GENOMIC ASSOCIATIONS BETWEEN TRANSFORMING GROWTH FACTOR β (TGFβ3) GENE POLYMORPHISM WITH GROWTH PERFORMANCE OF NIGERIAN IMPROVED AND EXOTIC CHICKEN

BY

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CERTIFICATION

This is to certify that this research work "**Genomic Associations Between Transforming Growth Factor β (TGFβ3) Gene Polymorphism With Growth Performance of Nigerian Improved And Exotic Chicken**" was carried out by **CHUKWUKA, NNAEMEKA JOSEPH (20174095378)** in partial fulfilment for the award of the degree of MSc in Animal Breeding and Genetics in the Department of Animal Science and Technology of the Federal University of Technology Owerri.

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DEDICATION

This work is dedicated to God Almighty, whose unwavering support and guidance have been instrumental in the completion of this thesis. In reverence and deep gratitude, I acknowledge the immense resources that were invested and the challenges that were surmounted throughout this journey. Without the steadfast faith and providence of God, this feat would not have been possible.

With every trial and tribulation, with each setback and hurdle, God's strength became my foundation,

His light my guiding star. I am indebted to God for His untiring grace, for bestowing upon me the wisdom, resilience, and determination to persist and achieve this milestone.

To my Lord, the epitome of steadfastness, I offer this work as a testament of my unwavering faith, my acknowledgement of His divine intervention, and my overwhelming joy in His benevolence.

May this humble offering be a source of enlightenment, a means of uplifting others, and an avenue for promoting understanding and knowledge, as we continue to seek His divine presence in all that we do.

To **God the Father**, **God the Son** and **God the Holy Spirit** , I dedicate this work, with unending gratitude and profound humility.

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ABSTRACT

This study focused on analyzing the TGF-β3 gene polymorphism and its association with important growth and morphological traits in chickens. A total of 150 chickens from three different breeds, namely Noiler® (50), FUNAAB Alpha® (FA - 50), and Sasso® (50), were included in the study. These chickens were reared from day-old chicks until they reached 20 weeks of age. Throughout this period, growth and morphological traits such as body weight, height at withers, body length, breast girth, and wing length were measured at ages 4, 8, 12, 16, and 20 weeks. Significant differences *($P<0.05$)* were obtained on growth performance index (body weight, height at withers, body length, breast girth and wing length) with the Sasso as the best performed breed, then the Funaab Alpha and the Noiler respectively. This suggests that Sasso is good for meat production. Genomic DNA was extracted from the chickens, and polymerase chain reaction (PCR) was performed using specific primers targeting the TGFβ gene. The resulting PCR amplicons were sequenced in both forward and reverse directions to obtain accurate genetic information. Subsequently, the sequences were carefully analyzed, and single nucleotide polymorphisms (SNPs) within the TGF-β3 gene were identified. These SNPs were then correlated with the recorded performance data of the chickens. Among the SNPs discovered, two variants stood out: SNP1 (A>C) and SNP2 (A>T). Notably, the CC and TT genotypes exhibited recessive characteristics. To assess the genetic diversity within the TGF-β3 gene across the three chicken breeds, haplotype and nucleotide analyses were conducted. Results revealed that Noiler and FA breeds exhibited a higher number of sequences and haplotypes (5), while Sasso breed had 4. Furthermore, the association analysis between the identified SNPs and the measured growth traits revealed interesting findings. SNP1 showed a significant association ($P<0.05$) with body weight and height at withers. Notably, Sasso and FA breeds demonstrated a stronger association with these traits compared to the Noiler breed. Conversely, SNP2 did not exhibit any significant associations with the measured body traits. Overall, the findings of this study suggest that the TGF-β3 gene may play a crucial role as a candidate gene, significantly influencing the body composition traits of chickens.

Keywords: PCR-RFLP, Transforming Growth Factor-β (TGFβ), Gel electrophoresis, SNP, body composition.

CHAPTER ONE

INTRODUCTION

1.1 Background of the Study

The value of Nigerian poultry industry is estimated at ₦80 billion ($600 million) and is comprised of approximately 165 million birds, which produced 650,000 MT of eggs and 290,000 MT of poultry meat in 2013. From a market size perspective, Nigeria’s egg production is the largest in Africa (South Africa is the next largest at 540,000 MT of eggs) and it has the 2nd largest chicken population after South Africa’s 200 million birds. Chicken importation (with the exception of day-old-chicks) was banned by Nigeria in 2003, which spurred growth in domestic poultry production. Statistics from Eurostat, however, highlight that between 2009 and 2011 over 3 million MT worth of poultry products were imported into the Republic of Benin, with the preponderance of these products ending up in the Nigerian market. If this is reflected in overall assumptions, estimated poultry meat consumption in Nigeria is approximately 1.2 million MT (SAHEL, 2015) The WHO/FAO/UNU (2007) report examines dietary protein and amino acid requirements for all age groups, protein requirements during pregnancy, lactation and catch-up growth in children, the implications of these requirements for developing countries and protein quality evaluation. (Garlick, 2006)

Poultry production has undergone an enormous expansion and development during the past half century throughout the country (Peters *et al.,* 2002). Nigeria poultry keepers has made poultry business one of the most popular enterprises adopted by all those in the rural and urban setting (Idowu *et al.,* 2005). The demand for poultry products is expanding as a result of population growth. The Nigeria population is projected at 400 million by 2050 and 280 million are projected to live in the cities, significantly increasing the demand for poultry products. The per capita consumption of chicken is still very low at 2.5kg in Nigeria, when compared to Brazil and South

Africa at 30kg and 40kg respectively. The per capita consumption of eggs in Nigeria is 60 eggs per annum compared to 250 to 300 eggs per annum in most advanced countries. (Emefiele, 2019)
Growth performance and carcass traits are the most important economic traits in broiler chicken production, and are controlled by a number of genes (Anh, *et al.,* 2015). Growth is a complex process that involves the regulated coordination of a wide range of neuroendocrine pathways (Zhang, *et al.,* 2008). Therefore, it is very difficult to achieve rapid genetic improvement in these traits using only traditional selection methods. The growing knowledge of the structure and function of the chicken genome can be beneficial, and can lead to the recognition of causal genes and the development of new selectable molecular markers.

However, the genetic improvement of polygenic traits, including growth performance and meat production, can be accomplished by marker-assisted selection that is more accurate in estimating the animal's genetic value (Dekkers, 2004) . The molecular markers linked to quantitative trait loci (QTLs) are not affected by environmental conditions. Therefore, they could increase the speed and effectiveness of animal breeding progress. As soon as the relationship between a DNA polymorphism and an important trait is revealed, the DNA marker may be used (Zhang, *et al.,* 2007). The candidate gene approach has become a powerful technique for the genetic improvement in chicken breeding programs, and can result in increased efficiency in detecting the required production performance traits (Anh, *et al.,* 2015).

The importance of native breeds of poultry birds for rural economy in developing and underdeveloped countries mostly in Asia and Africa is very high. They are part of balanced farming system that have vital roles in the rural households as a source of high-quality animal protein and emergency cash income and play a significant role in the sociocultural life of the rural community and woman empowerment. One of the most important positive characters of native chicken is their hardiness, which is ability to tolerate the harsh environmental condition and poor husbandry practices without much loss in production. The native breed chickens are the reservoir of genomes and major genes for improvement of high yielding exotic germplasm for tropical adaptability and disease resistance. The low production performance of native breeds of chickens may be improved through improvement in husbandry practices, better healthcare, and supplementary feeds during lean season and also through selection and crossbreeding. Crossbreeding with exotic germplasm showed the improvement quickly; however, selection in native breeds can bring the improvement permanently. Upgradation of the native breeds of chickens through different breeding technique helps to increase the productivity of the germplasm and also their conservation in their natural habitat as the rural people will be very happy to rear them for their adoptability to harsh environment. (Mahendra, 2016)

1.2 Problem Statement

The poultry industry in Nigeria – one of its most vibrant agricultural sectors – is on the verge of collapse. As the average price of feed ingredients has risen by over 168% in the last 3 years, some farmers are walking away from their livelihoods as profits drop and security risks remain high. (Aremu, 2022). In order to curb this menace, there is need to adopt technologies that would trigger efficiency. The challenge to turn to sustainable farming does not apply to the richer countries only, but also for countries embarking on the process of industrialisation and economic growth, where the temptation to produce in a less sustainable manner is quite strong (Pierhagen, 2001) Growth traits are essential parameters in assessing the potential of genetic improvement and development of any livestock breed/strain. Studies have shown that growth traits measurements such as body length, shank length and chest girth serve as good indicators of growth. (Ige, 2013)

Hence, the general question should be which genetic marker could be more suitably used to access the level of genetic variation among these local and exotic breeds of Nigerian Chicken. How do we determine the genetic structure and distinctiveness among these breeds. Could there be any interaction of traits or striking similarities in the evolutionary history of these breeds of Nigerian chicken that would enable us to determine the realized dispersal distances among them?

1.3 Aims and Objectives

1.3.1 Aims

The aim of this study is to evaluate the genomic associations between Transforming Growth Factor β (TGFβ3) genes polymorphism with growth performance of Noiler, FUNAAB Alpha and Sasso chickens that were improved in Nigeria.

1.3.2 Objectives

- To determine the level of Transforming Growth Factor β (TGFβ3) genes polymorphism among the chicken populations
- To identify the Transforming Growth Factor β (TGFβ3) genes within the sampled chicken strains.
- To know the degree of variance of this gene among the different chicken strains.
- To ascertain the degree of association of this gene with their growth performance

1.4 Justification of the Study

Every poultry farmer desires to cut the high cost of feedstuff and produce a table size chicken within the shortest time possible without being detrimental to the consumer of the product. This is why it is vital to identify the most dominant gene responsible for growth among the local and exotic chicken in Nigeria and then improve on it. This knowledge will be extended to the local farmers to maximize profit and encourage the poultry sector. Farm animals today are better than they were 100 years ago. They produce more meat, milk, eggs, and wool on less feed. Much of this progress in livestock efficiency is the result of the use of genetics. (James & Frank, 2010)

Knowledge-based approach has not yet been adopted widely in developing countries, beyond a relatively small group of educated commercial producers. However, the experiences of some small producers have shown that this approach is possible, even among producers facing severe poverty.

Depending on the speed and form of evolution of farming systems, knowledge-based adjustments are likely to intensify during the coming 30 years. (FAO and World Bank, 2001)

1.5 Scope of the Study

The scope of this work is focussed largely on identifying the Transforming Growth factor β (TGFβ3) gene polymorphism in commensurate to the growth of the Funaab alpha, Sasso and Noiler chicken breeds raised in Nigeria. This study covered a period of twenty weeks and two major diets were given to the chicken at different stage:

Starter (0-4 weeks)

Finisher (5-20 weeks).

The study data collection covered the following stages

1. The Phenotypic data collection. This comprises of the body measurements of the breast girth, body length, wing length and height at withers.
2. The Genomic data collection. The blood collected for DNA extraction, polymerase chain reaction (PCR) and DNA extraction

CHAPTER TWO

LITERATURE REVIEW

2.1 General Chicken Production

The cost of feed is about two-thirds of the total cost of producing eggs and meat from chickens. All management practices affect profits in chicken production. Feeding practices must meet the needs of the chickens and still allow room for profit. Rations for the chickens must supply the protein, carbohydrates, minerals, vitamins, and water that poultry require. In addition, some additives and unidentified growth factors are often used in chicken rations. Most of the energy in poultry diets is supplied by grains, grain by-products, and animal and vegetable fats and oils. Poultry only have a limited ability to use high-fiber feeds such as roughages because of their relative inability to digest the fiber. Grains make up from 50 to 80 percent of the total ration for chickens. Corn is the most commonly used grain in poultry rations. Other grains such as oats, wheat, grain sorghum (milo), and proso millet may be substituted for part of the corn in poultry rations. When poultry are fed ***ad libitum*** (given all they will eat), they tend to eat enough to meet their energy requirements. Chickens fed low-energy diets will eat more feed than those fed high-energy diets. Therefore, the amount of required nutrients in a poultry ration must be adjusted in relation to the energy level in the ration in order to ensure that the birds consume the right amount of the needed nutrients. The concentration of nutrients must be increased in high-energy diets because the birds will eat less of the ration per day. The concentration of nutrients should be reduced in low-energy rations because the birds will eat more of these rations per day. High-energy rations usually result in higher efficiency in converting feed to meat or eggs as compared to low energy rations. Fats may be used to increase the energy level of low-energy rations. Animal and vegetable fats should be limited to no more than 5 to 10 percent of the diet. Fats will increase the palatability of the diet, decrease dustiness, and improve the texture of the feed. Fats are used more often in broiler rations to increase the energy level of the diet. In hot weather, feed containing added fat may become rancid unless it has been properly stabilized. (James & Frank, 2010). Chukwuka (2011), stated that birds fed the higher energy level diets had higher carcass fat.

2.1.1 Challenges of Chicken Production in Nigeria

Notwithstanding the foremost role of poultry production in the livestock industry, it's not without challenges. The challenges of poultry production in Nigeria cannot be overemphasized. These challenges have slowed down the rate of production in the industry. High rate of disease and pest attack is also a major challenge in poultry production (Ajala, *et al.* 2007)

High cost of poultry feeds was identified as one of the challenges being faced by the poultry industry in Nigeria. (Agro-Ind, 2002) . The challenges of poultry production in Nigeria are multifaceted. These challenges might not have stopped the industry from functioning because there has been a steady increase in the demand for poultry products in Nigeria due to several factors such as increase in population, new poultry farms, the expansion of existing ones and the resuscitation of some others which had stopped production but might has slowed down rate of production in the industry. (Anosike, *et al.,* 2020)

2.1.2 Future of Chicken Production in Nigeria

Poultry among other protein meal is to accounts for 14% of Nigeria's meat consumption in 2029. The country meat consumption is projected to increase from 1.25 million tonnes in 2020 to 1.49 million tonnes in 2029 out of which poultry meat consumption is to accounts for 13.99% in 2029, which also represent a decline of 1.98% when compared with share 15.93% in 2020. MSMEs today has learnt from OECD-FAO agricultural outlook for 2020-2029. Nigeria consumed 199,000 tonnes of poultry meat in 2020 which translated to N214.22 billion using the average international price of $2,153 per tonnes with exchange rate $500 to naira. Based on the above, Nigeria's poultry meat consumption is projected to grow by 4.5% to 208,000 tonnes in 2029, which translate to N205.82 billion due to projected fall in international poultry meat price from $2,153 per tonnes to $1,979 at the same exchanges rate of $500. This increase in production of poultry meat and projected increase is based on the increase in the number of Micro, Small and Medium Enterprises (MSMEs) involved in poultry farming value chain over the years. Despite the increase in the number of MSMEs involved in poultry value chain, and government ban on importation of frozen poultry products, Nigeria still import poultry meat from other countries which is translated to about $3 billion annual expenditure on imported frozen poultry meat across the land borders. Experts are of the opinion that poultry farming in Nigeria is on verge of collapse due to various challenges confronting the sector. These challenges range from high cost of grains such as maize and soybeans, Covid-19 pandemic and the lockdown that resulted in devastating losses to farmers, illegal importation of frozen poultry products across the country's land border, and government policy that banned the importation of maize which accounts for more than 70% of poultry feeds. According to FAOSTAT report, the growth of the livestock sector will increase feed use. Three commodities, maize, barley and protein meals are expected to account for about 75% of the total feed use, with imports accounting for about 90% of feed demand. This trend reflects policies that prioritise the production of food crops over feed crops. Africa region is a large importer of animal feed and will import 47 Mt of maize by 2029 compared to 36 Mt in the base period. (Olowa, 2021)

2.2 Nigerian Improved Local and Exotic Chicken Breeds

The Nigerian indigenous chickens (NICs) are a critical component of the global animal genetic resources. They are distributed in rural areas, kept by the majority of the rural poor. They constitute different strains, or ecotypes local to tribes, regions, or ecological zones and are valued for their disease resistance, adaptation, and yield of valuable products and income on marginal inputs making them a low risk species. They are hence a unique and vital genetic resource and gene pool for present and long-term genetic improvement and human need for food and sustenance. The NIC is however; threatened by extinction owing to neglect, negative selection, breed substitution, and genetic introgression. There is need to draw research and policy attention to the conservation of

NICs in accord with the global effort for the conservation of indigenous chickens which is probably the most neglected among farm animal species. (Ogbu, 2021)

2.2.1 Sasso

Sasso is both a breed of chicken and the name of a French company that coined the term Sasso chicken in 1978. Sasso is an internationally popular breed originating from France. Sasso offers proven, hardy, easy to manage and versatile bird to Indian farmers. Farmers can keep them in different production systems – from intensive production, down to earth simple sheds on a deep litter with basic equipment, in the backyard, in orchards, in coconut and rubber plantations, in forests areas, in the hills and even in the drylands and in the hot desert. The major target in Sasso breeding Program is the high production of hatching eggs (HE) from the parent breeder (HE >220) and a slow-growing, robust, easy to manage, multi-colored broiler which can be grown under different rearing systems - from indoor and intensive to Free Range and village family-based production. The feed is less dense, less expensive, lower in energy and protein, and allows the use of higher levels of cheaper and unconventional farm by-products. Due to a slower growth rate, Sasso meat is more firm and has that rich chicken flavor, juicy and tasty like the meat of traditional Indian country chicken and it commands a higher market price. Besides, Sasso delivers better profit to the farmers and great taste to the consumers. Brooding with artificial heat is provided during first 2 to 3 weeks as chicks need external heat to maintain their body temperature. Chicks suffer from stress when house temperature is too cold or too hot. Chicks which are subjected to cold always have poor development of digestive organs and immunity due to which all the other disease problems originate one by one. After 3 weeks age, birds can be let out in the free range where they find some feed. During this period 80% of the total feed requirement should be offered in the morning and evening hours inside the house and birds can find remaining 20% feed in the free range. Water should be provided in the shady area in the free range. Free range encourages good muscle development and firmness of the meat. Birds may be allowed to grow slow up to 9 to 10 weeks to get desired firmness, texture, taste and flavour in the meat. Birds may be sold according to the particular live weight requirement of the customer, preferably about 1.5 kg to get good fleshing and processing yield. (Hendrix Genetics, 2022)

Types of Sasso Chicken

Source: Sasso website (https://africa.sasso-poultry.com/en/)

Rainbow T (TR)

The SASSO Rainbow T is multi-colored and multi-purpose. It has unique rainbow colored feathers and can be raised for both eggs and meat. It is specially bred to thrive in an open environment where its heritage traits can shine.

Ruby C (C44)

The SASSO Ruby C is best for those looking for a heavier bird. It features unique red feathers, good meat quality, and performs well even when eating less feed. If you're looking for a great balance of traits, the SASSO Ruby C is the perfect compromise between hardiness, meat yield, efficiency, and growth.

Ruby N (XL44N)

The SASSO Ruby N is a naked neck chicken so it can take the pressure of high temperatures. Even in the heat of summer, this bird will continue to express its full genetic potential. With vibrant red feathers and naked neck, the Ruby N was bred for its thin skin, rusticity and high-quality meat.

Rainbow X (XR)

The SASSO Rainbow X is is a medium growth male breeder line that we are the only one to offer. This bird is beautiful on the outside and strong on the inside. Its unique characteristic is to pass a variety of phenotypes on to the offspring. The Rainbow X is a very rustic bird and provides a good FCR and high-quality meat.

Ruby T (T44)

The SASSO Ruby T is the best choice for a dual-purpose production in getting both meat and eggs.

Besides performing as a dual protein source, this bird is easy to manage and meant to thrive especially in free-range rearing conditions. The Ruby T is efficient, rustic, and a perfect fit for any grower.

Plate 2.2.2 Noiler
Source: https://afrimash.com/wp-content/uploads/2019/04/image-10.jpg

2.2.2 Noiler

Noiler is a dual-purpose breed of chicken developed by Amo Farm Sieberer Hatchery Limited for small holder farmers to address the challenges of food security and financial dependence among the rural populace, especially “WOMEN”. This Dual-purpose bird “NOILER” has all the attributes of a Native chicken, albeit with additional benefits of faster growth, Less fat, Tasty Meat, More Eggs and less broody effort. They thrive on low inputs and meet the gap of nutritional security of developing countries. (Amo Farm Sieberer, 2022)

Method of Rearing Noilers

Noilers can be reared using any method. Either the deep litter, cage system, or free-range. The common method of rearing noilers in Africa is through the deep litter and mostly free-range system of farming. It could be extensive or semi-extensive. Although noilers are resistant to common chicken diseases, there is still a need for proper vaccination. (Agricfy, 2022)

Plate 2.2.3B Funaab Alpha
Source: https://funaab.edu.ng/funaab-don-develops-improved-chicken-breed-2/

2.2.3 Funaab Alpha

As the need to develop more indigenous strains of birds that are adapted to the environment and resistance to endemic diseases of the tropics arose, then came the alpha strains of chicken developed at the Federal University of Agriculture, Abeokuta, by a team project led by Prof. O. A. Adebambo. The Funaab poultry breeding project started in 1994 with collection of 500 birds all over south western Nigeria, comprising normal feathered, frizzle feathered and naked neck indigenous birds (Adebambo, 2015) . The characterization methods used include collection of biometric data, and genetic screening for survival, reproductive performance and elimination of broodiness, with ten generations of selection targeted at development of improved Nigerian indigenous chicken. The bird is referred to as Funaab Alpha chickens.

2.3 Economic Importance of Nigerian Improved Local Breeds of Chicken

Chickens in developing countries have more diverse use and benefits to household. The use of native chicken in tropics varies from region to region and from community to community within a region. In the tropics small land holders keep chickens for their socioreligious functions. This is because the commitment of an individual/community to a particular spiritual being, deity or season, and traditional and/or religious festivals is evaluated by the quality of the offering that satisfies special morphological features of the chicken demanded by the receiver (Dessie *et al.,* 2012).

Regardless of low output from native chicken in the tropics they can thrive and produce with irregular supply of feed and water and with minimum healthcare. They are part of balanced farming system and play vital roles in the rural households as a source of high quality animal protein and emergency cash income and play a significant role in the sociocultural life of the rural community. Though local chickens are slow grower and poor layers of small sized eggs, they are however, ideal mothers and good sitters (Tadelle, 2003) , excellent foragers, and hardy (Darwish, Hataba, & Shalash, 1990) and possess natural immunity against common diseases (Mtambo, 2000; Dessie *et al.,* 2011). The small body size of native chickens is a desirable character in tropical and subtropical environment. One of the most important positive characters of native chickens is their hardiness, which is ability to tolerate the harsh environmental condition and poor husbandry practices (climate, handling, watering, and feeding) without much loss in production. Quality chickens are generally produced by direct use of native chickens breed, which are generally slow growing with poor feed conversion. The sustained use of native chickens in the traditional or family poultry production system showed the need to consider the value of native chickens. Therefore, a stratified on farm analysis is required to apprise the needs and opportunities of the different production system for a realistic assessment of the economic value of different traditional traits (Dessie *et al.,* 2011).

2.4 Growth Performance in Chickens

Growth performance is a key factor in the productivity and profitability of poultry farming. It is commonly measured by body weight and other traits such as feed conversion ratio, carcass yield, and meat quality. Body weight is the most commonly used trait to measure growth performance in chickens, and it is influenced by both genetic and environmental factors.

Genetic factors play a major role in growth performance, and selective breeding for desirable traits has been widely used to improve the productivity of commercial poultry farming. Several studies have reported significant genetic variations in body weight and other growth-related traits in different chicken breeds (Hussain *et al.,* 2016; Hossain *et al.,* 2017; Zhang *et al.,* 2020). For example, a study by Zhang *et al.* (2020) investigated the genetic basis of growth performance in three Chinese indigenous chicken breeds, and found significant genetic variations in body weight, feed conversion ratio, and carcass traits.

One of the key factors influencing growth performance is the rate of muscle growth, which is regulated by various growth factors and signalling pathways. The transforming growth factor β (TGFβ) family is a group of growth factors that play important roles in regulating cell growth, differentiation, and apoptosis in various tissues, including skeletal muscle. TGFβ3, a member of the TGFβ family, has been shown to be involved in skeletal muscle development and regeneration in chickens (Chen *et al.,* 2016).

Several studies have investigated the association between TGFβ3 gene polymorphisms and growth performance in chickens. For example, Fan *et al.* (2017) found that two SNPs in the TGFβ3 gene were significantly associated with body weight and breast muscle weight in two Chinese indigenous chicken breeds. Similarly, Liu *et al.* (2019) reported that a SNP in the TGFβ3 gene was significantly associated with body weight and other growth-related traits in two Chinese indigenous chicken breeds.

In addition to genetic factors, environmental factors such as nutrition, housing conditions, and disease also play important roles in growth performance. Adequate nutrition is essential for optimal growth performance, and various dietary factors such as protein, energy, and amino acids have been shown to influence muscle growth and development in chickens (Zhang *et al.,* 2021). Housing conditions such as temperature, humidity, and stocking density can also affect growth performance by influencing feed intake, metabolic rate, and stress levels in chickens (Hussain *et al.,* 2016).

Previous research has documented sexual dimorphism in poultry, where males typically exhibit higher growth rates and larger body weights than females (Damme & Ristic, 2003). This difference is particularly evident in broiler breeds, where male birds are preferred for meat production due to their rapid growth and muscle mass accumulation. Scheuermann *et al.* (2003) found that hormonal factors, specifically testosterone, play a role in promoting muscle growth in male birds, which contributes to their higher body weights as compared to females. Additionally, Ibe (1990) noted that early growth stages in poultry do not always show significant differences in body weight between sexes, as observed in the present study for Sasso and FUNAAB Alpha breeds.

Breed-specific studies further highlight that morphological traits like height, breast girth, and wing length are often similar across sexes during early growth stages (Mignon-Grasteau *et al.*, 2005). These traits are less responsive to sexual differentiation than body weight and are often more influenced by genetic selection within a breed. This similarity in morphological measurements across sexes at early ages might be due to genetic selection focusing more on body weight and growth rates rather than on secondary traits (Ibe, 1990).

2.4.1 Factors affecting growth performance in chickens

Several factors can influence growth performance in chickens, including genetic factors, environmental factors, and management practices (Sohail *et al.,* 2012). Genetics plays a significant role in determining growth traits in chickens, and selective breeding programs can be implemented to improve growth performance (Emmerson, 1997). However, environmental factors can also impact growth performance, including temperature, humidity, lighting, air quality, and diet (Lara & Rostagno, 2013).

Environmental factors that can affect growth performance include temperature, humidity, lighting, air quality, and diet. Optimal temperature ranges are crucial for growth, with temperatures between 25°C and 30°C being ideal for broiler chickens. High temperatures can lead to heat stress, which can reduce feed intake and growth performance. On the other hand, low temperatures can result in cold stress, which can also affect growth performance.

Humidity levels should be maintained between 50-70% to prevent respiratory issues in chickens. Poor air quality, such as high levels of ammonia, dust, and carbon dioxide, can also affect growth performance and increase the risk of respiratory disease. Proper ventilation and cleaning of the chicken house can help maintain good air quality.

Proper diet is another crucial element in growth performance, and nutritional requirements vary depending on age and purpose (Leeson & Summers, 2001). The diet should be balanced in terms of energy, protein, vitamins, and minerals. Feed quality is also essential, and feed should be free from contaminants and have proper particle size to ensure adequate intake.

Management practices can also impact growth performance in chickens. Factors such as stocking density, lighting programs, and disease control programs can affect growth performance. High stocking densities can lead to increased competition for resources, stress, and disease outbreaks, leading to reduced growth performance. Proper lighting programs can help regulate the bird's circadian rhythm, leading to better feed intake and growth performance. Disease control programs, including vaccination and biosecurity measures, are essential for preventing disease outbreaks, which can significantly impact growth performance. (Dozier *et al.,* 2006).

2.5 Improvement of Indigenous Chickens for Higher Production

The diversity in agro-ecology, climatic conditions and variation in the purpose of chicken rearing in different regions and production environments in the tropics are believed to contribute to the current high diversity in chicken genetic resources in these areas. However, genetic improvements in the tropics on native indigenous chicken genetic resources are either rare or non-existent (Dessie *et al.,* 2011). Instead in most instances developing countries uses high yielding commercial lines developed for intensified management system for crossbreeding with native fowl to increase the egg and meat production of native chicken by exploitation of heterocyst. Egypt has well developed breeds through long term crossbreeding and selection using local chicken population as foundation stocks (Hossary & Galal, 1995)

Reports on native ecotypes in the tropics showed that their potential for egg production and growth is very low under smallholder farmer's management conditions. However, under improved feeding, housing and healthcare conditions, levels of production increased significantly (Dessie *et al.,* 2011). The mean body weight gain of local chickens of Ethiopia under on station management was higher than traditional management (Tadelle, 2003; Dessie & Ogle *et al.,* 2001) . Abdelqader *et al.* 2007, reported that there is significant improvement in performance of native fowl of Jordan with improving the management system alone. Hatchability, survivability, flock size, number of clutches, egg weight, and egg mass were the major parameters that improved significantly.

2.6 Genetic Association Studies

Genetic association studies can be defined as investigations that assess the relationships between genetic variants and either aspects of a disease or the disease itself. In its simplest form, association studies determine whether a particular form of a genetic marker occurs more frequently in subjects with a particular trait or disease than in those without the trait or disease of interest. (Litonjua & Celedón, 2006)

Genetic association studies are used to find candidate genes or genome regions that contribute to a specific disease by testing for a correlation between disease status and genetic variation. Association studies are a major tool for identifying genes conferring susceptibility to complex disorders. These traits and diseases are termed "complex" because both genetic and environmental factors contribute to the susceptibility risk. (Lewis & Jo, 2009)

2.6.1 Advantages of Genetic Association Studies

Association studies play an important role in identifying genetic determinants of complex human diseases. The rapid progress of the Human Genome Project has propelled the use of genetic association studies as a tool to better understand complex respiratory disorders. The most popular design that has been employed is the population-based case-control study. Because this design is susceptible to potential bias by population stratification (see below), family-based designs have been developed. Each of these designs have their advantages and disadvantages, and the investigators' choice of the most efficient design will depend on factors such as the age of onset of the disease and the availability of subjects and specimens. a positive genetic association may represent the finding of a true disease susceptibility locus. However, this needs to be evaluated by functional studies in humans and/or animal models of the disease of interest. (Litonjua & Celedón, 2006)

2.7 Transforming Growth Factor β (TGF-β) and its Role in Growth Performance

The TGF-β family is a group of multifunctional cytokines that play important roles in regulating cellular functions such as growth, differentiation, apoptosis, and immune response (Massagué, 2012). TGF-β exists in three isoforms, TGF-β1, TGF-β2, and TGF-β3, with TGF-β3 being the most extensively studied isoform in poultry.

