GENETIC ANALYSIS OF BODY WEIGHTS OF INDIGENOUS CHICKEN IN KENYA

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A Thesis submitted to the Graduate School in Fulfilment for the Requirements of the Master of Science Degree in Animal Production (Animal Breeding Option) of Egerton University

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DECLARATION AND APPROVAL

DECLARATION

This thesis is my original work and has not, wholly or in part, been presented for an award of a diploma or degree in any other university known to me.

Mwaura Magothe Signed: ..... Date: 28-2-2013

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APPROVAL

This thesis has received my approval for final submission as the official University Supervisor.

Prof. Dr. A. K. Kahi Signed: ..... Date: 28/2/2013

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At the beginning I prayed to the almighty, and at the end of the day, I thank God for this accomplishment.

DEDICATION

This work is dedicated to my parents, my wife, my children and all indigenous chicken producers.

ABSTRACT

Kenya has a large population of indigenous chicken (IC) comprising several genotypes that are adapted to various environmental conditions and exhibit high within genotype variations in production. However, genetic and nutritional interventions designed to improve their low productivity have been applied uniformly disregarding the apparent genotype differences and without a sound scientific basis to inform targeted manipulations of growth processes. This study analyzed body weights (BW) of IC genotypes intensively reared from hatch to 30 weeks of age to determine the influence of the crested-head (Cr), frizzle-feather (Fr), naked-neck (Na) and normal-feather (na) major genes on BW and growth patterns, estimate genetic parameters of the combined IC population, compare growth patterns of the entire body mass with selected body parts and determine the relationships between BW and linear measurements of the selected body parts. The influence of major genes was determined using linear models and growth patterns described using non-linear models fitting the Gompertz-Laird function. Genetic parameters were estimated using Restricted Maximum Likelihood (REML) procedure fitting a sire model with hatch and sex as fixed effects and sires as random effects in single and multi-traits models. The relationship between BW and linear measurements was determined by correlation and regression. The Cr gene significantly ($P<0.05$) depressed BW by between 52.2 and 112.3 g from 18 weeks onwards, had low absolute growth rate from 10 to 22 weeks than na and higher initial specific growth and maturation rates than the Na gene. The Fr gene significantly depressed BW by between 28.2 and 75.1 g from 8 to 16 weeks and had higher relative growth rates than Cr from 12 to 16 weeks. The Na gene depressed BW by between 24.7 and 134.6 g from 8 weeks onwards, thus indicating that IC genotypes have varied growth potentials and patterns that can be improved to increase production.The heritability estimates for body weights at 2, 4, 6, 12, 14, 16 and 26 weeks of age were 0.51±0.22, 0.65±0.24, 0.51±0.22, 0.35±0.20, 0.31±0.23, 0.29±0.20 and 0.11±0.10, respectively, indicating selection can be applied at these ages. Genetic correlations were all positive and ranged between 0.44 and 0.99, indicating improvement at one age would lead to improvements in other ages. All body parts displayed diminishing returns growth patterns and reached maximum growth between 3 and 6 weeks of age while the entire body mass had sigmoid growth pattern and reached maximum growth between 13 and 14 weeks. The correlation coefficients between body weight and each linear measurement ranged from low (-0.013) to high (0.879) and varied with age. All body weight prediction equations had high R^2 that ranged between 0.896 and 0.907, indicating adequate fit. The shank length and drumstick circumference were the better predictors of body weight from week 4 onwards, indicating that the equations can reliably be used to predict body weights in the absence of weighing scales.

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TABLE OF CONTENTS

DECLARATION AND APPROVAL ii
COPYRIGHT iii
ACKNOWLEDGEMENTS iv
DEDICATION v
ABSTRACT vi
LIST OF TABLES x
LIST OF FIGURES xi
LIST OF ABBREVIATIONS AND ACRONYMS xii
CHAPTER ONE 1
GENERAL INTRODUCTION 1
1.1 Background information 1
1.2 Objectives 3
1.3 Research questions 3
CHAPTER TWO 4
LITERATURE REVIEW 4
2.1 Indigenous chicken production in Kenya 4
2.1.1 Importance of indigenous chicken 4
2.1.2 Production systems 5
2.1.3 Marketing systems 6
2.1.4 Phenotypic characteristics 7
2.1.5 Challenges to indigenous chicken production 9
2.2 Major genes 9
2.3 Indigenous chicken traits of importance and their performances 11
2.4 Growth functions 13
2.5 Genetic and phenotypic parameters 13
2.6 Relationships between body weights and linear body measurements 16
CHAPTER THREE 18
INFLUENCE OF MAJOR GENES FOR CRESTED-HEAD, FRIZZLE-FEATHER AND NAKED-NECK ON BODY WEIGHTS AND GROWTH PATTERNS OF INDIGENOUS CHICKEN REARED INTENSIVELY IN KENYA 18
3.1 Introduction 18
3.2 Materials and Methods 19

3.2.1 Experimental procedure 19
3.2.2 Chicken management 19
3.2.3 Data collection 19
3.2.4 Statistical analyses 20
3.2.5 Growth patterns 20
3.3 Results 21
3.3.1 Body weights 21
3.3.2 Growth patterns 22
3.4 Discussion 27
3.4.1 Body weights 27
3.4.2 Growth patterns 29
3.5 Conclusions 31
CHAPTER FOUR 33
GENETIC PARAMETER ESTIMATES FOR EGG AND BODY WEIGHTS OF INDIGENOUS CHICKEN IN KENYA 33
4.1 Introduction 33
4.2 Materials and Methods 33
4.2.1 Data source and chicken management 33
4.2.2 Data collection and analyses 34
4.3 Results 35
4.3.1 Heritability estimates for egg and body weights 35
4.3.2 Correlation between egg and body weights 37
4.4 Discussion 38
4.4.1 Heritability estimates for egg weight and body weights 38
4.4.2 Correlation between egg weight and body weights 40
4.5 Conclusions 42
CHAPTER FIVE 43
GROWTH PATTERNS OF INDIGENOUS CHICKEN BODY PARTS AND THEIR RELATIONSHIPS WITH BODY MASS 43
5.1 Introduction 43
5.2 Materials and methods 43
5.2.1 Data collection 43
5.2.2 Statistical analyses 44
5.3 Results 46

5.3.1 Body mass and selected parts linear measurements 46
5.3.2 Specific growth patterns 48
5.3.3 Relationships between body weights and linear measurements 49
5.4 Discussion 52
5.4.1 Body mass and selected parts linear measurements 52
5.4.2 Specific growth patterns 54
5.4.3 Relationships between body weights and linear measurements 57
5.5 Conclusions 59
CHAPTER SIX 60
GENERAL DISCUSSION AND CONCLUSIONS 60
6.1 Aim of the study 60
6.1.1 Study methodology 61
6.2 The influence of major genes on body weights and growth patterns of indigenous chickens 62
6.2.1 Body weights 62
6.2.2 Growth parameters 63
6.2.3 Growth patterns 63
6.3 Estimation of genetic and phenotypic parameters 64
6.3.1 Heritability estimates 65
6.3.2 Genetic and phenotypic correlations 65
6.4 Growth patterns of indigenous chicken body parts and their relationships with body weight 66
6.4.1 Body mass and selected parts linear measurements 66
6.4.2 Specific growth patterns 67
6.4.3 Relationships between body weights and linear measurements 68
6.4.4 Conclusions 68
REFERENCES 71

LIST OF TABLES

Table 1. Phenotypic characteristics of indigenous chickens in Kenya 8
Table 2. Some major genes in chickens and their effects on different traits 10
Table 3. Mean production and reproduction performance of indigenous chickens 12
Table 4. Heritability, genetic and phenotypic correlations of some indigenous chicken traits15
Table 5. Least squares means for observed live body weights of indigenous chicken genotypes at different ages 22
Table 6. Least squares means for growth parameters of indigenous chicken genotypes 23
Table 7. Least squares means for absolute growth rates of indigenous chicken genotypes at different ages 24
Table 8. Least squares means for relative growth rates of indigenous chicken genotypes at different ages 26
Table 9. Single-trait estimates of sire, residual and phenotypic variances and heritability coefficients with standard error for egg weight and biweekly body weights 35
Table 10. Multi-trait estimates of sire, residual and phenotypic variances, and heritability coefficient with standard error for egg weight and body weights at various ages 37
Table 11. Genetic and phenotypic correlations between egg weight, juvenile body weights, grower body weights and mature body weight 37
Table 12. Least squares means for overall observed body weight and linear measurements at various ages 46
Table 13. Least squares means per sex for body weight, shank length, drumstick length, drumstick circumference and chest circumference at various ages 47
Table 14. Least squares means for growth parameters of each body measurement 49
Table 15. Correlation coefficients between body weight and each linear measurement per sex from hatch to 30 weeks of age 51
Table 16. Regression equations for predicting body weight of both males and females at any age 52

LIST OF FIGURES

Figure 1. Structure of the indigenous chicken value chain 7
Figure 2. Specific growth curves for normal-feather, crested-head, frizzle-feather and naked-neck indigenous chickens 23
Figure 3. Absolute growth rate curves for normal-feather, crested-head, frizzle-feather and naked-neck indigenous chickens 25
Figure 4. Relative growth rate curves for normal-feather, crested-head, frizzle-feather and naked-neck indigenous chickens 27
Figure 5. Changes in heritability coefficients and body weights of indigenous chickens with age 36
Figure 6. Growth patterns of whole body mass, shank length, drumstick length, drumstick circumference and chest circumference of male and female indigenous chickens. 50
Figure 7. Changes in correlation coefficients between body weight and shank length, drumstick length, drumstick circumference and chest circumference of indigenous chickens with age 52

LIST OF ABBREVIATIONS AND ACRONYMS

AFE	Age at First Egg
ASM	Age at Sexual Maturity
BW	Body Weight
BW_I	Body Weight at Inflection
EN	Egg Number
EW	Egg weight
FAO	Food Agricultural Organization of the united Nations
g	Grams
GDP	Gross Domestic Product
GoK	Government of Kenya
HW	Hatching Weight
IC	Indigenous Chicken
INCIP	Indigenous Chicken Improvement Project
KARI	Kenya Agricultural Research Institute
MALDM	Ministry of Agriculture, Livestock Development and Marketing
MOLD	Ministry of Livestock Development
MT	Metric Tonnes
NAHRC	National Animal Husbandry Research Centre
NPDP	National Poultry Development Programme
t_I	Age at Inflection

CHAPTER ONE
INTRODUCTION

1.1 Background information

Indigenous chicken (IC) are described as small, robust and highly adapted multi-coloured birds of no particular breed (Sonaiya and Swan, 2004). In Kenya, they are kept by over 90% of households in both rural and urban areas in small flocks averaging between 1 and 50 mature birds per household (Njenga, 2005; Olwande et al., 2010). The birds are reared in low to medium input production systems for various purposes that include nutritional, economic, social-cultural and spiritual (Maina, 2000; Njenga, 2005). Nutritionally, they are a source of cheaply available high quality protein while economically, they are a source of wealth creation at both household and national levels (Upton, 2000). In some parts of the country, they are used as gifts and for recreation, while in others they are important in performing funeral rites and spiritual cleansing (Maina, 2000). The IC has therefore been recognized as an important tool for nutritional security, wealth creation, socio-cultural and spiritual wellbeing of communities (Mack et al., 2005). However, despite their importance and increasing demand for their products, production and production efficiencies of IC are generally low and highly varied (Njenga, 2005; Olwande et al., 2010).

