 | 1.1545 | 199.79 | 186.30 | 213.70 | 36.7 | 199.50 | 199.18 | 230 |
| 11 | 4 | 4 | 2 | 5 | 1.4066 | 185.51 | 170.80 | 199.10 | 27.6 | 185.30 | 183.25 | 202 |
| 12 | 4 | 4 | 2 | 6 | 1.4324 | 228.76 | 212.60 | 245.40 | 35.2 | 228.70 | 225.58 | 200 |
| 13 | 4 | 4 | 2 | 7 | 3.0124 | 188.38 | 170.70 | 209.60 | 11.3 | 188.20 | 184.81 | 266 |
| 14 | 4 | 4 | 3 | 3 | 1.0658 | 291.96 | 274.50 | 310.50 | 77.0 | 291.90 | 290.33 | 54 |
| 15 | 4 | 4 | 3 | 4 | 1.1651 | 383.03 | 360.10 | 404.90 | 98.1 | 382.60 | 386.00 | 48 |
| 16 | 4 | 4 | 3 | 5 | 1.9298 | 371.92 | 345.90 | 396.90 | 47.6 | 371.60 | 366.51 | 92 |
| 17 | 4 | 4 | 3 | 6 | 1.5996 | 445.74 | 417.60 | 472.60 | 81.9 | 445.70 | 444.33 | 78 |
| 18 | 4 | 4 | 3 | 7 | 2.6781 | 350.75 | 321.30 | 377.20 | 29.3 | 350.90 | 351.29 | 184 |
| 19 | 4 | 4 | 4 | 4 | 2.7808 | 576.06 | 543.50 | 612.80 | 41.4 | 575.40 | 571.14 | 226 |
| 20 | 4 | 4 | 4 | 5 | 3.1025 | 601.25 | 562.60 | 639.40 | 42.2 | 600.50 | 598.66 | 124 |
| 21 | 4 | 4 | 4 | 6 | 2.7590 | 719.02 | 678.10 | 760.50 | 60.8 | 718.80 | 718.36 | 124 |
| 22 | 4 | 4 | 4 | 7 | 4.4462 | 557.68 | 519.40 | 602.20 | 23.6 | 556.50 | 554.25 | 194 |
| 23 | 4 | 4 | 5 | 5 | 4.1573 | 661.61 | 615.50 | 708.90 | 35.5 | 662.30 | 662.83 | 98 |
| 24 | 4 | 4 | 5 | 6 | 3.6033 | 789.26 | 742.50 | 837.30 | 47.7 | 788.90 | 793.03 | 124 |
| 25 | 4 | 4 | 5 | 7 | 3.5613 | 611.70 | 571.20 | 654.00 | 36.8 | 612.10 | 604.74 | 190 |
| 26 | 4 | 4 | 6 | 6 | 4.9282 | 1036.0 | 970.60 | 1099.0 | 44.5 | 1036.0 | 1036.0 | 124 |
| 27 | 4 | 4 | 6 | 7 | 6.5151 | 855.76 | 798.30 | 921.00 | 23.6 | 854.50 | 855.99 | 226 |
| 28 | 4 | 4 | 7 | 7 | 12.296 | 762.32 | 692.00 | 845.50 | 10.6 | 758.20 | 753.91 | 228 |
| 29 | 0 | 0 | 1 | 1 | 0.37606E-01 | 12.431 | 12.040 | 12.840 | 30.0 | 12.420 | 12.405 | 282 |
| 30 | 0 | 0 | 2 | 2 | 0.36575 | 46.051 | 42.630 | 50.080 | 27.7 | 45.980 | 45.843 | 140 |
| 31 | 0 | 0 | 3 | 3 | 0.66693 | 47.870 | 42.000 | 53.280 | 19.1 | 48.030 | 49.031 | 218 |