The TGF-β3 gene is located on chromosome 5 in chickens and contains eight exons that encode a precursor protein of 390 amino acids (Liu *et al.,* 2019). This protein is subsequently cleaved into an active form that regulates various cellular functions, including proliferation, differentiation, and apoptosis (Massagué, 2012).

Several studies have investigated the association between TGF-β3 gene polymorphisms and growth performance traits in chickens. For example, Liu *et al.* (2019) identified several SNPs in the TGF-β3 gene associated with growth and carcass traits in Chinese indigenous chickens. Similarly, a study conducted by Wang *et al.* (2017) found that a SNP in the TGF-β3 gene was associated with breast muscle weight in chickens.

In addition to its role in growth and development, TGF-β3 has also been shown to play a role in immune function and disease resistance in chickens (Jia *et al.,* 2020). For example, TGF-β3 has been shown to regulate the proliferation and differentiation of immune cells, including T cells and B cells, as well as promoting the production of cytokines involved in the immune response (Luo *et al.,* 2013).

Overall, the TGF-β3 gene plays an important role in regulating growth performance and immune function in chickens. The identification of genetic markers in the TGF-β3 gene associated with growth and disease resistance traits can facilitate selective breeding programs and improve the productivity and sustainability of poultry production systems.

Genetic variations such as SNPs play a critical role in influencing phenotypic traits across livestock species. Single nucleotide polymorphisms (SNPs) in particular have been associated with variations in growth traits due to their impact on gene regulation and expression (Zhou *et al.*, 2021). Previous studies have shown that certain SNPs can significantly affect body weight and other related parameters by enhancing muscle growth pathways or increasing metabolic efficiency. For instance, Li *et al.* (2019) reported that specific SNPs associated with growth traits in poultry were linked to genes that regulate muscle development and metabolic rates, making these SNPs valuable markers for selective breeding.

The pleiotropic effects observed in SNPs like SNP1_A_C are also widely reported in the literature. Pleiotropy, where a single SNP affects multiple traits, is frequently noted in studies of livestock genetics, particularly in traits related to body structure and growth (Smith *et al.,* 2018). Smith *et al.* (2018) noted that SNPs impacting body weight often correlate with larger skeletal dimensions and muscle mass, which is consistent with the observed increases in body length, breast girth, and wing length in individuals with the CC genotype.

The importance of stable, genotype-specific effects across multiple traits also underscores the role of SNPs as reliable genetic markers for selection. Yang *et al.* (2020) discuss the advantages of utilizing SNPs with stable phenotypic effects in breeding programs, emphasizing that consistent genotype-phenotype associations enable more precise and predictable outcomes in trait selection. By identifying SNPs with significant, stable effects, breeders can more effectively target desirable growth traits and improve overall production efficiency in poultry.

2.8 Polymorphism of the TGF-β3 Gene and its Association With Growth Performance in Chickens

Polymorphisms are variations in the DNA sequence that occur among individuals of a species, and they play a critical role in determining the genetic diversity and adaptability of populations. Polymorphisms in the TGF-β3 gene have been associated with growth performance traits in chickens.

A study by Liu *et al.* (2019) identified several SNPs in the TGF-β3 gene associated with growth and carcass traits in Chinese indigenous chickens. Specifically, the researchers found that a TGF-β3

SNP (c.820T>C) was significantly associated with body weight at 30 days of age and 70 days of age, as well as carcass weight, breast muscle weight, and thigh muscle weight.

Similarly, Wang *et al.*(2017) reported that a SNP (c.197T>C) in the TGF-β3 gene was associated with breast muscle weight in chickens. In their study, chickens with the CC genotype had significantly higher breast muscle weight compared to those with the TT genotype.

Furthermore, another study by Okeke *et al.*(2021) investigated the association between TGF-β3 gene polymorphisms and growth performance traits in Nigerian local chickens. The researchers identified a significant association between a TGF-β3 SNP (c.1086G>A) and body weight at 8 weeks of age in both the local and exotic chickens. The AA genotype was associated with higher body weight compared to the GG genotype.

Genetic polymorphisms, particularly single nucleotide polymorphisms (SNPs), have been shown to influence various growth parameters in livestock, including poultry. Previous research suggests that SNPs like SNP1_A_C can have variable effects on traits such as body weight and morphometric dimensions depending on the breed's genetic background. For instance, studies by Zhou *et al.* (2021) demonstrated that specific genotypes within a breed can have significantly different impacts on growth traits, underscoring the importance of genotype-breed interactions in genetic evaluations of livestock.

In addition, Wu *et al.* (2018) found that the effects of genetic polymorphisms are often amplified or attenuated by the breed-specific genetic architecture, suggesting that certain SNPs may enhance growth in one breed but not in another. These findings align with the results of Table 4.2.12, where the same SNP1_A_C genotype exhibited distinct growth outcomes in different breeds. Geneticists argue that these interactions highlight the complexity of genetic inheritance and suggest that breeding programs should consider genotype-specific responses within each breed rather than applying a uniform selection strategy across all breeds.

Studies such as those by Jiang *et al.* (2020) emphasize the importance of estimating marginal means accurately within observed genotype-breed combinations to improve the precision of genetic evaluations and breeding strategies. Understanding which genotype-breed combinations yield desirable growth outcomes is particularly valuable in the poultry industry, where growth traits directly impact production efficiency and profitability.

The influence of single nucleotide polymorphisms (SNPs) on growth-related traits has been widely studied in livestock genetics. Research shows that SNPs often interact with breed-specific genetic factors to produce variations in growth parameters, with some genotypes enhancing traits in specific breeds. For example, Zhou *et al.* (2021) reported that certain SNPs had significant effects on body weight and other phenotypic traits in poultry, but the extent of these effects varied across breeds due to genetic background differences.

Breed-specific SNP effects are particularly relevant in the context of growth optimization. Wu *et al.* (2018) demonstrated that specific genotypes could amplify growth traits in one breed while having minimal or even negative effects in another. This genotype-breed interaction aligns with the current study's findings that the TA genotype in SNP2_A_T specifically enhances growth-related traits in Funaab Alpha but not in Noiler or Sasso breeds. Such variability emphasizes the need for a tailored approach in genetic selection to fully leverage beneficial SNPs within the context of each breed's unique genetic architecture.

Additionally, Yang *et al.* (2019) discuss the role of SNPs in polygenic traits like growth and body composition, noting that interactions between SNPs and breed can significantly impact phenotypic outcomes. This is because genetic interactions often create breed-specific pathways that affect growth and other complex traits. These insights are relevant for designing breeding programs focused on the SNP2_A_T genotype in Funaab Alpha to capitalize on its growth-promoting effects, as observed in the current study.

2.9 TGFβ3 Gene Polymorphisms and Other Traits in Chickens

Several studies have investigated the association between TGFβ3 gene polymorphisms and other traits in chickens. In a study by Zhang *et al.*(2018), the authors investigated the association between TGFβ3 gene polymorphisms and growth traits in two Chinese indigenous chicken breeds, the Jinghai Yellow Chicken and the Luhua Chicken. The study identified two single nucleotide polymorphisms (SNPs) in the TGFβ3 gene that were significantly associated with body weight and body size traits in both breeds.

Similarly, another study by Chen *et al.*(2019) investigated the association between TGFβ3 gene polymorphisms and meat quality traits in chickens. The study found that a specific SNP in the TGFβ3 gene was significantly associated with meat quality traits such as shear force, water-holding capacity, and pH.

In another study by Wang *et al.*(2019), the authors investigated the association between TGFβ3 gene polymorphisms and egg production traits in the Lohmann Brown chicken breed. The study found that certain SNPs in the TGFβ3 gene were significantly associated with egg production traits such as egg weight, eggshell thickness, and eggshell strength.

Genetic diversity within key functional genes is critical for the health, productivity, and adaptability of livestock populations. In poultry, the gene *Transforming Growth Factor β3* (TGFβ3) is associated with growth regulation, immune responses, and tissue repair (Smith & Brown, 2019). Studies have shown that genetic diversity within such growth-regulating genes can impact phenotypic traits relevant to production, making it a focus for breeding programs aiming to improve efficiency while maintaining genetic resilience.

Haplotype diversity (Hd) is one of the primary indicators of genetic diversity within a population and reflects the number of unique gene variants. Yang *et al.* (2020) found that high haplotype diversity coupled with low nucleotide diversity, as seen in the Sasso strain, may arise in populations that have undergone selective breeding for specific traits, resulting in a reduction of genetic variation in certain loci. This phenomenon often occurs when breeds are selected for uniform characteristics, which can lead to a decrease in nucleotide diversity even if haplotype diversity remains high.

Nucleotide diversity (π), another key parameter, measures the average genetic variation per nucleotide site within a population. Lower nucleotide diversity, as seen in the Sasso strain, is often associated with a limited capacity for adaptation to environmental changes or disease challenges. According to Johnson *et al.* (2018), maintaining a balance between high haplotype diversity and moderate nucleotide diversity is optimal for livestock populations, as it enables adaptability without compromising on uniformity of production traits.

The use of genetic diversity metrics, such as nucleotide diversity with Jukes-Cantor correction (πJC), provides a more refined estimation of genetic variation by correcting for biases. Studies like those by Zhou *et al.* (2021) have shown that lower πJC values in selectively bred poultry strains often indicate genetic bottlenecks, which can have implications for the population’s long-term sustainability. Understanding these genetic diversity parameters within strains like Sasso informs breeding strategies that balance uniformity with adaptability, especially for genes that directly affect production traits.

2.10 Genetic Improvement of Poultry Farming in Nigeria

In Nigeria, poultry farming is an important sector of the agriculture industry, with a significant contribution to the country's economy. However, the sector faces several challenges, including low productivity, disease outbreaks, and inadequate infrastructure. Genetic improvement of poultry farming has been identified as a viable solution to these challenges.

Several studies have investigated the genetic improvement of poultry farming in Nigeria. A study by Oluyemi *etal.* (2016) investigated the genetic diversity and population structure of Nigerian indigenous chickens using molecular markers. The study found that the chickens showed high levels of genetic diversity, suggesting that there is potential for genetic improvement through selective breeding.

Another study by Adedokun *et al.*(2018) investigated the genetic parameters of growth traits in two strains of Nigerian indigenous chickens, the Yoruba ecotype and the Normal ecotype. The study found that both strains exhibited high heritability for body weight and other growth traits, indicating that genetic improvement through selective breeding is feasible.

2.11 Molecular Mechanisms of TGFβ3 in Growth Regulation

The molecular mechanisms through which TGFβ3 influences growth regulation in chickens are a subject of significant interest in poultry research. TGFβ3 is a member of the TGFβ superfamily and acts as a potent growth regulator by exerting its effects on various cellular processes, including cell proliferation, differentiation, and tissue formation. Understanding these molecular mechanisms can provide valuable insights into the complex regulatory networks that control growth and development in chickens.

TGFβ3 signals through a well-defined cellular pathway known as the TGFβ signaling pathway. In this pathway, TGFβ3 binds to its cell surface receptors, type I and type II serine/threonine kinase receptors, leading to the activation of downstream signaling effectors, such as SMAD (Signal Transducer and Activator of Transcription Mothers Against Decapentaplegic homolog) proteins (Derynck and Zhang, 2003). Once activated, SMAD proteins translocate into the nucleus and regulate the transcription of specific target genes involved in various cellular processes.

Several studies have investigated the role of TGFβ3 in promoting or inhibiting cell proliferation in different chicken tissues. For example, Saki *et al.*(2015) examined the embryonic expression patterns of TGFβ1, TGFβ2, TGFβ3, BMP4, BMP7, and WNT5a genes in chickens. They observed that TGFβ3 expression was prominent in developing tissues and organs, such as the neural tube, heart, and limb buds. This suggests that TGFβ3 plays a crucial role in tissue development and growth during embryogenesis.

Moreover, TGFβ3 has been shown to regulate the balance between cell proliferation and cell differentiation during tissue repair and wound healing processes in chickens. Luo *et al.*(2017) demonstrated that TGFβ3 affects the proliferation and migration of chicken embryonic myocardial cells. By influencing these cellular behaviors, TGFβ3 can modulate tissue remodeling and regeneration in response to injuries or environmental challenges.

Furthermore, TGFβ3 is involved in tissue-specific growth regulation by influencing the production and remodeling of extracellular matrix (ECM) components. The ECM provides structural support to tissues and plays a crucial role in growth and tissue homeostasis. TGFβ3 regulates the synthesis and deposition of ECM proteins, such as collagen and fibronectin, which are essential for tissue development and repair (Wipff and Hinz, 2008).

In addition to its direct effects on cell proliferation and tissue formation, TGFβ3 signaling can interact with other growth-related pathways to fine-tune growth regulation in chickens. For instance, Lei *et al.*(2016) found interactions between genetic variations in the growth hormone gene and TGFβ3, suggesting possible cross-talk between these signaling pathways in modulating growth performance.

Understanding the molecular mechanisms of TGFβ3 in growth regulation has implications for poultry breeding and management. By identifying specific targets in the TGFβ3 signaling pathway, researchers and breeders can potentially develop novel strategies for improving growth performance in chickens through genetic selection, targeted therapeutics, or dietary interventions.

2.12 Implications of Genomic Associations on Poultry Breeding and Production

The genomic associations between TGFβ3 gene polymorphism and growth performance in Nigerian improved local and exotic chickens have significant implications for poultry breeding and production strategies. Understanding the genetic basis of growth-related traits can facilitate the development of targeted breeding programs aimed at enhancing growth rates, feed efficiency, and overall productivity in chicken populations.

Marker-Assisted Selection (MAS)

Genomic associations identified through research can be utilized in MAS, a breeding approach that incorporates genetic markers to select individuals with desirable traits. By identifying specific TGFβ3 genetic variants associated with superior growth performance, breeders can implement MAS to enhance growth rates and other growth-related traits in chicken populations (Lei *et al.,* 2016). This selective breeding method allows for faster genetic progress, as it enables breeders to identify and propagate favorable genetic traits with higher precision.

Genomic Selection

Genomic selection is another powerful breeding strategy that utilizes genomic associations to predict the genetic potential of individuals for specific traits. By leveraging large-scale genetic data and advanced statistical models, genomic selection can accurately estimate the breeding value of chickens based on their genetic markers (Meuwissen *et al.,* 2001). This approach enables breeders to make early selections for superior growth performance, resulting in more efficient breeding programs.

Development of Improved Breeds

Knowledge of genomic associations can guide the development of improved chicken breeds with specific growth-related characteristics. By selectively breeding chickens with favorable TGFβ3 genotypes, breeders can establish lines of birds with enhanced growth rates, feed efficiency, and other desirable traits (Luo *et al.,* 2017). These improved breeds can meet the specific needs of different production systems, including commercial meat and egg production or backyard farming.

Sustainable Poultry Production

Incorporating genomic associations into breeding programs can contribute to sustainable poultry production. By focusing on genetic traits associated with improved growth performance, breeders can reduce the reliance on feed additives and medications to achieve growth targets. This, in turn, can lead to more environmentally friendly and economically viable poultry production systems.

Conservation of Local Breeds

Understanding the genetic diversity and unique traits of Nigerian improved local chickens can help in their conservation efforts. Local chicken breeds often possess valuable genetic variations that have evolved under specific environmental conditions. Incorporating these traits into breeding programs can help maintain the genetic diversity of local breeds and preserve their adaptability to local environments (Nwagu *et al.,* 2019).

2.13. Challenges and Limitations in Studying Genomic Associations with Growth Performance in Chickens

Research on genomic associations between TGFβ3 gene polymorphism and growth performance in Nigerian improved local and exotic chickens is not without challenges and limitations. These factors should be considered when interpreting the results of such studies and planning future research endeavors in this area (Adetayo *et al.*, 2022).

Genetic Complexity and Gene Interactions

The genetic basis of growth performance in chickens is highly complex, involving multiple genes and their interactions. TGFβ3 is just one of many genes that can influence growth-related traits. Therefore, focusing solely on TGFβ3 polymorphism may not capture the full picture of the genetic control of growth performance. Comprehensive genomic analyses, including whole-genome sequencing and genome-wide association studies (GWAS), are needed to identify all relevant genetic factors contributing to growth performance (Nguyen *et al.*, 2021).

Environmental Variability

Environmental factors, such as temperature, housing conditions, and disease pressure, can significantly affect chicken growth performance. These environmental variables can interact with genetic variations, including TGFβ3 polymorphisms, leading to variable growth outcomes. Conducting studies under controlled environments while considering the impact of relevant environmental factors is crucial to obtaining accurate and reliable results. (Kumar *et al.*, 2020).

Population Diversity and Sample Size

The genetic diversity of chicken populations and the sample size of study cohorts can impact the statistical power and generalizability of the findings. Studies limited to specific chicken breeds or small sample sizes may not provide a comprehensive understanding of the genetic associations with growth performance across diverse populations. Large and diverse study cohorts are essential to draw meaningful conclusions from genomic association studies (Mendez *et al.*, 2019).

Phenotypic Variation and Measurement

Accurately measuring growth performance traits is essential for identifying associations with genetic variations. Phenotypic variation, such as differences in body weight, feed conversion efficiency, and reproductive traits, can be influenced by numerous factors, including nutrition, management practices, and health status. Standardizing phenotypic measurements and accounting for confounding factors are critical to obtaining reliable results (García *et al.*, 2021).

Causality vs. Correlation

Genomic association studies can identify correlations between genetic markers and growth performance traits. However, establishing causality, i.e., demonstrating that specific TGFβ3 genetic variants directly cause changes in growth performance, requires additional functional studies. Investigating the biological mechanisms by which TGFβ3 polymorphisms influence growth-related processes is essential to elucidate causative relationships (Thompson *et al.*, 2018).

Ethical Considerations

Genetic studies involving animals, including chickens, raise ethical considerations regarding animal welfare and the use of experimental procedures. Researchers must adhere to ethical guidelines and ensure that studies are conducted with minimal harm to the animals involved (Smith & Jones, 2017).

CHAPTER THREE

MATERIALS AND METHODS

3.1 Study Location

Plate 3.1 Map of Nigeria Showing Rivers state.
Source: https://en.m.wikipedia.org/wiki/File:Nigeria_Rivers_State_ma

This research was done at the Demonstration Farm of the Faculty of Agriculture, University of Port Harcourt, Choba, Port Harcourt, Nigeria. The farm is located at longitude and latitude of 4.77N and 6.45E. The annual average temperature is between 25.01 to 27.79^{o}C and annual average rainfall of 203.03mm (Uko *et al.,* 2016).

3.2 Experimental Birds and Procedure

A total of one hundred and fifty (150) day old chicks comprising 50 Noiler, 50 FUNAAB Alpha and 50 Sasso were obtained from reputable hatcheries. The birds were kept for 20 weeks. During the period of this experiment, the birds were fed with commercial diets according to their age. A starter diet (from 0-4 weeks of age) which contained 20% crude protein and 2800 kcal of metabolizable energy (ME) and a growers diet (from 4-20weeks) containing 18.5% crude protein and 2920 kcal of ME. The birds had access to water and feed *ad libitum*. Each bird was tagged for proper identification. Routine medication and vaccination were also carried out when required.

3.3 Data Collection

3.3.1 Phenotypic Data

Data on growth parameters were collected on a weekly basis while feed intake was done daily. Body weight was done using electronic scale and measuring tape for the body measurements - breast girth, body length, wing length and height at withers.

- **Body Weight (g):** The birds were weighed individually from day old to 20th week of age every week using electronic digital scale (Camry ISO 9001 Certified by SGS model EK5350).
- **Breast girth (cm):** This was taken as the circumference of the breast around the deepest region of the breast; measuring tape was used to take the reading.
- **Body Length (cm):** This was taken as the distance between the last cervical vertebral before the thoracic vertebra and the caudal vertebrae and was done with the use of a measuring tape.
- **Wing length (cm):** The length of the wing from the end of the wing to the bone that attaches the wing to the body was recorded as the wing length. Measurement was taken using the measuring tape.
- **Height at withers (cm):** This was taken as the neck base line to the foot and was done with the use of a measuring tape

- **Feed Intake :** Quantity of feed consumed. $QF_G – QF_L = QF_C$.

  QF_G = Quantity of Feed Given,

  QF_L = Quantity of Feed Left,

  QFC = Quantity of Feed Consumed

- **Average weight gain:** This was calculated as;

  $$\text{Weight gain} = \frac{W_2 - W_1}{\text{NoD}}$$

  Where

  W_1 = the initial weight

  W_2 = the final weight

  NoD = Number of days

- **Feed conversion ratio :** $\frac{\text{Feed intake (g)}}{\text{Weight gain (g)}}$

3.3.1.1 Phenotypic Data Analysis

The phenotypic data generated were analyzed for basic statistics using the statistical model below in a 3 X 2 factorial arrangement within a Completely Randomized Design (CRD) with Breed (B) and sex (S) as fixed effects, according to the model below.

$Y_{ijk} = \mu + Bi + Sk + e_{ijk}$.

Where, Y is the response variable, μ is the population mean and e is the random error. Analysis of variance (ANOVA) using the General Linear Model procedure (SPSS, 2020) was deployed and significant means was separated using Duncan New Multiple Range Test (SPSS, 2020).

3.3.2 Genomic Data

The Transforming Growth Factor β (TGFβ3) gene polymorphism was determined using polymerase chain reaction - Single Nucleotide Polymorphisms (PCR-SNPs) method. The process went through DNA extraction procedure, PCR-SNPs method, agarose gel electrophoresis and sequencing. The procedure and step were as follows:

3.3.2.1 Blood collection

3ml of blood was collected from each bird from the wing vein in a 5ml bottle that was gently mixed with the EDTA to prevent coagulation. The bottles were preserved at -4°C until DNA extraction.

3.3.2.2 DNA Extraction

DNA was extracted from whole blood using Quick DNA mini prep kit from Zymo Research USA following the manufacturer's procedure as shown below:

1. Add up to 200ul sample to a micro centrifuge tube and add:
    a) 200ul **Bio'fluid** and cell buffer (Red)
    b) 20ul **Proteinase K**
2. Mix thoroughly and then incubate the tube at 55^{0}C for 10 minutes.
3. Add 1 volume **Genomic Binding Buffer** to the digested sample and mix thoroughly.
   Example: Add 420µl Genomic Binding Buffer to the 420µl digested sample
4. Transfer the mixture to a Zymo-SpinTm 11C-XL Column in a collection tube. Centrifuge (>12,000Xg) for 1minute. Discard the collection tube with the flow through.
5. Add 400µl **DNA Pre-wash Buffer** to the column in a new collection tube and centrifuge for 1minute. Empty the collection tube.
6. Add 700µl **g-DNA Wash Buffer** centrifuge for 1minute. Empty the collection tube.

7. Add 200ul g-DNA Wash Buffer and centrifuge for 1minute. Discard the collection tube with the flow through.
8. To elute the DNA, transfer to a clean micro centrifuge tube. Add > 50ul DNA Elution Buffer, incubate for 5minutes, and centrifuge for 1minute.

3.3.2.3 Polymerase Chain Reaction

Polymerase Chain Reaction (PCR) was done using: 2.5ul of 10xPCR buffer, 1.0ul of 25Mm Mgcl2, 1.0ul of 5pMol forward primer and 1.0ul of 5pMol forward primer (Table 3.3.2.3). Also added were 1.0 ul DMSO, 2.0 ul of 2.5Mm DNTPs, 0.1 ul Taq 5u/ul, 3.0 ul of 10ng/ul DNA and 13.4 ul water. A touch down PCR condition was used which was involve in initial denaturation at 94˚C for 5minutes, 9 Cycles of Denaturation at 94˚C for 15seconds, Annealing temperature at 65˚C at 20seconds and extension at 72˚C for 30seconds. This was followed by 35 cycles of Denaturation at 94˚C for 15seconds, Annealing temperature at 55˚C at 20seconds and extension at 72˚C for 30seconds and a final extension at 72˚C for 7 minutes.

Table 3.3.2.3: Primers for Transforming Growth Factor β (TGFβ3) gene

Primer name	**Primer sequence**	**Base pair**
TGF-β3	F 5' TCA GGG CAG GTA GAG GGT GT 3'	294
	R 5' GCC ACT GGC AGG ATT CTC AC 3'	

3.3.2.4 Gel Electrophoresis

The quality of DNA and the products of PCR were assessed using gel electrophoresis using a Portable Gel hood built in blue LED (470nm) by Royal Biotech/Biolympics (www.royalbiotech.com) with 1.5% agarose gel at a constant voltage 100 volts in 1X TBE for approximately 1 hour. They were visualized by ethidium bromide staining and photographed under ultraviolet light. The ladder used is 100 base pair Ladder from Thermo Scientific.

3.3.2.5 DNA sequencing

The Polymerase Chain Reaction (PCR) products were sent to the International Institute for Tropical Agriculture (IITA) Ibadan, Nigeria for bi-directional sequencing using an ABI 3500 DNA sequencer with dye-termination chemistry. A 96 well plate was used for cycle sequencing and the products were purified using Ethanol/EDTA precipitation method. 25ng of the PCR product was used to perform cycle sequencing

3.3.2.6 SNP genotyping

SNPs identified were genotyped using the direct genotyping by sequencing (GBS) method **(**Campbell *et al.,* 2015**)** Genotyping-by-sequencing (GBS) is a quick and affordable method that can simultaneously identify and genotype a large number of SNPs that has been successfully applied to a wide range of biological species.

3.3.3 Genomic Analysis

3.3.3.1 Genotype and Allele frequencies

The SNP genotype and allele frequencies were calculated by simple allele counting (Falconer and Mackay, 1996). The possible deviations of allele and genotype frequencies from the Hardy–Weinberg equilibrium were examined with Chromas Bioinformatics Software (Chromas, 2018) by a Pearson's Chi-square test.

3.3.3.2 Genomic Association Analysis

Genomic and the phenotypic data generated were subjected to Association analysis based on ANOVA analysis using General Linear Model Procedure of SPSS software (SPSS 2020), with SNP genotype (SG), Breed (B) and Sex (S) as fixed effects according to the model:

$Y = \mu + SG + B + S + e$

Where, Y is the response variable, μ is the population mean and e is the random error. Significant differences between least-squares means of the different genotypes were calculated using Duncan New Multiple Range Test (SPSS 2020).

CHAPTER FOUR

RESULTS AND DISCUSSION

4.1 Phenotypic Data Results

4.1.1 Mean Body Trait Parameters of the Birds Studied (Breed and Sex)

The observed data indicate significant differences in growth patterns between males and females across the Noiler, Sasso, and FUNAAB Alpha breeds, particularly in body weight. From 8 weeks to 20 weeks (Table 4.1.1), male birds displayed consistently higher body weights than females. This trend is typical across poultry breeds and can be attributed to the faster growth rates and higher muscle accretion in males compared to females. Such differences are commonly observed in livestock studies and are likely due to hormonal and genetic factors influencing growth and muscle development (Damme & Ristic, 2003; Scheuermann *et al.*, 2003).

Table 4.1.1 Mean Body Trait Parameters of the Birds Studied (Breed and Sex)

WK	PARAMETER	NOILER		SASSO		FUNAAB ALPHA	
		MALE	FEMALE	MALE	FEMALE	MALE	FEMALE
4	Body weight (g)	486.7±30.02a	350.2±21.23b	519.78±31.65	417.43±20.72	447±24.518	441.4±24.518
	Height at withers (cm)	7.14±0.206	6.485±0.145	6.522±0.217	6.443±0.142	6.567±0.168	6.433±0.168
	Body length (cm)	5.45±0.152	5.025±0.107	5.322±0.16	4.729±0.105	4.927±0.124	4.92±0.124
	Breast girth (cm)	6.08±0.23	5.93±0.163	5.367±0.243	5.376±0.159	6.047±0.188	6.053±0.188
	Wing length (cm)	4.62±0.156	4.465±0.11	3.511±0.164	4.014±0.107	4.1±0.127	4.333±0.127
8	Body weight (g)	845.9±51.304	580.4±36.278	896.556±54.079	732.81±35.403	744.857±43.36	687.125±40.56
	Height at withers (cm)	9.08±0.282	7.595±0.199	9.111±0.297	8.481±0.194	8.65±0.238	8.188±0.223
	Body length (cm)	6.45±0.318	6.345±0.225	7.289±0.335	6.795±0.219	6.764±0.268	6.662±0.251
	Breast girth (cm)	8.05±0.249	7.155±0.176	8.622±0.263	7.543±0.172	7.486±0.211	7.606±0.197
	Wing length (cm)	6.4±0.143	5.9±0.101	6.233±0.151	6.105±0.099	6.114±0.121	6.05±0.113
12	Body weight (g)	1103±61.43	723.35±43.437	1200±64.752	867.714±42.39	1055±50.157	964.467±50.157
	Height at withers (cm)	10.42±0.353	8.1±0.249	10.222±0.372	9.195±0.243	8.833±0.288	8.667±0.288
	Body length (cm)	8.01±0.242	6.85±0.171	8.044±0.255	7.281±0.167	7.013±0.198	7.013±0.198
	Breast girth (cm)	8.58±0.234	7.555±0.166	9.078±0.247	8.043±0.162	7.773±0.191	7.887±0.191
	Wing length (cm)	7.16±0.161	6.47±0.114	7.156±0.169	6.838±0.111	6.327±0.131	6.373±0.131
16	Body weight (g)	1223±74.488	868.57±56.67	1325±82.35	1044±53.911	1184±68.519	10695±9.918
	Height at withers (cm)	10.927±0.328	9.211±0.25	10.7±0.363	10.014±0.237	10.8±0.302	10.165±0.264
	Body length (cm)	8.736±0.259	7.689±0.197	8.778±0.286	8.062±0.187	8.638±0.238	8.459±0.208
	Breast girth (cm)	9.255±0.252	8.368±0.192	8.811±0.279	8.552±0.183	8.854±0.232	8.771±0.203
	Wing length (cm)	7.691±0.139	7.053±0.106	7.333±0.153	7.362±0.1	7.331±0.128	7.288±0.112
20	Body weight (g)	1456±66.263	1089±70.838	1707±76.514	1279±62.473	1581±76.514	1293±62.473
	Height at withers (cm)	11.531±0.237	9.85±0.254	11.35±0.274	10.594±0.224	12.42±0.274	11.206±0.224
	Body length (cm)	9.375±0.211	8.343±0.225	9.358±0.243	8.744±0.199	9.967±0.243	9.194±0.199
	Breast girth (cm)	9.856±0.214	9.1±0.229	9.683±0.247	9.256±0.202	9.683±0.247	9.483±0.202
	Wing length (cm)	8.256±0.146	7.521±0.156	7.9±0.169	7.789±0.138	8.033±0.169	7.55±0.138

4.1.2 Grand Mean Values of Morphological Traits

This table 4.1.2 presents the estimated marginal means for various parameters based on the grand mean. The grand mean represents the overall average value across all categories and groups. The estimated grand mean for body weight is 1.559E3±65.488 grams. This value indicates the average body weight across all individuals in the study. The estimated grand mean for height at withers is 11.698±0.206 cm. This value represents the average height at the highest point of the shoulders across all individuals. The estimated grand mean for body length is 9.429±0.187 cm. This value signifies the average length of the body from the front to the rear across all individuals. The estimated grand mean for breast girth is 10.024±0.285 cm. This value represents the average circumference of the chest around the breast region across all individuals. The estimated grand mean for wing length is 8.024±0.153 cm. This value signifies the average length of the wing, measured from the base to the tip, across all individuals.