Production performance of an animal is determined by the environmental conditions in which it performs and its genetic makeup (Falconer, 1989). Matching genotypes with environments has the potential to increase productivity in medium to low input production systems without significantly increasing the costs of production (FAO, 2007). Globally, several major genes conferring better adaptability to IC in adverse environmental conditions have been identified. Among these are the naked-neck gene (Na) responsible for feather reduction and the frizzle gene (Fr) responsible for feather curling (Horst, 1988). The genes cause changes in feather distribution and morphology leading to reduced body insulation and hence increased heat loss (Bartels, 2003). Genotypes possessing these genes, either singly or in combination have improved feed intake, feed conversion, immunocompetence and productivity in high ambient temperature environments due to reduced heat stress and pleiotropic gene effects (Bartels, 2003; N'dri et al., 2007b; Mahrous et al., 2008; El-Gendy, 2009). To increase growth and reproduction efficiency of IC by matching genotypes to their environments, the influence of the genes on the traits need to be evaluated.

Growth is an important trait in poultry due to its economic importance and the relative ease with which it can be improved (Emmerson, 1997; Menge, 2008). Improvement of IC

growth would therefore be expected to have positive impacts on the livelihoods of producers in any production system. However, growth is a complex process of changes in size of body mass, organs or tissues with time and is influenced by both genetic and non-genetic factors (Trenkle and Marple, 1983; Karkach, 2006). To describe growth patterns and characteristics, mathematical functions that summarize growth into a few biologically interpretable parameters are used (Trenkle and Marple, 1983; Goliomytis et al., 2003). The parameters are also necessary for modelling growth curves that describe growth patterns. Growth patterns and characteristics are useful in developing standard management and nutritional regimes necessary for achievement of innate growth potential (Cooper, 2005). Most importantly, growth patterns and characteristics of individual birds can be used as selection criteria in genetic improvement programmes (Mignon-Grasteau et al., 2000b; Cooper, 2005).

Genetic improvement involves a systematic exploitation of performance variation among individuals within or between populations (FAO, 2007). Phenotypic, genetic and environmental variances are important measures of variability of a trait and are important in describing properties of traits in a population. Genetic and phenotypic parameters are properties critical in determining breeding objectives, selection criteria and predicting the consequences of selection (Hill et al., 2007). Selection of superior individuals within a population has been suggested as the most efficient and sustainable genetic improvement strategy in medium to low input production systems (FAO, 2007). Accurate estimates of genetic and phenotypic parameters are therefore necessary in designing effective genetic improvement programmes. However, these parameters are lacking for the IC population in Kenya.

Growth is estimated through measurement of body weights at specified ages. In the absence of weighing scales, linear body parts measurements are particularly important in estimating live body weights of most livestock species (Kabir et al., 2006). It is a common practice to estimate live weight by measuring a part of the body trunk, with a good estimate being obtained by measuring the shank length in chicken, and the heart girth in cattle, horses and pigs (Latshaw and Bishop, 2001). In addition, the relationships between body weights and linear body parts measurements provide useful information on performance, productivity and carcass yield (Yang et al., 2006b; Raji et al., 2010). To estimate body weights of IC in the absence of weighing scales and understand possible carcass parts yield, it is necessary to evaluate growth of the most important body parts and determine their relationships with body weight (Nahashon et al., 2006b). However, this information is lacking for IC in Kenya. This information is important and can be used for genetic improvement and marketing of IC

especially in medium to low production systems where marketing is informal and poorly developed (Upton, 2000). Furthermore, the price of live chicken in Kenya largely depends on body weight (Njenga, 2005).

1.2 Objectives

The overall objective of this study was to contribute to improving IC productivity in Kenya through evaluating the genetics of body weights. The specific objectives were: -

i. To determine the influence of morphologically expressed major genes on body weights and to describe growth patterns of four IC genotypes.
ii. To estimate heritabilities of, and correlations between egg weight and live weights of IC at various ages.
iii. To determine the relationship between growth patterns of IC whole body mass and selected body parts at various ages and derive linear equations for predicting live body weight.

1.3 Research questions

i. How do the morphologically expressed major genes influence body weights and growth patterns of IC?
ii. What is the magnitude of the estimate of heritabilities of, and correlations between egg weight and body weights of IC?
iii. How are the growth patterns of IC whole body mass and selected body parts at various ages related?

CHAPTER TWO
LITERATURE REVIEW

2.1 Indigenous chicken production in Kenya

Indigenous chicken (IC) (*Gallus gallus domesticus*) occupy a unique and important position in the livelihood of rural households (Mack et al., 2005). In Kenya, non-descript local chicken strains and their crosses with exotic breeds are readily available and kept for various reasons in various production systems. Several terms, such as, "family chicken", "scavenging chicken", "village chicken", "local chicken" or "indigenous chicken", have been used to refer to these local fowl (Kitalyi, 1998; Safalaoh, 2001). The chickens have been kept by different communities from time immemorial and were present long before the introduction of European breeds (Maina, 2000). They have undergone both natural and human selection for a long time thus resulting to their adaptation to the prevailing environmental conditions (FAO, 2007).

Indigenous chicken tend to be robust and well adapted to survive and reproduce in unfavourable environmental conditions such as fluctuating weather, feed shortages, chronic diseases, heavy parasite loads and predator challenges (Guèye, 1998). They posses many advantageous traits that include good egg and meat quality characteristics, high fertility, excellent brooding and mothering ability, free-ranging and high-fibre feed utilization ability and resistance to some diseases, among others (Horst, 1988 and 1999; Tadelle et al., 2000). These traits make IC unique and immensely important in rural farming communities.

2.1.1 Importance of indigenous chicken

Indigenous chicken are the most numerous poultry species in Kenya (Upton, 2000; MOLD, 2008). They are kept for economic, nutritional, social-cultural and spiritual purposes by over 90% of households in both urban and rural areas (Maina, 2000; King'ori, 2004). At household level, IC provides additional income without competing for resources with other farm enterprises (Upton, 2000). Eggs and live chicken are sold whenever cash is required on short notice. Generally, more than 50% of households sell their eggs and live birds for an income (Ndegwa et al., 1998).

Apart from generating income, chicken meat and eggs are cheap and readily available sources of essential nutrients for human nutrition. Chicken meat is consumed mostly during important occasions such as banquets or ceremonies and whenever important guests visit a rural family. Generally, over 18% of the eggs laid and 30% of the household flock are consumed by the household (Ndegwa et al., 1998; Okitoi, 2000; Kaudia and Kitalyi, 2002).

Nevertheless, all birds that survive to maturity are ultimately either sold or consumed by the household. In addition, chicken are useful in a number of social, cultural and spiritual activities. These include gifts, funeral rites and spiritual cleansing (Njenga, 2005). In some communities, cock fighting is an exciting and popular entertainment sport for the rural folks (Maina, 2000; Bett et al., 2012). Other uses include kitchen waste disposal, manure production and being biological clocks for telling time of day especially early in the morning.

2.1.2 Production systems

Chicken production systems are classified according to production objectives, husbandry practices and levels of inputs (Guèye, 1998; Kitalyi, 1998). Depending on a households' land availability and the commercial value attached to the enterprise, three IC production systems are evident (Menge et al., 2005). These are: free-range system (FRS), semi-intensive system (SIS) and confined-full-ration system (CFRS).

In FRS, small flocks of less than 30 adult birds per household are kept for various uses that include provision of eggs and meat for consumption, source of income, capital investment and to meet social, cultural and spiritual obligations (Ndegwa et al., 1998; Njenga, 2005). The birds are let out of their night shelters in the morning to scavenge around the homestead. They are neither provided with any health care nor feed supplements (Ndegwa et al., 1998). Free-range feeds usually include; green forages, insects and earthworms, kitchen wastes, various seeds and any other consumable feed resource (Mwamachi et al., 2000; Birech, 2002). Night shelters include rudimentary coops, kitchens, stores and human habitats. Due to low inputs, free-range production system has relatively low outputs and is often considered supplementary to other agricultural enterprises. However, because the cost of production per unit of egg or meat is nearly negligible, returns for land, labour and capital is high (Upton, 2000; Menge et al., 2005). This can be considered as low inputs–low outputs production system.

In SIS, chicken are kept in small flocks of between 5 and 50 birds mainly for household consumption and sale (Ndegwa et al., 1998). Levels of inputs range from low to medium depending on the commercial value attached to the flock. The birds are left to scavenge around the homestead feeding on grass, insects, kitchen wastes and any other available feed resource. They are confined part of the time, especially during cropping seasons and supplemented with crop residues, grains, kitchen wastes, small quantities of commercial feeds and any other available feed resources (Siamba et al., 2000; Kaudia and

Kitalyi, 2002). The birds are usually provided with some form of housing but are not given any veterinary care except the use of traditional herbal medicines (Guèye, 1998).

In CFRS, flocks ranging between 100 and 500 adult birds are either confined totally in deep litter shelters, or partially in fenced runs with night shelters. The objective of this system is primarily commercial and mostly crossbred chicken are used (Owango, 1997). The birds are provided with commercial or homemade rations, given prophylactic cover and vaccinated against endemic diseases. Eggs and live birds are sold to readily available customers. Due to the costs of inputs and high levels of management required, this system is rare in rural areas (Menge et al., 2005).

2.1.3 Marketing systems

The willingness of producers to increase productivity is closely linked to the existence of efficient marketing systems for their produce (Gausi et al., 2004; Bett et al., 2012). Marketing is an important component of the IC value chain (Bett et al., 2012). Generally, any agribusiness value chain can be categorised into production, marketing, processing and consumption components. In Kenya, the IC marketing component is entirely a private sector business driven by the high demand for IC products by local consumers (Upton, 2000; Bett et al., 2009). The marketing system generally involves the producers, traders, processors and finally the consumers (Figure 1).

Most CFRS and SIS producers market their eggs and live chicken through itinerant traders (middle-traders, shops, hotels and supermarkets) while some market directly to processors and consumers. In these systems, decisions to market are entirely based on the availability of stocks for sale and the economics of profit and loss (Njenga, 2005). Although prices occasionally fluctuate due to market volatility, this marketing channel is relatively well developed and stable (Kitalyi, 1998; Upton, 2000).

In the FRS, eggs and live chicken marketing is undeveloped, erratic, unpredictable and largely informal. Producers depend on hawkers and middle-traders to purchase their eggs and live birds for subsequent sale to urban centres for a profit (Upton, 2000; Bett et al., 2009). Decisions to market are often dictated by the households' need for cash, disease outbreaks and the need to de-stock whenever the population exceeds the household carrying capacity (Njenga, 2005). Although egg prices are relatively constant, prices of live chicken fluctuate, being low during grain shortage seasons and high during festive seasons (Bett et al., 2012).