Variable B: Packed cell volume post-Gibbs

******** Monte Carlo Error by Time Series ********

| Pos. | eff1 | eff2 | trt1 | trt2 | MCE | Mean | HPD Interval (95%) | | Effective sample size | Median | Mode | Independent chain size |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 5 | 5 | 1 | 1 | 0.21316 | 5.3496 | 4.3510 | 6.5970 | 8.4 | 5.2510 | 4.9326 | 138 |
| 2 | 5 | 5 | 1 | 2 | 0.18314 | 2.5748 | 2.0150 | 3.1930 | 3.5 | 2.5200 | 2.3266 | 308 |
| 3 | 5 | 5 | 1 | 3 | 0.13992 | 3.4401 | 2.6480 | 4.2950 | 9.0 | 3.4210 | 3.3646 | 126 |
| 4 | 5 | 5 | 1 | 4 | 0.74981E-01 | 1.9692 | 1.5340 | 2.4150 | 9.0 | 1.9460 | 1.8714 | 258 |
| 5 | 5 | 5 | 1 | 5 | 0.46028 | 2.8868 | 1.7150 | 4.0730 | 2.6 | 2.7430 | 1.9985 | 316 |
| 6 | 5 | 5 | 2 | 2 | 0.13355 | 1.6337 | 1.3040 | 2.2310 | 3.8 | 1.5480 | 1.4226 | 300 |
| 7 | 5 | 5 | 2 | 3 | 0.68405E-01 | 1.8526 | 1.4530 | 2.2560 | 8.6 | 1.8340 | 1.7605 | 158 |
| 8 | 5 | 5 | 2 | 4 | 0.72562E-01 | 1.5664 | 1.1860 | 1.9360 | 7.3 | 1.5650 | 1.5790 | 188 |
| 9 | 5 | 5 | 2 | 5 | 0.18451 | 1.8814 | 1.3700 | 2.5260 | 3.3 | 1.7750 | 1.7029 | 306 |
| 10 | 5 | 5 | 3 | 3 | 0.15392 | 2.8790 | 1.9750 | 3.7870 | 7.4 | 2.8650 | 2.8925 | 152 |
| 11 | 5 | 5 | 3 | 4 | 0.12830 | 2.1507 | 1.6350 | 2.7500 | 5.5 | 2.1190 | 2.0431 | 378 |
| 12 | 5 | 5 | 3 | 5 | 0.99093E-01 | 2.1438 | 1.7000 | 2.7160 | 7.1 | 2.1410 | 1.9246 | 174 |
| 13 | 5 | 5 | 4 | 4 | 0.15485 | 2.5119 | 1.8330 | 3.1460 | 5.2 | 2.5040 | 2.5424 | 208 |
| 14 | 5 | 5 | 4 | 5 | 0.12599 | 2.0213 | 1.4610 | 2.5770 | 6.2 | 2.0590 | 2.1800 | 174 |
| 15 | 5 | 5 | 5 | 5 | 0.23657 | 3.0263 | 2.1660 | 3.9860 | 4.1 | 3.0270 | 2.6641 | 264 |
| 16 | 0 | 0 | 1 | 1 | 0.13081 | 10.119 | 8.6490 | 11.430 | 29.7 | 10.120 | 10.144 | 46 |
| 17 | 0 | 0 | 2 | 2 | 0.54274E-01 | 8.9626 | 8.2470 | 9.7730 | 49.7 | 8.9690 | 9.0085 | 72 |
| 18 | 0 | 0 | 3 | 3 | 0.66388E-01 | 8.8681 | 8.2240 | 9.6950 | 33.9 | 8.8520 | 8.7508 | 58 |
| 19 | 0 | 0 | 4 | 4 | 0.13365 | 7.2743 | 6.4930 | 8.0100 | 8.9 | 7.2880 | 7.2872 | 188 |
| 20 | 0 | 0 | 5 | 5 | 0.93654E-01 | 6.0013 | 5.0250 | 6.9500 | 25.6 | 5.9750 | 6.1224 | 58 |
| 21 | | | | h2 | 0.43140E-02 | 0.20280 | 0.17241 | 0.23086 | 11.6 | 0.20086 | 0.19712 | 130 |
| 22 | | | | h2 | 0.54566E-02 | 0.88100E-01 | 0.74261E-01 | 0.11268 | 3.8 | 0.83991E-01 | 0.80763E-01 | 300 |
| 23 | | | | h2 | 0.50408E-02 | 0.13435 | 0.10348 | 0.15957 | 6.4 | 0.13484 | 0.13540 | 216 |
| 24 | | | | h2 | 0.65104E-02 | 0.14308 | 0.11586 | 0.16744 | 4.7 | 0.14249 | 0.14226 | 220 |
| 25 | | | | h2 | 0.50823E-02 | 0.16784 | 0.14680 | 0.19612 | 7.2 | 0.16513 | 0.16443 | 252 |
| 26 | | | | rg12 | 0.20173E-01 | 0.87183 | 0.80379 | 0.93143 | 3.0 | 0.87766 | 0.89135 | 314 |
| 27 | | | | rg13 | 0.10907E-01 | 0.87785 | 0.82998 | 0.92067 | 5.2 | 0.88134 | 0.88919 | 222 |
| 28 | | | | rg14 | 0.22127E-01 | 0.54100 | 0.42316 | 0.63440 | 6.0 | 0.55041 | 0.57316 | 344 |
| 29 | | | | rg15 | 0.82451E-01 | 0.71364 | 0.48685 | 0.87428 | 2.6 | 0.74163 | 0.84889 | 336 |
| 30 | | | | rg23 | 0.40919E-01 | 0.86178 | 0.73044 | 0.93808 | 2.9 | 0.89106 | 0.92763 | 332 |
| 31 | | | | rg24 | 0.32092E-01 | 0.77744 | 0.69400 | 0.86350 | 3.0 | 0.78724 | 0.84445 | 304 |