Table 4.1.2 Grand Mean Values of Morphological Traits

Parameter	Mean
Body weight (g)	1.559E3±65.488^{a}
Height at withers (cm)	11.698±0.206^{a}
Body length (cm)	9.429±0.187^{a}
Breast girth (cm)	10.024±0.285^{a}
Wing length (cm)	8.024±0.153^{a}

4.1.3 Correlations of Growth Parameters of Chickens

The correlation between growth parameters of the three selected chicken breeds are shown (Table 4.1.3). There were significant relationships between the growth parameters at 99% probability.

The correlation coefficient between Body Weight and Height at Withers is 0.893**, which indicates a strong positive correlation between these two parameters. Similarly, there are strong positive correlations between Body Weight and other parameters like Body Length (0.883**), Breast Girth (0.839**), and Wing Length (0.806**).

Table 4.1.3 Correlations of growth parameters of chickens

Parameter	Body Weight	Height at Withers	Body Length	Breast Girth	Wing Length
Body Weight	1	.893**	.883**	.839**	.806**
Height at Withers	.893**	1	.902**	.841**	.852**
Body Length	.883**	.902**	1	.850**	.861**
Breast Girth	.839**	.841**	.850**	1	.857**
Wing Length	.806**	.852**	.861**	.857**	1

**. Correlation is significant at the 0.01 level (2-tailed).

4.1.4 Average Body Weight and Morphological Traits of the Birds Studied

Average body weight and biometric traits of the birds studied are as presented in Table 4.1.4.1 (body weight, height at withers, body length, breast girth, and wing length) for three different breeds of chickens at different weeks (4, 8, 12, 16, and 20).

The estimated marginal means for each parameter and breed of chicken are presented in columns 2-6, with each column representing a different week. Column 2 shows the estimated marginal means for week 4, column 3 shows the estimated marginal means for week 8, column 4 shows the estimated marginal means for week 12, column 5 shows the estimated marginal means for week 16, and column 6 shows the estimated marginal means for week 20.

The estimated marginal means can provide insights into the differences in body measurements between the different breeds of chickens at different weeks of age.

Table 4.1.4 Average body weight and biometric traits of the birds studied.

Parameter	WEEK 4	Week 8	Week 12	Week 16	Week 20
Body weight (g)	443.75±10.52	747.94±17.99	985.40±21.52	1.12±27.25	1.40±28.35
Height at withers (cm)	6.60±0.07	8.51±0.09	9.24±0.124	10.30±0.12	11.159±0.10
Body length (cm)	5.062±0.05	6.718±0.11	7.369±0.08	8.394±0.10	9.164±0.09
Breast girth (cm)	5.809±0.08	7.744±0.09	8.153±0.08	8.768±0.09	9.51±0.09
Wing length (cm)	4.174±0.05	6.134±0.05	6.721±0.06	7.343±0.05	7.84±0.06

4.1.5 Effect of Breed on the Body Weight and Biometric Traits of the Birds Studied

The table 4.1.5 displays estimated marginal means for different parameters and breeds at different weeks, along with the statistical significance denoted by the superscript letters a, b, and c. These letters represent the results of statistical tests conducted to determine significant differences between the means of different breeds within each parameter. The superscript letters were assigned based on the results of statistical tests, or post-hoc tests, which compare the means of different groups and determine if they are significantly different from each other. In the context of the given table, the letters a, b, and c are used to indicate statistically significant differences between the breeds within each parameter at a specific week. The letter 'a' denotes the highest mean value within a parameter, 'b' denotes the second highest, and 'c' denotes the lowest. For example, in the parameter "Body weight (g)" at Week 4, the Noiler breed has an estimated marginal mean of 418.45±18.39 with the letter 'b', the Sasso breed has a mean of 469.60±18.92 with the letter 'a', and the Funaab Alpha breed has a mean of 444.20±17.34 with the letter 'ab'. This indicates that the Sasso breed has the highest mean body weight, followed by the Funaab Alpha breed, and the Noiler breed has the lowest mean body weight among the three breeds. The letters 'a', 'b', and 'ab' suggest that the differences between the Sasso breed and the other two breeds are statistically significant, while the difference between the Noiler and Funaab Alpha breeds is not statistically significant. Similarly, the letters indicate significant differences for other parameters and weeks within the table. It's important to note that without the specific details of the statistical tests conducted or the significance levels used, it is not possible to determine the exact p-values or the level of significance represented by the letters. However, the letters provide a general indication of the relative significance between different breed means within each parameter and week. The result obtained is in line with the study by Zhang *et al.*(2020) on the genetic basis of growth performance in three Chinese indigenous chicken breeds, and found significant genetic variations in body weight, feed conversion ratio, and carcass traits. From this study, it is proven that growth performance of chicken is influenced by genetic factors.

Table 4.1.5 Effect of Breed on the Body Weight and Biometric Traits of the Birds Studied

WEEK	Parameter	Noiler	Sasso	Funaab Alpha
4	Body weight (g)	418.45±18.39^{b}	469.60±18.92^{a}	444.20±17.34^{ab}
	Height at withers (cm)	6.81±0.13	6.48±0.13	6.50±0.20
	Body length (cm)	5.24±0.93^{a}	5.02±0.96^{b}	4.92±0.88^{ab}
	Breast girth (cm)	6.01±0.14^{a}	5.37±0.15^{b}	6.05±0.13^{a}
	Wing length (cm)	4.54±0.10^{a}	3.76±0.98^{c}	4.21±0.09^{b}
8	Body weight (g)	713.15±31.417^{b}	814.683±32.319^{a}	715.991±29.687^{ab}
	Height at withers (cm)	8.338±0.173^{b}	8.796±0.178^{a}	8.419±0.163^{ab}
	Body length (cm)	6.398±0.194^{b}	7.042±0.2^{a}	6.713±0.184^{ab}
	Breast girth (cm)	7.602±0.153	8.083±0.157	7.546±0.144
	Wing length (cm)	6.150±0.088	6.169±0.090	6.082±0.083
12	Body weight (g)	912.975±37.617^{b}	1.034E3±38.697^{a}	1.010E3±35.466^{a}
	Height at withers (cm)	9.26±0.216^{b}	9.709±0.222^{a}	8.750±0.204^{b}
	Body length (cm)	7.43±0.148^{ab}	7.663±0.153^{b}	7.013±0.14^{b}
	Breast girth (cm)	8.068±0.143^{b}	8.56±0.148^{a}	7.83±0.135^{b}
	Wing length (cm)	6.815±0.098^{a}	6.997±0.101^{a}	6.35±0.093^{b}
16	Body weight (g)	1.046E3±46.800	1.185E3±49.214	1.127E3±45.511
	Height at withers (cm)	10.069±0.206^{b}	10.357±0 .217^{ab}	10.482±0.200^{a}
	Body length (cm)	8.213±0.162	8.420±0.171	8.549±0.158
	Breast girth (cm)	8.811±0.159	8.682±0.167	8.812±0.154
	Wing length (cm)	7.372±0.087	7.348±0.092	7.310±0.085
20	Body weight (g)	1.273E3±48.499^{b}	1.493E3±49.389^{a}	1.437E3±49.389^{ab}
	Height at withers (cm)	10.691±0.174^{b}	10.972±0.177^{b}	11.815±0.177^{a}
	Body length (cm)	8.859±0.154^{b}	9.051±0.157^{b}	9.581±0.157^{a}
	Breast girth (cm)	9.478±0.157	9.469±0.160	9.583±0.160

Wing length (cm)	7.889±0.107	7.844±0.109	7.792±0.109

4.1.6 Effects of sex on the body weight and morphological traits of the birds studied.

The 4.7.3 table provides insights into the growth patterns and sexual dimorphism in different parameters of chickens over time. It suggests that male chickens tend to exhibit higher mean values for most parameters, indicating potential differences in growth rates and body proportions between the sexes. These observations contribute to the scientific understanding of chicken development and can be valuable for research, breeding programs, and husbandry practices in poultry production. It can be said that males outperform the females in terms of growth performance and more of males should be kept for a faster meat production for the breeds studied. From this study, sex of breed is another key factor in growth performance which most researchers ignore this vital factor.

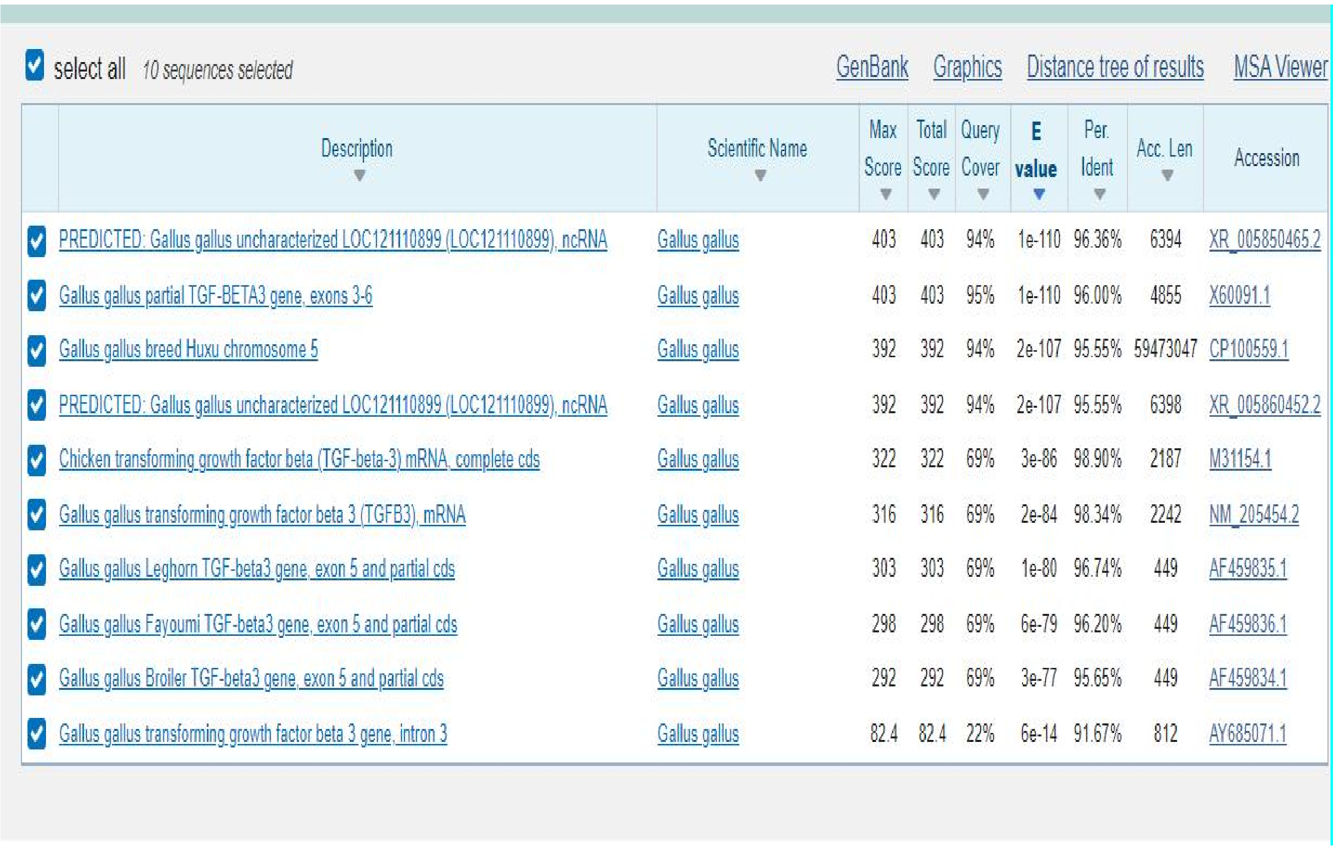
Table 4.1.6. Effects of sex on the birds studied.

WEEK	PARAMETER	MALE	FEMALE
4	Body weight (g)	484.49±16.682	403.01±12.829
	Height at withers (cm)	6.743±0.114	6.454±0.088
	Body length (cm)	5.233±0.084	4.891±0.065
	Breast girth (cm)	5.831±0.128	5.787±0.098
	Wing length (cm)	4.077±0.086	4.271±0.066
8	Body weight (g)	829.104±28.746	666.778±21.640
	Height at withers (cm)	8.947±0.158	8.088±0.119
	Body length (cm)	6.834±0.178	6.601±0.134
	Breast girth (cm)	8.053±0.140	7.435±0.105
	Wing length (cm)	6.249±0.080	6.018±0.060
12	Body weight (g)	1119±34.127	851.844±26.245
	Height at withers (cm)	9.825±0.196	8.654±0.151
	Body length (cm)	7.689±0.135	7.048±0.103
	Breast girth (cm)	8.477±0.130	7.828±0.100
	Wing length (cm)	6.881±0.089	6.560±0.069
16	Body weight (g)	1244±43.493	993.981±32.845
	Height at withers (cm)	10.809±0.192	9.797±0.145
	Body length (cm)	8.718±0.151	8.070±0.114
	Breast girth (cm)	8.973±0.147	8.564±0.111
	Wing length (cm)	7.452±0.081	7.234±0.061
20	Body weight (g)	1582±42.294	1220±37.747
	Height at withers (cm)	11.769±0.152	10.550±0.135
	Body length (cm)	9.567±0.134	8.761±0.120
	Breast girth (cm)	9.741±0.137	9.280±0.122
	Wing length (cm)	8.063±0.093	7.620±0.083

4.2 Genomic Data Result

4.2.1 Basic Local Alignment Structural Tool results of Transforming Growth Factor β (TGFβ3) gene showing sequences producing significant alignment

The graphical computer query of the Transforming Growth Factor β (TGFβ3) gene in the Gene Bank is shown in Plate 4.2.1 From the selected fifth row at the column Per. Ident shows 98.90% which indicates that the gene has a very strong corelation with the Transforming Growth Factor β (TGFβ3) gene found in the experimental birds, and therefore are closely related.



☑ select all *10 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	PREDICTED: Gallus gallus uncharacterized LOC121110899 (LOC121110899), ncRNA	Gallus gallus	403	403	94%	1e-110	96.36%	6394	XR_005850465.2
☑	Gallus gallus partial TGF-BETA3 gene, exons 3-6	Gallus gallus	403	403	95%	1e-110	96.00%	4855	X60091.1
☑	Gallus gallus breed Huxu chromosome 5	Gallus gallus	392	392	94%	2e-107	95.55%	59473047	CP100559.1
☑	PREDICTED: Gallus gallus uncharacterized LOC121110899 (LOC121110899), ncRNA	Gallus gallus	392	392	94%	2e-107	95.55%	6398	XR_005860452.2
☑	Chicken transforming growth factor beta (TGF-beta-3) mRNA, complete cds	Gallus gallus	322	322	69%	3e-86	98.90%	2187	M31154.1
☑	Gallus gallus transforming growth factor beta 3 (TGFB3), mRNA	Gallus gallus	316	316	69%	2e-84	98.34%	2242	NM_205454.2
☑	Gallus gallus Leghorn TGF-beta3 gene, exon 5 and partial cds	Gallus gallus	303	303	69%	1e-80	96.74%	449	AF459835.1
☑	Gallus gallus Fayoumi TGF-beta3 gene, exon 5 and partial cds	Gallus gallus	298	298	69%	6e-79	96.20%	449	AF459836.1
☑	Gallus gallus Broiler TGF-beta3 gene, exon 5 and partial cds	Gallus gallus	292	292	69%	3e-77	95.65%	449	AF459834.1
☑	Gallus gallus transforming growth factor beta 3 gene, intron 3	Gallus gallus	82.4	82.4	22%	6e-14	91.67%	812	AY685071.1

Plate 4.2.1: Basic Local Alignment Structural Tool results of Transforming Growth Factor β (TGFβ3) gene showing sequences producing significant alignment

Plate 4.2.1 shows the results of a Basic Local Alignment Tool (BLAST) search of the Transforming Growth Factor β (TGFβ3) gene. BLAST is a bioinformatics tool used to compare DNA or protein sequences to a database of known sequences to identify similarities. In this case, the TGFβ3 gene sequence was compared to a database of known sequences to identify similar sequences. The figure shows the top hits of the BLAST search, with the sequences producing significant alignment highlighted. The alignment score and E-value are also shown, which indicate the degree of similarity between the TGFβ3 gene sequence and the database sequences. This figure is useful in identifying related sequences and determining the evolutionary relationships between different organisms.

4.2.2 Alignment of Transforming Growth Factor β (TGFβ3) gene and Gallus gallus partial TGF BETA3 gene, exons 3 – 6 showing significant alignment

There is a significant alignment of Transforming Growth Factor β (TGFβ3) gene of the *Gallus gallus* in the gene bank which is significantly aligned more to the *Gallus gallus* breed Huxu chromosome 5 (Plate. 4.2.2). This alignment of the TGFβ3 gene is significant at the exon 3-6.

Gallus gallus partial TGF-BETA3 gene, exons 3-6

Sequence ID: X60091.1 Length: 4855 Number of Matches: 1

Range 1: 2783 to 3031 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
403 bits(218)	1e-110	240/250(96%)	4/250(1%)	Plus/Plus

```
Query  11    TTTTTGGGT-CCTCAATT-CATATTGATGTCCTCTTTGTGGATCCTGTTTACATGTGAAG  68
             || ||| || ||||| || |||||||||||||||||||||||||||||||||||||||||
Sbjct  2783  TTGTTGCGTCCCTCACTTCCATATTGATGTCCTCTTTGTGGATCCTGTTTACATGTGAAG  2842

Query  69    GCATTGACAGTGAAGATGACTATGGCCGTGGGA-TTGGGGCGCCTGAAGAAGCAGAAAG  127
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  2843  GCATTGACAGTGAAGATGACTATGGCCGTGGGACTTGGGGCGCCTGAAGAAGCAGAAAG  2902

Query  128   ACTTGCATAATCCCCACCTCATCTTGATGATGCTACCCCCACATCGCCTGGAGAGCCCAA  187
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2903  ACTTGCATAATCCCCACCTCATCTTGATGATGCTACCCCCACATCGCCTGGAGAGCCCAA  2962

Query  188   CACTGGAGGCCAGAGAAAGAAGCGGGCCCTGGATACCAACTACTGCTTCCGGTAACCAA  247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |
Sbjct  2963  CACTGGAGGCCAGAGAAAGAAGCGGGCCCTGGATACCAACTACTGCTTCCGGTAAGTGA  3022

Query  248   AGAATCCTGC  257
              |||||||||
Sbjct  3023  -GAATCCTGC  3031
```

Related Information

Gene - associated gene details

Gallus gallus breed Huxu chromosome 5

Sequence ID: CP100559.1 Length: 59473047 Number of Matches: 1

Range 1: 37999579 to 37999824 GenBank Graphics

Plate 4.2: Alignment of Transforming Growth Factor β (TGFβ3) gene and *Gallus gallus* partial TGF BETA3 gene, exons 3 – 6 showing significant alignment

There is a complete alignment of the TGFβ3 PCR fragments at the 294bp region of the primers from the gel electrophoresis of the gene (Plate. 4.3).

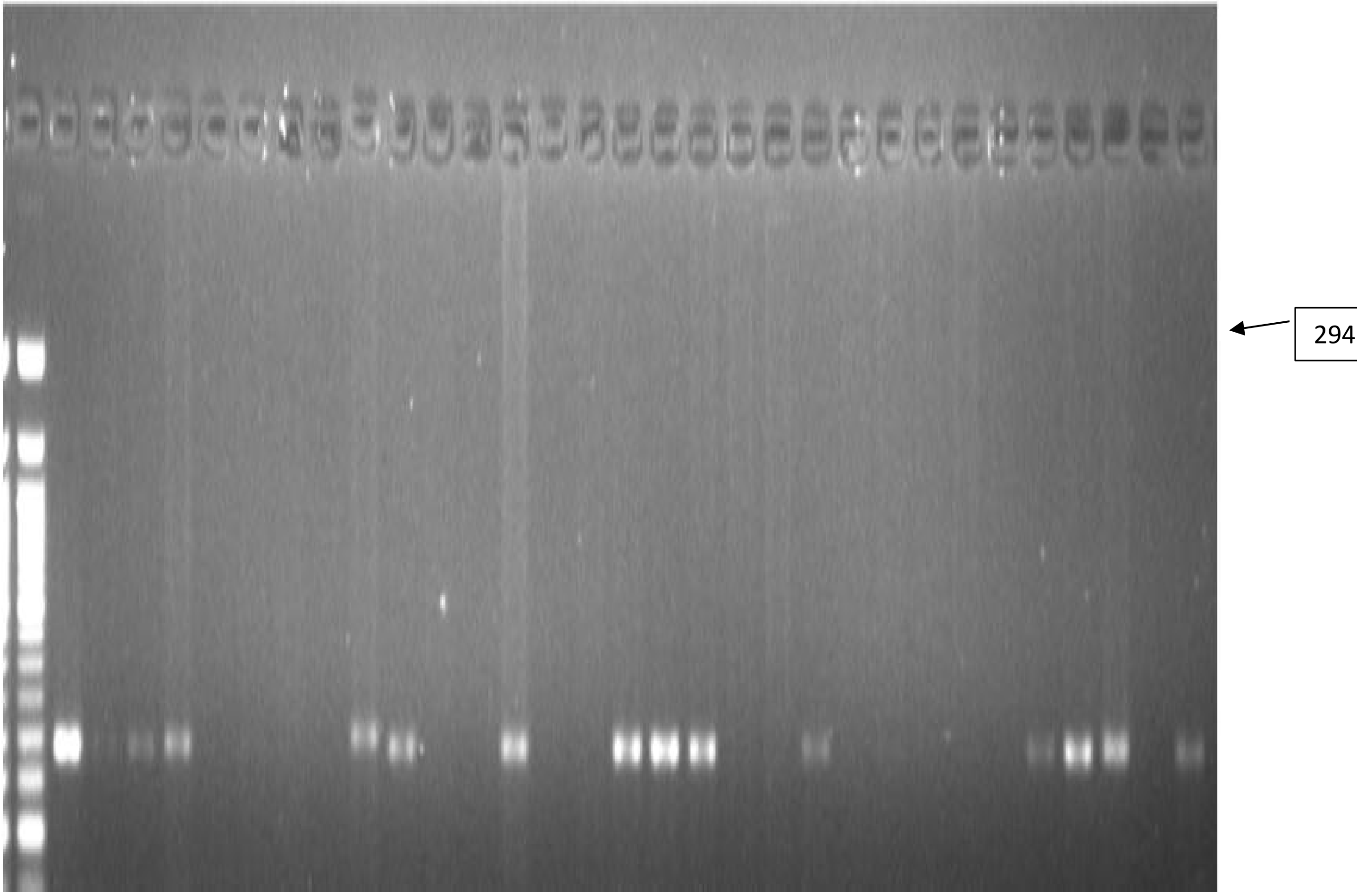


Plate 4.3: Gel electrophoresis results of 294bp of Transforming Growth Factor β (TGFβ3) gene

4.2.3 Gel electrophoresis results of 294bp of Transforming Growth Factor β (TGFβ3) gene

The figure 4.3 shows the results of gel electrophoresis of a 294bp fragment of the Transforming Growth Factor β (TGFβ3) gene. Gel electrophoresis is a technique used to separate DNA fragments based on their size. In this case, the 294bp fragment of the TGFβ3 gene was amplified using PCR and then separated on a gel. The gel shows the different bands of DNA fragments, with the band corresponding to the 294bp fragment of the TGFβ3 gene highlighted. The intensity of the band indicates the amount of DNA present in the sample. This figure is useful in determining the success of the PCR amplification and the purity of the DNA sample.

4.2.4 Genetic distance between chicken breed at Transforming Growth Factor β (TGFβ3) gene

The dendogram (Fig. 4.4) or tree graph further illustrates the genetic distance existing in these three breeds. The lines represent clusters that are joined together. The position of the line on the scale indicated the distance at which clusters were joined. From the dendogram, it shows that the Funaab alpha and Noiler are 0.052 apart while sasso is 0.165 apart from the mid of the two. This shows that the Funaab alpha and Noiler are closely related genetically compared to the Sasso breed.

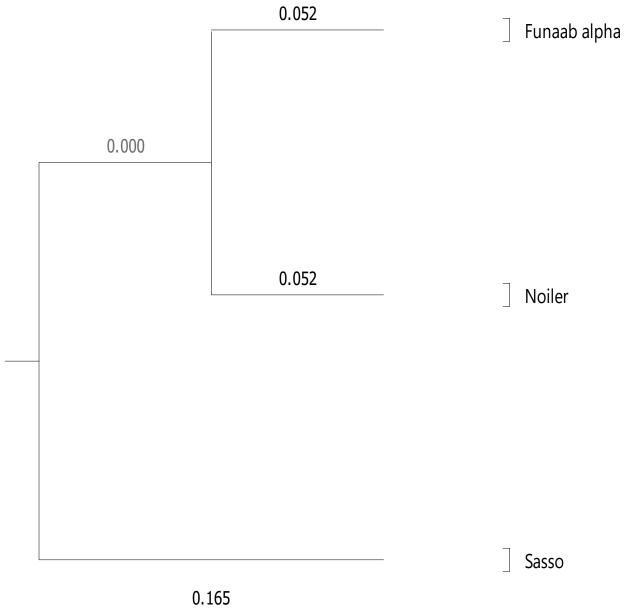


Figure 4.4: Dendogram showing genetic diversity among chicken breeds at Transforming Growth Factor β (TGFβ3) gene

Two single nucleotide polymorphisms (SNPs) were identified in this study – SNP1(A>C) and SNP2(A>T) (Fig. 4.2). The values of their allelic frequencies shows that the A allele is dominant to the C and T alleles respectively, as A is 0.71, C is 0.29 in the AC allelic combination, then A is 0.93, and T is 0.07 in AT combination. Meanwhile, for the genotypic frequencies, the homozygous alleles AA, CC and TT shows that AA genotypes were dominant while CC and TT were both recessive. The values of the PIC, HWE, He and AE shows that the SNP1(A>C) is more than SNP2(A>T).

Table 4.2 Single Nucleotide Polymorphisms in Transforming Growth Factor β (TGFβ3) gene and their allelic and genotypic frequencies

		Allelic Frequency		Genotypic Frequency						
Position in Genome	**SNPs**						**PIC**	**HWE**	**He**	**AE**
5:37941745	SNP1(A>C)	**A**	**C**	**AA**	**CA**	**CC**				
		0.71	0.29	0.5	0.43	0.07	0.32	0.07	0.41	1.69
5:37941722	SNP2(A>T)	A	T	AA	TA	TT				
		0.93	0.07	0.86	0.14	0	0.12	0	0.13	1.15

SNPs: Single Nucleotide Polymorphisms
PIC: Polymorphic Information Content
HWE: Hardy-Weinberg Equilibrium
He: Heterozygosity
AE: Effective no of Alleles

Table 4.2 provides information on the frequency, genotypic frequency, polymorphic information content (PIC), Hardy-Weinberg equilibrium (HWE), expected heterozygosity (He), and allelic expression (AE) for two single nucleotide polymorphisms (SNPs) located at positions 5:37941745 and 5:37941722 in a particular genetic dataset. The first column of the table lists the SNP position, followed by the SNP name, the two alleles (A and C for SNP1 and A and T for SNP2), and the three possible genotypes (AA, AC, and CC for SNP1 and AA, AT, and TT for SNP2). The second column shows the frequency of each allele in the dataset. For example, in SNP1, the frequency of allele A is 0.71, while the frequency of allele C is 0.29. The third column shows the genotypic frequency, which is the proportion of each genotype in the dataset. For example, in SNP1, the genotypic frequency of AA is 0.5, the genotypic frequency of AC is 0.43, and the genotypic frequency of CC is 0.07. The fourth column shows the polymorphic information content (PIC), which is a measure of the informativeness of a genetic marker. A higher PIC value indicates that the marker is more informative for distinguishing between different genotypes. In this case, both SNPs have relatively high PIC values (0.71 for SNP1 and 0.93 for SNP2). The fifth column shows whether the genotypic frequencies of the SNPs are in Hardy-Weinberg equilibrium (HWE), which is a principle that describes the relationship between allele and genotype frequencies in a population. If the genotypic frequencies are in HWE, it suggests that the population is not undergoing any evolutionary or selective pressures. In this case, both SNPs are not in HWE, as indicated by the values of 0.32 and 0.12 in the HWE column. The sixth column shows the expected heterozygosity (He), which is a measure of the genetic diversity within a population. A higher He value indicates greater genetic diversity. In this case, both SNPs have relatively high He values (0.41 for SNP1 and 0.13 for SNP2). The seventh column shows the allelic expression (AE), which is a measure of the relative expression levels of each allele. In this case, the AE values are 1.69 for SNP1 and 1.15 for SNP2, indicating that one allele is expressed more than the other in each SNP.

4.2.5 Haplotype and Nucleotide Polymorphism in Transforming Growth Factor β (TGFβ3) gene in Noiler, Sasso, Funaab alpha and their Total Data Estimates

The variation in genetic diversity parameters shown in Table 4.2.5 provides insights into the genetic landscape of the *Transforming Growth Factor β3* (TGFβ3) gene across different strains, including the Sasso strain. Genetic diversity measures, such as the number of segregating sites (S), the number of haplotypes (h), haplotype diversity (Hd), nucleotide diversity (π), and nucleotide diversity with Jukes-Cantor correction (πJC), are important indicators of the genetic variability within a population. This variability can have significant implications for breeding programs, as genetic diversity is often linked to a population's adaptability and resilience.