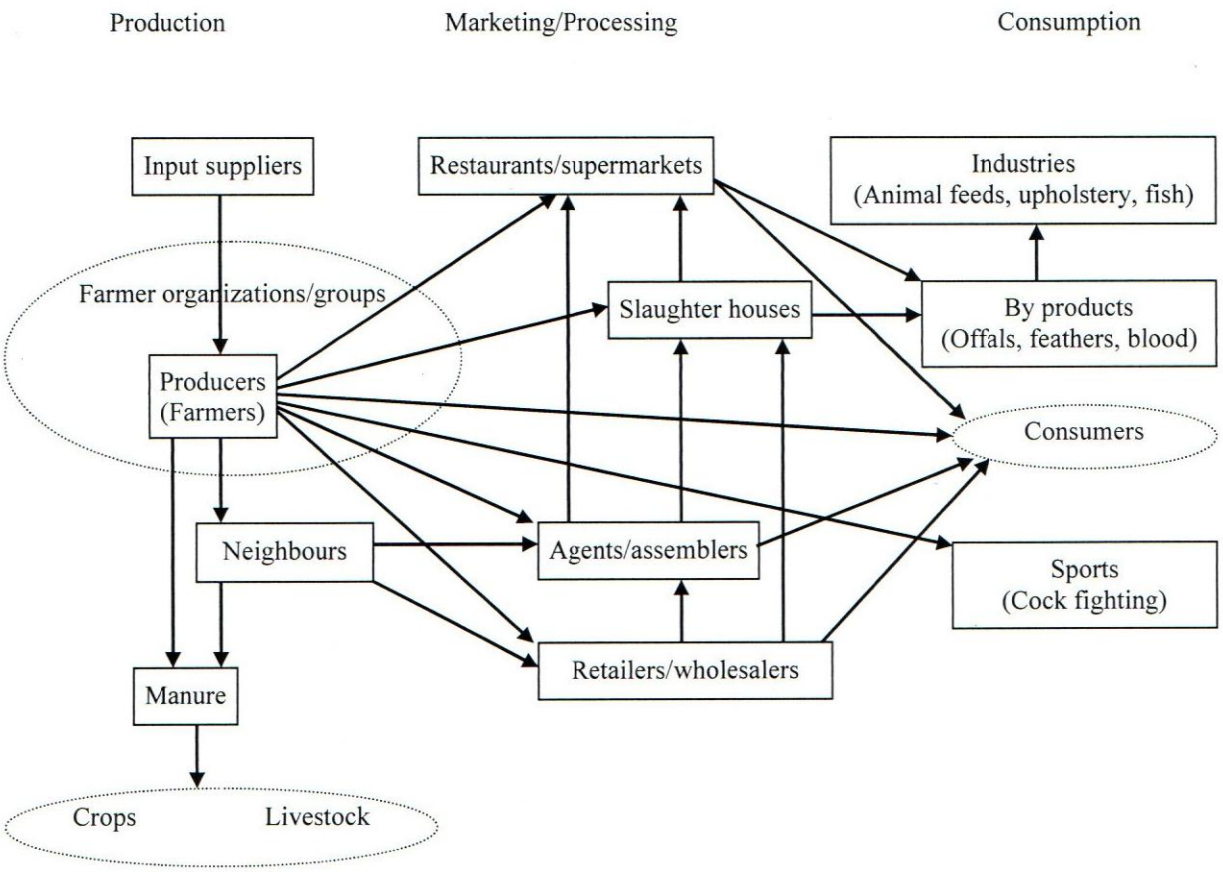


Figure 1. Structure of the indigenous chicken value chain

Source: Bett et al. (2012)

2.1.4 Phenotypic characteristics

Indigenous chicken constitute a heterogeneous population with various characteristics for both quantitative and qualitative traits (Sonaiya and Swan, 2004). They exhibit wide phenotypic variations in body weight, size, plumage colour, comb shape, shank colour and other parameters. Although IC in Kenya have not been conclusively described, several phenotypes have been identified based on morphological characteristics (Table 1). Although some of the phenotypes are known to be due to presence or absence of major genes (Tixier-Boichard, 2002), it is generally assumed that these phenotypic variations have a genetic base hence the name genotype (Falconer, 1989). However, some phenotypic differences may be due to environmental influences and need to be confirmed through detailed gene typing studies.

Several genotypes have been identified and include normal-feather, naked-neck, frizzle-feather, dwarf, crested and feathered-shanks, among others (Ndegwa and Kimani, 1996; Chemjor, 1998; Maina, 2000; Njenga, 2005). Maina (2000) concluded that although

the genotypes were not isolated reproductively, they were significantly distinct from each other, with the crested genotype being more distinct, while the naked-neck and feathered-shanks being more genetically close. Therefore, the different genotypes are indicators of a wide genetic variability within the unselected IC population.

Table 1. Phenotypic characteristics of indigenous chickens in Kenya

Characteristic	Phenotypes	Reference
Body weight	Heavy	Chemjor (1998); Maina (2000)
	Medium	
	Light	
Body size	Tall	Maina (2000)
	Medium	
	Dwarf	
Plumage colour	Black	Chemjor (1998); Maina (2000)
	White	
	Brown	
	Golden	
	Red	
	Yellow	
	Mixed colours	
Comb shape	Single	Maina (2000)
	Rose	
	Strawberry	
	Pea	
Shank colour	Black	Maina (2000)
	Yellow	
	White	
Eye colour	Black	Maina (2000)
	Brown	
	Yellow	
	Red	
Head appearance	Normal head	Maina (2000)
	Crested head	
Neck appearance	Feathered neck	Chemjor (1998); Maina (2000); Njenga (2005)
	Naked neck	
Plumage appearance	Normal feather	Chemjor (1998); Maina (2000); Njenga (2005)
	Frizzle feather	
Shank appearance	Feathered shank	Maina (2000)
	Unfeathered shank	

2.1.5 Challenges to indigenous chicken production

Despite their importance, IC production in Kenya encounters wide range of challenges that may be summarised into production and management related constraints. Production related constraints refer to factors that negatively influence production and productivity of IC and include inadequate nutrition and low genetic ability (Ndegwa et al., 1998; Okitoi et al., 2000). In both CFRS and FRS, IC energy and protein requirements have been determined and nutrient intake quantified (Chemjor, 1998; Birech, 2002; King'ori, 2004).

Protein intake by free-ranging IC has been found to be deficient leading to calls for supplementation (Mwamachi et al., 2000; Juma and Ondwasy, 2002; King'ori et al., 2007). However, although supplementation increases growth and egg production, the increases would not be expected to surpass genetically determined levels. Growth and egg production performance of confined IC fed commercial rations are lower than for commercial pure breeds due to their low genetic ability (Halima et al., 2006a; Lwelamira et al., 2008; Marle-Köster et al., 2008). The low genetic ability is mainly due to lack of sustainable genetic improvement strategies.

Management constraints relate to factors that reduce survival rates of IC and include poor housing and, inadequate nutrition and disease control. These constraints are more severe in SIS and FRS production conditions. Unconfined birds are predisposed to abiotic and biotic stresses that include harsh weather conditions, deficient nutrient intakes, parasites, predators and diseases, leading to high mortalities (Olwande et al., 2010). In addition, diseases and parasites are rarely controlled. The most important diseases causing severe losses include New Castle disease (NCD), chronic respiratory disease (CRD), fowl pox, coccidiosis, fowl typhoid, salmonellosis, infectious coryza and pollorum (Ndegwa et al., 1998; Kaudia and Kitalyi, 2002; Njenga, 2005). Although both internal and external parasites are common and usually cause insignificant mortalities, they reduce growth rate and egg production. The common parasites include helminths and coccidia, lice, fleas, ticks and mites (Ondwasy et al., 2000; Njenga, 2005; Mungube et al., 2008).

2.2 Major genes

According to the theory of quantitative genetics, quantitative traits are affected by many genes, each exerting infinitesimally small effects that they are unidentifiable (Falconer, 1989). The inheritance of such quantitative traits as growth rate and egg production in chicken cannot be explained by Mendelian laws of inheritance. However, some genes exert

large or at least measurable effects on the phenotypic expression of a trait and segregate in Mendelian pattern (Etches, 2001). Such genes are referred to as major genes, and several affecting quantitative traits and many morphological variants in chickens have been described and most mapped in the classical genome map (Tixier-Boichard, 2002; Bartels, 2003). Some major genes affecting growth rate, egg production, broodiness, feather color, feather structure, feather pattern, comb shape, skin color, and numerous other morphological traits are summarized in Table 2.

Table 2. Some major genes in chickens and their effects on different traits

Major gene	Mode of inheritance	Direct effects	Indirect effects	References
Na: naked-neck	Incomplete dominant	- Loss of neck feathers - Reduced pterylae width - Reduced secondary feathering	- Increased sensible heat loss - Improved adult fitness	Horst (1988); Yahav et al. (1998)
sc: scaleless	Recessive	- Complete loss of feathers	- Improved sensible heat loss	Bartels (2003); Cahaner et al. (2008)
dw: dwarf	Recessive, sex linked, multiple allelic	- Reduced body size	- Reduced metabolism - Improved fitness	Horst (1988); Tixier-Boichard (2002)
K: slow feathering	Dominant, sex linked, multiple allelic	- Delayed feathering	- Reduced protein requirement - Increased heat loss in early growth	Horst (1988); Khosravinia (2008)
F: frizzle	Incomplete dominant with modifiers	- Culled feathers - Reduced feathering	- Increased heat loss - Reduced hypodermal fat deposits	Horst (1988); Bartels (2003)
Fsh: feathered shank	Dominant with modifiers, multiple allelic	- Feathers on shank	- Reduced heat loss	Ikeobi et al. (2001); Bartels (2003)
Cr: crest	Incomplete dominant with modifiers	- Crest	- Impaired sight	Bartels (2003)
id: non-inhibitor	Recessive, sex linked, multiple allelic	- Dermal melanin deposition in skin and shank	- Increased radiation protection	Horst (1988)
Et: ear tuft	Incomplete dominant, multiple allelic	- Feather-covered skin appendages near the ear	- Reduced heat loss through ear opening	Bartels (2003)

The origin of most major genes in chickens has been attributed to mutations, and their existence in a population to subsequent natural and human selection (Etches, 2001; Tixier-Boichard, 2002; Bartels, 2003). However, evidence also suggests that some of the major genes may have been present but dormant in the wild chicken ancestors and were activated in the process of domestication and adaptation to various climatic environments (Kraublich, 2000). Whereas natural selection favors adapted individuals, humans on the other hand, have for centuries selected chickens based on a diverse range of desirable characteristics (Etches, 2001; Siegel et al., 2006). In the tropics, most of these major genes are available in free-ranging local chickens and confer direct and indirect effects on productive adaptability (Horst, 1988).

Genes exert their effects directly through synthesis of proteins that regulate biological responses affecting a trait. Most major genes, however, affect more than one trait through linkage and pleiotropic effects (Falconer, 1989; Hull and Harvey, 1999). Therefore, presence or absence of a particular major gene leads to phenotypic consequences and hence variation (Tixier-Boichard, 2002). In addition, some major genes exert indirect effects on traits through physical mechanisms that confer adaptive advantages in challenging environments (Bartels, 2003; Khosravinia, 2008). To improve production in such environments, it is important to understand the influence of such major genes on traits of importance.

2.3 Indigenous chicken traits of importance and their performances

Indigenous chicken producers are faced with the challenge of identifying important traits that directly influence profitability, which collectively form the breeding goal (Menge et al., 2005). Because IC are kept in a wide range of challenging environmental conditions, knowledge of such traits would help producers improve on production efficiency of their flocks. The traits are broadly classified as production and functional traits (Cardellino and Boyazoglu, 2009). Production traits influence productivity and include annual egg number, live weights at various ages, age at sexual maturity, feed conversion efficiency, clutch size, clutch length and egg weight. The functional traits include fertility, hatchability, broodiness, mothering instinct and disease resistance, and play a central role in the generation and survival of replacement stock within the production systems (Menge, 2008). Table 3 shows the performance of IC in Kenya.

The performances of various traits are low and highly varied compared to performance of exotic pure breeds and hybrids. In the free-range and semi-intensive production systems, age at first egg ranges from 180 to 240 days compared to a range of 155

to 164 days for hybrids (Sharifi et al., 2010). However, this has been shown to reduce to 166 days under intensive management. This apparent growth rate improvement under intensive management is an indicator of genotype x environment interaction (Besbes, 2009). Males are heavier than females with an average mature body weight of 2.2 and 1.6 kg, respectively (Chemjor, 1998). Indigenous chicken hens lay about 45 eggs per year with a range of between 30 and 75 eggs under free range and semi-free range systems (Kaudia and Kitalyi, 2002). However, some lay up to 120 eggs when supplemented with concentrates compared to 260-300 egg per year for modern hybrid layers. Egg weights in all production systems average between 45 and 47 grams with a range of between 36 and 52 grams (Njenga, 2005). There are about 3 clutches per year with an average of 15 eggs per clutch before incubation. In all the production systems, chicks are produced by natural incubation using broody hens. Fertility and hatchability is usually above 70% but hatching weights are often low, ranging between 25 and 43 grams (King'ori, 2004).