Variable C: Bodyweight and Packed cell volume post-Gibbs

******** Monte Carlo Error by Time Series ********

| Pos. | eff1 | eff2 | trt1 | trt2 | MCE | Mean | HPD Interval (95%) | | Effective sample size | Median | Mode | Independent chain size |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 5 | 5 | 1 | 1 | 1.3860 | 249.68 | 231.10 | 269.90 | 51.4 | 249.30 | 247.36 | 402 |
| 2 | 5 | 5 | 1 | 2 | 0.80230 | 333.46 | 312.80 | 357.10 | 202.1 | 333.30 | 334.86 | 92 |
| 3 | 5 | 5 | 1 | 3 | 1.0629 | 346.05 | 323.10 | 369.40 | 131.4 | 345.80 | 349.24 | 242 |
| 4 | 5 | 5 | 1 | 4 | 1.8718 | 336.50 | 311.10 | 362.80 | 50.0 | 336.60 | 338.65 | 352 |
| 5 | 5 | 5 | 1 | 5 | 2.3957 | 310.48 | 280.00 | 340.70 | 42.9 | 310.00 | 308.26 | 292 |
| 6 | 5 | 5 | 1 | 6 | 1.0778 | 18.548 | 12.810 | 24.970 | 8.4 | 18.260 | 17.900 | 1038 |
| 7 | 5 | 5 | 1 | 7 | 0.51528 | 14.588 | 10.810 | 18.400 | 14.8 | 14.570 | 14.526 | 984 |
| 8 | 5 | 5 | 1 | 8 | 0.59032 | 3.9715 | -0.21480 | 8.3450 | 12.5 | 3.9200 | 3.7893 | 940 |
| 9 | 5 | 5 | 1 | 9 | 0.34476 | 4.2009 | 0.60720 | 7.7290 | 29.5 | 4.2580 | 4.4454 | 400 |
| 10 | 5 | 5 | 1 | 10 | 0.93816 | -4.8964 | -10.470 | 1.7750 | 12.3 | -5.3610 | -5.7696 | 490 |
| 11 | 5 | 5 | 2 | 2 | 3.2974 | 475.84 | 441.00 | 513.50 | 32.4 | 475.50 | 473.37 | 398 |
| 12 | 5 | 5 | 2 | 3 | 2.4293 | 509.31 | 474.60 | 544.80 | 55.7 | 508.70 | 507.19 | 398 |
| 13 | 5 | 5 | 2 | 4 | 2.9073 | 504.66 | 465.20 | 541.80 | 46.6 | 504.30 | 503.97 | 318 |
| 14 | 5 | 5 | 2 | 5 | 3.6308 | 470.47 | 427.10 | 514.90 | 38.9 | 470.00 | 471.26 | 310 |
| 15 | 5 | 5 | 2 | 6 | 1.2433 | 23.094 | 15.880 | 31.580 | 10.5 | 22.570 | 21.398 | 1086 |
| 16 | 5 | 5 | 2 | 7 | 0.47192 | 25.957 | 20.910 | 31.310 | 33.5 | 25.790 | 25.739 | 342 |
| 17 | 5 | 5 | 2 | 8 | 0.37840 | 10.057 | 5.3980 | 15.900 | 44.7 | 9.9430 | 10.253 | 272 |
| 18 | 5 | 5 | 2 | 9 | 0.41983 | 6.6326 | 1.8490 | 11.510 | 36.3 | 6.7410 | 7.0031 | 302 |
| 19 | 5 | 5 | 2 | 10 | 1.4102 | -3.3444 | -11.310 | 5.9640 | 10.7 | -3.7980 | -5.2433 | 570 |
| 20 | 5 | 5 | 3 | 3 | 3.6914 | 588.33 | 544.20 | 635.20 | 40.7 | 587.20 | 580.81 | 424 |
| 21 | 5 | 5 | 3 | 4 | 3.3082 | 587.47 | 541.00 | 632.80 | 50.7 | 586.90 | 587.21 | 350 |
| 22 | 5 | 5 | 3 | 5 | 4.0654 | 559.71 | 507.20 | 611.50 | 43.7 | 559.00 | 554.32 | 288 |
| 23 | 5 | 5 | 3 | 6 | 0.90630 | 20.676 | 12.540 | 28.920 | 20.5 | 20.790 | 21.022 | 402 |
| 24 | 5 | 5 | 3 | 7 | 0.55830 | 27.081 | 21.480 | 32.730 | 28.2 | 26.990 | 27.415 | 412 |
| 25 | 5 | 5 | 3 | 8 | 0.81954 | 19.350 | 13.210 | 26.630 | 16.3 | 19.210 | 19.095 | 836 |
| 26 | 5 | 5 | 3 | 9 | 0.57633 | 8.4100 | 2.4320 | 13.760 | 26.1 | 8.5810 | 9.9276 | 378 |
| 27 | 5 | 5 | 3 | 10 | 0.98595 | 0.19214 | -7.0390 | 8.5580 | 17.7 | -0.13520 | -0.65640 | 424 |
| 28 | 5 | 5 | 4 | 4 | 9.6767 | 677.25 | 603.70 | 742.90 | 14.0 | 679.70 | 680.61 | 904 |
| 29 | 5 | 5 | 4 | 5 | 5.0823 | 672.79 | 608.50 | 736.80 | 39.8 | 673.20 | 677.79 | 318 |
| 30 | 5 | 5 | 4 | 6 | 1.2113 | 12.583 | 3.0560 | 21.710 | 16.6 | 12.750 | 14.950 | 414 |
| 31 | 5 | 5 | 4 | 7 | 0.61670 | 26.508 | 20.170 | 32.270 | 25.8 | 26.460 | 25.271 | 456 |