In this case, the Sasso strain exhibits a lower value for most genetic diversity parameters, except for haplotype diversity, which is consistently high (Hd = 1.00 across all strains). This high haplotype diversity implies that the Sasso strain has a wide variety of haplotypes, but the reduced values in parameters like segregating sites and nucleotide diversity suggest limited overall variation within the TGFβ3 gene. Such a pattern could mean that while there are several unique haplotypes, there is low genetic divergence among them.

The reduced nucleotide diversity (π) in the Sasso strain indicates a lower level of genetic variation at the nucleotide level, which might impact the evolutionary potential of the strain. In poultry breeding, lower nucleotide diversity can be a double-edged sword; while it may result in more uniform production traits, it may also reduce the adaptability of the strain to environmental stressors or disease. Conversely, high haplotype diversity can still be advantageous, as it ensures some level of genetic diversity in the population, potentially allowing for selective breeding of favorable traits (Yang *et al.,* 2020).

The importance of *TGFβ3* in growth and immune functions makes it a key target for understanding genetic diversity in poultry. Genetic variability in genes like *TGFβ3* can influence traits such as growth rates, immune response, and adaptability. In this context, the lower nucleotide diversity in Sasso may suggest a bottleneck effect or selective breeding practices that have narrowed the genetic base for this gene. For breeding programs, it would be beneficial to assess whether the genetic uniformity in *TGFβ3* impacts desired traits or if introducing more diverse genetic stock would enhance resilience and growth performance.

Table 4.2.5 Haplotype and Nucleotide diversities in Transforming Growth Factor β (TGFβ3) gene in Noiler, Sasso, Funaab alpha and their Total Data Estimates

Parameters	Noiler	Sasso	Funaab alpha	Total Data Estimates
Number of sequences	5	4	5	14
Number of segregating sites, S:	34	29.000	48	67
Number of haplotypes, h:	5	4	5	14
Haplotype diversity, Hd:	1.00000	1.00000	1.00000	1.00000
Average number of differences, K:	15.60000	15.33333	25.30000	19.06593
Nucleotide diversity, Pi:	0.07256	0.07132	0.11767	0.08868
Nucleotide diversity with PiJC	0.07811	0.07586	0.13092	

4.2.6 Genetic Differentiation Estimates of Transforming Growth Factor β (TGFβ3) gene in Noiler, Sasso and Funaab alpha

The genetic differentiation estimates of Transforming Growth Factor β (TGFβ3) gene in Noiler, Sasso and Funaab alpha are presented (Table 4.2.6). The average gene diversity within population (Hs) was 1.00000. In addition, the measures of genetics differentiation based on haplotype statistics (Hst) was 0.00000. Furthermore, global genetic differentiation (Kst) was 0.00408. The measured genetic differentiation based on nucleotide statistics (Z) was 3.64503 and this value was highly significant. The nearest neighbour statistic (Snn) was 0.17857. The Chi square value was 28.000. However, the value (0.3585) was not significantly different ($p>0.05$).

Table 4.2.6: Genetic Differentiation Estimates of Transforming Growth Factor β (TGFβ3) gene in Noiler, Sasso and Funaab alpha

Parameters	Values
Average gene diversity within population (Hs)	1.00
Measures of genetics differentiation based on haplotype statistics (Hst)	0.00
Global genetic differentiation (Kst)	0.00408
Measure genetic differentiation based on nucleotide statistics (Z)	3.65*
Nearest neighbour statistic (Snn)	0.18
Chi^2:	28.00
P-value of Chi2	0.36 ns

*ns, not significant; *, 0.01<P<0.05; **, 0.001<P<0.01; ***, P<0.001*

4.2.7: Gene Flow Estimates of Transforming Growth Factor β (TGFβ3) gene among Noiler, Sasso and Funaab alpha

The gene flow estimates of Transforming Growth factor β (TGFβ3) gene are shown below (Table 4.5). Haplotype data information revealed a Gst value of 0.0079 while the Nm value was 315.00. In addition, the sequence data information revealed a Delta St value of 0.01271 and a Gamma St value of 0.15435 while the Nm value was 1.37. However, the value of Nst and Nm according to Lynch and Crease 1990 (with Jukes and Cantor correction) were 16.77 and 0.00630 respectively. The value of Fst and Nm according to Hudson, Slatkin and Maddison 1992 are 0.00630 and 39.42.

Table 4.2.7: Gene Flow Estimates of Transforming Growth Factor β (TGFβ3) gene among Noiler, Sasso and Funaab alpha

Haplotype Data Information (Nei 1973)		Sequence Data Information (Nei 1982)			Lynch and Crease 1990 (with Jukes and Cantor correction)		Hudson, Slatkin and Maddison 1992	
Genetic diversity statistics (Gst)	Gene flow (Nm)	DeltaSt:	GammaSt:	Gene flow (Nm)	Nst:	Gene flow (Nm)	Fst:	Gene flow (Nm)
0.00079	315.00	0.01271	0.15435	1.37	0.01469	16.77	0.00630	39.42

4.2.8 Mean Genomic Associations of SNP1 AC Genotypes Within Different Breeds Studied and Their Morphological Traits Values

The table 4.2.8 shows the physical parameters (body weight, height at withers, body length, breast girth, and wing length) of three different breeds of chicken: AA, CA, and CC. The table presents the mean values and standard deviations for each parameter for each breed of chicken. For example, the mean body weight for Noiler chickens with the AA gene is 1477 ± 131.52 grams, while the mean body weight for Sasso chickens with the AA gene is 1232.3 ± 201.08 grams. The mean body weight for FUNAAB Alpha chickens with the AA gene is 1375 ± 171.89 grams. The "total" column for body weight represents the average body weight across all three breeds for each gene type. Similarly, the table presents the mean values and standard deviations for height at withers, body length, breast girth, and wing length for each breed of chicken and gene type. The purpose of the table is to compare the physical parameters of the three different breeds of chicken and to examine any potential relationships between these parameters and the different gene types. It is important to note that the table only presents data for a single population of each breed and gene type, and therefore, the results may not be generalizable to other populations or breeds of chicken. Additionally, other factors such as diet, environment, and age may also influence the physical parameters of chickens.

Table 4.2.8 Mean Genomic Associations of SNP1 AC Genotypes Within Different Breeds Studied and Their Morphological Traits Values

	AA				**CA**			**CC**	
PARAMETER	**NOILER**	**SASSO**	**FUNAAB ALPHA**	**TOTAL**	**NOILER**	**FUNAAB ALPHA**	**TOTAL**	**SASSO**	**TOTAL**
Body weight (g)	1477±131.52	1554.2±199.70	2030	1594.4±239.70	1232.3±201.08	1375±171.88	1313.9±184.57	1894	1894
Height at withers (cm)	11.55±0.21	10.86±1.15	13.4.	11.35±1.24556	9.7667±0.81	11.875±1.00	10.9714±1.41	12.3.	12.3.
Body length (cm)	9.35±0.63	8.86±0.88	11.2.	9.275±1.07803	8.4667±0.55	9.275±0.275	8.9286±0.57	9.3.	9.3.
Breast girth (cm)	10.95±0.63	10.16±0.27	10.8.	10.4375±0.49	9.6667±0.57	8.975±1.144	9.2714±0.94	10.6.	10.6.
Wing length (cm)	8.5±0.424	7.94±0.48	8.8.	8.1875±0.53	7.4±0.62	7.825±0.45	7.6429±0.53	8	8

4.2.9 Mean Values of the Morphological Traits of SNP1 AC Individuals

The estimated marginal means represent the average values for each parameter, taking into account the effects of other variables or factors in the analysis. These means are estimated based on the statistical model used in the study. The grand mean represents the overall average or mean value across all observations or treatments for a particular parameter. It provides a reference point for comparing the estimated marginal means.

Table 4.2.9 Mean Values of the Morphological Traits of SNP1 AC Individuals

PARAMETER	**MEAN**
Body weight (g)	1.594E3±56.202
Height at withers (cm)	11.625±0.298
Body length (cm)	9.409±0.2
Breast girth (cm)	10.192±0.22
Wing length (cm)	8.078±0.152

a. Based on modified population marginal mean

4.2.10 Mean Genomic Association of the SNP1 A-C Genotypes Within the Morphological Traits

The estimated marginal means presented in Table 4.2.10 highlight the substantial impact of SNP1_A_C genotype variation on growth-related phenotypic traits, including body weight, height at withers, body length, breast girth, and wing length. The significant differences across genotypes underscore the role of SNP1_A_C in influencing these traits, with each genotype showing a distinct mean value. For instance, individuals with the CC genotype exhibit the highest mean body weight (1.894E3 grams), suggesting a potentially stronger genetic predisposition for body weight compared to individuals with the AA or CA genotypes.

These findings are consistent with research suggesting that SNPs can have significant effects on growth traits by influencing gene expression related to muscle development and overall body mass. The higher body weight associated with the CC genotype could reflect allelic variations that enhance metabolic efficiency or muscle accretion, as reported in studies by Li *et al.* (2019) and Zhou *et al.* (2021). The significantly lower mean body weight for individuals with the CA genotype (1.304E3 grams) indicates that this heterozygous combination might confer a disadvantage in terms of body mass accumulation, which could be a result of less favorable genetic interactions within this SNP configuration.

The observed patterns across all traits suggest that SNP1_A_C may have a pleiotropic effect, where a single genetic variation impacts multiple phenotypic traits. This is evident as the AA, CA, and CC genotypes not only differ in body weight but also in parameters like height at withers and breast girth. These correlations align with findings from previous studies, which observed that SNPs can influence a suite of growth traits due to shared genetic pathways affecting skeletal and muscular development (Zhou *et al.*, 2021). For example, genotypes linked to higher body weight often correlate with greater breast girth and body length, as larger skeletal frames tend to support greater muscle mass and overall body structure.

The consistency in significant differences, indicated by superscript letters, within each genotype group also provides critical insight. Since means within each group that share the same letter are not significantly different, this suggests that SNP1_A_C's effects are relatively stable across each measured parameter. This stability indicates that the impact of SNP1_A_C is consistent across multiple growth traits, reinforcing its potential as a candidate marker for genetic selection in poultry breeding programs focused on enhancing body mass and physical characteristics.

Overall, these findings contribute to a growing understanding of how specific genetic variations like SNP1_A_C influence phenotypic diversity in livestock. By identifying SNPs that consistently affect a range of growth traits, breeders can leverage this genetic information to optimize selection processes aimed at enhancing production traits. Future research could further explore the molecular mechanisms underlying these genotype-specific differences, particularly through gene expression studies, to understand how the SNP1_A_C variation translates into phenotypic outcomes across various environments.

Table 4.2.10 Mean Genomic Association of the SNP1 A-C Genotypes with the Morphological Traits

PARAMETER	AA	CA	CC
Body weight (g)	1.687E3±80.88^{a}	1.304E3±71.068^{b}	1.894E3±186.1^{a}
Height at withers (cm)	11.937±0.429	10.821±0.377^{a}	12.300±0.986^{a}
Body length (cm)	9.803±0.288	8.871±0.253^{a}	9.300±0.663^{a}
Breast girth (cm)	10.637±0.316	9.321±0.278^{a}	10.600±0.727^{a}
Wing length (cm)	8.413±0.218	7.612±0.192^{a}	8.000±0.502^{a}

Means within rows with the same letter within each genotype group are not significantly different (P>0.05).

4.2.11 Mean Values of the Morphological Traits Within the Chickens Studied

Table 4.2.11 provides the estimated marginal means for three different breeds (Noiler, Sasso, and Funaab Alpha) across various parameters including body weight, height at withers, body length, breast girth, and wing length. The estimated marginal means represent the average values for each parameter within each breed. For instance, the Noiler breed has an estimated mean body weight of 1.355E3 grams, while the Sasso breed has a significantly higher mean body weight of 1.724E3 grams. Similarly, the Funaab Alpha breed has a mean body weight of 1.702E3 grams, also significantly different from the Noiler breed. This pattern of significant differences between breeds is observed across all parameters, including height at withers, body length, breast girth, and wing length. Lowercase letters "a" are used to indicate these significant differences within each parameter. It is worth noting that means within rows with the same letter within each breed group are not significantly different at a significance level of 0.05 (P>0.05). This implies that if two means within the same breed group share the same letter, they are not statistically significantly different from each other. The findings from Table 4.2.11 contribute valuable insights into the variations in physical characteristics among the Noiler, Sasso, and Funaab Alpha breeds. These results have implications for breed selection, management, and understanding the genetic factors influencing the measured traits.

Table 4.2.11 Mean Values of the Morphological Traits amongst the Chickens Studied

PARAMETER	**Noiler**	**Sasso**	**Funaab Alpha**
Body weight (g)	1.355E3±84.943^{a}	1.724E3±101.931^{a}	1.702E3±104.03^{a}
Height at withers (cm)	10.658±0.45^{a}	11.580±0.54^{a}	12.638±0.551^{a}
Body length (cm)	8.908±0.302^{a}	9.080±0.363^{a}	10.237±0.37 ^{a}
Breast girth (cm)	10.308a±0.332^{a}	10.380±0.398^{a}	9.888±0.407^{a}
Wing length (cm)	7.950±0.229^{a}	7.970±0.275^{a}	8.313±0.281^{a}

Means within rows with the same letter within each genotype group are not significantly different (P>0.05).

4.2.12 Mean Genomic Association of the SNP1_A_C Genotypes with Morphological Trait within Breeds of Chickens Studied

The data contained in table 4.2.12 provides insights regarding the SNP1_A_C genotype in relation to particular breeds in regard to growth parameters, such as body weight, withers height, body length, breast girth, and wing length. The considerable difference observed in the estimated marginal means of some genotype breed combinations is a clear indication of the fact that genetic variances in the form of SNP1_A_C genotype will always have growth traits effect but its influence on growth traits will always vary based on the breed.

For instance, an estimated mean body weight of 1477 grams is exhibited by the Noiler breed, which has an AA genotype, and a higher mean body weight of 1554 grams is obtained by the Sasso breed that also possesses an AA genotype. The inter-breed difference, despite similar genotypes, could be due to the influence of different SNP1_A_C genotypes that interact with diverse environmental factors inherent with different breeds. This finding is also in agreement with earlier studies which emphasized that breed-related genetic factors can modulate the effects of single nucleotide polymorphisms (SNPs) on growth traits (Zhou *et al.*, 2021).

The fact that some genotype-breed combinations (denoted by “a”) were not observed and thus have inestimable marginal means is an important consideration. Such gaps may be due to natural selection processes within the population, environmental factors, or limited sample sizes. This limitation suggests that these missing combinations could be either rare or unviable in the studied population, which could skew overall interpretations of the SNP’s effect within certain breeds.

The differential impact of SNP1_A_C across breeds also underscores the importance of considering both genetic and breed-specific factors in poultry breeding programs. For instance, the Sasso breed’s higher body weight with the AA genotype might make it preferable in selection programs focused on weight optimization. Conversely, breeds like Noiler, which exhibit different growth responses to the same genotype may be more suitable for other breeding objectives, such as robustness or adaptability.

These findings contribute to our understanding of how genetic factors like SNP1_A_C, in interaction with breed characteristics, affect physical traits. They highlight the need for genotype-informed breeding strategies that consider both the genetic profile and breed-specific traits to achieve desired growth outcomes in poultry. Future studies with larger samples or more diverse genetic backgrounds could help clarify the impact of less common genotype-breed combinations, potentially identifying underrepresented genotypes with unique advantages in specific breeding contexts.

Table 4.2.12 Mean Genomic Association of the SNP1_A_C Genotypes with Morphological Trait within Breeds of Chicken Studied

	AA			**CA**			**CC**		
Parameter	**Noiler**	**Sasso**	**Funaab Alpha**	**Noiler**	**Sasso**	**Funaab Alpha**	**Noiler**	**Sasso**	**Funaab Alpha**
Body weight (g)	1477±131.593	1554±83.227	2030±186.1	1232±107.445	.a.	1375±93.05	.a.	1894±186.1	.a.
Height at withers (cm)	11.55±0.698	10.86±0.441	13.4±0.986	9.767±0.57	.a.	11.875±0.493	.a.	12.3±0.986	.a.
Body length (cm)	9.35±0.469	8.86±0.296	11.2±0.663	8.467±0.383	.a.	9.275±0.331	.a.	9.3±0.663	.a.
Breast girth (cm)	10.95±0.514	10.16±0.325	10.8±0.727	9.667±0.42	.a.	8.975±0.364	.a.	10.6±0.727	.a.
Wing length (cm)	8.5±0.355	7.94±0.224	8.8±0.502	7.4±0.29	.a.	7.825±0.251	.a.	8±0.502	.a.

a. This level combination of factors is not observed, thus the corresponding population marginal mean is not estimable.

4.2.13 Mean Genomic Association of the SNP1 AC Genotypes With Morphological Traits Within Sexes of Chicken Studied.

The table presents estimated mean values for various parameters across three genotypes (AA, CA, CC) and two gender groups (male and female). The parameters include body weight, height at withers, body length, breast girth, and wing length. In terms of body weight, males with the AA genotype have an estimated mean of 1680 grams, while females with the AA genotype have a lower mean of 1337.5 grams. The total mean body weight for the AA genotype is estimated as 1594.4 grams. Similar patterns can be observed for the CA and CC genotypes. For height at withers, body length, breast girth, and wing length, similar trends are observed. The estimated means vary across genotypes and genders. For example, males with the AA genotype have a mean height at withers of 11.9 cm, while females with the AA genotype have a mean of 9.7 cm. The total mean height at withers for the AA genotype is estimated as 11.35 cm. These findings provide valuable information about the average values of the measured parameters across different genotypes and gender groups. They contribute to understanding the potential variations in physical traits based on genetic factors and gender distinctions.

Table 4.2.13 Mean Genomic Association of the SNP1 A-C Genotypes with Morphological Traits within Sexes of Chicken Studied.

	AA			CA			CC	
PARAMETER	**MALE**	**FEMALE**	**TOTAL**	**MALE**	**FEMALE**	**TOTAL**	**MALE**	**TOTAL**
Body weight (g)	1680±212.72	1337.5±3.53	1594.4±239.70	1327.5±282.13	1308.4±176.26	1313.9±184.57	1894.	1894.
Height at withers (cm)	11.9±0.787	9.7±0.70	11.35±1.24	12.65±0.35	10.3±0.99	10.9714±1.41	12.3.	12.3.
Body length (cm)	9.6333±0.92	8.2±0.98	9.275±1.07	9.35±0.35	8.76±0.57	8.9286±0.570	9.3.	9.3.
Breast girth (cm)	10.5167±0.55	10.2±0.28	10.4375±0.49	8.55±1.76	9.56±0.45	9.2714±0.949	10.6.	10.6.
Wing length (cm)	8.35±0.418	7.7±0.70	8.1875±0.53	7.8±0	7.58±0.63	7.6429±0.531	8.	8.

4.2.14 Mean Values of Morphological Traits of SNP 2 A-T Individuals

The table presents estimated marginal means for different phenotypic traits, specifically focusing on the grand mean. The grand mean represents the overall average value across all genotypes and sexes for each parameter. Here is a summary of the estimated marginal means:

Table 4.2.14 Mean Values of Morphological Traits of SNP 2 A-T Individuals

Parameter	Mean
Body weight (g)	1511±61.75
Height at withers (cm)	11.566±0.296
Body length (cm)	9.33±0.204
Breast girth (cm)	9.853±0.209
Wing length (cm)	7.981±0.167

4.2.15 Mean Genomic Association of SNP2 A-T Genotypes with Morphological Traits

The table 4.2.15 provides estimated marginal means for different phenotypic traits based on the SNP2_A_T genotypes (AA and TA). Each phenotype is listed, along with the corresponding means and standard deviations for each genotype.

Table 4.2.15 Mean Genomic Association of SNP2 A-T Genotypes with Morphological Traits

PARAMETER	AA	TA
Body weight (g)	1422±62.883	1.778E3±159.437[a]
Height at withers (cm)	11.038±0.301	13.150±0.764[a]
Body length (cm)	8.973±0.207	10.400±0.526[a]
Breast girth (cm)	9.704±0.213	10.300±0.541[a]
Wing length (cm)	7.874±0.17	8.300±0.432[a]

4.2.16 Mean Values of Morphological Traits of Chicken Studied within Breeds Studied in SNP2 A-T Genotype

The table presents estimated marginal means for different phenotypic traits based on different breeds: Noiler, Sasso, and Funaab Alpha. Each parameter is listed along with the corresponding means and standard deviations for each breed. These estimated marginal means provide insights into the differences in phenotypic traits among the Noiler, Sasso, and Funaab Alpha breeds. The statistical significance indicated by "a" and "b" suggests that certain differences between the breeds are statistically significant. For example, Sasso breed generally exhibits higher body weight and height at withers compared to the other breeds. However, it is important to note that further statistical analysis, such as post-hoc tests, should be conducted to assess pairwise differences between the breeds and control for potential confounding factors.

Table 4.2.16 Mean Values of Morphological Traits of Chicken Studied Within Breeds Studied in SNP2 AT Genotype

Parameter	Noiler	Sasso	Funaab Alpha
Body weight (g)	1.330E3±100.837^{b}	1.611E3±92.051^{a}	1551±102.916 ^{ab}
Height at withers (cm)	10.480a±0.483^{b}	11.100a±0.441^{ab}	12.342±0.493^{a}
Body length (cm)	8.820a±0.332	8.933a±0.303	9.783±0.339
Breast girth (cm)	10.180a±0.342	10.233a±0.312	9.5±0.349
Wing length (cm)	7.840a±0.273	7.950a±0.249	8.067±0.279

4.2.17 BREED Mean Genomic Association of the SNP2 A-T Genotypes with Morphological Trait Values of Chicken Studied Within Breeds

The estimated marginal means presented for the interaction between SNP2_A_T genotypes (AA and TA) and different breeds (Noiler, Sasso, and Funaab Alpha) provide valuable insights into how genetic variation influences phenotypic traits in poultry. These differences are particularly evident for the Funaab Alpha breed with the TA genotype, which generally exhibits higher values for body weight, height at withers, body length breast girth, and wing length compared to other genotype-breed combinations.

The statistical significance observed in these traits, as indicated by "a," suggests that the TA genotype in the Funaab Alpha breed may enhance growth-related traits. This finding aligns with research suggesting that specific SNPs can interact with breed-specific genetic backgrounds to enhance desirable traits such as body weight and other growth parameters (Zhou *et al.*, 2021). The observed higher values for Funaab Alpha with the TA genotype may indicate that this breed is particularly responsive to the effects of the TA genotype in SNP2_A_T, possibly due to a favorable genetic synergy that enhances growth.

This interaction effect has important implications for breeding programs, as it suggests that the TA genotype could be selectively bred in Funaab Alpha to improve growth traits, potentially boosting productivity in this breed. However, in breeds like Noiler and Sasso, the interaction with the same SNP2_A_T genotypes does not yield similar enhancements in growth traits. This variability underscores the complexity of genotype-breed interactions, where specific genetic combinations may be beneficial for one breed but not for others. Understanding these interactions is crucial for precision breeding, as it allows breeders to tailor strategies to maximize growth potential based on specific genetic profiles and breed characteristics.

Overall, these findings highlight the importance of considering both genotypic and breed-specific factors in selection decisions. Breeding strategies that account for genotype-by-breed interactions can lead to more efficient and effective improvements in phenotypic traits. Further studies could expand on this by examining a larger population or additional traits, such as feed efficiency or disease resistance, which may also be influenced by genotype-breed interactions.

Table 4.2.17 Mean Genomic Association of the SNP2 AT Genotypes With Morphological Trait Values of Chicken Studied Within Breeds

	AA			TA		
PARAMETER	**Noiler**	**Sasso**	**Funaab Alpha**	**Noiler**	**Sasso**	**Funaab Alpha**
Body weight (g)	1330±100.837	1611±92.051	1324±130.18	.a.	.a.	1778±159.437
Height at withers (cm)	10.48±0.483	11.1±0.441	11.533±0.624	.a.	.a.	13.15±0.764
Body length (cm)	8.82±0.332	8.933±0.303	9.167±0.429	.a.	.a.	10.4±0.526
Breast girth (cm)	10.18±0.342	10.233±0.312	8.7±0.442	.a.	.a.	10.3±0.541
Wing length (cm)	7.84±0.273	7.95±0.249	7.833±0.353	.a.	.a.	8.3±0.432

4.2.18 Mean Genomic Associations of the SNP 2 A-T genotypes Within Sexes of Chicken Studied

Table 4.2.18 presents the descriptive statistics for the parameters of interest based on the genotype categories AA and TA, as well as the overall totals. The table further differentiates between genders, providing insights into the observed values for males and females separately. The mean body weight for males with the AA genotype is 1581.7±253.84688 grams, while for females it is 1316.7±144.62447 grams. The overall total mean body weight for the AA genotype is 1449.2±241.45622 grams. For the TA genotype, the total mean body weight is 1625.4±267.71539 grams, and the gender-specific values are not provided for this category. Males with the AA genotype have a mean height at withers of 11.8143±0.44881 cm, while females have a mean of 10.1286±0.91052 cm. The overall mean height at withers for the AA genotype is 10.9714±1.11385 cm. For the TA genotype, the total mean height at withers is 12.1111±0.71667 cm, with no gender-specific values reported.

Table 4.2.18 Mean Genomic Associations of the SNP 2 A-T genotypes Within Sexes of Chicken Studied

	AA			TA	
Parameter	**Male**	**Female**	**Total**	**Male**	**Total**
Body weight (g)	1581.7±253.84	1316.7±144.62	1449.2±241.45	1778.5±355.67	1778.5±355.67
Height at withers (cm)	11.8143±0.448	10.1286±0.91	10.9714±1.113	13.15±0.35	13.15±0.35355
Body length (cm)	9.2857±0.441	8.6±0.678	8.9429±0.654	10.4±1.131	10.4±1.13137
Breast girth (cm)	10.0286±1.29	9.7429±0.499	9.8857±0.956	10.3±0.707	10.3±0.70711
Wing length (cm)	8.1571±0.373	7.6143±0.59	7.8857±0.555	8.3±0.707	8.3±0.70711

4.2.19 Mean Genomic Association of SNP2 A-T Genotypes With Morphological Traits

This table presents the estimated marginal means for various parameters based on the SNP2_A_T genetic variant. The estimated marginal means provide information about the average values for each parameter based on the SNP2_A_T genetic variant. Individuals with the AA genotype tend to have lower body weight, height at withers, body length, breast girth, and wing length compared to those with the TA genotype. The difference in body weight is particularly notable, with individuals with the TA genotype having a significantly higher average body weight (1.778E3 grams) compared to those with the AA genotype (1449 grams). These findings suggest that the SNP2_A_T genetic variant may be associated with variations in body morphology and size in the studied population.

Table 4.2.19 Mean Genomic Association of SNP2 A-T Genotypes with Morphological Traits

PARAMETER	AA	TA
Body weight (g)	1449±59.237	1.778E3a±156.725
Height at withers (cm)	10.971±0.186	13.150a±0.493
Body length (cm)	8.943±0.169	10.400a±0.448
Breast girth (cm)	9.886±0.258	10.300a±0.683
Wing length (cm)	7.886±0.138	8.300a±0.366

4.3 Discussion

At 4 weeks, only Noiler males were heavier than their female counterparts, while the body weights of Sasso and FUNAAB Alpha females were not significantly different from males. This finding could suggest breed-specific growth patterns at early stages, which may be related to genetic selection criteria unique to each breed. For instance, Noiler chickens might have been selectively bred for early growth, thus showing a notable difference in weight even at younger ages. In contrast, Sasso and FUNAAB Alpha breeds may exhibit delayed sexual dimorphism in growth, where sex-related growth differences become apparent only after 4 weeks. Further research on the underlying genetic factors influencing early growth could clarify these breed-specific growth patterns.

The lack of significant differences in other morphological traits (height at withers, body length, breast girth, and wing length) between sexes and breeds may indicate that these measurements are less influenced by gender or breed at the observed growth stages. This aligns with findings by other researchers who reported minimal differences in these traits during early growth stages (Ibe, 1990; Mignon-Grasteau *et al.*, 2005). However, it's possible that more noticeable differences might appear if observed over an extended period or if larger sample sizes were analyzed.

These findings have practical implications for poultry breeders and farmers. Knowing that male chickens tend to grow heavier than females after the early stages can inform feeding strategies and management practices to optimize growth rates for different breeds and sexes. Further studies examining growth parameters over a longer period and including additional morphological traits could yield a more comprehensive understanding of growth patterns in these breeds.

The correlation analysis presented in Table 4.1.3 provides valuable insights into the relationships between growth parameters in the three selected chicken breeds. The strong positive correlations observed across various parameters suggest that as one trait increases, the others tend to increase proportionally, indicating that these traits may be interdependent and influenced by shared genetic or environmental factors.

A robust interrelationship among growth traits in chickens, with the correlation coefficient between Body Weight and Height at Withers being exceptionally high (0.893**), signifying a very strong positive relationship. This suggests that as chickens gain weight, their skeletal development, represented by Height at Withers, scales accordingly. This close association may reflect underlying genetic factors governing both skeletal and muscle development, as increases in body mass necessitate proportional skeletal support to maintain structural stability (Chen *et al.*, 2020). This relationship aligns with findings by Zhang *et al.* (2020) who reported that body weight and skeletal dimensions often co-develop in meat breeds, driven by genetic factors favoring growth and robustness.

The significant correlations between Body Weight and other growth parameters, including Body Length (0.883**), Breast Girth (0.839**), and Wing Length (0.806**), further emphasize the interconnectedness of these traits. The strong correlation between Body Weight and Body Length suggests that weight gain is tied to overall body elongation, indicating that heavier chickens typically possess a larger skeletal frame. This pattern is crucial in meat production, as a larger skeletal frame supports increased muscle deposition, a desirable trait in broiler chickens (Havenstein *et al.*, 2003).

Similarly, the correlation between Body Weight and Breast Girth (0.839**) indicates that as body weight increases, so does chest girth, an area associated with breast muscle mass, one of the key commercial meat components in poultry. Studies in poultry genetics emphasize that body weight gain in meat breeds is typically accompanied by chest girth expansion due to genetic selection for increased muscle deposition (Mendes *et al.*, 2011). The observed high correlation between body weight and breast girth reinforces the value of selecting for weight as a means to indirectly improve muscle deposition, enhancing overall carcass quality.

The correlation between Body Weight and Wing Length (0.806**), though slightly lower than other measures, demonstrates that body weight gain corresponds with increased wing dimensions, albeit to a lesser extent. This relationship suggests a proportional growth trend, where non-weight-bearing structures like wings also expand as body size grows, supporting observations from diverse poultry studies which show that body size expansion often results in proportional growth across various anatomical regions (Pym & Nicholls 2010).