Table 3. Mean production and reproduction performance of indigenous chickens

Trait	Mean performance			References
	Confined full ration system	Semi-intensive system	Free-range system	
Age at first egg (days)	166.0	203.0	224.0	Ndegwa and Kimani (1996); Siamba et al. (2000)
No. of clutches/year	4.0	3.0	2.5	Ndegwa et al. (1998); Juma and Ondwasy (2002); Kaudia and Kitalyi (2002)
No. of eggs/clutch	30.0	21.2	11.1	Kaudia and Kitalyi (2002); Juma and Ondwasy (2002); Njenga (2005)
Egg weight (g)	42.7	-	-	Njenga (2005)
Fertility (%)	61.8	-	-	Njenga (2005)
Hatchability (%)	74.2	77.0	84.0	Okitoi et al. (2000); Kaudia and Kitalyi (2002); King'ori (2004); Njenga (2005)
Annual egg production	120.0	75.0	40.0	Ndegwa et al. (1998); Juma and Ondwasy (2002); Kaudia and Kitalyi (2002)
Body weight at first egg (g)	1630.0	-	-	Ndegwa and Kimani (1996)
Mature body weight (g)[1]	[m] 2210.0 [f] 1660.0	-	[m] 1770.0 [f] 1320.0	Chemjor (1998); Njenga (2005)

[1] m- male, f- female

2.4 Growth functions

Growth is a priority trait in the poultry industry (Emmerson, 1997). It is defined as an increase in size (e.g. length, width, weight, etc) with age and is affected by both non-genetic and genetic factors. The non-genetic factors include environmental factors such as climate, nutrition and health, intrinsic factors such as sex and physiological status, and extrinsic factors such as maternal effects (Trenkle and Marple, 1983; Sengul and Kuraz, 2005). The genetic factors include presence or absence and the switching on or off of particular genes or gene combinations that influence growth (Nie et al., 2005; Le Rouzic et al., 2008).

Mathematical functions are used to summarize the entire spectrum of whole body mass or body parts growth into a few parameters that can be interpreted biologically (Maruyama et al., 2001; Goliomytis et al., 2003). The parameters are useful in describing various growth characteristics such as specific growth, absolute growth and relative growth rates. In addition, the parameters are useful in modelling growth curves that describe the pattern of growth. The most commonly used growth functions utilize three or four parameters. Three parameter functions include the Gompertz, logistic and von Bertalanffy functions while four parameter functions include the Richards, Morgan-Mercer-Flodin, Janoschek and Weibull functions, among others (Maruyama et al., 2001). Historically, the Gompertz has been the function of choice for describing growth in chicken because of its overall fit and the biological meaning of the model parameters (Mignon-Grasteau et al., 1999).

Poultry growth can be broadly characterized into four phases; exponential growth phase, linear growth phase, diminishing growth phase and antithesis phase through senescence (Goliomytis et al., 2003; Brown et al., 2007). These phases represent a sigmoid growth pattern. Other patterns frequently observed include the exponential pattern usually observed soon after hatch, asymptotic pattern characterized by a positive and steadily decreasing growth rate and bell-shaped pattern observed in organs that show degeneration and involution (Lopez et al., 2000; Hyankova et al., 2001; Kuhi et al., 2003; Aggrey, 2004). Growth characteristics and patterns are useful as they provide information used to estimate feed requirements, understand the effects of environmental stress on growth and manipulate the desired body composition at a given age.

2.5 Genetic and phenotypic parameters

Genetic and phenotypic parameters are useful measures of variation in a population (Falconer, 1989). They include heritability, genetic and phenotypic correlations, and

repeatability coefficients. These parameters interpret the genetic properties of traits; hence their estimation is synonymous with (co)variance components estimation (Shaw, 1987). Unbiased heritability estimates of and accurate correlations between traits are mandatory when designing genetic improvement programmes. They are necessary in the definition of breeding goals and selection criteria, prediction of response to selection and genetic gain expected from selection programmes, selection of various breeding strategies and evaluation of breeding programmes.

Heritability refers to the proportion of the phenotypic variance that can be attributed to gene effects. It is a measure of the extent to which additive genes influence phenotypic observation of a particular trait. Therefore, traits with high heritability can be improved through selection, with response to selection and genetic gain expected to be high. However, heritability is not only a property of a trait, but also of a population and the environment in which individuals live (Falconer, 1989; Castillo and Segura-Correa, 2004).

Heritability estimates of a trait vary between and within populations as shown in Table 4. The variations are attributed to differences in gene frequencies, selection history, prevailing environmental conditions and methods of estimation. For instance, the heritability estimate for AFE differ between the Kuchi of Tanzania (0.42) and a native chicken strain of Korea (0.24), as does the estimate for HW within the same Creole population. It is therefore important that estimates from one population be treated with caution when used in other populations, and statistical models that best describe the mating structure and the phenotypic observations are used (Thompson, 2008). Generally, heritability estimates for body weights range from low (0.13) to high (0.68) within a population, while the heritability estimates for production traits are higher than for reproduction traits (Table 4).

Table 4. Heritability, genetic and phenotypic correlations of some indigenous chicken traits

Breed type	Country	Method used[1]	Trait 1[2]	Trait 2[2]	Parameter estimates[3]				Source
					$h^2_{trait\ 1}$	$h^2_{trait\ 2}$	$r_{a(1,2)}$	$r_{p(1,2)}$	
Kuchi	Tanzania	MTSM	AFE	EW	0.42		0.32	0.12	Lwelamira et al. (2009)
Native chicken strain RB	Korea	MTAM	AFE	EN39	0.24	0.24	-0.81	-0.59	Sang et al. (2006)
Native chicken	Iran	MVAM	AFE	EN12	0.49		-0.85		Kamali et al. (2007)
Venda	South Africa	STAM	BW10		0.41				Norris and Ngambi (2006)
Kuchi	Tanzania	MTSM	BW12	BW16	0.41		0.78	0.68	Lwelamira et al. (2009)
Native chicken	Iran	MVAM	BW12	EN12	0.68	0.40	0.11		Kamali et al. (2007)
Kuchi	Tanzania	MTSM	BW16	BW20	0.44		0.93	0.74	Lwelamira et al. (2009)
Kuchi	Tanzania	MTSM	BW20	AFE	0.45		-0.20	-0.16	Lwelamira et al. (2009)
Native chicken strain RB	Korea	MTAM	BW39	EN39	0.43		-0.47	-0.16	Sang et al. (2006)
Venda	South Africa	STAM	BW4		0.25				Norris and Ngambi (2006)
Kuchi	Tanzania	MTSM	BW8	EN13	0.38	0.31	-0.06	-0.02	Lwelamira et al. (2009)
Native chicken strain RB	Korea	MTAM	BWFE	EN39	0.39		-0.48	-0.07	Sang et al. (2006)
Kuchi	Tanzania	MTSM	EW	EN13	0.43		-0.19	-0.13	Lwelamira et al. (2009)
Native chicken	Iran	MTAM	EW	AEP	0.59	0.35	-0.09	-0.03	Kiani-Manesh et al. (2002)
Native chicken	Iran	MVAM	EW	EN12	0.64		-0.09		Kamali et al. (2007)
Native chicken strain RB	Korea	MTAM	EW	EN39	0.37		-0.30	-0.10	Sang et al. (2006)
Creole chicken	Mexico	MVAM	HW		0.40				Castillo and Segura-Correa (2004)
Creole chicken	Mexico	STSM	HW		0.13				Castillo and Segura-Correa (2004)
Venda	South Africa	STAM	HW		0.36				Norris and Ngambi (2006)

[1]MTSM- multiple trait sire model, MTAM- multiple trait animal model, MVAM- multivariate animal model, STAM- single trait animal model, STSM- single trait sire model

[2]AFE- age at first egg, BW4- body weight at 4 weeks, BW8- body weight at 8 weeks, BW10- body weight at 10 weeks, BW12- body weight at 12 weeks, BW16- body weight at 16 weeks, BW20- body weight at 20 weeks, BW39- body weight at 39 weeks, BWFE- body weight at first egg, EW- egg weight, HW- hatching weight, EN12- egg number at 12 weeks, EN13- egg number at 13 weeks, EN39- egg number at 39 weeks, AEP- annual egg production

[3]h^2- heritability estimate, r_a-genetic correlation, r_p- phenotypic correlation

Phenotypic, genetic and environmental correlations are measures of the strength of the relationship between traits and environmental effects. Genetic and environmental correlations together give the phenotypic correlation (Falconer, 1989). Phenotypic correlations indicate the gross relationships between traits that include both the environment and the genetic portions of the covariance. On the other hand, genetic correlations indicate how two traits are affected by similar genes regulating physiological processes. Correlations are useful in connecting traits within the selection criteria with traits in the breeding goal and aid in the prediction of response to selection in a trait due to direct selection in another. Furthermore, genetic correlations of traits recorded in different environments indicate presence and importance of genotype by environment (G x E) interactions (N'dri et al., 2007a).

Table 4 shows some genetic and phenotypic correlations for various IC traits. A positive correlation implies that an improvement in one trait would result in an improvement in the correlated trait, while a negative correlation would result in the deterioration of the correlated trait. For example, increasing AFE would result in EW improvement while reducing EN. It is therefore necessary to estimate the correlations between IC traits in Kenya before any meaningful genetic improvement programmes can be implemented.

2.6 Relationships between body weights and linear body measurements

Live body weights and linear body parts contribute significantly to the lifetime performance of an animal (Chineke, 2005). Body linear measurements are useful in describing body conformation and carcass composition (Lukaszewicz et al., 2008; Larivière et al., 2009). The associations between body weights and linear measurements are also important in evaluating breed performance and predicting live weights at various ages (Saatci and Tilki, 2007; Olawunmi et al., 2008). In addition, the measurements are also important in determining the relationships among economic characteristics and reproductive performance and the associations and interactions between heredity and environment (Ojedapo et al., 2008).

The associations between live body measurements are established through correlations, regressions and allometry (Yang et al., 2006b; Lukaszewicz et al., 2008). Correlations measure the type and strength of a relationship between two or more variables, while regressions establishes the extent to which one variable depends on other variables. Whereas correlations establish the general strength of an association between variables, regressions predict the outcome of one variable given a set of other variables. Allometry, on the other hand, is the change in relative dimensions of parts of an organism that are correlated

with changes in the overall size (Gayon, 2000). It measures the relationship between changes in an organisms shape and its overall size.

In livestock production, the relationships between body weights and linear body measurements provide information on performance, space requirements, selection and breeding, health and body condition score, feed requirements and carcass yield (Chineke, 2005; Yang et al., 2006b). In addition, regression equations are used to estimate live body weights from a linear measurement of a part of the body trunk, especially in the absence of weighing scales (Latshaw and Bishop, 2001). In most rural areas, weighing scales are not readily available. There is the need therefore to establish the type and strength of relationships between live body weights and linear body parts measurements, and formulate equations that can be used to estimate live body weights.