POSTGIBBS for Posterior Distribution Statistics

Variable D: Milk yield post-Gibbs

******** Monte Carlo Error by Time Series ********

| Pos. | eff1 | eff2 | trt1 | trt2 | MCE | Mean | HPD Interval (95%) | | Effective sample size | Median | Mode | Independent chain size |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 3 | 3 | 1 | 1 | 0.43882 | 3.4535 | 1.5520 | 5.4010 | 6.6 | 3.2840 | 2.5135 | 1644 |
| 2 | 3 | 4 | 1 | 1 | 0.20767 | -1.3027 | -2.4380 | -0.40330 | 7.0 | -1.1940 | -1.1181 | 1426 |
| 3 | 4 | 4 | 1 | 1 | 0.24877 | 1.0540 | 0.39090 | 1.9500 | 3.4 | 0.98150 | 0.47386 | 2568 |
| 4 | 5 | 5 | 1 | 1 | 0.10088 | 0.91672 | 0.40650 | 1.3060 | 6.2 | 0.93690 | 1.0673 | 1996 |
| 5 | 0 | 0 | 1 | 1 | 0.24434 | 2.3354 | 1.0120 | 3.5370 | 7.7 | 2.4090 | 2.6264 | 1686 |
| 6 | | | | h2 | 0.43715E-01 | 0.43799 | 0.24003 | 0.63014 | 6.3 | 0.43071 | 0.35579 | 1734 |
| 7 | | | | h2 | 0.29438E-01 | 0.13418 | 0.52813E-01 | 0.22012 | 3.2 | 0.13102 | 0.77469E-01 | 2526 |
| 8 | | | | h2 | 0.14862E-01 | 0.11885 | 0.50905E-01 | 0.17718 | 5.0 | 0.11919 | 0.13506 | 2092 |
| 9 | | | | rg | 0.56073E-01 | -0.69541 | -0.90512 | -0.45822 | 5.0 | -0.69761 | -0.85583 | 1568 |

******** Posterior Standard Deviation ********

| Pos. | eff1 | eff2 | trt1 | trt2 | PSD | Mean | PSD Interval (95%) | | Geweke diagnostic | Autocorrelations lag: 1 | 10 | 50 | Independent # batches |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 3 | 3 | 1 | 1 | 1.1281 | 3.4535 | 1.2425 | 5.6645 | 0.08 | 0.997 | 0.982 | 0.927 | 4 |
| 2 | 3 | 4 | 1 | 1 | 0.54940 | -1.3027 | -2.3795 | -0.22588 | 0.37 | 0.996 | 0.977 | 0.907 | 4 |
| 3 | 4 | 4 | 1 | 1 | 0.46126 | 1.0540 | 0.14991 | 1.9580 | -1.71 | 0.998 | 0.983 | 0.929 | 2 |
| 4 | 5 | 5 | 1 | 1 | 0.25187 | 0.91672 | 0.42305 | 1.4104 | 1.14 | 0.995 | 0.957 | 0.795 | 3 |
| 5 | 0 | 0 | 1 | 1 | 0.67849 | 2.3354 | 1.0056 | 3.6653 | -0.00 | 0.989 | 0.940 | 0.862 | 4 |
| 6 | | | | h2 | 0.10986 | 0.43799 | 0.22266 | 0.65331 | 0.26 | 0.998 | 0.983 | 0.930 | 4 |
| 7 | | | | h2 | 0.52340E-01 | 0.13418 | 0.31592E-01 | 0.23676 | -2.01 | 0.998 | 0.984 | 0.937 | 2 |
| 8 | | | | h2 | 0.33337E-01 | 0.11885 | 0.53512E-01 | 0.18419 | 1.29 | 0.994 | 0.955 | 0.801 | 3 |
| 9 | | | | rg | 0.12594 | -0.69541 | -0.94226 | -0.44857 | -0.76 | 0.997 | 0.980 | 0.917 | 4 |

## Variable E: Age at first calving post-Gibbs

******** Monte Carlo Error by Time Series ********

| Pos. | eff1 | eff2 | trt1 | trt2 | MCE | Mean | HPD Interval (95%) | | Effective sample size | Median | Mode | Independent chain size |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 1 | 1 | 1 | 1 | 2.6741 | 87.809 | 58.140 | 121.60 | 36.2 | 87.250 | 95.291 | 112 |
| 2 | 0 | 0 | 1 | 1 | 2.1987 | 138.24 | 110.10 | 165.60 | 42.8 | 138.30 | 142.50 | 114 |
| 3 | | | | h2 | 0.11039E-01 | 0.38778 | 0.26836 | 0.52740 | 35.6 | 0.38686 | 0.41853 | 114 |

******** Posterior Standard Deviation ********

| Pos. | eff1 | eff2 | trt1 | trt2 | PSD | Mean | PSD Interval (95%) | | Geweke diagnostic | Autocorrelations lag: 1 | 10 | 50 | Independent # batches |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 1 | 1 | 1 | 1 | 16.094 | 87.809 | 56.264 | 119.35 | -0.01 | 0.969 | 0.816 | 0.339 | 26 |
| 2 | 0 | 0 | 1 | 1 | 14.393 | 138.24 | 110.03 | 166.45 | -0.00 | 0.899 | 0.677 | 0.288 | 26 |
| 3 | | | | h2 | 0.65891E-01 | 0.38778 | 0.25864 | 0.51693 | -0.01 | 0.974 | 0.822 | 0.349 | 26 |