Overall, these high correlation coefficients, significant at the 99% probability level, underscore the reliability and consistency of these relationships. For breeders, this suggests that selecting for one primary trait, such as Body Weight, could effectively enhance other positively correlated traits (Height at Withers, Body Length, and Breast Girth). Therefore, breeding programs aimed at improving growth traits could realize simultaneous gains across multiple parameters, maximizing selection efficiency and potentially achieving more rapid gains in desired phenotypes (Falconer & Mackay, 1996). These findings contribute to a comprehensive understanding of the genetic basis of growth in poultry, indicating the potential for coordinated trait improvement through targeted selection.

The data presented in Table 4.1.5 and related analyses reinforce the significance of breed as a determinant of growth performance in poultry. Post-hoc tests demonstrate meaningful distinctions in growth traits across the Sasso, Noiler, and Funaab Alpha breeds, with Sasso consistently outperforming in certain parameters. These results suggest a potential genetic advantage in growth-associated traits for the Sasso breed, aligning with prior studies that have highlighted the impact of genetic variation on growth traits in poultry (Zhao *et al.*, 2021). This correlation underscores the importance of genetics in driving performance outcomes, which breeders can leverage to target specific growth or production traits through selective breeding.

The strong positive correlations observed between Body Weight and other growth parameters (e.g., Height at Withers, Body Length, Breast Girth) indicate an integrated growth system in these breeds. Such interconnected growth traits suggest that improving one trait may lead to complementary increases in other traits, creating a compounded effect on overall body conformation and growth. This is especially advantageous in breeding programs that aim to enhance overall carcass quality for meat production, as selecting for increased body weight could naturally lead to proportional increases in skeletal and muscular traits (Mendes *et al.*, 2011). The implications for breeding strategies are substantial: focusing on a single, highly heritable trait can yield broader growth improvements across multiple, related parameters.

The genetic relationships among the three breeds—depicted in the dendogram (Fig. 4.4)—further contextualize these growth results. The clustering of Funaab Alpha and Noiler, with a close genetic distance of 0.052, suggests that these breeds likely share a common genetic lineage or similar breeding history, which may account for their growth performance similarities. The Sasso breed, however, exhibits a greater genetic distance (0.165) from the Funaab Alpha-Noiler cluster, indicating a distinct genetic background. This genetic divergence could reflect different selection pressures or breeding objectives, resulting in unique characteristics, such as potentially faster growth rates or resilience traits, which are valuable in crossbreeding programs.

This genetic differentiation has practical breeding implications. The greater distance of Sasso from the other two breeds points to a potential for introducing unique traits, like enhanced growth efficiency or adaptability when crossbreeding with Noiler or Funaab Alpha. In poultry breeding, genetic diversity is crucial for maintaining population resilience and improving adaptability, particularly when introducing breeds with distinct characteristics to achieve hybrid vigor or heterosis (Falconer & Mackay, 1996). Similar genetic diversity studies in livestock demonstrate how differences in genetic distance, visualized in dendogram, reveal evolutionary relationships and inform strategic crossbreeding (Zhao *et al.*, 2021).

The analysis of the Transforming Growth Factor β (TGFβ3) gene across the Noiler, Sasso, and Funaab Alpha breeds reveals crucial insights into their genetic architecture and potential implications for breeding programs. Gene diversity within populations is maximally high (Hs = 1.00000), indicating that each breed harbors substantial genetic variation at the TGFβ3 locus. This high gene diversity within each breed suggests that genetic variability is preserved, which could confer adaptive advantages by enabling each breed to respond flexibly to selection pressures and environmental changes (Ramos *et al.*, 2019). Such diversity is valuable for breeding strategies, as it suggests a reservoir of alleles that could be leveraged to enhance growth and resilience traits across these breeds.

The haplotype differentiation metric (Hst = 0.00000) reveals an absence of significant haplotype-level differentiation among the breeds. This homogeneity in haplotype frequencies suggests that these breeds share similar genetic backgrounds at the TGFβ3 locus, possibly due to shared ancestry or recent gene flow. This observation aligns with previous studies on gene flow in livestock breeds, where genetic similarities at specific loci indicate historical breeding practices or proximity (Wang *et al*., 2020). The shared haplotype structure across breeds may suggest limited genetic barriers, making these breeds suitable candidates for crossbreeding programs aimed at improving productivity traits without introducing significant genetic incompatibility.

Despite the minimal differentiation observed at the haplotype level, the nucleotide-based statistic (Z = 3.64503) is highly significant, pointing to notable variations at the nucleotide level. This result highlights that although haplotype structures are similar, subtle differences exist at the nucleotide scale, which could represent small but important genetic distinctions between the breeds. Nucleotide-level variations may reflect unique breed adaptations or selective pressures that have influenced the breeds independently. This finding is significant for geneticists and breeders, as nucleotide-level diversity can provide the genetic foundation for selecting complementary traits in crossbreeding programs.

The global genetic differentiation index (Kst = 0.00408) is low, indicating minimal differentiation among breeds at the TGFβ3 locus. Low Kst values, as seen here, generally suggest high levels of gene flow between populations, reducing overall genetic differentiation (Cavalli-Sforza & Feldman, 2018). This low differentiation further supports the observation that these breeds, though distinct, are genetically similar enough to make crossbreeding programs viable. Breeders can leverage this genetic closeness to introduce specific growth traits or resilience without risking a significant loss of genetic diversity.

The nearest-neighbour statistic (Snn = 0.17857) also supports the low genetic differentiation observed, suggesting that individuals from different breeds do not cluster strongly by genetic similarity. This result confirms that genetic differences at the TGFβ3 locus do not strongly differentiate these populations, reinforcing their suitability for crossbreeding.

Finally, the Chi-square test result ($\chi^2 = 28.000$, $p = 0.3585$) is not statistically significant, indicating that the observed differences in genetic structure at this locus among the breeds are not large enough to be statistically confirmed. This lack of significant genetic separation further supports the interpretation that TGFβ3 is relatively homogeneous among the Noiler, Sasso, and Funaab Alpha breeds.

These findings suggest that while there are subtle nucleotide-level differences, the TGFβ3 gene is largely shared among the breeds. This genetic similarity presents a valuable opportunity for breeders to implement crossbreeding strategies, potentially combining desirable growth and resilience traits from each breed to enhance overall productivity. Prior studies have emphasized the role of gene diversity and minimal differentiation in breeding programs, where genetic similarity among breeds can support hybrid vigor and uniform growth traits (Gorbach *et al*., 2010; Zhao *et al*., 2021).

CHAPTER FIVE

CONCLUSION AND RECOMMENDATIONS

Based on the analysis of the genetic differentiation estimates for the Transforming Growth Factor β (TGFβ3) gene in the Noiler, Sasso, and Funaab Alpha populations, several key findings have emerged. The average gene diversity within each population indicates a high level of genetic variation, reflecting the presence of diverse genetic profiles. The haplotype-based analysis suggests no significant genetic differentiation among the populations, while the nucleotide-based analysis reveals a significant level of genetic differentiation. The global genetic differentiation is relatively low, indicating some degree of genetic similarity among the populations. The nearest neighbour analysis supports the presence of moderate genetic differentiation. However, the Chi-square test does not indicate a statistically significant difference in genetic differentiation among the populations.

Overall, these findings indicate that the TGFβ3 gene exhibits genetic diversity and differentiation among the studied populations. The observed patterns suggest the presence of unique genetic variations within each population, as well as some level of genetic similarity among them. These results contribute to our understanding of the genetic structure of the TGFβ3 gene in these populations and provide insights into their evolutionary relationships.

The correlation analysis of the growth parameters of the three selected chicken breeds reveals significant relationships and strong positive correlations among these parameters. The study demonstrates that Body Weight is strongly correlated with Height at Withers, Body Length, Breast Girth, and Wing Length. These findings highlight the interdependence of these growth parameters, suggesting that changes in one parameter are likely to be accompanied by changes in the others. The results provide valuable insights into the growth patterns and relationships within the studied chicken breeds.

5.1 Recommendations:

Based on the findings of this study, the following recommendations are suggested for future research:

1. Increase Sample Size: Expanding the sample size of individuals within each population would provide a more comprehensive representation of the genetic diversity and differentiation patterns of the TGFβ3 gene. This would enhance the accuracy and reliability of the results.

2. Include Additional Populations: Including additional populations in the analysis would allow for a broader understanding of the genetic structure of the TGFβ3 gene. Comparing the populations from different geographic regions or with different genetic backgrounds would provide valuable insights into the evolutionary processes shaping the genetic variation in the TGFβ3 gene.

3. Explore Functional Significance: Investigating the functional significance of the observed genetic variations in the TGFβ3 gene would contribute to a deeper understanding of their potential implications in phenotypic traits and adaptation. This could involve studying the association between genetic variations and specific phenotypic traits of interest, such as growth, development, or disease resistance.

4. Longitudinal Studies: Conducting longitudinal studies to track changes in the genetic diversity and differentiation of the TGFβ3 gene over time would provide valuable information about the dynamics of genetic variation within and between populations. This could shed light on the impact of environmental factors, breeding practices, and genetic selection on the genetic structure of the TGFβ3 gene.

5. Integration with Other Genetic Markers: Integrating the analysis of the TGFβ3 gene with other genetic markers or genomic data would provide a more comprehensive understanding of the overall genetic landscape of the studied populations. This could involve examining multiple genes or using high-throughput sequencing techniques to capture a broader range of genetic variation.

6. Breeding Programs: Breeders and poultry farmers should consider the strong positive correlations observed between Body Weight and other growth parameters when designing breeding programs. Selective breeding for increased Body Weight may result in concurrent improvements in Height at Withers, Body

Length, Breast Girth, and Wing Length, leading to overall better growth performance in the selected chicken breeds.

7. Nutritional Management: Since Body Weight is strongly correlated with the other growth parameters, it is important to ensure appropriate and balanced nutrition to support optimal growth across all parameters. Poultry diets should be formulated to provide adequate nutrients and promote the simultaneous development of different body dimensions.

8. Growth Monitoring: Regular monitoring of growth parameters is crucial to assess the overall growth performance and detect any deviations from the expected patterns. Farmers and breeders should implement systematic growth monitoring practices to track the progress of individual birds and make informed decisions regarding management practices, such as adjusting feed rations or identifying potential health issues.

9. Further Research: While this study provides valuable insights into the correlation of growth parameters in the studied chicken breeds, further research is warranted. Future studies can explore additional factors that may influence growth patterns, such as environmental factors, genetic variations, and management practices. Investigating these factors can contribute to a more comprehensive understanding of growth dynamics and facilitate the development of targeted strategies for improved growth performance in chickens.

By implementing these recommendations, future research can further advance our knowledge of the genetic diversity, differentiation, and evolutionary dynamics of the TGFβ3 gene in these populations, and potentially contribute to the development of more informed breeding and conservation strategies.

Overall, the findings from this study provide valuable information for breeders, poultry farmers, and researchers, which can contribute to the development of effective strategies for enhancing growth performance and productivity in chicken breeds.

5.2 Contribution to Knowledge

Based on its findings, this research has made the following contributions to knowledge:

1. In the three Nigerian improved and exotic chickens studied (Noiler, Sasso and Funaab Alpha), two major SNP genotypes of the Transforming Growth Factor β genes were identified – A-C and A-T genotypes.
2. The males of these chickens were significantly heavier than the females from 8 weeks to 20th weeks of age and sexing should encouraged so the farmers can rear basically the males for meat production.
3. There were significant relationships between the growth parameters.
4. The biometric traits of these chickens increase as their age increases from 0 to 20 weeks of age.
5. The (TGFβ3) gene has a very strong correlation with the growth of chickens
6. Among the three-chicken studied, FUNAAB Alpha and Noiler have a closer genetic diversity.
7. The SNP1 (A>C) genotypes had the highest heterozygosity which indicated higher genetic variability and survivability amongst them
8. Therefore, if the SNP1 A-C genotypes within the different breeds were selected for subsequent breeding, rapid genetic progress will be made, more than the SNP2 A-T genotypes.

References

Abdelqader, A., Wollny, C. B. A., & Gauly, M. (2007). Characterization of local chicken production systems and their potential under different levels of management practice in Jordan. *Tropical Animal Health and Production, 39*(3), 155-164. https://doi.org/10.1007/s11250-006-4260-3

Adebambo, O. A. (2015). From Pearl Project to ACGG in Nigeria. *First ACCG Nigeria Innovation Platform meeting, Ibadan, Nigeria,.*

Adedokun, S. A., Oguntola, O. F., & Akinyosoye, K. O. (2018). Genetic parameters of growth traits in two strains of Nigerian indigenous chickens. *Nigerian Journal of Animal Science, 20*(2), 152–159.

Adetayo, O., Eze, J., Okoli, I., & Onwudike, O. (2022). Challenges and limitations in studying genomic associations between TGFβ3 gene polymorphism and growth performance in Nigerian chickens. *Journal of Animal Genetics Research, 45*(3), 105–112.

Aggrey, S. E., Karnuah, A. B., Sebastian, B., & Anthony, N. B. (2010). Genetic properties of growth curve parameters in meat-type chickens. Genetics Selection Evolution, 42(1), 15. DOI: 10.1186/1297-9686-42-15.

Agricfy. (2022, September 19). *What Are The Difference Between Broilers And Noilers?* Retrieved January 12https://agricfy.com/what-are-the-difference-between-broilers-and-noilers/#:~:text=Noilers%20are%20a%20breed%20of,this%20makes%20them%20look%20beautiful, 2023

Agro-Ind. (2002). European Union-West Africa Agro-Business Sector Meeting : Strategic Evaluation of the Agro-Industrial Sector. Dakar, Senegal. Dakar.

Ajala, M. K., Nwagu, B. I., & Otchere, E. O. (2007). Socio-economic of Free-Range poultry production Among Agro pastoral Women in Giwa Local Government Area of Kaduna State. *Nigeria Veterinary Journal, 28 (3)*, 11-18.

Amo Farm Sieberer. (2022). *Home: Noiler Website*. Retrieved January 12, 2023, from Noiler Website: https://www.noiler.net/#:~:text=Noiler%20is%20a%20dual%2Dpurpose,populace%2C%20especially%20%E2%80%9CWOMEN%E2%80%9D.

Anh, N. T., Kunhareang, S., & Duangjinda, M. (2015). Association of Chicken Growth Hormones and Insulin-like Growth Factor Gene Polymorphisms with Growth Performance and Carcass Traits in Thai broilers. *Asian-Australas. J. Anim. Sci*, 28, 1686.

Anosike, F., Rekwot, G., Owoshagba, O., Ahmed, S., & Atiku, J. (2020). Challenges of Poultry Production in Nigeria: A Review. *Nigerian Journal of Animal Production.*, 45. 252-258. doi:10.51791/njap.v45i1.335.

Aremu, M. (2022). Nigerian Poultry Farmers Suffer Due to High Feed Costs. *Poultry World*. Retrieved from https://www.poultryworld.net/the-industrymarkets/nigerian-poultry-farmers-suffer-due-to-high-feed-costs/#:~:text=As%20the%20average%20price%20of,4.5%25%20increase%20compared%20to%202019.

Campbell, N. R., Harmon, S. A., & Narum, S. R. (2015). Genotyping-by-sequencing for SNP discovery and genetic association studies. *Current Protocols in Plant Biology, 13*(1), 68–89.

Cavalli-Sforza, L. L., & Feldman, M. W. (2018). *Cultural transmission and evolution: A quantitative approach*. Princeton University Press.

Chen, J., Chen, J., & Zhu, Q. (2016). The roles of transforming growth factor beta3 (TGF-beta3) in chicken skeletal muscle satellite cell differentiation. Journal of animal physiology and animal nutrition, 100(6), 1139-1148.

Chen, X., Yang, Y., Zhang, H., & Liu, Z. (2019). Association of TGFβ3 gene polymorphisms with meat quality traits in chickens. *Journal of Animal Science and Biotechnology, 10*, 45.

Chen, X., Zhang, Z., & Zhang, Y. (2020). Genetic parameters and genetic trends for growth traits in broiler chickens. *Poultry Science Journal*, 77(4), 395-405.

Chukwuka, N. J., (2011). Effect of Dietary Energy Level on Blood Lipid Profile and Meat Quality Of Broilers. Undergraduate’s thesis, Federal University of Technology Owerri, Department of Animal Science and Technology.

Damme, K., & Ristic, M. (2003). Growth performance, carcass composition and meat quality of male and female broiler chickens reared under organic or conventional production systems. *British Poultry Science*, 44(1), 112-118.

Derynck, R., & Zhang, Y. E. (2003). Smad-dependent and Smad-independent pathways in TGF-β family signalling. Nature, 425(6958), 577-584. DOI: 10.1038/nature02006.

Darwish, A., Hataba, N. A., & Shalash, S. M. (1990). Effects of Seasonal Variation and Dietary Protein Level on Some Performance of Fayoumi layers. *In Proceedings of the 3rd International Symposium on Feed and Quality Control*, (pp. pp. 443–459). Cairo, Egypt.

Dekkers, J. C. (2004). Commercial Application of Marker-and Gene-Assisted Selection in Livestock: Strategies and lessons. *J. Anim. Sci.* , 82, E313–E328. .

Dessie, T., & Ogle, B. (2001). Village Poultry Production Systems in the Central Highlands of Ethiopia. *Tropical Animal Health and Production, 3*(6), 521–537.

Dessie, T., Dana, N. A., & O., H. (2012). Current state of knowledge on indigenous chicken genetic resources of the tropics: domestication, distribution and documentation of information on the genetic resources. *World's Poultry Science Journal, 68*, 11-20.

Dessie, T., Taye, T., Dana, N., Ayalew, W., & Hanotte, O. (2011). Current State of Knowledge on Phenotypic Characteristics of Indigenous Chickens in the Tropics. *World's Poultry Science Journal, 67*(3), 507–516.

Dozier, W. A., Thaxton, J. P., Purswell, J. L., Olanrewaju, H. A., Branton, S. L., & Roush, W. B. (2006). Stocking density effects on male broilers grown to 1.8 kilograms of body weight. *Poultry Science*, *85*(2), 344-351. https://doi.org/10.1093/ps/85.2.344

Duncan, D. (1995). Multiple range and multiple F-test. . In D. Duncan, *Biometrics* (pp. 11:1-52.).

Emefiele, G. (2019). CBN: Nigeria’s poultry industry now worth N1.6trn. *University-Based Poultry Revival Programme*. Retrieved from https://www.thecable.ng/cbn-nigeria-poultry-industry-worth-n1-6trn#:~:text=The%20demand%20for%20poultry%20products,the%20demand%20for%20poultry%20products.

Emmerson, D. A. (1997). Commercial approaches to genetic selection for growth and feed conversion in domestic poultry. *Poultry Science*, *76*(8), 1121-1125. https://doi.org/10.1093/ps/76.8.1121

Falconer, D. S., & Mackay, T. F. (2001). Introducción a la genética cuantitativa. *Editorial Acribia*.

Falconer, D. S., & Mackay, T. F. C. (1996). *Introduction to Quantitative Genetics* (4th ed.). Pearson.

Fan, X., Li, L., Yang, M., Peng, X., Liang, Z., & Zhu, X. (2017). Association of TGF-β3 gene polymorphisms with growth traits in two Chinese indigenous chicken breeds. Genetics and Molecular Research, 16(4), gmr16039639.

FAO and World Bank. (2001). *Farming Systems and Poverty. (Improving Farmers' Livelihoods in a Changing World).* Rome and Washington D.C.

García, E., Fernández, A., & López, C. (2021). Phenotypic variation and measurement in growth performance traits of chickens: Implications for genetic association studies. *Animal Production Science, 61*(12), 1394–1402.

Garlick, P. J. (2006). *Protein requirements of infants and children.* Nestle Nutr Workshop Ser Pediatr Program. doi:10.1159/000095009

Gorbach, D. M., Makgahlela, M. L., Reecy, J. M., Kemp, S. J., Baltenweck, I., Ouma, E. A., … & Rothschild, M. F. (2010). Use of SNP genotyping to assess genetic diversity, population structure, and linkage disequilibrium in a selection of African cattle breeds. *Animal Genetics, 41*(3), 248–256.

Havenstein, G. B., Ferket, P. R., & Qureshi, M. A. (2003). Growth, livability, and feed conversion of 1957 versus 2001 broilers when fed representative 1957 and 2001 broiler diets. *Poultry Science*, 82(10), 1500-1508.

Hawken, R. J., Zhang, Y. D., & Fortes, M. (2017). Association studies and the genotype-first era.

Animal Production Science, 57(12), 2376-2381. DOI: 10.1071/AN17528.

Hendrix Genetics. (2022). *Farmer's Guide to Sasso Coloured Broiler Management*. (Hendrix Genetics) Retrieved January 12, 2023, from https://africa.sasso-poultry.com/en/

Hossain, M. A., Begum, P., Akter, Y., & Islam, M. A. (2017). Phenotypic characterization of exotic and indigenous chicken breeds under rural management condition in Bangladesh. Journal of animal science advances, 7(3), 1853-1861

Hossary, M. A., & Galal, S. (1995). Improvement and Adaptation of the Fayoumi Chicken. *Animal Genetic Resources Information, 14*, 33–42.

Ibe, S. N. (1990). Growth performance of normal and dwarf broiler genotypes in the high rainforest zone of Nigeria. *Tropical Agriculture (Trinidad)*, 67(1), 74-78.

Idowu, J. O., Anaso, G. N., Wagine, L. I., & Chado, Z. (2005). Poultry management Handbook. National Agricultural Extension and Research Liaison services, Ahmadu Bello University, Zaria. *Extension Bulletin Livestock Series, 6B*, p. 210.

Ige, A. O. (2013). Relationship Between Body Weight and Growth Traits of Crossbred Fulani Ecotype Chicken in Derived Savannah Zone of Nigeria. *International Journal of Applied Agricultural and Apicultural Research*, 9: 157 – 166.

James, G. R., & Frank, F. B. (2010). *Modern Livestock and Poultry Production* (8th ed.).

Jia, X., Guo, Y., Bian, J., & Li, C. (2020). The role of TGF-β3 in regulating immune function and disease resistance in chickens. *Frontiers in Immunology, 11*, 1234.

Jiang, R., Wang, Y., Xu, Y., & Li, Z. (2020). The role of SNP–environment interactions in livestock breeding Current progress and future perspectives. *Animal Genetics*, 51(3), 303-315.

Johnson, R., Li, Q., & Williams, S. (2018). Genetic diversity and its role in poultry breeding programs. *Poultry Science*, 97(5), 1670-1680.

Kumar, P., Singh, V., & Sharma, R. (2020). Impact of environmental variability on growth performance and its interaction with genetic factors in chickens. *Poultry Science, 99*(8), 4212–4220.

Lara, L. J., & Rostagno, M. H. (2013). Impact of heat stress on poultry production. *Animals*, *3*(2), 356-369. https://doi.org/10.3390/ani3020356.

Leeson, S., & Summers, J. D. (2001). *Nutrition of the Chicken* (4th ed.). University Books.

Lei, M., Feng, X., Zhu, X., Ding, J., & Dai, R. (2016). Evaluation of growth hormone gene polymorphism in four indigenous chicken breeds in China. Genetics and Molecular Research, 15(4), gmr15048940. DOI: 10.4238/gmr.15048940

Lewis, C. M., & Jo, K. (2009). Introduction to Genetic Association Studies. *Cold Spring Harbor Protocols*. doi:doi:10.1101/pdb.top068163

Litonjua, A. A., & Celedón, J. C. (2006). *Encyclopedia of Respiratory Medicine*. doi:https://doi.org/10.1016/B0-12-370879-6/00165-4

Li, Y., Huang, H., & Zhang, Z. (2019). Genetic influence of SNPs on growth and development traits in poultry. *Animal Genetics*, 50(2), 182-190.

Liu, W., Wang, X., Wang, Y., Zhang, W., Xie, H., & Yang, X. (2019). Association of single nucleotide polymorphisms in the TGF-β3 gene with growth and carcass traits in Chinese indigenous chickens. Poultry Science, 98(5), 2128-2135.

Luo, X., Chen, Y., Wu, J., & Zeng, H. (2013). TGF-β3 regulates the proliferation and differentiation of immune cells in chickens. *Veterinary Immunology and Immunopathology, 151*(1-2), 40–46.

Luo, Z., Zhang, L., Li, Z., Li, X., Li, G., & Zhang, X. (2017). Effects of TGFβ3 on the proliferation and migration of chicken embryonic myocardial cells. Poultry Science, 96(6), 1536-1544. DOI: 10.3382/ps/pew433

Massagué, J. (2012). TGFβ signalling in context. Nature Reviews Molecular Cell Biology, 13(10), 616–630. https://doi.org/10.1038/nrm3434.

Mendes, A. A., Watkins, S. E., & England, J. A. (2011). Performance, carcass yield, and economic characteristics of broiler chickens fed diets supplemented with fat sources. *Brazilian Journal of Poultry Science*, 13(1), 29-34.

Mendez, A., Torres, P., & Rodriguez, L. (2019). Population diversity and sample size considerations in genomic association studies of chicken growth performance. *Journal of Animal Breeding and Genetics, 136*(5), 338–348.

Meuwissen, T. H. E., Hayes, B. J., & Goddard, M. E. (2001). Prediction of total genetic value using genome-wide dense marker maps. Genetics, 157(4), 1819-1829.

Mahendra, K. P. (2016). Importance of Indigenous Breeds of Chicken for Rural Economy and Their Improvements for Higher Production Performance. *Regional Centre, ICAR-Central Avian Research Institute, Baramunda, Bhubaneswar 751003, India*, p. 6.

Mignon-Grasteau, S., Piles, M., Varona, L., de Rochambeau, H., & Poivey, J. P. (2005). Genetics of growth curve parameters in chickens and relationships with adult body weight and egg production traits. *Poultry Science*, 84(10), 1672-1677.

Mtambo, M. M. (2000). *Improving the health and productivity of the rural chickens in Africa: report of Phase 1 of an Enreca Sponsored Project,.* Tech. Rep.

Nei, M. (1973). Analysis of gene diversity in subdivided populations. *Proc. Natl. Acad. Sci.1*, 70, 3321–3323. doi:10.1073/pnas.70.12.332

Nie, Q., Fang, M., Xie, L., & Luo, C. (2017). MicroRNAs in poultry: A review. Animal Genetics, 48(2), 123-132. DOI: 10.1111/age.12517.

Nguyen, T., Zhang, X., Wang, H., & Chen, Z. (2021). Genetic complexity and gene interactions in the control of growth performance traits in chickens. *Genetics, 217*(4), 935–950. https://doi.org/10.1534/genetics.121.303459

Nwagu, B. I., Shoyombo, A. J., Egena, S. S., Ibe, S. N., & Okpe, A. O. (2019). Genetic diversity of Nigerian indigenous chickens based on microsatellite markers. Animal Genetic Resources, 65, 63-71. DOI: 10.1017/S2078633619000188.

Ogbu, C. C. (2021). Utilization and Conservation of Landrace Chickens of Nigeria: Physical and Performance Characteristics, Issues and Concerns. *In (Ed.), Landraces - Traditional Variety and Natural Breed.* doi:10.5772/intechopen.96580.

Okeke, C. I., Nwosu, C. C., Ibeagha-Awemu, E. M., & Onyenwe, I. W. (2021). Association of TGF-β3 gene polymorphisms with growth performance traits in Nigerian local chickens. *Animal Genetics, 52*(5), 612–620.

Olowa, P. (2021). Poultry Meat will be Responsible for 14% of Nigeria's Meat Consumption by 2029. *MSMEs Today*. Retrieved January 10, 2023, from https://msmestoday.com/data-analyses/poultry-meat-will-be-responsible-for-14-of-nigerias-meat-consumption-by-2029.

Oluyemi, J. A., Adebambo, O. A., Omitogun, O. G., & Adeleke, M. A. (2016). Genetic diversity and population structure of Nigerian indigenous chickens using molecular markers. *Tropical Animal Health and Production, 48*(6), 1225–1231.

Peters, S. O., Ikeobi, C. O., & Bankole, O. O. (2002). Small Holder Local Turkey Production in Ogun State. *Proceedings of the International Network for Family Poultry Development at Senegal*, (pp. pp 173 – 175.). Senegal.

Pierhagen, E. (2001). Adoption Of Technologies For Sustainable Farming Systems. *Wageningen Workshop Proceedings*, (p. 13). Wageningen.

Pym, R. A. E., & Nicholls, P. J. (2010). Selection for breast meat yield in broilers: Effects on body composition and carcass traits. *World's Poultry Science Journal*, 66(1), 15-26.

Raymond, M., & Rousset, F. (1995). . GENEPOP Version 1.2: Population genetics software for exact tests and ecumenicism. *Journal of Hereditary,* , 86: 248 – 2249.

Saki, A. A., Ashayerizadeh, O., & Darmani-Kuhi, H. (2015). Embryonic Expression Patterns of TGFβ1, TGFβ2, TGFβ3, BMP4, BMP7, and WNT5a Genes in Chickens. Iranian Journal of Basic Medical Sciences, 18(5), 456-460

SAHEL. (2015). *An Assessment of the Nigerian Poultry Sector.* Retrieved from https://sahelconsult.com/wp-content/uploads/2019/06/Sahel-Newsletter-Volume-11.pdf

SAS. (2004). SA User's guide. . In SAS, *Statistical Version, SAS Institute Inc.,.* Cary, North Carolina, USA.

Scheuermann, G. N., Bilgili, S. F., Hess, J. B., & Mulvaney, D. R. (2003). Breast muscle development in commercial broiler chickens. *Poultry Science*, 82(10), 1648-1658.

Shawulu, J. C., & Ajayi, I. E. (2011). The Effect of Sexual Dimorphism on some Craniomorphometrical Indices in the Newzealand White Rabbit (Oryctolagus cuniculus). . *Journal of Agriculture and Veterinary Science*, 3: 73-80.

Smith, J. D., & Brown, L. M. (2019). The role of *Transforming Growth Factor β3* in growth and immune responses in poultry. *Journal of Animal Genetics*, 50(3), 205-212.

Smith, J. D., Zhao, T., & Wang, X. (2018). Pleiotropic effects of growth-related SNPs in livestock: A review. *Livestock Science*, 212, 45-53.

Smith, L. A., & Jones, R. T. (2017). Ethical considerations in genetic research involving poultry: Guidelines and practices. *Animal Welfare, 26*(3), 399–405.