CHAPTER THREE

INFLUENCE OF MAJOR GENES FOR CRESTED-HEAD, FRIZZLE-FEATHER AND NAKED-NECK ON BODY WEIGHTS AND GROWTH PATTERNS OF INDIGENOUS CHICKEN REARED INTENSIVELY IN KENYA

3.1 Introduction

Domestic chickens are thought to have been introduced in Kenya at around 100 BC and have been undergoing both natural and to some extent human selection ever since (Maina, 2000). As a result, several distinct genotypes able to survive and reproduce in various environmental conditions developed with time and are still present despite introduction of exotic breeds. Some of the major genotypes available to date include the crested, frizzle, naked-neck, dwarf, tailless and feathered-shank, among others (Maina, 2000; Njenga, 2005). These genotypes possess major genes known to significantly contribute to adaptability and fitness of IC in the tropics (Horst, 1988). They therefore need to be exploited and utilized so as to increase production to meet the ever-increasing demand for IC products and to conserve them for present and future use (Bett et al., 2012). However, in Kenya the influence of major genes on traits of IC has not been determined.

Growth traits are important in any IC production system and an improvement in these traits would be expected to have a greater positive impact on the livelihoods of farmers (Menge, 2008). Growth is defined as an increase in entire body, body parts or individual organ's unit size per unit time (Yang et al., 2006a). Growth is described using mathematical functions that give biologically interpretable parameters. The Laird form of the Gompertz function is most commonly used in chicken as it depends on 3 parameters, each having a biological meaning (Mignon-Grasteau et al., 1999). These parameters are used to model growth curves that describe growth patterns. Accurate growth patterns of target animals are of importance to both producers and breeders in livestock production. Information on growth patterns is necessary and can be applied to determine feeding and management plans and design breeding strategies to improve capability of whole growth process (Lambe et al., 2006). Growth patterns of IC in Kenya have not been described. In this Chapter, the influence of morphologically expressed major genes on growth is determined and growth patterns of four IC genotypes described.

3.2 Materials and Methods

3.2.1 Experimental procedure

The study was conducted at the National Animal Husbandry Research Centre (NAHRC), Naivasha, Kenya. The centre has a mean annual temperature of 18°C with wide daily variations ranging from 8 to 26°C (NAHRC, 2000). The experimental birds were produced from unselected, random mating IC reared intensively at the centre. The flock comprised of birds collected from Western, North Rift, Central Rift, Mt. Kenya and Coastal regions of the country. Thirty three cocks (6 crested-head, 6 frizzle-feather, 7 naked-neck and 14 normal-feather) were randomly sampled from the flock. Each cock was allocated between 5 and 10 unrelated normal-feather hens and housed together in deep litter pens to produce the study population. Genotypes were identified according to the morphological expression of major genes for crested-head (Cr), frizzle-feather (Fr) and naked-neck (Na). Birds without any expression of the three major genes were classified as normal-feather (na).

3.2.2 Chicken management

Eggs were collected daily, labelled to identify an individual egg and its cock family and stored at room temperature for at most 14 days before incubation. The eggs were first-candled on the 7th day of incubation. After the 2nd candling on the 18th day of incubation, each egg was placed into an individual compartment for hatching. At hatch, chicks were tagged with numbered wing-tags and randomly placed into electric brooder compartments for brooding. At week 6 of age, genotypes were morphologically classified as normal-feather (nana nana, nana crcr and nana frfr), crested-head (nana Crcr), frizzle-feather (nana Frfr) or naked-neck (nana Nana). At week 9, chicks from a particular brooder compartment were transferred together into a randomly selected deep litter pen for rearing. Sex was determined by physiological appearance on the 8th and 14th weeks of age. All chicks were reared under natural light. Standard commercial feeds and clean water were supplied *ad libitum* at all ages and other standard management practises such as vaccinations and treatments applied procedurally.

3.2.3 Data collection

Each egg was weighed before incubation. Each bird was weighed at hatch and thereafter every 2 weeks up to 30 weeks of age using a digital weighing scale calibrated to the nearest 1 gram. Each bird had a total of 16 weight records starting from live body weight at hatch (BW0) and ending with live body weight at 30 weeks of age (BW30). A total of 511

birds (100 crested-head, 35 frizzle-feather, 87 naked-neck and 289 normal-feather) produced from 7 hatchings and with records up to 30 weeks of age were available for analysis.

3.2.4 Statistical analyses

Analysis of variance for live body weights at each age was performed using PROC GLM of SAS (SAS, 1998). A model that accounted for the fixed-effects parameters of hatch, genotype, sex and genotype nested within sex was fitted to determine the influence of genotype on live body weights. In the analysis of body weight at hatch, egg weight was fitted as a covariate, while in all other ages, body weight at hatch was fitted as a covariate. Least squares means were separated using the probability differences option. The model was:

$$\mathbf{Y_{ijkl} = \mu + H_i + G_j + S_k + G(S)_{jk} + \varepsilon_{ijkl}} \quad [1]$$

where: Y_{ijkl} = body weight of the l^{th} bird at a particular age; μ= overall mean; H_i = effect of the i^{th} hatch (i = 1…, 7); G_j = effect of the j^{th} genotype (j = crested-head, frizzle-feather, naked-neck, normal-feather); S_k = effect of the k^{th} sex (k = male, female); $G(S)_{jk}$= effect of genotype nested within sex; ε_{ijkl} = error term associated with each measurement.

Due to large differences in the genotype sample sizes, the power of the statistical test in Eq. 1 was analyzed. A post hoc power statistical analysis was conducted to determine the achieved power to reject the null hypothesis of no differences given the sample sizes, small to large genotype effect sizes and a constant alpha (Faul et al., 2007). The effect sizes (f) considered were small (f=0.1), moderate (f=0.25) and large (f=0.4) while alpha (α) was 0.05. In the absence of local population effect sizes, standard effect size parameters for the F-statistic are widely used (Faul et al., 2007). The F-statistic had a low power (0.45) to detect small effect sizes and very high powers (0.99 to 1.00) to detect moderate to high effect sizes between genotypes. The high power achieved showed that the statistic was able to detect medium to high effect size differences and reliably discriminate between the null and the alternate hypotheses despite the sample sizes of the genotypes.

3.2.5 Growth patterns

The growth pattern of each genotype was described by the Gompertz-Laird function (Aggrey, 2004) as:

$$\mathbf{BWt = BW0 \times \exp\left((L/K) \times \left(1 - \exp(-K \times t)\right)\right)} \quad [2]$$

where: BWt = live body weight at age t; BW0 = estimated body weight at hatch; L = initial specific growth rate; K = exponential rate of decay of the initial specific growth rate; and t = age in days.

Recorded body weights from hatch to 30 weeks of age were fitted into Eq. 2 and growth parameters BW0, L and K estimated for each bird using PROC NLIN of SAS (SAS, 1998). The estimated parameters were fitted into the function so as to model body weights at particular ages for each bird. In addition, age at inflection (t_I), body weight at inflection (BW_I), absolute growth rate (AGR) and relative growth rate (RGR) parameters were computed for each bird as (Aggrey, 2002 and 2004):

$$\mathbf{t_I = (L/K) \times \ln(L/K)} \quad [3]$$

$$\mathbf{BW_I = BW0 \times \exp((L/K) - 1)} \quad [4]$$

$$\mathbf{AGR = dBWt/dt = L \times \exp(-K \times t) \times BWt} \quad [5]$$

$$\mathbf{RGR = (dBWt/dt) \times (1/BWt) \times 100\% = L \times \exp(-K \times t) \times 100\%} \quad [6]$$

Analysis of variance for modelled body weights and for each parameter was performed according to Eq. 1 above. The least squares means for each genotype were then plotted against age to obtain growth curve patterns.

3.3 Results

3.3.1 Body weights

The least squares means of observed body weights for each genotype are presented in Table 5. The overall mean body weights at hatch (BW0), 6 weeks (BW6), 12 weeks (BW12), 18 weeks (BW18), 24 weeks (BW24) and 30 weeks (BW30) were 32.7, 309.5, 668.8, 1112.6, 1525.7 and 1741.0 g, respectively. The body weights from hatch to the 6th week of age were not significantly different ($P \geq 0.05$) between genotypes. The influence of major genes was apparent from the 8th week onwards. Whereas the Crcr genotype was significantly lighter than nana from the 18th week onwards, the Nana genotype was significantly lighter ($P<0.05$) than nana from the 8th week onwards and the Frfr genotype was significantly lighter than nana between the 8th and the 16th weeks only. However, the Crcr, Frfr and Nana genotypes had body weights that were similar at all ages.

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Table 5. Least squares means (LSM±se) for observed live body weights of indigenous chicken genotypes at different ages

BWt traits[1]	Average age in days (sd)	Genotypes[2]				Overall means
		Nana	Crcr	Frfr	Nana	
BW0	1.0	32.6±0.12^{a}	33.0±0.21^{a}	33.0±0.32^{a}	33.0±0.23^{a}	32.7±0.13
BW2	13.7(0.76)	78.2±0.74^{a}	75.7±1.31^{a}	76.4±2.00^{a}	75.3±1.45^{a}	77.9±0.79
BW4	27.8(0.85)	175.6±1.83^{a}	175.0±3.26^{a}	169.1±4.99^{a}	168.0±3.61^{a}	172.5±1.32
BW6	41.5(0.81)	312.7±3.40^{a}	303.9±6.04^{a}	296.8±9.25^{a}	301.7±6.68^{a}	309.5±2.61
BW8	56.0(0.70)	454.6±4.38^{a}	442.7±7.79^{ab}	426.4±11.94^{b}	429.9±8.62^{b}	438.9±3.67
BW10	70.2(1.80)	588.8±5.65^{a}	566.4±10.05^{ab}	539.4±15.40^{b}	551.2±11.13^{b}	558.9±4.83
BW12	83.6(1.58)	703.5±7.26^{a}	682.5±12.89^{ab}	640.8±19.77^{b}	658.3±14.28^{b}	668.8±6.11
BW14	98.2(1.38)	837.0±8.32^{a}	818.9±14.78^{ab}	771.1±22.66^{b}	783.7±16.37^{b}	789.6±7.64
BW16	112.4(0.85)	1007.9±9.70^{a}	979.5±17.24^{ab}	932.8±26.42^{b}	937.0±19.09^{b}	956.1±8.12
BW18	126.0(1.31)	1161.9±10.90^{a}	1109.7±19.37^{b}	1108.1±29.70^{ab}	1070.0±21.46^{b}	1112.6±8.87
BW20	140.1(1.48)	1356.8±13.62^{a}	1269.0±24.21^{b}	1289.1±37.12^{ab}	1235.0±26.81^{b}	1330.2±12.26
BW22	153.8(1.51)	1471.0±15.19^{a}	1358.7±26.99^{b}	1389.9±41.37^{ab}	1336.4±29.89^{b}	1419.9±13.28
BW24	168.1(1.17)	1570.0±16.58^{a}	1464.9±29.47^{b}	1497.6±45.18^{ab}	1450.9±32.64^{b}	1525.7±13.52
BW26	181.2(1.05)	1669.4±16.92^{a}	1568.3±30.07^{b}	1593.6±46.09^{ab}	1540.8±33.30^{b}	1629.0±13.67
BW28	195.2(1.23)	1735.0±17.39^{a}	1636.2±30.91^{b}	1645.2±47.39^{ab}	1620.8±34.23^{b}	1692.8±14.09
BW30	210.0(1.98)	1789.1±18.23^{a}	1690.4±32.40^{b}	1686.1±49.66^{ab}	1676.0±35.88^{b}	1741.0±14.49

[1]BWt- live body weight (g) at age t in weeks

[2]nana- normal-feather, Crcr- crested-head, Frfr- frizzle-feather, Nana- naked-neck

^{abc} means in a row with one or more superscripts in common are not significantly different ($P \geq 0.05$)

3.3.2 Growth patterns

The least squares means of the Gompertz-Laird growth parameters are presented in Table 6 and the specific growth curve in Figure 2. The estimated body weight at hatch (BW0), age at inflection (t_I) and body weight at inflection (BW_I) were not significantly different between genotypes. The nana, Frfr and Nana genotypes on one hand and nana, Frfr and Crcr on the other hand, had initial specific growth rate (L) and the exponential rate of decay of the initial specific growth rate (K) that were not significantly different. However, Crcr genotype had L and K that were significantly higher than Nana. The specific growth pattern had a characteristic sigmoid shape with a slow initial phase, followed by a rapid exponential growth phase and a final slow growth towards mature body weight (Figure 2). The nana, Crcr and Frfr genotypes had curves that were close to each other although the Frfr tended to have a higher body weight towards the asymptote.The Nana genotype however, had a lower growth curve than nana, Crcr and Frfr genotypes.