## Variable F: Average daily gain post-Gibbs

******** Monte Carlo Error by Time Series ********

| Pos. | eff1 | eff2 | trt1 | trt2 | MCE | Mean | HPD Interval (95%) | | Effective sample size | Median | Mode | Independent chain size |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 3 | 3 | 1 | 1 | 0.41292E-04 | 0.57066E-03 | 0.30200E-03 | 0.83020E-03 | 12.6 | 0.55980E-03 | 0.53206E-03 | 1072 |
| 2 | 3 | 4 | 1 | 1 | 0.20183E-04 | -0.19033E-03 | -0.34070E-03 | -0.48620E-04 | 15.3 | -0.18670E-03 | -0.16991E-03 | 510 |
| 3 | 4 | 4 | 1 | 1 | 0.14656E-04 | 0.26701E-03 | 0.15000E-03 | 0.39400E-03 | 17.7 | 0.26160E-03 | 0.23614E-03 | 428 |
| 4 | 0 | 0 | 1 | 1 | 0.21930E-04 | 0.50239E-03 | 0.32870E-03 | 0.70050E-03 | 19.1 | 0.49760E-03 | 0.46880E-03 | 550 |
| 5 | | | | h2 | 0.25687E-01 | 0.42158 | 0.24004 | 0.56722 | 11.7 | 0.42399 | 0.37715 | 1098 |
| 6 | | | | h2 | 0.89753E-02 | 0.19806 | 0.12476 | 0.27067 | 17.4 | 0.19720 | 0.18635 | 458 |
| 7 | | | | rg | 0.32712E-01 | -0.47448 | -0.74192 | -0.23191 | 16.9 | -0.48793 | -0.48764 | 526 |

******** Posterior Standard Deviation ********

| Pos. | eff1 | eff2 | trt1 | trt2 | PSD | Mean | PSD Interval (95%) | | Geweke diagnostic | Autocorrelations lag: 1 | 10 | 50 | Independent # batches |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 3 | 3 | 1 | 1 | 0.14657E-03 | 0.57066E-03 | 0.28339E-03 | 0.85794E-03 | -0.12 | 0.995 | 0.969 | 0.874 | 6 |
| 2 | 3 | 4 | 1 | 1 | 0.78873E-04 | -0.19033E-03 | -0.34492E-03 | -0.35737E-04 | 0.14 | 0.996 | 0.971 | 0.862 | 13 |
| 3 | 4 | 4 | 1 | 1 | 0.61660E-04 | 0.26701E-03 | 0.14615E-03 | 0.38786E-03 | 0.11 | 0.995 | 0.959 | 0.829 | 16 |
| 4 | 0 | 0 | 1 | 1 | 0.95754E-04 | 0.50239E-03 | 0.31471E-03 | 0.69007E-03 | 0.09 | 0.975 | 0.890 | 0.770 | 12 |
| 5 | | | | h2 | 0.87930E-01 | 0.42158 | 0.24924 | 0.59393 | -0.17 | 0.995 | 0.967 | 0.867 | 6 |
| 6 | | | | h2 | 0.37480E-01 | 0.19806 | 0.12460 | 0.27152 | 0.14 | 0.991 | 0.941 | 0.814 | 15 |
| 7 | | | | rg | 0.13455 | -0.47448 | -0.73819 | -0.21077 | 0.26 | 0.995 | 0.963 | 0.825 | 13 |

## Variable G: Calving interval post-Gibbs

******** Monte Carlo Error by Time Series ********

| Pos. | eff1 | eff2 | trt1 | trt2 | MCE | Mean | HPD Interval (95%) | | Effective sample size | Median | Mode | Independent chain size |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 4 | 4 | 1 | 1 | 384.75 | 3937.9 | 2504.0 | 5683.0 | 5.0 | 3790.0 | 3494.2 | 1766 |
| 2 | 5 | 5 | 1 | 1 | 369.81 | 1157.9 | 81.560 | 2506.0 | 4.0 | 1071.0 | 403.10 | 1938 |
| 3 | 0 | 0 | 1 | 1 | 82.905 | 22857. | 21400. | 24280. | 79.9 | 22830. | 22660. | 386 |
| 4 | | | | h2 | 0.13344E-01 | 0.14065 | 0.92202E-01 | 0.19999 | 4.8 | 0.13541 | 0.12587 | 1784 |
| 5 | | | | h2 | 0.13191E-01 | 0.41435E-01 | 0.28924E-02 | 0.88668E-01 | 4.0 | 0.38508E-01 | 0.14577E-01 | 1942 |

******** Posterior Standard Deviation ********

| Pos. | eff1 | eff2 | trt1 | trt2 | PSD | Mean | PSD Interval (95%) | | Geweke diagnostic | Autocorrelations lag: 1 | 10 | 50 | Independent # batches |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 4 | 4 | 1 | 1 | 858.00 | 3937.9 | 2256.2 | 5619.6 | 0.88 | 0.994 | 0.946 | 0.792 | 3 |
| 2 | 5 | 5 | 1 | 1 | 739.02 | 1157.9 | -290.60 | 2606.3 | -1.23 | 0.999 | 0.989 | 0.948 | 3 |
| 3 | 0 | 0 | 1 | 1 | 741.20 | 22857. | 21405. | 24310. | 0.13 | 0.489 | 0.270 | 0.207 | 15 |
| 4 | | | | h2 | 0.29226E-01 | 0.14065 | 0.83370E-01 | 0.19794 | 0.92 | 0.986 | 0.941 | 0.796 | 3 |
| 5 | | | | h2 | 0.26277E-01 | 0.41435E-01 | -0.10067E-01 | 0.92937E-01 | -1.23 | 0.998 | 0.987 | 0.947 | 3 |