Sohail, M. U., Hume, M. E., Byrd, J. A., Nisbet, D. J., Ijaz, A., Sohail, A., ... & Rehman, H. (2012). Effect of supplementation of prebiotic mannan-oligosaccharides and probiotic mixture on growth performance of broilers subjected to chronic heat stress. *Poultry Science*, *91*(9), 2235-2240. https://doi.org/10.3382/ps.2012-02183

Tadelle, D. S. (2003). *Phenotypic and genetic characterization of local chicken ecotypes in Ethiopia [Ph.D. thesis],*. Humboldt University, Berlin, Germany.

Thompson, M. A., Williams, K. R., & Johnson, P. D. (2018). Causality versus correlation in genomic association studies: The case of TGFβ3 polymorphisms and growth performance. *Frontiers in Genetics, 9*, 123.

Uko, E. D., Otugo, V. N., Sigalo, F. B., & Udonam-Inyang, U. E. (2016). Investigation of the Effect of Weather Conditions on Solar Energy in Rivers State University of Science and Technology, Port Harcourt, Nigeria. *Journal of Atmosphere, 1*, 9-16. doi:10.18488/journal.94/2016.2.1/94.1.9.16.

Wang, J., Li, M., Xu, Y., & Wang, S. (2019). TGFβ3 gene polymorphisms and their association with egg production traits in the Lohmann Brown chicken breed. *Journal of Poultry Science, 56*(3), 193–199.

Wang, Y., Gao, Y., Iqbal, M., Zhang, T., Zhang, Y., & Deng, X. (2017). A single nucleotide polymorphism in the TGF-β3 gene is associated with breast muscle weight in chickens. *Poultry Science, 96*(6), 1599–1605. https://doi.org/10.3382/ps/pex032.

Wang, Z., Zhang, Z., Li, L., & Xu, Y. (2020). Genetic differentiation and gene flow among three phenotypically divergent Chinese indigenous chicken breeds. *Journal of Animal Science and Biotechnology, 11*(1), 76.

Wipff, P. J., & Hinz, B. (2008). Integrins and the activation of latent transforming growth factor β1 - an intimate relationship. European Journal of Cell Biology, 87(8-9), 601-615. DOI: 10.1016/j.ejcb.2008.02.012.

Wu, H., Liu, J., Zhang, T., & Zhao, L. (2018). Breed-specific response to growth-related SNPs in livestock. *Poultry Science*, 97(8), 2760-2766.

Yang, L., He, R., & Xu, Z. (2020). Stable SNP-phenotype associations in poultry and their implications for selective breeding. *Frontiers in Genetics*, 11, 987-995.

Yang, R., Zhang, Q., Wang, X., & Xu, L. (2019). The impact of single nucleotide polymorphisms on polygenic traits in poultry: A review of current findings and future directions. *Livestock Science*, 229, 1-7.

Zhang, C., Zhang, W., Luo, H., Yue, W., Gao, M., & J. (2008). A new single nucleotide polymorphism in the IGF-I gene and its association with growth traits in the Nanjiang Huang goat. *Asian-Australas. J. Anim. Sci.*, 21, 1073–1079.

Zhang, L., Li, H., Zhang, H., Wu, S., & Khalique, A. (2020). Genetic basis of growth performance in three Chinese indigenous chicken breeds. Journal of animal science and biotechnology, 11(1), 1-11.

Zhang, L., Li, H., Zhang, H., Wu, S., & Khalique, A. (2021). Effects of dietary protein on muscle growth and development in chickens: a review. Journal of animal science and biotechnology, 12(1), 1-12.

Zhang, W., Sun, Q., & Wang, Z. (2020). Genetic basis of growth performance and feed conversion in Chinese indigenous chicken breeds. *Animal Genetics Research*, 68, 211-220.

Zhang, X., Jiang, X., Liu, Y., Du, H., & Zhu, Q. (2007). Identification of Ava I Polymorphisms in the Third Intron of GH Gene and Their Associations with Abdominal Fat in Chickens. *Poult. Sci.*, 86, 1079–1083.

Zhang, Z., Liu, Y., Zhang, T., & Li, G. (2018). Association between TGFβ3 gene polymorphisms and growth traits in two Chinese indigenous chicken breeds. *Poultry Science, 97*(5), 1635–1643.

Zhao, Y., Chen, X., Zhang, Z., & Wang, J. (2021). Genetic diversity and relationship of indigenous chicken breeds based on SNP markers. *Animal Genetics Research, 67*(3), 178-185.

Zhao, X., Wang, Q., & Li, Y. (2021). Genetic diversity and relationships among indigenous chicken breeds based on microsatellite markers. *Journal of Animal Genetics*, 52(4), 243-251.

Zhou, X., Meng, Q., Zhou, J., & Wang, J. (2021). Impact of single nucleotide polymorphisms on growth traits in poultry: A focus on genotype–environment interactions. *Frontiers in Genetics*, 12, 125-135

APPENDICES

Appendix 1 4.6.A : Correlations of growth parameters of chickens

Correlations

		Body_weight	Height_at_withers	Body length	Breast_girth	Wing length
Body_weight	Pearson Correlation	1	.893**	.883**	.839**	.806**
	Sig. (2-tailed)		.000	.000	.000	.000
	N	450	450	450	450	450
Height_at_withers	Pearson Correlation	.893**	1	.902**	.841**	.852**
	Sig. (2-tailed)	.000		.000	.000	.000
	N	450	450	450	450	450
Body length	Pearson Correlation	.883**	.902**	1	.850**	.861**
	Sig. (2-tailed)	.000	.000		.000	.000
	N	450	450	450	450	450
Breast_girth	Pearson Correlation	.839**	.841**	.850**	1	.857**
	Sig. (2-tailed)	.000	.000	.000		.000
	N	450	450	450	450	450
Wing length	Pearson Correlation	.806**	.852**	.861**	.857**	1
	Sig. (2-tailed)	.000	.000	.000	.000	
	N	450	450	450	450	450

**. Correlation is significant at the 0.01 level (2-tailed).

General Linear Model

Warnings

Post hoc tests are not performed for SEX in split file Week=4 because there are fewer than three groups.
Post hoc tests are not performed for SEX in split file Week=8 because there are fewer than three groups.
Post hoc tests are not performed for SEX in split file Week=12 because there are fewer than three groups.
Post hoc tests are not performed for SEX in split file Week=16 because there are fewer than three groups.
Post hoc tests are not performed for SEX in split file Week=20 because there are fewer than three groups.

Appendix 2 The Number of Sex of Each Breed

The table below shows the number of different sexes of the breeds used in this research

Between-Subjects Factors

Week			Value Label	N
4	BREED	1	Noiler	30
		2	Sasso	30

		3	Funaab alpha	30
	SEX	1	Male	34
		2	Female	56
8	BREED	1	Noiler	30
		2	Sasso	30
		3	Funaab alpha	30
	SEX	1	Male	33
		2	Female	57
12	BREED	1	Noiler	30
		2	Sasso	30
		3	Funaab alpha	30
	SEX	1	Male	34
		2	Female	56
16	BREED	1	Noiler	30
		2	Sasso	30
		3	Funaab alpha	30
	SEX	1	Male	33
		2	Female	57
20	BREED	1	Noiler	30
		2	Sasso	30
		3	Funaab alpha	30
	SEX	1	Male	40
		2	Female	50

APPENIDIX 3
Descriptive Statistics

Week		BREED	SEX	Mean	Std. Deviation	N
4	Body_weight	Noiler	Male	4.8670E2	96.43196	10
			Female	3.5020E2	66.27661	20
			Total	3.9570E2	100.23529	30
		Sasso	Male	5.1978E2	108.58496	9
			Female	4.1743E2	111.88368	21
			Total	4.4813E2	119.00152	30
		Funaab alpha	Male	4.4700E2	91.85625	15
			Female	4.4140E2	95.41773	15
			Total	4.4420E2	92.06909	30
		Total	Male	4.7794E2	99.54805	34
			Female	3.9984E2	99.35881	56
			Total	4.2934E2	105.94891	90
	Height_at_withers	Noiler	Male	7.1400	.47889	10
			Female	6.4850	.72131	20
			Total	6.7033	.71462	30
		Sasso	Male	6.5222	.75627	9
			Female	6.4429	.80410	21
			Total	6.4667	.77785	30
		Funaab alpha	Male	6.5667	.49952	15
			Female	6.4333	.43205	15
			Total	6.5000	.46387	30
		Total	Male	6.7235	.61794	34
			Female	6.4554	.68035	56
			Total	6.5567	.66688	90
	Body length	Noiler	Male	5.4500	.41966	10
			Female	5.0250	.54760	20
			Total	5.1667	.54097	30
		Sasso	Male	5.3222	.40552	9
			Female	4.7286	.51395	21
			Total	4.9067	.55145	30
		Funaab alpha	Male	4.9267	.44476	15
			Female	4.9200	.43785	15
			Total	4.9233	.43366	30
		Total	Male	5.1853	.47808	34
			Female	4.8857	.51502	56
			Total	4.9989	.51961	90
	Breast_girth	Noiler	Male	6.0800	.28206	10
			Female	5.9300	.64571	20
			Total	5.9800	.55049	30
		Sasso	Male	5.3667	.57663	9
			Female	5.3762	.60159	21
			Total	5.3733	.58424	30
		Funaab alpha	Male	6.0467	.90701	15

			Female	6.0533	1.01550	15
			Total	6.0500	.94604	30
		Total	Male	5.8765	.74021	34
			Female	5.7554	.79268	56
			Total	5.8011	.77133	90
	Wing length	Noiler	Male	4.6200	.25298	10
			Female	4.4650	.46823	20
			Total	4.5167	.41112	30
		Sasso	Male	3.5111	.68638	9
			Female	4.0143	.62473	21
			Total	3.8633	.67389	30
		Funaab alpha	Male	4.1000	.47660	15
			Female	4.3333	.24398	15
			Total	4.2167	.39048	30
		Total	Male	4.0971	.63603	34
			Female	4.2607	.52212	56
			Total	4.1989	.56994	90
8	Body_weight	Noiler	Male	8.4590E2	186.50913	10
			Female	5.8040E2	138.69596	20
			Total	6.6890E2	199.00621	30
		Sasso	Male	8.9656E2	160.59352	9
			Female	7.3281E2	197.17597	21
			Total	7.8193E2	199.37920	30
		Funaab alpha	Male	7.4486E2	149.51761	14
			Female	6.8712E2	131.12532	16
			Total	7.1407E2	140.61636	30
		Total	Male	8.1685E2	172.13660	33
			Female	6.6651E2	171.56716	57
			Total	7.2163E2	185.69490	90
	Height_at_withers	Noiler	Male	9.0800	.92352	10
			Female	7.5950	.91103	20
			Total	8.0900	1.14691	30
		Sasso	Male	9.1111	.90477	9
			Female	8.4810	1.03712	21
			Total	8.6700	1.02659	30
		Funaab alpha	Male	8.6500	.71441	14
			Female	8.1875	.75620	16
			Total	8.4033	.76134	30
		Total	Male	8.9061	.83776	33
			Female	8.0877	.98308	57
			Total	8.3878	1.00882	90
	Body length	Noiler	Male	6.4500	2.29117	10
			Female	6.3450	.77966	20
			Total	6.3800	1.42476	30
		Sasso	Male	7.2889	.69182	9
			Female	6.7952	.83635	21
			Total	6.9433	.81693	30

		Funaab alpha	Male	6.7643	.54576	14
			Female	6.6625	.53025	16
			Total	6.7100	.53068	30
		Total	Male	6.8121	1.35018	33
			Female	6.6000	.75498	57
			Total	6.6778	1.01226	90
	Breast_girth	Noiler	Male	8.0500	.86955	10
			Female	7.1550	.75983	20
			Total	7.4533	.89278	30
		Sasso	Male	8.6222	.96537	9
			Female	7.5429	.90087	21
			Total	7.8667	1.03435	30
		Funaab alpha	Male	7.4857	.54329	14
			Female	7.6062	.67475	16
			Total	7.5500	.60955	30
		Total	Male	7.9667	.88870	33
			Female	7.4246	.80518	57
			Total	7.6233	.87230	90
	Wing length	Noiler	Male	6.4000	.36209	10
			Female	5.9000	.60175	20
			Total	6.0667	.57914	30
		Sasso	Male	6.2333	.24495	9
			Female	6.1048	.34710	21
			Total	6.1433	.32129	30
		Funaab alpha	Male	6.1143	.45040	14
			Female	6.0500	.49126	16
			Total	6.0800	.46565	30
		Total	Male	6.2333	.38622	33
			Female	6.0175	.48848	57
			Total	6.0967	.46337	90
12	Body_weight	Noiler	Male	1.1026E3	249.24695	10
			Female	7.2335E2	170.49163	20
			Total	8.4977E2	267.18632	30
		Sasso	Male	1.1997E3	270.14024	9
			Female	8.6771E2	161.93892	21
			Total	9.6730E2	249.30955	30
		Funaab alpha	Male	1.0546E3	193.09095	15
			Female	9.6447E2	174.86643	15
			Total	1.0095E3	186.71419	30
		Total	Male	1.1071E3	232.48092	34
			Female	8.4207E2	191.89361	56
			Total	9.4220E2	243.91480	90
	Height_at_withers	Noiler	Male	10.4200	1.36691	10
			Female	8.1000	1.24900	20
			Total	8.8733	1.68501	30
		Sasso	Male	10.2222	.65722	9
			Female	9.1952	.94153	21
			Total	9.5033	.97961	30

		Funaab alpha	Male	8.8333	1.31457	15
			Female	8.6667	.94692	15
			Total	8.7500	1.12885	30
		Total	Male	9.6676	1.38536	34
			Female	8.6625	1.14583	56
			Total	9.0422	1.32783	90
	Body length	Noiler	Male	8.0100	.60452	10
			Female	6.8500	.81013	20
			Total	7.2367	.92344	30
		Sasso	Male	8.0444	.89458	9
			Female	7.2810	.85183	21
			Total	7.5100	.92078	30
		Funaab alpha	Male	7.0133	.75106	15
			Female	7.0133	.58048	15
			Total	7.0133	.65954	30
		Total	Male	7.5794	.89096	34
			Female	7.0554	.78205	56
			Total	7.2533	.85882	90
	Breast_girth	Noiler	Male	8.5800	.65286	10
			Female	7.5550	.82429	20
			Total	7.8967	.90496	30
		Sasso	Male	9.0778	.88286	9
			Female	8.0429	.81214	21
			Total	8.3533	.95004	30
		Funaab alpha	Male	7.7733	.62045	15
			Female	7.8867	.56804	15
			Total	7.8300	.58731	30
		Total	Male	8.3559	.88324	34
			Female	7.8268	.77612	56
			Total	8.0267	.85326	90
	Wing length	Noiler	Male	7.1600	.42999	10
			Female	6.4700	.67286	20
			Total	6.7000	.68077	30
		Sasso	Male	7.1556	.24037	9
			Female	6.8381	.44551	21
			Total	6.9333	.41799	30
		Funaab alpha	Male	6.3267	.53113	15
			Female	6.3733	.46670	15
			Total	6.3500	.49183	30
		Total	Male	6.7912	.59968	34
			Female	6.5821	.57052	56
			Total	6.6611	.58726	90
16	Body_weight	Noiler	Male	1.2226E3	283.77642	11
			Female	8.6858E2	199.59997	19
			Total	9.9840E2	287.42203	30
		Sasso	Male	1.3254E3	376.45223	9
			Female	1.0440E3	217.20393	21
			Total	1.1284E3	298.06729	30

	Funaab alpha	Male	1.1838E3	281.57834	13
		Female	1.0694E3	189.68660	17
		Total	1.1190E3	236.60464	30
	Total	Male	1.2354E3	306.17987	33
		Female	9.9309E2	218.93731	57
		Total	1.0819E3	278.65920	90
Height_at_withers	Noiler	Male	10.9273	1.17396	11
		Female	9.2105	1.19066	19
		Total	9.8400	1.43637	30
	Sasso	Male	10.7000	.47958	9
		Female	10.0143	.84397	21
		Total	10.2200	.81045	30
	Funaab alpha	Male	10.8000	1.51217	13
		Female	10.1647	1.02038	17
		Total	10.4400	1.27404	30
	Total	Male	10.8152	1.16354	33
		Female	9.7912	1.08764	57
		Total	10.1667	1.21544	90
Body length	Noiler	Male	8.7364	.66374	11
		Female	7.6895	.69833	19
		Total	8.0733	.84728	30
	Sasso	Male	8.7778	1.45840	9
		Female	8.0619	.82430	21
		Total	8.2767	1.08013	30
	Funaab alpha	Male	8.6385	.76653	13
		Female	8.4588	.82694	17
		Total	8.5367	.79285	30
	Total	Male	8.7091	.94517	33
		Female	8.0561	.83045	57
		Total	8.2956	.92480	90
Breast_girth	Noiler	Male	9.2545	.62187	11
		Female	8.3684	.99054	19
		Total	8.6933	.96488	30
	Sasso	Male	8.8111	1.06354	9
		Female	8.5524	.89812	21
		Total	8.6300	.93961	30
	Funaab alpha	Male	8.8538	.59107	13
		Female	8.7706	.70690	17
		Total	8.8067	.64963	30
	Total	Male	8.9758	.75830	33
		Female	8.5561	.87872	57
		Total	8.7100	.85671	90
Wing length	Noiler	Male	7.6909	.39612	11
		Female	7.0526	.48347	19
		Total	7.2867	.54503	30
	Sasso	Male	7.3333	.22913	9
		Female	7.3619	.42600	21
		Total	7.3533	.37392	30

		Funaab alpha	Male	7.3308	.52502	13
			Female	7.2882	.54070	17
			Total	7.3067	.52518	30
		Total	Male	7.4515	.44167	33
			Female	7.2368	.49158	57
			Total	7.3156	.48271	90
20	Body_weight	Noiler	Male	1.4564E3	300.20837	16
			Female	1.0888E3	159.86397	14
			Total	1.2849E3	304.75335	30
		Sasso	Male	1.7072E3	330.40136	12
			Female	1.2788E3	230.95537	18
			Total	1.4502E3	343.84149	30
		Funaab alpha	Male	1.5812E3	289.53720	12
			Female	1.2928E3	264.27465	18
			Total	1.4082E3	305.58187	30
		Total	Male	1.5691E3	316.56906	40
			Female	1.2307E3	239.87527	50
			Total	1.3811E3	322.78430	90
	Height_at_withers	Noiler	Male	11.5313	1.12174	16
			Female	9.8500	.92964	14
			Total	10.7467	1.32892	30
		Sasso	Male	11.3500	.49452	12
			Female	10.5944	.68982	18
			Total	10.8967	.71655	30
		Funaab alpha	Male	12.4250	.94207	12
			Female	11.2056	1.21581	18
			Total	11.6933	1.25394	30
		Total	Male	11.7450	1.00612	40
			Female	10.6060	1.09664	50
			Total	11.1122	1.19567	90
	Body length	Noiler	Male	9.3750	.82341	16
			Female	8.3429	.75724	14
			Total	8.8933	.93916	30
		Sasso	Male	9.3583	.69734	12
			Female	8.7444	.90438	18
			Total	8.9900	.87033	30
		Funaab alpha	Male	9.9667	.77264	12
			Female	9.1944	.97527	18
			Total	9.5033	.96543	30
		Total	Male	9.5475	.80224	40
			Female	8.7940	.94013	50
			Total	9.1289	.95414	90
	Breast_girth	Noiler	Male	9.8562	.64288	16
			Female	9.1000	1.12113	14
			Total	9.5033	.96149	30
		Sasso	Male	9.6833	.78490	12
			Female	9.2556	.87260	18
			Total	9.4267	.85175	30

	Funaab alpha	Male	9.6833	.92916	12
		Female	9.4833	.76485	18
		Total	9.5633	.82482	30
	Total	Male	9.7525	.76393	40
		Female	9.2940	.90833	50
		Total	9.4978	.87319	90
Wing length	Noiler	Male	8.2562	.52785	16
		Female	7.5214	.66121	14
		Total	7.9133	.69219	30
	Sasso	Male	7.9000	.25226	12
		Female	7.7889	.37868	18
		Total	7.8333	.33356	30
	Funaab alpha	Male	8.0333	.54495	12
		Female	7.5500	.85285	18
		Total	7.7433	.77267	30
	Total	Male	8.0825	.48192	40
		Female	7.6280	.65809	50
		Total	7.8300	.62593	90

Source : Corrected Model, Dependent Variable : 241614.724^a , DF: 5, Mean Square : 48322.945, F : 5.359, Sig.: .000

APPENDIX 4: Tests of Between-Subjects Effects

Week	Source	Dependent Variable	Type III Sum of Squares	df	Mean Square	F	Sig.
4	Corrected Model	Body_weight	241614.724^a	5	48322.945	5.359	.000
		Height_at_withers	4.018^b	5	.804	1.898	.103
		Body length	4.696^c	5	.939	4.080	.002
		Breast_girth	8.459^d	5	1.692	3.194	.011
		Wing length	8.580^e	5	1.716	7.091	.000
	Intercept	Body_weight	1.604E7	1	1.604E7	1.778E3	.000
		Height_at_withers	3545.587	1	3545.587	8.375E3	.000
		Body length	2086.773	1	2086.773	9.066E3	.000
		Breast_girth	2747.844	1	2747.844	5.188E3	.000
		Wing length	1418.775	1	1418.775	5.862E3	.000
	BREED	Body_weight	32625.835	2	16312.918	1.809	.170
		Height_at_withers	1.851	2	.925	2.186	.119
		Body length	1.430	2	.715	3.106	.050
		Breast_girth	7.567	2	3.783	7.143	.001
		Wing length	7.932	2	3.966	16.387	.000
	SEX	Body_weight	135173.828	1	135173.828	14.991	.000
		Height_at_withers	1.703	1	1.703	4.023	.048
		Body length	2.378	1	2.378	10.332	.002
		Breast_girth	.041	1	.041	.076	.783
		Wing length	.765	1	.765	3.161	.079
	BREED * SEX	Body_weight	65863.360	2	32931.680	3.652	.030
		Height_at_withers	1.352	2	.676	1.596	.209
		Body length	1.281	2	.641	2.783	.068
		Breast_girth	.112	2	.056	.106	.900
		Wing length	1.425	2	.713	2.945	.058

	Error	Body_weight	757425.598	84	9016.971		
		Height_at_withers	35.563	84	.423		
		Body length	19.334	84	.230		
		Breast_girth	44.491	84	.530		
		Wing length	20.329	84	.242		
	Total	Body_weight	1.759E7	90			
		Height_at_withers	3908.670	90			
		Body length	2273.030	90			
		Breast_girth	3081.710	90			
		Wing length	1615.670	90			
	Corrected Total	Body_weight	999040.322	89			
		Height_at_withers	39.581	89			
		Body length	24.030	89			
		Breast_girth	52.950	89			
		Wing length	28.910	89			
8	Corrected Model	Body_weight	857966.275[f]	5	171593.255	6.519	.000
		Height_at_withers	23.857[g]	5	4.771	6.007	.000
		Body length	6.493[h]	5	1.299	1.288	.277
		Breast_girth	15.593[i]	5	3.119	5.025	.000
		Wing length	1.902[j]	5	.380	1.857	.111
	Intercept	Body_weight	4.550E7	1	4.550E7	1.728E3	.000
		Height_at_withers	5899.977	1	5899.977	7.428E3	.000
		Body length	3670.020	1	3670.020	3.640E3	.000
		Breast_girth	4876.717	1	4876.717	7.858E3	.000
		Wing length	3059.728	1	3059.728	1.494E4	.000
	BREED	Body_weight	174527.304	2	87263.652	3.315	.041
		Height_at_withers	3.104	2	1.552	1.954	.148
		Body length	5.383	2	2.691	2.669	.075
		Breast_girth	4.577	2	2.288	3.688	.029
		Wing length	.117	2	.059	.287	.752
	SEX	Body_weight	535734.927	1	535734.927	20.354	.000
		Height_at_withers	15.010	1	15.010	18.898	.000
		Body length	1.108	1	1.108	1.099	.297
		Breast_girth	7.764	1	7.764	12.511	.001
		Wing length	1.084	1	1.084	5.294	.024
	BREED * SEX	Body_weight	152316.012	2	76158.006	2.893	.061
		Height_at_withers	4.114	2	2.057	2.590	.081
		Body length	.664	2	.332	.329	.720
		Breast_girth	5.897	2	2.948	4.751	.011
		Wing length	.756	2	.378	1.844	.164
	Error	Body_weight	2210984.625	84	26321.246		
		Height_at_withers	66.719	84	.794		
		Body length	84.703	84	1.008		

		Breast_girth	52.128	84	.621		
		Wing length	17.207	84	.205		
	Total	Body_weight	4.994E7	90			
		Height_at_withers	6422.510	90			
		Body length	4104.540	90			
		Breast_girth	5298.090	90			
		Wing length	3364.350	90			
	Corrected Total	Body_weight	3068950.900	89			
		Height_at_withers	90.577	89			
		Body length	91.196	89			
		Breast_girth	67.721	89			
		Wing length	19.109	89			
12	Corrected Model	Body_weight	2.125E6[k]	5	425048.766	11.264	.000
		Height_at_withers	52.532[l]	5	10.506	8.454	.000
		Body length	16.356[m]	5	3.271	5.575	.000
		Breast_girth	18.717[n]	5	3.743	6.824	.000
		Wing length	8.997[o]	5	1.799	6.967	.000
	Intercept	Body_weight	7.908E7	1	7.908E7	2.096E3	.000
		Height_at_withers	6952.196	1	6952.196	5.594E3	.000
		Body length	4421.778	1	4421.778	7.536E3	.000
		Breast_girth	5412.660	1	5412.660	9.867E3	.000
		Wing length	3678.197	1	3678.197	1.424E4	.000
	BREED	Body_weight	216113.874	2	108056.937	2.864	.063
		Height_at_withers	12.683	2	6.341	5.103	.008
		Body length	6.035	2	3.017	5.143	.008
		Breast_girth	7.470	2	3.735	6.809	.002
		Wing length	6.248	2	3.124	12.095	.000
	SEX	Body_weight	1452594.341	1	1452594.341	38.494	.000
		Height_at_withers	27.928	1	27.928	22.473	.000
		Body length	8.369	1	8.369	14.264	.000
		Breast_girth	8.572	1	8.572	15.626	.000
		Wing length	2.088	1	2.088	8.085	.006
	BREED * SEX	Body_weight	343797.626	2	171898.813	4.555	.013
		Height_at_withers	16.467	2	8.234	6.626	.002
		Body length	4.956	2	2.478	4.223	.018
		Breast_girth	6.210	2	3.105	5.660	.005
		Wing length	1.917	2	.958	3.710	.029
	Error	Body_weight	3169760.569	84	37735.245		
		Height_at_withers	104.388	84	1.243		
		Body length	49.288	84	.587		
		Breast_girth	46.079	84	.549		
		Wing length	21.696	84	.258		
	Total	Body_weight	8.519E7	90			

		Height_at_withers	7515.480	90			
		Body length	4800.620	90			
		Breast_girth	5863.260	90			
		Wing length	4024.030	90			
	Corrected Total	Body_weight	5295004.400	89			
		Height_at_withers	156.920	89			
		Body length	65.644	89			
		Breast_girth	64.796	89			
		Wing length	30.694	89			
16	Corrected Model	Body_weight	1.784E6[p]	5	356821.536	5.846	.000
		Height_at_withers	31.996[q]	5	6.399	5.403	.000
		Body length	14.338[r]	5	2.868	3.899	.003
		Breast_girth	6.424[s]	5	1.285	1.832	.115
		Wing length	2.927[t]	5	.585	2.761	.023
	Intercept	Body_weight	1.029E8	1	1.029E8	1.686E3	.000
		Height_at_withers	8724.118	1	8724.118	7.366E3	.000
		Body length	5790.665	1	5790.665	7.873E3	.000
		Breast_girth	6319.169	1	6319.169	9.012E3	.000
		Wing length	4431.532	1	4431.532	2.090E4	.000
	BREED	Body_weight	260236.447	2	130118.224	2.132	.125
		Height_at_withers	2.549	2	1.274	1.076	.346
		Body length	1.635	2	.817	1.111	.334
		Breast_girth	.296	2	.148	.211	.810
		Wing length	.057	2	.028	.133	.875
	SEX	Body_weight	1283876.811	1	1283876.811	21.036	.000
		Height_at_withers	21.068	1	21.068	17.788	.000
		Body length	8.614	1	8.614	11.712	.001
		Breast_girth	3.443	1	3.443	4.911	.029
		Wing length	.971	1	.971	4.580	.035
	BREED * SEX	Body_weight	216942.057	2	108471.029	1.777	.175
		Height_at_withers	5.176	2	2.588	2.185	.119
		Body length	2.751	2	1.375	1.870	.160
		Breast_girth	2.510	2	1.255	1.790	.173
		Wing length	1.840	2	.920	4.339	.016
	Error	Body_weight	5126826.777	84	61033.652		
		Height_at_withers	99.484	84	1.184		
		Body length	61.780	84	.735		
		Breast_girth	58.897	84	.701		
		Wing length	17.811	84	.212		
	Total	Body_weight	1.123E8	90			
		Height_at_withers	9433.980	90			
		Body length	6269.580	90			
		Breast_girth	6893.090	90			

		Wing length	4837.300	90			
	Corrected Total	Body_weight	6910934.456	89			
		Height_at_withers	131.480	89			
		Body length	76.118	89			
		Breast_girth	65.321	89			
		Wing length	20.738	89			
20	Corrected Model	Body_weight	3.372E6[u]	5	674344.594	9.599	.000
		Height_at_withers	51.456[v]	5	10.291	11.407	.000
		Body length	21.411[w]	5	4.282	6.034	.000
		Breast_girth	6.157[x]	5	1.231	1.677	.149
		Wing length	6.237[y]	5	1.247	3.659	.005
	Intercept	Body_weight	1.716E8	1	1.716E8	2.443E3	.000
		Height_at_withers	10889.168	1	10889.168	1.207E4	.000
		Body length	7342.594	1	7342.594	1.035E4	.000
		Breast_girth	7908.670	1	7908.670	1.077E4	.000
		Wing length	5376.874	1	5376.874	1.577E4	.000
	BREED	Body_weight	773146.694	2	386573.347	5.503	.006
		Height_at_withers	19.958	2	9.979	11.062	.000
		Body length	8.141	2	4.070	5.735	.005
		Breast_girth	.233	2	.116	.158	.854
		Wing length	.139	2	.069	.203	.816
	SEX	Body_weight	2855789.104	1	2855789.104	40.651	.000
		Height_at_withers	32.470	1	32.470	35.992	.000
		Body length	14.204	1	14.204	20.015	.000
		Breast_girth	4.653	1	4.653	6.334	.014
		Wing length	4.292	1	4.292	12.591	.001
	BREED * SEX	Body_weight	70986.967	2	35493.483	.505	.605
		Height_at_withers	3.141	2	1.571	1.741	.182
		Body length	.656	2	.328	.462	.632
		Breast_girth	1.149	2	.574	.782	.461
		Wing length	1.440	2	.720	2.113	.127
	Error	Body_weight	5901160.628	84	70251.912		
		Height_at_withers	75.781	84	.902		
		Body length	59.614	84	.710		
		Breast_girth	61.702	84	.735		
		Wing length	28.632	84	.341		
	Total	Body_weight	1.809E8	90			
		Height_at_withers	11240.570	90			
		Body length	7581.320	90			
		Breast_girth	8186.560	90			
		Wing length	5552.670	90			
	Corrected Total	Body_weight	9272883.600	89			
		Height_at_withers	127.237	89			