Table 6. Least squares means (LSM±se) for growth parameters of indigenous chicken genotypes

Parameters[1]	Genotypes[2]				Overall means
	Nana	Crcr	Frfr	Nana	
BW0	50.3±1.67[a]	49.1±3.00[a]	48.0±4.54[a]	56.7±3.24[a]	49.8±1.16
L	0.0603±0.00145[ab]	0.0633±0.00260[a]	0.0602±0.00394[ab]	0.0548±0.00281[b]	0.0599±0.00099
K	0.0153±0.00026[ab]	0.0161±0.00046[a]	0.0149±0.00070[ab]	0.0143±0.00050[b]	0.0150±0.00018
t_I	94.0±2.0[a]	91.0±3.0[a]	97.0±5.0[a]	98.0±3.0[a]	97.0±1.2
BW_I	837.4±17.97[a]	788.0±32.25[a]	807.4±48.80[a]	828.9±34.82[a]	840.6±13.03

[1]BW0- estimated body weight at hatch (g), L- initial specific growth rate (g/day) K- exponential rate of decay of the initial specific growth rate (g/day), t_I- age at inflection (days), BW_I- body weight at inflection (g)

[2] nana- normal-feather, Crcr- crested-head, Frfr- frizzle-feather, Nana- naked-neck

[abc]means in a row with one or more superscripts in common are not significantly different (P≥ 0.05)

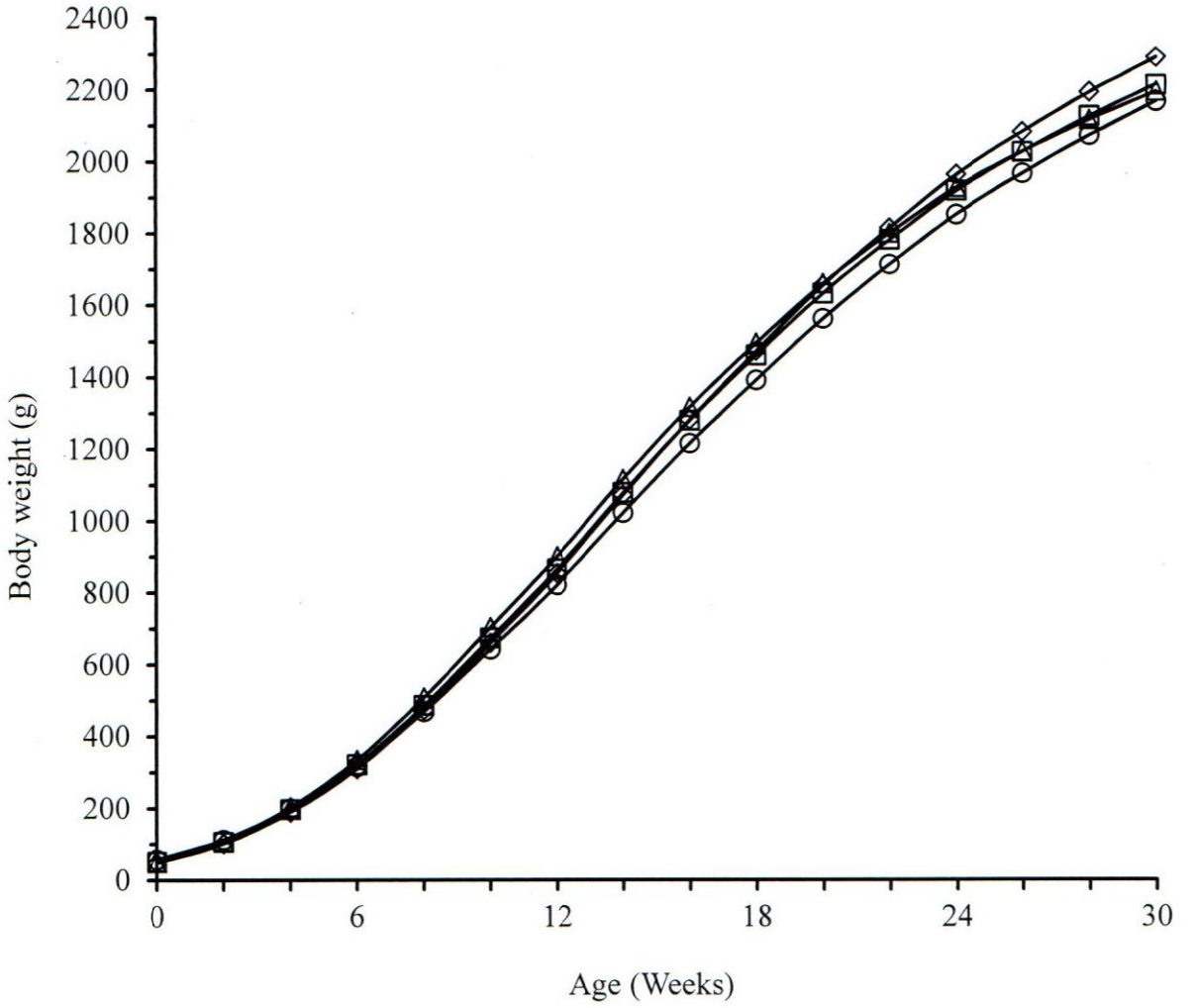


Figure 2. Specific growth curves for normal-feather (□), crested-head (Δ), frizzle-feather (◊) and naked-neck (○) indigenous chickens

The least squares means of absolute growth rate (AGR) for each genotype are presented in Table 7 and the growth patterns in Figure 3. All genotypes had similar AGR at hatch and from the 24th week onwards. From the 2nd to the 22nd week of age, the Crcr, Frfr and Nana genotypes had similar AGR. The Nana genotype however, grew at significantly lower rates ($P<0.05$) than nana between the 4th and the 18th week of age, while the Frfr grew at significantly lower rates than nana between the 2nd and the 6th week of age only. The Crcr genotype had significantly lower AGR than nana between the 10th week and the 22nd week, with the rates being similar in all other ages. The genotypes reached maximum AGR between the 12th and the 14th week (Figure 3). At these ages, the nana and Frfr genotypes on one hand, and the Crcr, Frfr and Nana on the other hand, had similar AGR. However, the Crcr and Nana genotypes had significantly higher maximum AGR than the nana genotype.

Table 7. Least squares means (LSM±se) for absolute growth rates of indigenous chicken genotypes at different ages

AGRt traits[1]	Genotypes[2]				Overall means
	Nana	Crcr	Frfr	Nana	
AGR0	2.74±0.046[a]	2.68±0.081[a]	2.53±0.125[a]	2.77±0.090[a]	2.63±0.034
AGR2	4.37±0.056[a]	4.33±0.100[ab]	3.99±0.153[b]	4.27±0.109[ab]	4.17±0.045
AGR4	6.47±0.081[a]	6.41±0.145[ab]	5.90±0.222[b]	6.09±0.158[b]	6.15±0.067
AGR6	8.43±0.110[a]	8.29±0.195[ab]	7.73±0.300[b]	7.77±0.213[b]	8.01±0.087
AGR8	10.08±0.128[a]	9.75±0.228[ab]	9.35±0.350[ab]	9.16±0.249[b]	9.60±0.100
AGR10	11.09±0.133[a]	10.53±0.238[b]	10.43±0.365[ab]	10.02±0.259[b]	10.60±0.103
AGR12	11.48±0.133[a]	10.74±0.238[b]	10.92±0.365[ab]	10.37±0.259[b]	11.04±0.105
AGR14	11.37±0.135[a]	10.50±0.241[b]	10.93±0.370[ab]	10.33±0.263[b]	11.02±0.110
AGR16	10.86±0.141[a]	9.95±0.251[b]	10.53±0.386[ab]	9.97±0.274[b]	10.63±0.117
AGR18	10.15±0.150[a]	9.26±0.267[b]	9.88±0.409[ab]	9.44±0.291[b]	10.02±0.125
AGR20	9.27±0.160[a]	8.45±0.284[b]	9.05±0.436[ab]	8.76±0.310[ab]	9.24±0.132
AGR22	8.37±0.169[a]	7.66±0.302[b]	8.17±0.463[ab]	8.04±0.329[ab]	8.42±0.136
AGR24	7.44±0.179[a]	6.87±0.320[a]	7.24±0.490[a]	7.27±0.348[a]	7.55±0.140
AGR26	6.63±0.189[a]	6.19±0.337[a]	6.43±0.516[a]	6.57±0.367[a]	6.78±0.144
AGR28	5.83±0.201[a]	5.55±0.358[a]	5.63±0.549[a]	5.87±0.390[a]	6.02±0.148
AGR30	5.09±0.217[a]	4.96±0.387[a]	4.87±0.593[a]	5.17±0.422[a]	5.30±0.156

[1]AGRt- absolute growth rate (g/day) at age t in weeks

[2]nana- normal-feather, Crcr- crested-head, Frfr- frizzle-feather, Nana- naked-neck

[abc]means in a row with one or more superscripts in common are not significantly different ($P\geq 0.05$)