## Variable H: Weaning weight post-Gibbs

******** Monte Carlo Error by Time Series ********

| Pos. | eff1 | eff2 | trt1 | trt2 | MCE | Mean | HPD Interval (95%) | | Effective sample size | Median | Mode | Independent chain size |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 3 | 3 | 1 | 1 | 7.7390 | 102.94 | 56.820 | 145.90 | 8.3 | 101.40 | 105.43 | 882 |
| 2 | 3 | 4 | 1 | 1 | 0.51167 | -7.5110 | -10.140 | -4.8520 | 8.0 | -7.4520 | -7.3979 | 988 |
| 3 | 4 | 4 | 1 | 1 | 0.40987E-01 | 0.73055 | 0.46310 | 0.99110 | 13.2 | 0.72960 | 0.72276 | 518 |
| 4 | 5 | 5 | 1 | 1 | 3.8910 | 17.727 | 4.0580 | 31.650 | 4.3 | 18.480 | 6.6313 | 1718 |
| 5 | 0 | 0 | 1 | 1 | 4.4770 | 93.398 | 64.770 | 122.20 | 11.9 | 94.340 | 95.537 | 624 |
| 6 | | | | h2 | 0.32071E-01 | 0.47728 | 0.28959 | 0.65471 | 8.2 | 0.47374 | 0.47049 | 884 |
| 7 | | | | h2 | 0.18716E-03 | 0.34025E-02 | 0.20917E-02 | 0.45242E-02 | 13.4 | 0.33992E-02 | 0.31809E-02 | 504 |
| 8 | | | | h2 | 0.18600E-01 | 0.82873E-01 | 0.18470E-01 | 0.14608 | 4.2 | 0.85089E-01 | 0.30004E-01 | 1718 |
| 9 | | | | rg | 0.32121E-01 | -0.87196 | -0.95024 | -0.74931 | 3.7 | -0.88480 | -0.94047 | 2008 |

******** Posterior Standard Deviation ********

| Pos. | eff1 | eff2 | trt1 | trt2 | PSD | Mean | PSD Interval (95%) | | Geweke diagnostic | Autocorrelations lag: 1 | 10 | 50 | Independent # batches |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 3 | 3 | 1 | 1 | 22.316 | 102.94 | 59.200 | 146.68 | 0.32 | 0.993 | 0.975 | 0.913 | 7 |
| 2 | 3 | 4 | 1 | 1 | 1.4448 | -7.5110 | -10.343 | -4.6792 | -1.02 | 0.990 | 0.967 | 0.890 | 6 |
| 3 | 4 | 4 | 1 | 1 | 0.14898 | 0.73055 | 0.43856 | 1.0225 | 0.45 | 0.992 | 0.968 | 0.886 | 12 |
| 4 | 5 | 5 | 1 | 1 | 8.0847 | 17.727 | 1.8815 | 33.573 | -0.71 | 0.998 | 0.984 | 0.918 | 3 |
| 5 | 0 | 0 | 1 | 1 | 15.459 | 93.398 | 63.099 | 123.70 | -0.01 | 0.968 | 0.882 | 0.793 | 10 |
| 6 | | | | h2 | 0.91836E-01 | 0.47728 | 0.29728 | 0.65727 | 0.33 | 0.994 | 0.972 | 0.914 | 7 |
| 7 | | | | h2 | 0.68515E-03 | 0.34025E-02 | 0.20596E-02 | 0.47454E-02 | 0.41 | 0.992 | 0.960 | 0.878 | 12 |
| 8 | | | | h2 | 0.38044E-01 | 0.82873E-01 | 0.83059E-02 | 0.15744 | -0.73 | 0.997 | 0.981 | 0.916 | 3 |
| 9 | | | | rg | 0.61870E-01 | -0.87196 | -0.99323 | -0.75070 | -1.76 | 0.998 | 0.984 | 0.932 | 3 |