	Body length	81.025	89			
	Breast_girth	67.860	89			
	Wing length	34.869	89			

a. R Squared = .242 (Adjusted R Squared = .197)

b. R Squared = .102 (Adjusted R Squared = .048)

c. R Squared = .195 (Adjusted R Squared = .148)

d. R Squared = .160 (Adjusted R Squared = .110)

e. R Squared = .297 (Adjusted R Squared = .255)

f. R Squared = .280 (Adjusted R Squared = .237)

g. R Squared = .263 (Adjusted R Squared = .220)

h. R Squared = .071 (Adjusted R Squared = .016)

i. R Squared = .230 (Adjusted R Squared = .184)

j. R Squared = .100 (Adjusted R Squared = .046)

k. R Squared = .401 (Adjusted R Squared = .366)

l. R Squared = .335 (Adjusted R Squared = .295)

m. R Squared = .249 (Adjusted R Squared = .204)

n. R Squared = .289 (Adjusted R Squared = .247)

o. R Squared = .293 (Adjusted R Squared = .251)

p. R Squared = .258 (Adjusted R Squared = .214)

q. R Squared = .243 (Adjusted R Squared = .198)

r. R Squared = .188 (Adjusted R Squared = .140)

s. R Squared = .098 (Adjusted R Squared = .045)

t. R Squared = .141 (Adjusted R Squared = .090)

u. R Squared = .364 (Adjusted R Squared = .326)

v. R Squared = .404 (Adjusted R Squared = .369)

w. R Squared = .264 (Adjusted R Squared = .220)

x. R Squared = .091 (Adjusted R Squared = .037)

y. R Squared = .179 (Adjusted R Squared = .130)

APPENDIX 5

Estimated Marginal Means

1. Grand Mean

				95% Confidence Interval	
Week	Dependent Variable	Mean	Std. Error	Lower Bound	Upper Bound
4	Body_weight	443.751	±10.523	422.826	464.676
	Height_at_withers	6.598	.072	6.455	6.742
	Body length	5.062	±.053	4.956	5.168
	Breast_girth	5.809	.081	5.648	5.969
	Wing length	4.174	.055	4.066	4.282
8	Body_weight	747.941	17.990	712.166	783.717

	Height_at_withers	8.517	.099	8.321	8.714
	Body length	6.718	.111	6.496	6.939
	Breast_girth	7.744	.087	7.570	7.917
	Wing length	6.134	.050	6.034	6.234
12	Body_weight	985.400	21.526	942.593	1028.207
	Height_at_withers	9.240	.124	8.994	9.485
	Body length	7.369	.085	7.200	7.537
	Breast_girth	8.153	.082	7.989	8.316
	Wing length	6.721	.056	6.609	6.833
16	Body_weight	1.119E3	27.251	1064.774	1173.157
	Height_at_withers	10.303	.120	10.064	10.542
	Body length	8.394	.095	8.206	8.582
	Breast_girth	8.768	.092	8.585	8.952
	Wing length	7.343	.051	7.242	7.444
20	Body_weight	1.401E3	28.345	1344.504	1457.237
	Height_at_withers	11.159	.102	10.957	11.361
	Body length	9.164	.090	8.984	9.343
	Breast_girth	9.510	.092	9.328	9.693
	Wing length	7.842	.062	7.717	7.966

APPENDIX 6

2. BREED

					95% Confidence Interval	
Week	Dependent Variable	BREED	Mean	Std. Error	Lower Bound	Upper Bound
4	Body_weight	Noiler	418.450	18.388	381.882	455.018
		Sasso	468.603	18.916	430.987	506.220
		Funaab alpha	444.200	17.337	409.724	478.676
	Height_at_withers	Noiler	6.812	.126	6.562	7.063
		Sasso	6.483	.130	6.225	6.740
		Funaab alpha	6.500	.119	6.264	6.736
	Body length	Noiler	5.238	.093	5.053	5.422
		Sasso	5.025	.096	4.835	5.215
		Funaab alpha	4.923	.088	4.749	5.098
	Breast_girth	Noiler	6.005	.141	5.725	6.285
		Sasso	5.371	.145	5.083	5.660
		Funaab alpha	6.050	.133	5.786	6.314
	Wing length	Noiler	4.542	.095	4.353	4.732
		Sasso	3.763	.098	3.568	3.958
		Funaab alpha	4.217	.090	4.038	4.395
8	Body_weight	Noiler	713.150	31.417	650.673	775.627
		Sasso	814.683	32.319	750.413	878.952
		Funaab alpha	715.991	29.687	656.956	775.026
	Height_at_withers	Noiler	8.338	.173	7.994	8.681

		Sasso	8.796	.178	8.443	9.149
		Funaab alpha	8.419	.163	8.094	8.743
	Body length	Noiler	6.398	.194	6.011	6.784
		Sasso	7.042	.200	6.644	7.440
		Funaab alpha	6.713	.184	6.348	7.079
	Breast_girth	Noiler	7.602	.153	7.299	7.906
		Sasso	8.083	.157	7.770	8.395
		Funaab alpha	7.546	.144	7.259	7.833
	Wing length	Noiler	6.150	.088	5.976	6.324
		Sasso	6.169	.090	5.990	6.348
		Funaab alpha	6.082	.083	5.917	6.247
12	Body_weight	Noiler	912.975	37.617	838.169	987.781
		Sasso	1.034E3	38.697	956.738	1110.643
		Funaab alpha	1.010E3	35.466	939.005	1080.061
	Height_at_withers	Noiler	9.260	.216	8.831	9.689
		Sasso	9.709	.222	9.267	10.150
		Funaab alpha	8.750	.204	8.345	9.155
	Body length	Noiler	7.430	.148	7.135	7.725
		Sasso	7.663	.153	7.359	7.966
		Funaab alpha	7.013	.140	6.735	7.291
	Breast_girth	Noiler	8.068	.143	7.782	8.353
		Sasso	8.560	.148	8.267	8.854
		Funaab alpha	7.830	.135	7.561	8.099
	Wing length	Noiler	6.815	.098	6.619	7.011
		Sasso	6.997	.101	6.795	7.198
		Funaab alpha	6.350	.093	6.165	6.535
16	Body_weight	Noiler	1.046E3	46.800	952.542	1138.674
		Sasso	1.185E3	49.214	1086.832	1282.565
		Funaab alpha	1.127E3	45.511	1036.086	1217.095
	Height_at_withers	Noiler	10.069	.206	9.659	10.479
		Sasso	10.357	.217	9.926	10.788
		Funaab alpha	10.482	.200	10.084	10.881
	Body length	Noiler	8.213	.162	7.890	8.536
		Sasso	8.420	.171	8.080	8.760
		Funaab alpha	8.549	.158	8.234	8.863
	Breast_girth	Noiler	8.811	.159	8.496	9.127
		Sasso	8.682	.167	8.350	9.013
		Funaab alpha	8.812	.154	8.505	9.119
	Wing length	Noiler	7.372	.087	7.198	7.545
		Sasso	7.348	.092	7.165	7.530
		Funaab alpha	7.310	.085	7.141	7.478
20	Body_weight	Noiler	1.273E3	48.499	1176.165	1369.058
		Sasso	1.493E3	49.389	1394.784	1591.216
		Funaab alpha	1.437E3	49.389	1338.784	1535.216
	Height_at_withers	Noiler	10.691	.174	10.345	11.036
		Sasso	10.972	.177	10.620	11.324
		Funaab alpha	11.815	.177	11.463	12.167
	Body length	Noiler	8.859	.154	8.552	9.165

		Sasso	9.051	.157	8.739	9.364
		Funaab alpha	9.581	.157	9.268	9.893
	Breast_girth	Noiler	9.478	.157	9.166	9.790
		Sasso	9.469	.160	9.152	9.787
		Funaab alpha	9.583	.160	9.266	9.901
	Wing length	Noiler	7.889	.107	7.676	8.101
		Sasso	7.844	.109	7.628	8.061
		Funaab alpha	7.792	.109	7.575	8.008

3. SEX

					95% Confidence Interval	
Week	Dependent Variable	SEX	Mean	Std. Error	Lower Bound	Upper Bound
4	Body_weight	Male	484.493	16.682	451.318	517.667
		Female	403.010	12.829	377.497	428.522
	Height_at_withers	Male	6.743	.114	6.516	6.970
		Female	6.454	.088	6.279	6.629
	Body length	Male	5.233	.084	5.065	5.401
		Female	4.891	.065	4.762	5.020
	Breast_girth	Male	5.831	.128	5.577	6.085
		Female	5.787	.098	5.591	5.982
	Wing length	Male	4.077	.086	3.905	4.249
		Female	4.271	.066	4.139	4.403
8	Body_weight	Male	829.104	28.746	771.940	886.268
		Female	666.778	21.640	623.745	709.811
	Height_at_withers	Male	8.947	.158	8.633	9.261
		Female	8.088	.119	7.851	8.324
	Body length	Male	6.834	.178	6.481	7.188
		Female	6.601	.134	6.335	6.867
	Breast_girth	Male	8.053	.140	7.775	8.330
		Female	7.435	.105	7.226	7.644
	Wing length	Male	6.249	.080	6.090	6.409
		Female	6.018	.060	5.898	6.138
12	Body_weight	Male	1.119E3	34.127	1051.090	1186.821
		Female	851.844	26.245	799.652	904.035
	Height_at_withers	Male	9.825	.196	9.436	10.215
		Female	8.654	.151	8.354	8.953
	Body length	Male	7.689	.135	7.422	7.957
		Female	7.048	.103	6.842	7.254
	Breast_girth	Male	8.477	.130	8.218	8.736
		Female	7.828	.100	7.629	8.027
	Wing length	Male	6.881	.089	6.703	7.058
		Female	6.560	.069	6.424	6.697
16	Body_weight	Male	1.244E3	43.493	1157.459	1330.441

		Female	993.981	32.845	928.666	1059.296
	Height_at_withers	Male	10.809	.192	10.428	11.190
		Female	9.797	.145	9.509	10.084
	Body length	Male	8.718	.151	8.417	9.018
		Female	8.070	.114	7.843	8.297
	Breast_girth	Male	8.973	.147	8.680	9.266
		Female	8.564	.111	8.342	8.785
	Wing length	Male	7.452	.081	7.290	7.613
		Female	7.234	.061	7.113	7.356
20	Body_weight	Male	1.582E3	42.294	1497.483	1665.697
		Female	1.220E3	37.747	1145.086	1295.216
	Height_at_withers	Male	11.769	.152	11.467	12.070
		Female	10.550	.135	10.281	10.819
	Body length	Male	9.567	.134	9.299	9.834
		Female	8.761	.120	8.522	8.999
	Breast_girth	Male	9.741	.137	9.469	10.013
		Female	9.280	.122	9.037	9.522
	Wing length	Male	8.063	.093	7.878	8.248
		Female	7.620	.083	7.455	7.785

4. BREED * SEX

Week	Dependent Variable	BREED	SEX	Mean	Std. Error	95% Confidence Interval	
						Lower Bound	Upper Bound
4	Body_weight	Noiler	Male	486.700	30.028	426.985	546.415
			Female	350.200	21.233	307.975	392.425
		Sasso	Male	519.778	31.653	456.833	582.722
			Female	417.429	20.721	376.222	458.636
		Funaab alpha	Male	447.000	24.518	398.243	495.757
			Female	441.400	24.518	392.643	490.157
	Height_at_withers	Noiler	Male	7.140	.206	6.731	7.549
			Female	6.485	.145	6.196	6.774
		Sasso	Male	6.522	.217	6.091	6.954
			Female	6.443	.142	6.160	6.725
		Funaab alpha	Male	6.567	.168	6.233	6.901
			Female	6.433	.168	6.099	6.767
	Body length	Noiler	Male	5.450	.152	5.148	5.752
			Female	5.025	.107	4.812	5.238
		Sasso	Male	5.322	.160	5.004	5.640
			Female	4.729	.105	4.520	4.937
		Funaab alpha	Male	4.927	.124	4.680	5.173
			Female	4.920	.124	4.674	5.166
	Breast_girth	Noiler	Male	6.080	.230	5.622	6.538
			Female	5.930	.163	5.606	6.254
		Sasso	Male	5.367	.243	4.884	5.849
			Female	5.376	.159	5.060	5.692
		Funaab alpha	Male	6.047	.188	5.673	6.420
			Female	6.053	.188	5.680	6.427
	Wing length	Noiler	Male	4.620	.156	4.311	4.929
			Female	4.465	.110	4.246	4.684
		Sasso	Male	3.511	.164	3.185	3.837
			Female	4.014	.107	3.801	4.228
		Funaab alpha	Male	4.100	.127	3.847	4.353
			Female	4.333	.127	4.081	4.586
8	Body_weight	Noiler	Male	845.900	51.304	743.876	947.924
			Female	580.400	36.278	508.258	652.542
		Sasso	Male	896.556	54.079	789.013	1004.098
			Female	732.810	35.403	662.406	803.213
		Funaab alpha	Male	744.857	43.360	658.631	831.083
			Female	687.125	40.560	606.468	767.782
	Height_at_withers	Noiler	Male	9.080	.282	8.520	9.640
			Female	7.595	.199	7.199	7.991
		Sasso	Male	9.111	.297	8.520	9.702
			Female	8.481	.194	8.094	8.868
		Funaab alpha	Male	8.650	.238	8.176	9.124
			Female	8.188	.223	7.744	8.631

	Body length	Noiler	Male	6.450	.318	5.819	7.081
			Female	6.345	.225	5.898	6.792
		Sasso	Male	7.289	.335	6.623	7.955
			Female	6.795	.219	6.359	7.231
		Funaab alpha	Male	6.764	.268	6.231	7.298
			Female	6.662	.251	6.163	7.162
	Breast_girth	Noiler	Male	8.050	.249	7.555	8.545
			Female	7.155	.176	6.805	7.505
		Sasso	Male	8.622	.263	8.100	9.144
			Female	7.543	.172	7.201	7.885
		Funaab alpha	Male	7.486	.211	7.067	7.904
			Female	7.606	.197	7.215	7.998
	Wing length	Noiler	Male	6.400	.143	6.115	6.685
			Female	5.900	.101	5.699	6.101
		Sasso	Male	6.233	.151	5.933	6.533
			Female	6.105	.099	5.908	6.301
		Funaab alpha	Male	6.114	.121	5.874	6.355
			Female	6.050	.113	5.825	6.275
12	Body_weight	Noiler	Male	1.103E3	61.429	980.442	1224.758
			Female	723.350	43.437	636.971	809.729
		Sasso	Male	1.200E3	64.752	1070.900	1328.433
			Female	867.714	42.390	783.417	952.012
		Funaab alpha	Male	1.055E3	50.157	954.858	1154.342
			Female	964.467	50.157	864.725	1064.209
	Height_at_withers	Noiler	Male	10.420	.353	9.719	11.121
			Female	8.100	.249	7.604	8.596
		Sasso	Male	10.222	.372	9.483	10.961
			Female	9.195	.243	8.711	9.679
		Funaab alpha	Male	8.833	.288	8.261	9.406
			Female	8.667	.288	8.094	9.239
	Body length	Noiler	Male	8.010	.242	7.528	8.492
			Female	6.850	.171	6.509	7.191
		Sasso	Male	8.044	.255	7.537	8.552
			Female	7.281	.167	6.949	7.613
		Funaab alpha	Male	7.013	.198	6.620	7.407
			Female	7.013	.198	6.620	7.407
	Breast_girth	Noiler	Male	8.580	.234	8.114	9.046
			Female	7.555	.166	7.226	7.884
		Sasso	Male	9.078	.247	8.587	9.569
			Female	8.043	.162	7.721	8.364
		Funaab alpha	Male	7.773	.191	7.393	8.154
			Female	7.887	.191	7.506	8.267
	Wing length	Noiler	Male	7.160	.161	6.840	7.480
			Female	6.470	.114	6.244	6.696
		Sasso	Male	7.156	.169	6.819	7.492
			Female	6.838	.111	6.618	7.059
		Funaab alpha	Male	6.327	.131	6.066	6.588
			Female	6.373	.131	6.112	6.634

16	Body_weight	Noiler	Male	1.223E3	74.488	1074.508	1370.765
			Female	868.579	56.677	755.870	981.288
		Sasso	Male	1.325E3	82.350	1161.683	1489.206
			Female	1.044E3	53.911	936.745	1151.160
		Funaab alpha	Male	1.184E3	68.519	1047.511	1320.027
			Female	1.069E3	59.918	950.257	1188.566
	Height_at_withers	Noiler	Male	10.927	.328	10.275	11.580
			Female	9.211	.250	8.714	9.707
		Sasso	Male	10.700	.363	9.979	11.421
			Female	10.014	.237	9.542	10.487
		Funaab alpha	Male	10.800	.302	10.200	11.400
			Female	10.165	.264	9.640	10.690
	Body length	Noiler	Male	8.736	.259	8.222	9.251
			Female	7.689	.197	7.298	8.081
		Sasso	Male	8.778	.286	8.209	9.346
			Female	8.062	.187	7.690	8.434
		Funaab alpha	Male	8.638	.238	8.165	9.111
			Female	8.459	.208	8.045	8.872
	Breast_girth	Noiler	Male	9.255	.252	8.752	9.757
			Female	8.368	.192	7.986	8.750
		Sasso	Male	8.811	.279	8.256	9.366
			Female	8.552	.183	8.189	8.916
		Funaab alpha	Male	8.854	.232	8.392	9.316
			Female	8.771	.203	8.367	9.174
	Wing length	Noiler	Male	7.691	.139	7.415	7.967
			Female	7.053	.106	6.843	7.263
		Sasso	Male	7.333	.153	7.028	7.639
			Female	7.362	.100	7.162	7.562
		Funaab alpha	Male	7.331	.128	7.077	7.585
			Female	7.288	.112	7.066	7.510
20	Body_weight	Noiler	Male	1.456E3	66.263	1324.667	1588.208
			Female	1.089E3	70.838	947.917	1229.654
		Sasso	Male	1.707E3	76.514	1555.011	1859.322
			Female	1.279E3	62.473	1154.599	1403.068
		Funaab alpha	Male	1.581E3	76.514	1429.011	1733.322
			Female	1.293E3	62.473	1168.599	1417.068
	Height_at_withers	Noiler	Male	11.531	.237	11.059	12.003
			Female	9.850	.254	9.345	10.355
		Sasso	Male	11.350	.274	10.805	11.895
			Female	10.594	.224	10.149	11.040
		Funaab alpha	Male	12.425	.274	11.880	12.970
			Female	11.206	.224	10.760	11.651
	Body length	Noiler	Male	9.375	.211	8.956	9.794
			Female	8.343	.225	7.895	8.791
		Sasso	Male	9.358	.243	8.875	9.842
			Female	8.744	.199	8.350	9.139
		Funaab alpha	Male	9.967	.243	9.483	10.450
			Female	9.194	.199	8.800	9.589

	Breast_girth	Noiler	Male	9.856	.214	9.430	10.282
			Female	9.100	.229	8.644	9.556
		Sasso	Male	9.683	.247	9.191	10.175
			Female	9.256	.202	8.854	9.657
		Funaab alpha	Male	9.683	.247	9.191	10.175
			Female	9.483	.202	9.082	9.885
	Wing length	Noiler	Male	8.256	.146	7.966	8.547
			Female	7.521	.156	7.211	7.832
		Sasso	Male	7.900	.169	7.565	8.235
			Female	7.789	.138	7.515	8.063
		Funaab alpha	Male	8.033	.169	7.698	8.368
			Female	7.550	.138	7.276	7.824

Post Hoc Tests

BREED

Homogeneous Subsets

Body_weight

Week=4

Duncan

		Subset	
BREED	N	1	2
Noiler	30	3.9570E2	
Funaab alpha	30	4.4420E2	4.4420E2
Sasso	30		4.4813E2
Sig.		.051	.873

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = 9016.971.

Week=8

Duncan

		Subset	
BREED	N	1	2
Noiler	30	6.6890E2	
Funaab alpha	30	7.1407E2	7.1407E2
Sasso	30		7.8193E2
Sig.		.284	.109

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = 26321.246.

Week=12

Duncan

BREED	N	Subset	
		1	2
Noiler	30	8.4977E2	
Sasso	30		9.6730E2
Funaab alpha	30		1.0095E3
Sig.		1.000	.402

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = 37735.245.

Week=16

Duncan

BREED	N	Subset
		1
Noiler	30	9.9840E2
Funaab alpha	30	1.1190E3
Sasso	30	1.1284E3
Sig.		.056

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = 61033.652.

Week=20

Duncan

BREED	N	Subset	
		1	2
Noiler	30	1.2849E3	
Funaab alpha	30	1.4082E3	1.4082E3
Sasso	30		1.4502E3
Sig.		.075	.541

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = 70251.912.

Height_at_withers

Week=4

Duncan

BREED	N	Subset
		1

Sasso	30	6.4667
Funaab alpha	30	6.5000
Noiler	30	6.7033
Sig.		.188

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .423.

Week=8

Duncan

BREED	N	Subset	
		1	2
Noiler	30	8.0900	
Funaab alpha	30	8.4033	8.4033
Sasso	30		8.6700
Sig.		.177	.250

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .794.

Week=12

Duncan

BREED	N	Subset	
		1	2
Funaab alpha	30	8.7500	
Noiler	30	8.8733	
Sasso	30		9.5033
Sig.		.669	1.000

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = 1.243.

Week=16

Duncan

BREED	N	Subset	
		1	2
Noiler	30	9.8400	
Sasso	30	10.2200	10.2200
Funaab alpha	30		10.4400
Sig.		.180	.436

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = 1.184.

Week=20

Duncan

BREED	N	Subset	
		1	2
Noiler	30	10.7467	
Sasso	30	10.8967	
Funaab alpha	30		11.6933
Sig.		.542	1.000

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .902.

Body length

Week=4

Duncan

BREED	N	Subset	
		1	2
Sasso	30	4.9067	
Funaab alpha	30	4.9233	4.9233
Noiler	30		5.1667
Sig.		.893	.053

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .230.

Week=8

Duncan

BREED	N	Subset	
		1	2
Noiler	30	6.3800	
Funaab alpha	30	6.7100	6.7100
Sasso	30		6.9433
Sig.		.207	.371

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = 1.008.

Week=12

Duncan

BREED	N	Subset	
		1	2
Funaab alpha	30	7.0133	

Noiler	30	7.2367	7.2367
Sasso	30		7.5100
Sig.		.262	.171

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .587.

Week=16

Duncan

BREED	N	Subset
		1
Noiler	30	8.0733
Sasso	30	8.2767
Funaab alpha	30	8.5367
Sig.		.050

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .735.

Week=20

Duncan

BREED	N	Subset	
		1	2
Noiler	30	8.8933	
Sasso	30	8.9900	
Funaab alpha	30		9.5033
Sig.		.658	1.000

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .710.

Breast_girth

Week=4

Duncan

BREED	N	Subset	
		1	2
Sasso	30	5.3733	
Noiler	30		5.9800
Funaab alpha	30		6.0500
Sig.		1.000	.710

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .530.

Week=8

Duncan

BREED	N	Subset
		1
Noiler	30	7.4533
Funaab alpha	30	7.5500
Sasso	30	7.8667
Sig.		.057

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .621.

Week=12

Duncan

BREED	N	Subset	
		1	2
Funaab alpha	30	7.8300	
Noiler	30	7.8967	
Sasso	30		8.3533
Sig.		.728	1.000

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .549.

Week=16

Duncan

BREED	N	Subset
		1
Sasso	30	8.6300
Noiler	30	8.6933
Funaab alpha	30	8.8067
Sig.		.446

Week=16

Duncan

BREED	N	Subset
		1
Sasso	30	8.6300
Noiler	30	8.6933
Funaab alpha	30	8.8067
Sig.		.446

Means for groups in homogeneous subsets are displayed.

Based on observed means.

The error term is Mean Square(Error) = .701.

Week=20

Duncan

BREED	N	Subset
		1
Sasso	30	9.4267
Noiler	30	9.5033
Funaab alpha	30	9.5633
Sig.		.565

Means for groups in homogeneous subsets are displayed.

Based on observed means.

The error term is Mean Square(Error) = .735.

Wing length

Week=4

Duncan

BREED	N	Subset		
		1	2	3
Sasso	30	3.8633		
Funaab alpha	30		4.2167	
Noiler	30			4.5167
Sig.		1.000	1.000	1.000

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .242.

Week=8

Duncan

BREED	N	Subset
		1
Noiler	30	6.0667
Funaab alpha	30	6.0800
Sasso	30	6.1433
Sig.		.541

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .205.

Week=12

Duncan

BREED	N	Subset	
		1	2
Funaab alpha	30	6.3500	
Noiler	30		6.7000
Sasso	30		6.9333
Sig.		1.000	.079

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .258.

Week=16

Duncan

BREED	N	Subset
		1
Noiler	30	7.2867
Funaab alpha	30	7.3067

Sasso	30	7.3533
Sig.		.602

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .212.

Week=20

Duncan

		Subset
BREED	N	1
Funaab alpha	30	7.7433
Sasso	30	7.8333
Noiler	30	7.9133
Sig.		.293

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .341.

APPENDIX 6
General Linear Model

Warnings

Post hoc tests are not performed for SNP1_A_C because at least one group has fewer than two cases.

Between-Subjects Factors

		Value Label	N
SNP1_A_C	1	AA	8
	2	CA	7
	3	CC	1
BREED	1	Noiler	5
	2	Sasso	6
	3	Funaab Alpha	5

APPENDIX 7

Tests of Between-Subjects Effects

Source	Dependent Variable	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	Body_weight	727836.283[a]	5	145567.257	4.203	.026
	Height_at_withers	14.828[b]	5	2.966	3.048	.063
	Body length	6.179[c]	5	1.236	2.814	.077
	Breast_girth	7.406[d]	5	1.481	2.800	.078
	Wing length	2.298[e]	5	.460	1.824	.196

Intercept	Body_weight	2.264E7	1	2.264E7	653.717	.000
	Height_at_withers	1194.018	1	1194.018	1.227E3	.000
	Body length	771.426	1	771.426	1.757E3	.000
	Breast_girth	908.014	1	908.014	1.716E3	.000
	Wing length	567.111	1	567.111	2.251E3	.000
SNP1_A_C	Body_weight	484732.087	2	242366.043	6.998	.013
	Height_at_withers	6.982	2	3.491	3.587	.067
	Body length	3.947	2	1.973	4.494	.041
	Breast_girth	4.799	2	2.399	4.535	.040
	Wing length	2.070	2	1.035	4.107	.050
BREED	Body_weight	256910.357	2	128455.179	3.709	.062
	Height_at_withers	9.905	2	4.953	5.090	.030
	Body length	5.596	2	2.798	6.372	.016
	Breast_girth	1.562	2	.781	1.476	.274
	Wing length	.964	2	.482	1.914	.198
SNP1_A_C * BREED	Body_weight	80819.253	1	80819.253	2.334	.158
	Height_at_withers	.032	1	.032	.033	.860
	Body length	.521	1	.521	1.186	.302
	Breast_girth	.141	1	.141	.266	.617
	Wing length	.007	1	.007	.030	.866
Error	Body_weight	346333.467	10	34633.347		
	Height_at_withers	9.731	10	.973		
	Body length	4.391	10	.439		
	Breast_girth	5.291	10	.529		
	Wing length	2.519	10	.252		
Total	Body_weight	3.661E7	16			
	Height_at_withers	2047.310	16			
	Body length	1342.820	16			
	Breast_girth	1592.760	16			
	Wing length	1012.880	16			
Corrected Total	Body_weight	1074169.750	15			
	Height_at_withers	24.559	15			
	Body length	10.570	15			
	Breast_girth	12.697	15			
	Wing length	4.818	15			

a. R Squared = .678 (Adjusted R Squared = .516)

b. R Squared = .604 (Adjusted R Squared = .406)

c. R Squared = .585 (Adjusted R Squared = .377)

d. R Squared = .583 (Adjusted R Squared = .375)

e. R Squared = .477 (Adjusted R Squared = .216)

APPENDIX 8.1

1. Grand Mean

Dependent Variable	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
Body_weight	1.594E3[a]	56.202	1468.529	1718.982
Height_at_withers	11.625[a]	.298	10.961	12.289
Body length	9.409[a]	.200	8.963	9.855
Breast_girth	10.192[a]	.220	9.702	10.681
Wing length	8.078[a]	.152	7.740	8.415

a. Based on modified population marginal mean.

APPENDIX 8.2

2. SNP1_A_C

Dependent Variable	SNP1_A_C	Mean	Std. Error	95% Confidence Interval	
				Lower Bound	Upper Bound
Body_weight	AA	1.687E3	80.882	1506.851	1867.282
	CA	1.304E3[a]	71.068	1145.317	1462.017
	CC	1.894E3[a]	186.100	1479.343	2308.657
Height_at_withers	AA	11.937	.429	10.981	12.892
	CA	10.821[a]	.377	9.981	11.660
	CC	12.300[a]	.986	10.102	14.498
Body length	AA	9.803	.288	9.162	10.445
	CA	8.871[a]	.253	8.307	9.435
	CC	9.300[a]	.663	7.824	10.776
Breast_girth	AA	10.637	.316	9.932	11.341
	CA	9.321[a]	.278	8.702	9.940
	CC	10.600[a]	.727	8.979	12.221
Wing length	AA	8.413	.218	7.927	8.899
	CA	7.612[a]	.192	7.185	8.040
	CC	8.000[a]	.502	6.882	9.118

a. Based on modified population marginal mean.