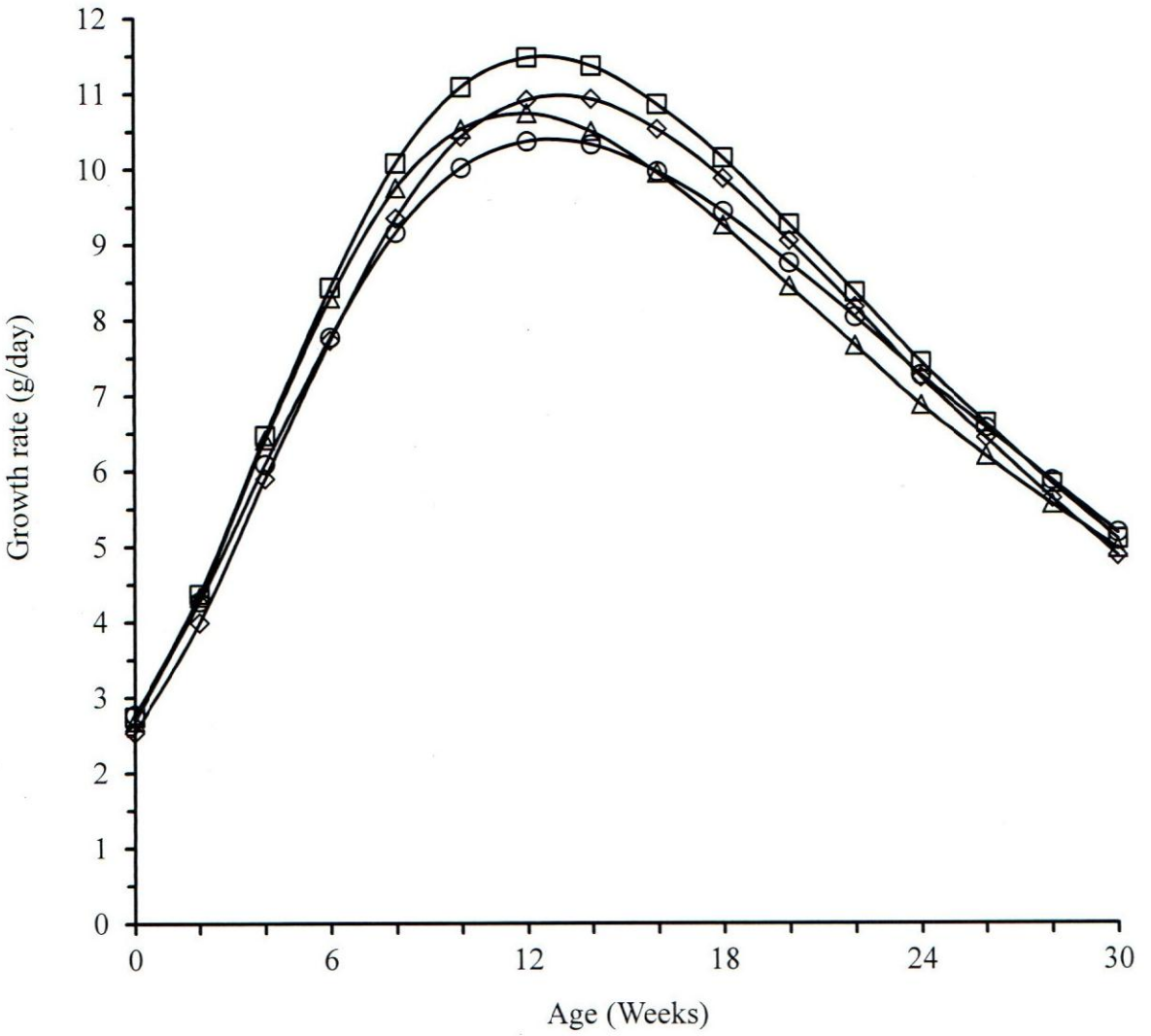


Figure 3. Absolute growth rate curves for normal-feather (□), crested-head (Δ), frizzle-feather (◊) and naked-neck (○) indigenous chickens

The least squares means of relative growth rate (RGR) for each genotype are presented in Table 8 and the corresponding growth curves in Figure 4. The genotypes displayed differences in RGR from hatch to the 16th week of age, with the highest growth rate being from hatch to the 2nd week of age. At hatch, whereas the Crcr genotype had a significantly higher RGR than Nana, the rate was similar to nana and Frfr. The Crcr had significantly higher RGR than Nana from hatch to the 2nd week but the rates were not significantly different thereafter. The Nana genotype had RGR that were significantly lower than nana between the 2nd and the 10th week of age while Crcr had significantly lower RGR than nana between the 12th and the 16th week of age. The Frfr genotype tended to have higher RGR than nana, Crcr and Nana genotypes at all ages. Whereas Frfr grew at a significantly higher RGR than Crcr between the 12th and the 16th week, it grew at significantly higher RGR

than Nana between the 8th and the 12th weeks of age. However, Frfr and nana genotypes did not have significantly different RGR at all ages.

Table 8. Least squares means (LSM±se) for relative growth rates of indigenous chicken genotypes at different ages

RGRt traits[1]	Genotypes[2]				Overall means
	Nana	Crcr	Frfr	Nana	
RGR0	5.94±0.145^{ab}	6.11±0.259^{a}	5.85±0.397^{ab}	5.34±0.282^{b}	5.86±0.099
RGR2	4.82±0.100^{a}	4.89±0.177^{a}	4.80±0.271^{ab}	4.37±0.193^{b}	4.77±0.068
RGR4	3.84±0.065^{a}	3.84±0.115^{ab}	3.85±0.177^{ab}	3.52±0.126^{b}	3.81±0.045
RGR6	3.09±0.042^{a}	3.05±0.076^{ab}	3.12±0.116^{ab}	2.86±0.082^{b}	3.07±0.030
RGR8	2.46±0.027^{a}	2.41±0.049^{ab}	2.50±0.075^{a}	2.31±0.053^{b}	2.46±0.020
RGR10	1.97±0.018^{a}	1.92±0.033^{ab}	2.02±0.051^{a}	1.88±0.036^{b}	1.98±0.014
RGR12	1.61±0.014^{ab}	1.55±0.025^{c}	1.65±0.038^{a}	1.55±0.027^{bc}	1.62±0.012
RGR14	1.29±0.012^{a}	1.24±0.021^{b}	1.33±0.032^{a}	1.26±0.023^{ab}	1.31±0.010
RGR16	1.05±0.011^{ab}	1.00±0.020^{b}	1.08±0.031^{a}	1.04±0.022^{ab}	1.07±0.009
RGR18	0.86±0.011^{a}	0.82±0.020^{a}	0.89±0.030^{a}	0.86±0.022^{a}	0.88±0.009
RGR20	0.70±0.011^{a}	0.67±0.020^{a}	0.73±0.030^{a}	0.71±0.021^{a}	0.72±0.009
RGR22	0.58±0.011^{a}	0.56±0.019^{a}	0.60±0.030^{a}	0.60±0.021^{a}	0.60±0.008
RGR24	0.47±0.010^{a}	0.46±0.019^{a}	0.49±0.029^{a}	0.49±0.021^{a}	0.49±0.008
RGR26	0.39±0.010^{a}	0.38±0.018^{a}	0.41±0.028^{a}	0.42±0.020^{a}	0.41±0.008
RGR28	0.33±0.010^{a}	0.32±0.018^{a}	0.34±0.027^{a}	0.35±0.019^{a}	0.34±0.007
RGR30	0.27±0.010^{a}	0.27±0.017^{a}	0.28±0.027^{a}	0.29±0.019^{a}	0.28±0.007

[1]RGRt- relative growth rate (%) at age t in weeks

[2] nana- normal-feather, Crcr- crested-head, Frfr- frizzle-feather, Nana- naked-neck

^{abc}means in a row with one or more superscripts in common are not significantly different ($P \geq 0.05$)

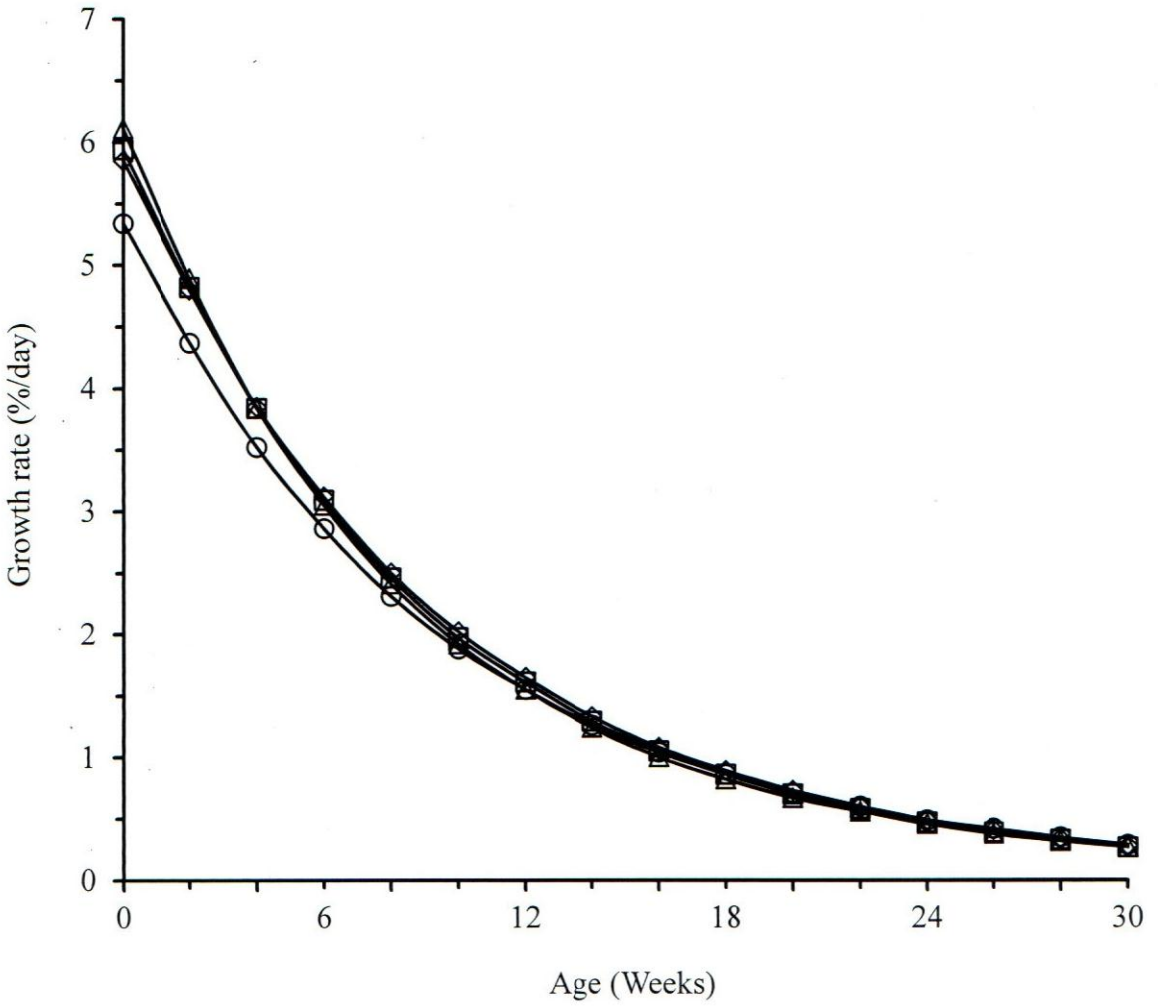


Figure 4. Relative growth rate curves for normal-feather (□), crested-head (Δ), frizzle-feather (◊) and naked-neck (○) indigenous chickens

3.4 Discussion

3.4.1 Body weights

The observed overall mean hatching weight and the overall mean body weights at all ages in this study were higher than reported for indigenous chickens in the tropics (Adedokun and Sonaiya, 2001; Msoffe et al., 2004; Fayeye et al., 2005; Halima et al., 2006b; Thakur et al., 2006). The weights were lower than for selected commercial breeds (N'dri et al., 2006), Athens-Canadian chickens (Aggrey, 2002), indigenous Creole chickens (Segura-Correa et al., 2004 and 2005), Chinese Jinghai yellow chickens (Yang et al., 2006a) and crosses between Egyptian local and European breeds (Mekky et al., 2008). However, the weights were comparable to crosses between indigenous chickens and European breeds (Azharul et al., 2005; Chatterjee et al., 2007), crosses of various indigenous chicken breeds in Egypt (Iraqi et al., 2002) and strains of commercial layers reported by Ojedapo et al. (2008). The overall mean body weights across the ages suggest that birds from most regions of the country are

not strictly indigenous but non-descript crosses between the original indigenous birds and European breeds. Indeed, the crosses are as a result of an exotic cockerel exchange programme that operated between 1978 and 1996 in most regions of the country (Nyange, 1995).