## Variable H: Milk yield and weaning weight post-Gibbs _ Posterior Standard Deviation

******** Posterior Standard Deviation ********

| Pos. | eff1 | eff2 | trt1 | trt2 | PSD | Mean | PSD Interval (95%) | | Geweke diagnostic | Autocorrelations lag: 1 | 10 | 50 | Independent # batches |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 6 | 6 | 1 | 1 | 0.17246E-01 | 0.11867 | 0.84869E-01 | 0.15247 | -0.46 | 0.962 | 0.818 | 0.486 | 7 |
| 2 | 6 | 6 | 1 | 2 | 0.42715 | 1.7242 | 0.88696 | 2.5614 | -0.67 | 0.976 | 0.861 | 0.571 | 6 |
| 3 | 6 | 7 | 1 | 1 | 0.11763E-01 | 0.51648E-01 | 0.28593E-01 | 0.74703E-01 | 0.06 | 0.963 | 0.799 | 0.317 | 8 |
| 4 | 6 | 8 | 1 | 1 | 0.72077E-02 | 0.59783E-01 | 0.45656E-01 | 0.73911E-01 | 0.85 | 0.927 | 0.789 | 0.365 | 7 |
| 5 | 6 | 9 | 1 | 1 | 0.53358E-02 | -0.19918E-01 | -0.30376E-01 | -0.94595E-02 | 1.18 | 0.957 | 0.860 | 0.548 | 3 |
| 6 | 6 | 6 | 2 | 2 | 10.005 | 31.995 | 12.386 | 51.604 | -0.80 | 0.982 | 0.878 | 0.597 | 6 |
| 7 | 6 | 7 | 2 | 1 | 0.22558 | 0.43237 | -0.97709E-02 | 0.87451 | 0.45 | 0.964 | 0.798 | 0.344 | 7 |
| 8 | 6 | 8 | 2 | 1 | 0.15709 | 0.33669 | 0.28782E-01 | 0.64459 | 0.92 | 0.934 | 0.749 | 0.355 | 2 |
| 9 | 6 | 9 | 2 | 1 | 0.14792 | -0.47538 | -0.76530 | -0.18546 | 1.10 | 0.971 | 0.870 | 0.580 | 3 |
| 10 | 7 | 7 | 1 | 1 | 0.13944E-01 | 0.84720E-01 | 0.57389E-01 | 0.11205 | -0.65 | 0.965 | 0.787 | 0.572 | 5 |
| 11 | 7 | 8 | 1 | 1 | 0.66275E-02 | 0.58207E-01 | 0.45217E-01 | 0.71197E-01 | -0.63 | 0.922 | 0.668 | 0.374 | 5 |
| 12 | 7 | 9 | 1 | 1 | 0.56968E-02 | 0.13076E-01 | 0.19104E-02 | 0.24242E-01 | 0.57 | 0.965 | 0.853 | 0.458 | 6 |
| 13 | 8 | 8 | 1 | 1 | 0.43011E-02 | 0.96044E-01 | 0.87614E-01 | 0.10447 | 0.29 | 0.839 | 0.680 | 0.290 | 7 |
| 14 | 8 | 9 | 1 | 1 | 0.27501E-02 | 0.27552E-01 | 0.22161E-01 | 0.32942E-01 | 0.90 | 0.911 | 0.778 | 0.535 | 3 |
| 15 | 9 | 9 | 1 | 1 | 0.32763E-02 | 0.31917E-01 | 0.25495E-01 | 0.38338E-01 | 0.94 | 0.965 | 0.909 | 0.640 | 4 |
| 16 | 10 | 10 | 1 | 1 | 0.10197E-01 | 0.74179E-01 | 0.54193E-01 | 0.94165E-01 | 0.23 | 0.920 | 0.680 | 0.207 | 6 |
| 17 | 10 | 11 | 1 | 1 | 0.10207E-01 | -0.20444E-01 | -0.40450E-01 | -0.43754E-03 | -0.04 | 0.938 | 0.740 | 0.228 | 9 |
| 18 | 10 | 12 | 1 | 1 | 0.12601E-01 | 0.50192E-01 | 0.25495E-01 | 0.74889E-01 | -0.70 | 0.947 | 0.706 | 0.176 | 10 |
| 19 | 10 | 13 | 1 | 1 | 0.69189E-02 | -0.17533E-01 | -0.31094E-01 | -0.39715E-02 | -0.06 | 0.902 | 0.575 | 0.102 | 7 |
| 20 | 10 | 10 | 2 | 2 | 19.867 | 46.082 | 7.1440 | 85.021 | -1.46 | 0.987 | 0.917 | 0.834 | 3 |
| 21 | 10 | 11 | 2 | 1 | 0.57061 | -0.52733 | -1.6457 | 0.59107 | -1.57 | 0.985 | 0.861 | 0.390 | 2 |
| 22 | 10 | 12 | 2 | 1 | 0.40672 | 0.39535 | -0.40182 | 1.1925 | -1.41 | 0.974 | 0.815 | 0.583 | 3 |
| 23 | 10 | 13 | 2 | 1 | 0.23801 | 0.23906 | -0.22744 | 0.70556 | -0.67 | 0.946 | 0.706 | 0.174 | 3 |
| 24 | 11 | 11 | 1 | 1 | 0.30573E-01 | 0.10871 | 0.48791E-01 | 0.16864 | 0.51 | 0.974 | 0.821 | 0.473 | 3 |
| 25 | 11 | 12 | 1 | 1 | 0.18532E-01 | 0.12204E-01 | -0.24119E-01 | 0.48528E-01 | 0.24 | 0.978 | 0.828 | 0.408 | 7 |
| 26 | 11 | 13 | 1 | 1 | 0.11287E-01 | 0.47731E-02 | -0.17350E-01 | 0.26896E-01 | 0.60 | 0.952 | 0.763 | 0.488 | 5 |
| 27 | 12 | 12 | 1 | 1 | 0.19340E-01 | 0.80216E-01 | 0.42309E-01 | 0.11812 | -0.27 | 0.966 | 0.770 | 0.229 | 8 |
| 28 | 12 | 13 | 1 | 1 | 0.10531E-01 | -0.32699E-03 | -0.20968E-01 | 0.20314E-01 | 0.46 | 0.956 | 0.715 | 0.271 | 6 |
| 29 | 13 | 13 | 1 | 1 | 0.36502E-01 | 0.55884E-01 | -0.15660E-01 | 0.12743 | 0.21 | 0.296 | 0.040 | -0.011 | 23 |
| 30 | 0 | 0 | 1 | 1 | 0.29333E-02 | 0.14502 | 0.13927 | 0.15077 | -0.11 | 0.185 | 0.118 | -0.026 | 70 |
| 31 | 0 | 0 | 2 | 2 | 26.192 | 117.07 | 65.736 | 168.41 | 1.39 | 0.975 | 0.892 | 0.779 | 3 |