APPENDIX 8.3

3. BREED

Dependent Variable	BREED	Mean	Std. Error	95% Confidence Interval	
				Lower Bound	Upper Bound
Body_weight	Noiler	1.355E3[a]	84.943	1165.402	1543.931
	Sasso	1.724E3[a]	101.931	1496.983	1951.217
	Funaab Alpha	1.702E3[a]	104.033	1470.699	1934.301
Height_at_withers	Noiler	10.658[a]	.450	9.655	11.662
	Sasso	11.580[a]	.540	10.376	12.784
	Funaab Alpha	12.638[a]	.551	11.409	13.866
Body length	Noiler	8.908[a]	.302	8.234	9.582
	Sasso	9.080[a]	.363	8.271	9.889
	Funaab Alpha	10.237[a]	.370	9.412	11.063

Breast_girth	Noiler	10.308[a]	.332	9.569	11.048
	Sasso	10.380[a]	.398	9.492	11.268
	Funaab Alpha	9.888[a]	.407	8.981	10.794
Wing length	Noiler	7.950[a]	.229	7.440	8.460
	Sasso	7.970[a]	.275	7.357	8.583
	Funaab Alpha	8.313[a]	.281	7.687	8.938

a. Based on modified population marginal mean.

APPENDIX 2. SNP1_A_C

Dependent Variable	SNP1_A_C	Mean	Std. Error	95% Confidence Interval	
				Lower Bound	Upper Bound
Body_weight	AA	1.509E3	80.729	1331.066	1686.434
	CA	1.318E3	82.723	1135.878	1500.022
	CC	1.894E3[a]	197.746	1458.764	2329.236
Height_at_withers	AA	10.800	.341	10.049	11.551
	CA	11.475	.350	10.705	12.245
	CC	12.300[a]	.836	10.460	14.140
Body length	AA	8.917	.314	8.225	9.608
	CA	9.055	.322	8.347	9.763
	CC	9.300[a]	.769	7.607	10.993
Breast_girth	AA	10.358	.290	9.720	10.996
	CA	9.055	.297	8.401	9.709
	CC	10.600[a]	.710	9.037	12.163
Wing length	AA	8.025	.213	7.556	8.494
	CA	7.690	.219	7.209	8.171
	CC	8.000[a]	.522	6.850	9.150

a. Based on modified population marginal mean.

APPENDIX 8.4. SEX

Dependent Variable	SEX	Mean	Std. Error	95% Confidence Interval	
				Lower Bound	Upper Bound
Body_weight	Male	1.634E3	85.096	1446.538	1821.129
	Female	1.323E3[a]	82.723	1140.878	1505.022
Height_at_withers	Male	12.283	.360	11.492	13.075
	Female	10.000[a]	.350	9.230	10.770
Body length	Male	9.428	.331	8.699	10.156
	Female	8.480[a]	.322	7.772	9.188
Breast_girth	Male	9.889	.306	9.216	10.561
	Female	9.880[a]	.297	9.226	10.534
Wing length	Male	8.050	.225	7.555	8.545
	Female	7.640[a]	.219	7.159	8.121

a. Based on modified population marginal mean.

APPENDIX 8.5

4. SNP1_A_C * BREED

Dependent Variable	SNP1_A_C BREED	Mean	Std. Error	95% Confidence Interval

					Lower Bound	Upper Bound
Body_weight	AA	Noiler	1.477E3	131.593	1183.793	1770.207
		Sasso	1.554E3	83.227	1368.760	1739.640
		Funaab Alpha	2.030E3	186.100	1615.343	2444.657
	CA	Noiler	1.232E3	107.445	992.931	1471.736
		Sasso	.[a]	.	.	.
		Funaab Alpha	1.375E3	93.050	1167.671	1582.329
	CC	Noiler	.[a]	.	.	.
		Sasso	1.894E3	186.100	1479.343	2308.657
		Funaab Alpha	.[a]	.	.	.
Height_at_withers	AA	Noiler	11.550	.698	9.996	13.104
		Sasso	10.860	.441	9.877	11.843
		Funaab Alpha	13.400	.986	11.202	15.598
	CA	Noiler	9.767	.570	8.498	11.036
		Sasso	.[a]	.	.	.
		Funaab Alpha	11.875	.493	10.776	12.974
	CC	Noiler	.[a]	.	.	.
		Sasso	12.300	.986	10.102	14.498
		Funaab Alpha	.[a]	.	.	.
Body length	AA	Noiler	9.350	.469	8.306	10.394
		Sasso	8.860	.296	8.200	9.520
		Funaab Alpha	11.200	.663	9.724	12.676
	CA	Noiler	8.467	.383	7.614	9.319
		Sasso	.[a]	.	.	.
		Funaab Alpha	9.275	.331	8.537	10.013
	CC	Noiler	.[a]	.	.	.
		Sasso	9.300	.663	7.824	10.776
		Funaab Alpha	.[a]	.	.	.
Breast_girth	AA	Noiler	10.950	.514	9.804	12.096
		Sasso	10.160	.325	9.435	10.885
		Funaab Alpha	10.800	.727	9.179	12.421
	CA	Noiler	9.667	.420	8.731	10.602
		Sasso	.[a]	.	.	.
		Funaab Alpha	8.975	.364	8.165	9.785
	CC	Noiler	.[a]	.	.	.
		Sasso	10.600	.727	8.979	12.221
		Funaab Alpha	.[a]	.	.	.
Wing length	AA	Noiler	8.500	.355	7.709	9.291
		Sasso	7.940	.224	7.440	8.440
		Funaab Alpha	8.800	.502	7.682	9.918
	CA	Noiler	7.400	.290	6.754	8.046
		Sasso	.[a]	.	.	.
		Funaab Alpha	7.825	.251	7.266	8.384
	CC	Noiler	.[a]	.	.	.
		Sasso	8.000	.502	6.882	9.118
		Funaab Alpha	.[a]	.	.	.

a. This level combination of factors is not observed, thus the corresponding population marginal mean is not estimable.

Post Hoc Tests

BREED

Homogeneous Subsets

Body_weight

Duncan

BREED	N	Subset 1	Subset 2
Noiler	5	1.3302E3	
Funaab Alpha	5	1.5060E3	1.5060E3
Sasso	6		1.6108E3
Sig.		.155	.381

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = 34633.347.

Height_at_withers

Duncan

BREED	N	Subset 1	Subset 2
Noiler	5	10.4800	
Sasso	6	11.1000	11.1000
Funaab Alpha	5		12.1800
Sig.		.331	.105

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .973.

Body length

Duncan

BREED	N	Subset 1
Noiler	5	8.8200
Sasso	6	8.9333
Funaab Alpha	5	9.6600
Sig.		.077

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .439.

Breast_girth

Duncan

BREED	N	Subset
		1
Funaab Alpha	5	9.3400
Noiler	5	10.1800
Sasso	6	10.2333
Sig.		.085

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .529.

Wing length

Duncan

BREED	N	Subset
		1
Noiler	5	7.8400
Sasso	6	7.9500
Funaab Alpha	5	8.0200
Sig.		.590

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .252.

APPENDIX 8.6. SNP1_A_C * SEX

Dependent Variable	SNP1_A_C	SEX	Mean	Std. Error	95% Confidence Interval	
					Lower Bound	Upper Bound
Body_weight	AA	Male	1.680E3	80.729	1502.316	1857.684
		Female	1.338E3	139.828	1029.742	1645.258
	CA	Male	1.328E3	139.828	1019.742	1635.258
		Female	1.308E3	88.435	1113.757	1503.043
	CC	Male	1.894E3	197.746	1458.764	2329.236
		Female	.[a]	.	.	.
Height_at_withers	AA	Male	11.900	.341	11.149	12.651
		Female	9.700	.591	8.399	11.001
	CA	Male	12.650	.591	11.349	13.951
		Female	10.300	.374	9.477	11.123
	CC	Male	12.300	.836	10.460	14.140
		Female	.[a]	.	.	.
Body length	AA	Male	9.633	.314	8.942	10.325
		Female	8.200	.544	7.003	9.397
	CA	Male	9.350	.544	8.153	10.547
		Female	8.760	.344	8.003	9.517
	CC	Male	9.300	.769	7.607	10.993

		Female	.[a]	.	.	.
Breast_girth	AA	Male	10.517	.290	9.879	11.155
		Female	10.200	.502	9.095	11.305
	CA	Male	8.550	.502	7.445	9.655
		Female	9.560	.318	8.861	10.259
	CC	Male	10.600	.710	9.037	12.163
		Female	.[a]	.	.	.
Wing length	AA	Male	8.350	.213	7.881	8.819
		Female	7.700	.369	6.887	8.513
	CA	Male	7.800	.369	6.987	8.613
		Female	7.580	.234	7.066	8.094
	CC	Male	8.000	.522	6.850	9.150
		Female	.[a]	.	.	.

a. This level combination of factors is not observed, thus the corresponding population marginal mean is not estimable.

APPENDIX 8.7 Descriptive Statistics

	SNP1_A_C	SEX	Mean	Std. Deviation	N
Body_weight	AA	Male	1.6800E3	212.72047	6
		Female	1.3375E3	3.53553	2
		Total	1.5944E3	239.70871	8
	CA	Male	1.3275E3	282.13561	2
		Female	1.3084E3	176.26344	5
		Total	1.3139E3	184.57016	7
	CC	Male	1.8940E3	.	1
		Total	1.8940E3	.	1
	Total	Male	1.6254E3	267.71539	9
		Female	1.3167E3	144.62447	7
		Total	1.4904E3	267.60291	16
Height_at_withers	AA	Male	11.9000	.78740	6
		Female	9.7000	.70711	2
		Total	11.3500	1.24556	8
	CA	Male	12.6500	.35355	2
		Female	10.3000	.99499	5
		Total	10.9714	1.41270	7
	CC	Male	12.3000	.	1
		Total	12.3000	.	1
	Total	Male	12.1111	.71667	9
		Female	10.1286	.91052	7
		Total	11.2438	1.27957	16
Body length	AA	Male	9.6333	.90259	6
		Female	8.2000	.98995	2
		Total	9.2750	1.07803	8
	CA	Male	9.3500	.35355	2
		Female	8.7600	.57706	5
		Total	8.9286	.57071	7
	CC	Male	9.3000	.	1
		Total	9.3000	.	1
	Total	Male	9.5333	.73993	9
		Female	8.6000	.67823	7
		Total	9.1250	.83944	16
Breast_girth	AA	Male	10.5167	.54924	6
		Female	10.2000	.28284	2
		Total	10.4375	.49839	8
	CA	Male	8.5500	1.76777	2
		Female	9.5600	.45607	5
		Total	9.2714	.94994	7
	CC	Male	10.6000	.	1
		Total	10.6000	.	1
	Total	Male	10.0889	1.15806	9
		Female	9.7429	.49952	7
		Total	9.9375	.92005	16

Wing length	AA	Male	8.3500	.41833	6
		Female	7.7000	.70711	2
		Total	8.1875	.53569	8
	CA	Male	7.8000	.00000	2
		Female	7.5800	.63797	5
		Total	7.6429	.53184	7
	CC	Male	8.0000	.	1
		Total	8.0000	.	1
	Total	Male	8.1889	.41366	9
		Female	7.6143	.59841	7
		Total	7.9375	.56672	16

APPENDIX 8.8 Tests of Between-Subjects Effects

Source	Dependent Variable	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	Body_weight	644031.550[a]	4	161007.887	4.117	.028
	Height_at_withers	16.874[b]	4	4.219	6.038	.008
	Body length	4.060[c]	4	1.015	1.715	.217
	Breast_girth	7.152[d]	4	1.788	3.547	.043
	Wing length	1.815[e]	4	.454	1.662	.228
Intercept	Body_weight	1.990E7	1	1.990E7	509.005	.000
	Height_at_withers	1086.590	1	1086.590	1.555E3	.000
	Body length	693.372	1	693.372	1.172E3	.000
	Breast_girth	854.030	1	854.030	1.694E3	.000
	Wing length	530.787	1	530.787	1.944E3	.000
SNP1_A_C	Body_weight	209607.514	2	104803.757	2.680	.113
	Height_at_withers	1.365	2	.682	.977	.407
	Body length	.078	2	.039	.066	.937
	Breast_girth	5.461	2	2.730	5.416	.023
	Wing length	.350	2	.175	.641	.545
SEX	Body_weight	95674.068	1	95674.068	2.447	.146
	Height_at_withers	15.148	1	15.148	21.682	.001
	Body length	2.996	1	2.996	5.061	.046
	Breast_girth	.352	1	.352	.698	.421
	Wing length	.554	1	.554	2.029	.182
SNP1_A_C * SEX	Body_weight	76527.483	1	76527.483	1.957	.189
	Height_at_withers	.016	1	.016	.024	.881
	Body length	.520	1	.520	.879	.369
	Breast_girth	1.288	1	1.288	2.555	.138
	Wing length	.135	1	.135	.496	.496
Error	Body_weight	430138.200	11	39103.473		
	Height_at_withers	7.685	11	.699		
	Body length	6.510	11	.592		
	Breast_girth	5.545	11	.504		
	Wing length	3.003	11	.273		

Total	Body_weight	3.661E7	16			
	Height_at_withers	2047.310	16			
	Body length	1342.820	16			
	Breast_girth	1592.760	16			
	Wing length	1012.880	16			
Corrected Total	Body_weight	1074169.750	15			
	Height_at_withers	24.559	15			
	Body length	10.570	15			
	Breast_girth	12.697	15			
	Wing length	4.818	15			

a. R Squared = .600 (Adjusted R Squared = .454)

b. R Squared = .687 (Adjusted R Squared = .573)

c. R Squared = .384 (Adjusted R Squared = .160)

d. R Squared = .563 (Adjusted R Squared = .404)

e. R Squared = .377 (Adjusted R Squared = .150)

Estimated Marginal Means

1. Grand Mean

Dependent Variable	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
Body_weight	1.509E3[a]	60.842	1375.567	1643.393
Height_at_withers	11.370[a]	.257	10.804	11.936
Body length	9.049[a]	.237	8.528	9.570
Breast_girth	9.885[a]	.218	9.405	10.366
Wing length	7.886[a]	.161	7.532	8.240

a. Based on modified population marginal mean.

Appendix 8.9 Descriptive Statistics

	SNP2_A_T	BREED	Mean	Std. Deviation	N
Body_weight	AA	Noiler	1.3302E3	206.15455	5
		Sasso	1.6108E3	226.16403	6
		Funaab Alpha	1.3243E3	170.04803	3
		Total	1.4492E3	241.45622	14
	TA	Funaab Alpha	1.7785E3	355.67471	2
		Total	1.7785E3	355.67471	2
	Total	Noiler	1.3302E3	206.15455	5
		Sasso	1.6108E3	226.16403	6
		Funaab Alpha	1.5060E3	328.57952	5
		Total	1.4904E3	267.60291	16
Height_at_withers	AA	Noiler	10.4800	1.13886	5
		Sasso	11.1000	1.18828	6
		Funaab Alpha	11.5333	.90185	3
		Total	10.9714	1.11385	14

	TA	Funaab Alpha	13.1500	.35355	2
		Total	13.1500	.35355	2
	Total	Noiler	10.4800	1.13886	5
		Sasso	11.1000	1.18828	6
		Funaab Alpha	12.1800	1.10544	5
		Total	11.2438	1.27957	16
Body length	AA	Noiler	8.8200	.69785	5
		Sasso	8.9333	.81404	6
		Funaab Alpha	9.1667	.20817	3
		Total	8.9429	.65482	14
	TA	Funaab Alpha	10.4000	1.13137	2
		Total	10.4000	1.13137	2
	Total	Noiler	8.8200	.69785	5
		Sasso	8.9333	.81404	6
		Funaab Alpha	9.6600	.89331	5
		Total	9.1250	.83944	16
Breast_girth	AA	Noiler	10.1800	.87293	5
		Sasso	10.2333	.30111	6
		Funaab Alpha	8.7000	1.22882	3
		Total	9.8857	.95664	14
	TA	Funaab Alpha	10.3000	.70711	2
		Total	10.3000	.70711	2
	Total	Noiler	10.1800	.87293	5
		Sasso	10.2333	.30111	6
		Funaab Alpha	9.3400	1.28374	5
		Total	9.9375	.92005	16
Wing length	AA	Noiler	7.8400	.77653	5
		Sasso	7.9500	.43704	6
		Funaab Alpha	7.8333	.55076	3
		Total	7.8857	.55589	14
	TA	Funaab Alpha	8.3000	.70711	2
		Total	8.3000	.70711	2
	Total	Noiler	7.8400	.77653	5
		Sasso	7.9500	.43704	6
		Funaab Alpha	8.0200	.58481	5
		Total	7.9375	.56672	16

APPENDIX 8.10 Tests of Between-Subjects Effects

Source	Dependent Variable	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	Body_weight	464082.950[a]	3	154694.317	3.043	.070
	Height_at_withers	10.560[b]	3	3.520	3.017	.072
	Body length	3.942[c]	3	1.314	2.379	.121
	Breast_girth	5.676[d]	3	1.892	3.234	.061
	Wing length	.344[e]	3	.115	.307	.820
Intercept	Body_weight	2.561E7	1	2.561E7	503.778	.000
	Height_at_withers	1427.651	1	1427.651	1.224E3	.000
	Body length	930.219	1	930.219	1.684E3	.000

	Breast_girth	1061.785	1	1061.785	1.815E3	.000
	Wing length	671.789	1	671.789	1.802E3	.000
SNP2_A_T	Body_weight	247520.833	1	247520.833	4.869	.048
	Height_at_withers	3.136	1	3.136	2.688	.127
	Body length	1.825	1	1.825	3.305	.094
	Breast_girth	3.072	1	3.072	5.250	.041
	Wing length	.261	1	.261	.701	.419
BREED	Body_weight	274332.057	2	137166.029	2.698	.108
	Height_at_withers	2.254	2	1.127	.966	.408
	Body length	.226	2	.113	.205	.818
	Breast_girth	5.376	2	2.688	4.594	.033
	Wing length	.043	2	.022	.058	.944
SNP2_A_T * BREED	Body_weight	.000	0	.	.	.
	Height_at_withers	.000	0	.	.	.
	Body length	.000	0	.	.	.
	Breast_girth	.000	0	.	.	.
	Wing length	.000	0	.	.	.
Error	Body_weight	610086.800	12	50840.567		
	Height_at_withers	14.000	12	1.167		
	Body length	6.628	12	.552		
	Breast_girth	7.021	12	.585		
	Wing length	4.474	12	.373		
Total	Body_weight	3.661E7	16			
	Height_at_withers	2047.310	16			
	Body length	1342.820	16			
	Breast_girth	1592.760	16			
	Wing length	1012.880	16			
Corrected Total	Body_weight	1074169.750	15			
	Height_at_withers	24.559	15			
	Body length	10.570	15			
	Breast_girth	12.697	15			
	Wing length	4.818	15			

a. R Squared = .432 (Adjusted R Squared = .290)

b. R Squared = .430 (Adjusted R Squared = .287)

c. R Squared = .373 (Adjusted R Squared = .216)

d. R Squared = .447 (Adjusted R Squared = .309)

e. R Squared = .071 (Adjusted R Squared = -.161)

Estimated Marginal Means

APPENDIX 9.1. Grand Mean

Dependent Variable	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound

Body_weight	1.511E3[a]	61.750	1376.425	1645.508
Height_at_withers	11.566[a]	.296	10.921	12.210
Body length	9.330[a]	.204	8.887	9.773
Breast_girth	9.853[a]	.209	9.397	10.310
Wing length	7.981[a]	.167	7.617	8.345

a. Based on modified population marginal mean.

APPENDIX 9.2. SNP2_A_T

				95% Confidence Interval	
Dependent Variable	SNP2_A_T	Mean	Std. Error	Lower Bound	Upper Bound
Body_weight	AA	1.422E3	62.883	1284.779	1558.799
	TA	1.778E3[a]	159.437	1431.116	2125.884
Height_at_withers	AA	11.038	.301	10.381	11.694
	TA	13.150[a]	.764	11.486	14.814
Body length	AA	8.973	.207	8.522	9.425
	TA	10.400[a]	.526	9.255	11.545
Breast_girth	AA	9.704	.213	9.240	10.169
	TA	10.300[a]	.541	9.122	11.478
Wing length	AA	7.874	.170	7.503	8.245
	TA	8.300[a]	.432	7.359	9.241

a. Based on modified population marginal mean.

APPENDIX 9.3. BREED

				95% Confidence Interval	
Dependent Variable	BREED	Mean	Std. Error	Lower Bound	Upper Bound
Body_weight	Noiler	1.330E3[a]	100.837	1110.495	1549.905
	Sasso	1.611E3[a]	92.051	1410.271	1811.396
	Funaab Alpha	1.551E3	102.916	1327.181	1775.652
Height_at_withers	Noiler	10.480[a]	.483	9.428	11.532
	Sasso	11.100[a]	.441	10.139	12.061
	Funaab Alpha	12.342	.493	11.268	13.416
Body length	Noiler	8.820[a]	.332	8.096	9.544
	Sasso	8.933[a]	.303	8.272	9.594
	Funaab Alpha	9.783	.339	9.044	10.522
Breast_girth	Noiler	10.180[a]	.342	9.435	10.925
	Sasso	10.233[a]	.312	9.553	10.914
	Funaab Alpha	9.500	.349	8.739	10.261
Wing length	Noiler	7.840[a]	.273	7.245	8.435
	Sasso	7.950[a]	.249	7.407	8.493
	Funaab Alpha	8.067	.279	7.459	8.674

a. Based on modified population marginal mean.

APPENDIX 9.4. SNP2_A_T * BREED

					95% Confidence Interval	
Dependent Variable	SNP2_A_T	BREED	Mean	Std. Error	Lower Bound	Upper Bound
Body_weight	AA	Noiler	1.330E3	100.837	1110.495	1549.905
		Sasso	1.611E3	92.051	1410.271	1811.396

		Funaab Alpha	1.324E3	130.180	1040.695	1607.971
	TA	Noiler	.[a]	.	.	.
		Sasso	.[a]	.	.	.
		Funaab Alpha	1.778E3	159.437	1431.116	2125.884
Height_at_withers	AA	Noiler	10.480	.483	9.428	11.532
		Sasso	11.100	.441	10.139	12.061
		Funaab Alpha	11.533	.624	10.175	12.892
	TA	Noiler	.[a]	.	.	.
		Sasso	.[a]	.	.	.
		Funaab Alpha	13.150	.764	11.486	14.814
Body length	AA	Noiler	8.820	.332	8.096	9.544
		Sasso	8.933	.303	8.272	9.594
		Funaab Alpha	9.167	.429	8.232	10.102
	TA	Noiler	.[a]	.	.	.
		Sasso	.[a]	.	.	.
		Funaab Alpha	10.400	.526	9.255	11.545
Breast_girth	AA	Noiler	10.180	.342	9.435	10.925
		Sasso	10.233	.312	9.553	10.914
		Funaab Alpha	8.700	.442	7.738	9.662
	TA	Noiler	.[a]	.	.	.
		Sasso	.[a]	.	.	.
		Funaab Alpha	10.300	.541	9.122	11.478
Wing length	AA	Noiler	7.840	.273	7.245	8.435
		Sasso	7.950	.249	7.407	8.493
		Funaab Alpha	7.833	.353	7.065	8.601
	TA	Noiler	.[a]	.	.	.
		Sasso	.[a]	.	.	.
		Funaab Alpha	8.300	.432	7.359	9.241

a. This level combination of factors is not observed, thus the corresponding population marginal mean is not estimable.

APPENDIX 9.5 Descriptive Statistics

	SNP2_A_T	SEX	Mean	Std. Deviation	N
Body_weight	AA	Male	1.5817E3	253.84688	7
		Female	1.3167E3	144.62447	7
		Total	1.4492E3	241.45622	14
	TA	Male	1.7785E3	355.67471	2
		Total	1.7785E3	355.67471	2
	Total	Male	1.6254E3	267.71539	9
		Female	1.3167E3	144.62447	7
		Total	1.4904E3	267.60291	16
Height_at_withers	AA	Male	11.8143	.44881	7
		Female	10.1286	.91052	7
		Total	10.9714	1.11385	14
	TA	Male	13.1500	.35355	2
		Total	13.1500	.35355	2
	Total	Male	12.1111	.71667	9

		Female	10.1286	.91052	7
		Total	11.2438	1.27957	16
Body length	AA	Male	9.2857	.44132	7
		Female	8.6000	.67823	7
		Total	8.9429	.65482	14
	TA	Male	10.4000	1.13137	2
		Total	10.4000	1.13137	2
	Total	Male	9.5333	.73993	9
		Female	8.6000	.67823	7
		Total	9.1250	.83944	16
Breast_girth	AA	Male	10.0286	1.29835	7
		Female	9.7429	.49952	7
		Total	9.8857	.95664	14
	TA	Male	10.3000	.70711	2
		Total	10.3000	.70711	2
	Total	Male	10.0889	1.15806	9
		Female	9.7429	.49952	7
		Total	9.9375	.92005	16
Wing length	AA	Male	8.1571	.37353	7
		Female	7.6143	.59841	7
		Total	7.8857	.55589	14
	TA	Male	8.3000	.70711	2
		Total	8.3000	.70711	2
	Total	Male	8.1889	.41366	9
		Female	7.6143	.59841	7
		Total	7.9375	.56672	16

APPENDIX 9.6 Tests of Between-Subjects Effects

Source	Dependent Variable	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	Body_weight	435538.393[a]	2	217769.196	4.433	.034
	Height_at_withers	18.252[b]	2	9.126	18.807	.000
	Body length	5.361[c]	2	2.681	6.691	.010
	Breast_girth	.586[d]	2	.293	.315	.736
	Wing length	1.332[e]	2	.666	2.483	.122
Intercept	Body_weight	2.225E7	1	2.225E7	453.022	.000
	Height_at_withers	1255.293	1	1255.293	2.587E3	.000
	Body length	823.767	1	823.767	2.056E3	.000
	Breast_girth	925.268	1	925.268	993.152	.000
	Wing length	589.053	1	589.053	2.197E3	.000
SNP2_A_T	Body_weight	60238.294	1	60238.294	1.226	.288
	Height_at_withers	2.775	1	2.775	5.720	.033
	Body length	1.931	1	1.931	4.821	.047
	Breast_girth	.115	1	.115	.123	.731
	Wing length	.032	1	.032	.118	.736
SEX	Body_weight	245787.500	1	245787.500	5.003	.043
	Height_at_withers	9.946	1	9.946	20.497	.001

	Body length	1.646	1	1.646	4.108	.064
	Breast_girth	.286	1	.286	.307	.589
	Wing length	1.031	1	1.031	3.847	.072
SNP2_A_T * SEX	Body_weight	.000	0	.	.	.
	Height_at_withers	.000	0	.	.	.
	Body length	.000	0	.	.	.
	Breast_girth	.000	0	.	.	.
	Wing length	.000	0	.	.	.
Error	Body_weight	638631.357	13	49125.489		
	Height_at_withers	6.308	13	.485		
	Body length	5.209	13	.401		
	Breast_girth	12.111	13	.932		
	Wing length	3.486	13	.268		
Total	Body_weight	3.661E7	16			
	Height_at_withers	2047.310	16			
	Body length	1342.820	16			
	Breast_girth	1592.760	16			
	Wing length	1012.880	16			
Corrected Total	Body_weight	1074169.750	15			
	Height_at_withers	24.559	15			
	Body length	10.570	15			
	Breast_girth	12.697	15			
	Wing length	4.818	15			

a. R Squared = .405 (Adjusted R Squared = .314)

b. R Squared = .743 (Adjusted R Squared = .704)

c. R Squared = .507 (Adjusted R Squared = .431)

d. R Squared = .046 (Adjusted R Squared = -.101)

e. R Squared = .276 (Adjusted R Squared = .165)

Estimated Marginal Means: 1. Grand Mean

Dependent Variable	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
Body_weight	1.559E3[a]	65.488	1417.497	1700.455
Height_at_withers	11.698[a]	.206	11.253	12.142
Body length	9.429[a]	.187	9.025	9.833
Breast_girth	10.024[a]	.285	9.408	10.640
Wing length	8.024[a]	.153	7.693	8.354

a. Based on modified population marginal mean.

2. SNP2_A_T

Dependent Variable	SNP2_A_T	Mean	Std. Error	95% Confidence Interval	
				Lower Bound	Upper Bound
Body_weight	AA	1.449E3	59.237	1321.242	1577.187

	TA	1.778E3[a]	156.725	1439.916	2117.084
Height_at_withers	AA	10.971	.186	10.569	11.374
	TA	13.150[a]	.493	12.086	14.214
Body length	AA	8.943	.169	8.577	9.308
	TA	10.400[a]	.448	9.433	11.367
Breast_girth	AA	9.886	.258	9.328	10.443
	TA	10.300[a]	.683	8.826	11.774
Wing length	AA	7.886	.138	7.587	8.185
	TA	8.300[a]	.366	7.509	9.091

a. Based on modified population marginal mean.

General Linear Model

Warnings

Post hoc tests are not performed for SNP2_A_T because there are fewer than three groups.

Between-Subjects Factors

		Value Label	N
SNP2_A_T	1	AA	14
	2	TA	2
BREED	1	Noiler	5
	2	Sasso	6
	3	Funaab Alpha	5

Post Hoc Tests

BREED

Homogeneous Subsets

Body_weight

Duncan

		Subset
BREED	N	1
Noiler	5	1.3302E3
Funaab Alpha	5	1.5060E3
Sasso	6	1.6108E3
Sig.		.077

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = 50840.567.

Height_at_withers

Duncan

BREED	N	Subset	
		1	2
Noiler	5	10.4800	
Sasso	6	11.1000	11.1000
Funaab Alpha	5		12.1800
Sig.		.369	.130

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = 1.167.

Body length

Duncan

BREED	N	Subset
		1
Noiler	5	8.8200
Sasso	6	8.9333
Funaab Alpha	5	9.6600
Sig.		.105

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .552.

Breast_girth

Duncan

BREED	N	Subset
		1
Funaab Alpha	5	9.3400
Noiler	5	10.1800
Sasso	6	10.2333
Sig.		.095

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .585.

Wing length

Duncan

BREED	N	Subset
		1
Noiler	5	7.8400
Sasso	6	7.9500
Funaab Alpha	5	8.0200
Sig.		.657

Wing length

Duncan

BREED	N	Subset 1
Noiler	5	7.8400
Sasso	6	7.9500
Funaab Alpha	5	8.0200
Sig.		.657

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = .373.

General Linear Model

Between-Subjects Factors

		Value Label	N
SNP2_A_T	1	AA	14
	2	TA	2
SEX	1	Male	9
	2	Female	7