Variable J: Genetic and phenotypic correlations W7_BW_airemlf90

```
 Correlations from inverse of AI matrix
    1.0000      0.49131E-01  0.44609E-02 -0.38441     -0.26816E-02
   0.49131E-01   1.0000      0.46362E-01  0.10934E-01 -0.89260E-02
   0.44609E-02  0.46362E-01   1.0000     -0.66601E-03 -0.82077
  -0.38441      0.10934E-01 -0.66601E-03   1.0000      0.47673E-03
  -0.26816E-02 -0.89260E-02 -0.82077      0.47673E-03   1.0000
 SE for G
   0.13437      0.65757
   0.65757       6.5852
 SE for R
   0.21282       0.0000
    0.0000       4.4842

 Sampling variances of covariances function of random effects (n=10000)

 h2  - Fucntion: g_4_4_1_1/(g_4_4_1_1+g_4_4_1_2+r_1_1)
   Mean:   0.52143E-01
   Sample Mean:   0.52063E-01
   Sample SD:   0.91650E-02

 h2  - Fucntion: g_4_4_2_2/(g_4_4_2_2+g_4_4_1_2+r_2_2)
   Mean:   0.58442
   Sample Mean:   0.58322
   Sample SD:   0.38989E-01

 rg12  - Fucntion: g_4_4_1_2/(g_4_4_1_1*g_4_4_2_2)^0.5
   Mean:   0.19089
   Sample Mean:   0.19369
   Sample SD:   0.87769E-01
```

## Appendix D. Abstract of conference paper

Variable A: Animal Production Society of Kenya 2023 Scientific Symposium

Tuesday 24th October, 2023 Best Western Hotel, KISUMU

### Non-Genetic Factors Influencing Growth, Milk Quality and Disease Resistance in the N'dama Cattle in Gambia

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**Abstract**

Cattle production in vast areas of sub-Saharan Africa is limited by tsetse-transmitted trypanosomiasis, which is regarded as the single most important constraint to cattle production. The aim of this study was to identify factors that influence growth, milk quality and disease resistance traits in the N'dama cattle in the Gambia. Data on birth weight (BW), fat %, protein percent and pack cell volume (PCV) were obtained from the International Trypanotolerance Centre (ITC), now WALIC, under an Open Nucleus Breeding Scheme in The Gambia, a genetic improvement program with the goal of improving the N'Dama breed. A total of 5689, 1720, 1753 and 3904 records of BW, fat %, protein % and PCV





were analysed by fitting generalized linear models in SAS software. Where applicable the model consisted of year of birth, year of milking, month of birth or milking, herd, parity and sex of the animal. The results indicate that all the fixed effects had a significant effect ($P<0.05$) on the traits studied. Male calves were significantly heavier ($P<0.001$) than female calves at birth with the respective weights being 17.04±0.31 and 16.31±0.31 kg. The mean Fat%, protein% and PCV were 4.03±1.46%, 3.4±0.83% and 23.25±3.55%. From the present study herd, year of birth, year of milking and sex of animal were important non-genetic effects that should be accounted for when identifying superior animals for genetic improvement of growth, milk quality and trypanotolence in the N'dama cattle.

**Key words:** *fat percent; packed cell volume; protein percent; trypanotolerance*

15TH BIENNIAL INTERNATIONAL CONFERENCE

# Genetic parameters for growth traits of the n'dama cattle in the Gambia

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## ABSTRACT

The N'dama cattle are adapted to poor-quality feed resources and tsetse-infested (both *Glossina palpalis gambiensis* and *Glossina morsitans submorsitans species*) areas in the West African region, including The Gambia. The breed can therefore contribute significantly to the livelihoods of resource-limited households. Genetic variance is a key prerequisite for sustainable genetic improvement in a population. In beef cattle, maternal genetic effects play an important role in the growth and survival of calves. These effects stem from the genetic contribution of the dam and can significantly impact the traits of economic importance such as reproductive traits which include calving interval, age at weaning, and fertility. It also has a direct impact on growth rate, calf performance, and maternal care. Focusing on maternal genetics and its effects on traits related to reproduction, maternal care, and calf performance can enhance the overall efficiency and productivity of cattle herds. Previous studies that estimated genetic parameters did not consider maternal genetic effects for early growth traits. The objective of this study was therefore to estimate genetic co-variance components and parameters for growth traits along the growth curve in the N'dama cattle in the Gambia. A total of 5,173, 3,130, 2,488, 2,422, 2,442, 1,471, 1,934, and 1,452 records for birth weight (BW) weight at 7 months (WT7), 12 months (WT12), 16 months (WT16), 18 months (WT18), 24 months (WT24), 36 months (WT36) and 50 months (WT50), were used for analysis. The effect of fixed factors and least square means were estimated using a general linear model of the Statistical Analysis System (SAS 2004) fitting herd-year-season of birth and sex as fixed