Although the Crcr, Frfr and Nana genotypes tended to have slightly higher body weights at hatch, the differences were not statistically significant. The lack of significant differences between genotypes from hatch to 6 weeks of age agrees with the findings of Padhi et al. (1999) for Nana and nana Andaman chicken genotypes in India. However, Segura-Correa et al. (2005) reported similarity in body weights from hatch to 18 weeks of age between Nana and nana Creole chicken genotypes in Mexico. Missohou et al. (2003) reported no significant differences between Frfr and nana at hatch while Mahrous et al. (2008) reported no significant differences between Frfr and nana genotypes from hatch to 4 weeks of age. The results were however, in contrast with Mahrous et al. (2008) who also reported significant differences between Nana and nana from hatch to 12 weeks and between Nana and Frfr from hatch to 4 weeks of age. The different results obtained by the various authors may be attributed to genetic diversity of the populations, age and size of hens used to produce the experimental birds and the prevailing environmental conditions especially ambient temperatures. It is an established fact that egg weights are positively correlated with hatching weights and age of hen at lay (Van den Brand, et al., 2004; Saatci et al., 2005; Ojedapo et al., 2008). In this study, diurnal ambient temperature variations were wide and the hens were of various ages.

When compared to na, the Na gene had between 24.7g and 134.6g body weight depression effect from the 8^{th} week onwards while the Fr gene had between 28.2g and 75.1g body weight depression effect from the 8^{th} to the 16^{th} week only. Njenga (2005) found significant differences in body weights of mature Nana, Frfr and nana genotypes in coastal Kenya. In that study, Nana genotype had significantly heavier mature body weight than nana, while the weight of Frfr genotype was similar to that of Nana and nana. In addition, Nana and Frfr genotypes tended to be heavier than nana at the 5^{th} week of age, although the differences were not significant. It is worthwhile to note that coastal Kenya has an average mean temperature of $26^{o}C$ (Njenga, 2005). Missohou et al. (2003) on the other hand, noted significant body weight depression effects attributed to the Fr gene at 20 and 44 weeks of age.

The naked-neck and frizzle-feather genes, either singly or in combination have been shown to confer consistent superiority in body weights, feed conversion, egg production and

disease resistance at moderate (25°C) to high (32°C) ambient temperatures. Missohou et al. (2003) showed that heterozygous frizzle-feather layers consistently produced more eggs than their normal-feather counterparts. Mahrous et al. (2008) reported that the frizzle-feather, naked-neck and naked-neck-frizzle genotypes had significantly heavier body weights, improved feed conversion ratio and increased total antibody titre against sheep red blood cells compared to their normal-feather counterparts. However, at moderate (20°C) to low (12°C) ambient temperatures, the genes have equal or inferior performance compared to their normal-feather counterparts (Yahav et al., 1998; Raju et al., 2004; El-Safty et al., 2006). The Na and Fr genes exert their effects physiologically due to reduced body insulation (Bartels, 2003). The superior performance of Nana and Frfr genotypes at high ambient temperatures are due to their ability to dissipate heat by convection, thus leading to less heat stress than nana genotypes (Yahav et al., 1998; Deeb and Cahaner, 1999; Adedeji et al., 2006). The inferior performance of heterozygous Nana and Frfr genotypes in the current study is an expected consequence of reduced body insulation leading to increased heat loss at low to moderate environmental temperatures (Yahav et al., 1998). The recovery of the Frfr genotype from the 18th week onwards is possibly due to a decrease in heat loss resulting from a possible increase in feather coverage with age, unlike the Nana genotype. The two genotypes are therefore not ideal for environments with low ambient temperatures. Interestingly, Crcr genotype had significantly lower body weights than nana from the 18th week onwards, with body weight depression effects ranging between 52.2g and 112.3g. Both genotypes were normal-feather and the only morphological difference was the presence of a tuft of feathers on the head of Crcr genotype. There is scarcity of information on the performance of Crcr genotypes in literature. It is however proposed that the low body weights may be due to possible pleiotropic effects of the Cr gene, genetic linkage or gene x gene interactions. There is therefore the need for further investigations. Furthermore, since many reports have shown that light strains of birds are good layers (Adedeji et al., 2006), the crested-head genotype may also be a good layer.

3.4.2 Growth patterns

Estimated BW0 were higher than measured for all genotypes. However, BW0 for nana, Crcr and Frfr (50.3g, 49.1g and 48.0g, respectively) were close to 46.1g reported by Aggrey (2002) for unselected random mating Athens-Canadian chicken population and higher than 39.6g reported by Mignon-Grasteau et al. (1999) for selected meat-type chickens. The Gompertz-Laird growth function usually overestimates BW0 and it has been suggested

that BW0 should be measured rather than estimated or be constrained by weighting with the inverse of the variance (Aggrey, 2002). However, constraining BW0 has been shown not to improve the fitting of Gompertz-Laird model, and results in estimating model parameters that are out of parameter space (Koncagul and Cadirci, 2010).

Growth parameters L, K and BW_I for all genotypes in this study were lower, while t_I was higher than for improved chickens (Mignon-Grasteau et al., 1999; Aggrey, 2002). In addition, all genotypes had maximum AGR that were lower than reported for broilers (Santos et al., 2005), and RGR were also lower than for Athens-Canadian chickens reported by Aggrey (2004). This implies that IC in Kenya, on average, grow and mature slowly (0.06 g/day and 0.02 g/day, respectively), have low body weights (840.6g) when growth rate is at its maximum and takes longer (14 weeks) to attain the body weights when growth rate is at its maximum. This confirms the fact that unselected IC have slow growth (King'ori et al., 2007). However, the growth of Nana was significantly lower than Crcr genotype yet the body weights across ages, and body weight and age at inflection were not significantly different. The Naked-neck breed in South Africa has been reported to have a higher growth rate, early maturity and a lighter mature weight as opposed to the Venda breed with a lower growth rate, late maturity but a heavier mature weight (Norris et al., 2007). The Nana genotype in the current study may have consumed more feeds to generate body heat than the other genotypes so as to compensate for heat loss (Yahav et al., 1998). Investigations on feed efficiencies of the genotypes are therefore warranted.

The growth trajectories (Figure 2, 3 and 4) obtained in this study were similar to curves reported for chickens (Kuhi et al., 2003; Aggrey, 2004; Santos et al., 2005; Norris et al., 2007), ducks (Maruyama et al., 2001), quails (Hyankova et al., 2001) and guinea fowls (Nahashon et al., 2006b). The specific growth curves (Figure 2) had a characteristic sigmoid shape (Kuhi et al., 2003), with initial slow growth from hatch to 2 weeks, exponential growth from week 2 to week 20 and a final slow growth thereafter towards the asymptote. The absolute growth curves (Figure 3) had a characteristic bell-shape (Hyankova et al., 2001) with growth rate accelerating phase from hatch towards maximum growth, a maximum growth phase between week 12 and 14, and a growth rate decline phase thereafter. The relative growth curves (Figure 4) had a characteristic diminishing-returns shape (Aggrey, 2004) with the highest growth at hatch, followed by a decline with age. Whereas specific growth curves describe the relationship between cumulative live body weights with age, absolute growth curves describe the change in body weight per unit time while relative

growth curves describe the ratio of the change in body weight to the achieved body weight at a given age (Kuhi et al., 2003; Aggrey, 2004).

Growth curve patterns have been used to improve performance of domestic birds. Growth parameters are known to be heritable (Mignon-Grasteau et al., 2000b) and selection strategies have long been used to modify the shapes of growth curves, leading to rapid growth in broilers, quails and ducks (Hyankova et al., 2001; Maruyama et al., 2001). In Kenya, IC have not been systematically improved through selective breeding (King'ori et al., 2007). The growth characteristics will contribute to efforts of genetically improving the performance of IC in Kenya. In addition, understanding growth characteristics will aid in designing feeding schemes for environments utilizing the various genotypes to maximize production efficiency while minimizing production costs of this very important genetic resource.

3.5 Conclusions

The first step in any livestock improvement endeavour is to determine current optimal performance levels. The overall mean body weights across the ages in this study indicated that IC from most regions of the country may not strictly be indigenous but are non-descript crosses between the original indigenous birds and various European breeds. Therefore, there exists already some level of body weight improvement that should be exploited.

Unfavorable environmental temperatures constrain chicken performance in both intensive and extensive production systems. Determining the performance of IC genotypes is important in matching them to suitable environments for increased productivity. This study revealed that major genes influence growth and growth patterns of IC at different ages from 8 weeks of age. At moderate to low environmental temperatures, the frizzle and naked neck genes depress growth performance and are not ideal for cool environments even in the tropics. Although the crested gene also depresses growth, the crested genotype may be a candidate for egg production.

The study demonstrated that the specific growth of IC displays a characteristic sigmoid pattern. The low average L and K, and the high t_I confirmed that IC grow and mature slowly although wide variations exist between genotypes and individuals within genotypes leading to differences in growth patterns. The highest absolute growth occurred at between 8 and 18 weeks of age while the highest growth efficiencies occurred between hatch and 16 weeks of age. The differences in growth patterns between genotypes and individuals within genotypes can be used in the development of parental lines in a breeding programme. Therefore, breeding programmes aimed at altering the shape of growth curves should be

established and selection strategies formulated to improve growth performance of the various IC genotypes. In addition, feed rations and feeding strategies aimed at optimizing absolute growth should be formulated.

CHAPTER FOUR

GENETIC PARAMETER ESTIMATES FOR EGG AND BODY WEIGHTS OF INDIGENOUS CHICKEN IN KENYA

4.1 Introduction

Several attempts have been made to increase production performance of IC in Kenya. These attempts have focused mainly on genetic improvement through crossbreeding with exotic breeds, mortality reduction through improved housing and vaccinations, and nutritional improvement through feed supplementation (Nyange, 1995; Okitoi et al., 2000; Juma and Ondwasy, 2002). However, no attempt has ever focused on genetic improvement through selection yet selection strategies have been used to improve growth and egg production of commercial chickens (Siegel et al., 2006; Nwagu, et al., 2007). In addition, breeding programmes utilizing appropriate selection strategies have been used to improve growth and egg production of native chickens in Egypt, Korea and Iran (Kosba et al., 2006; Sang et al., 2006; Kamali et al., 2007). Despite slow and usually small genetic achievements through selection, the changes realized are always permanent and cumulative unlike in crossbreeding or upgrading (FAO, 2007).

Improvement through selection requires estimates of genetic parameters. Even in case of inadequate information and data, some attempt at estimating genetic and phenotypic parameters is better than no attempt. Therefore, this Chapter provides preliminary estimates of heritabilities and correlations between egg weight and body weights necessary for the establishment of a breeding programme for IC based on quantified parameter estimates. These estimates would be improved as more performance and pedigree data becomes available.

4.2 Materials and Methods

4.2.1 Data source and chicken management

The data source and chicken management is as described in Chapter 3. Briefly, the experimental birds were produced from unselected, random mating IC reared intensively at the centre. The flock comprised of birds collected from Western, North Rift, Central Rift, Mt. Kenya and Coastal regions of the country. Thirty three cocks were randomly sampled from the flock, each allocated between 5 and 10 unrelated hens and housed together in deep litter pens to produce the study population.

4.2.2 Data collection and analyses

Data collection is as presented in Chapter 3. The study population of 511 birds produced in 7 hatchings and with records up to 30 weeks of age were progenies of 33 sires and 136 dams. Significant fixed effects and covariates to be fitted were determined using PROC GLM (SAS, 1998). Estimates of heritabilities and correlations were based on the sire model with variance components estimated using Derivative-Free Restricted Maximum Likelihood (DFREML) method (Meyer, 1997).

Variance components were first estimated for egg weight (EW) and body weight at each age using single trait procedures. Three juvenile (BW2, BW4 and BW6), three growing (BW12, BW14 and BW16) and one mature body weight (BW26) with the highest heritabilities were further analysed using multiple trait procedures to re-estimate heritabilities and estimate correlation coefficients. In both analyses, sire and residual effects were fitted as random effects. In the analysis of hatching weight (BW0), hatch number was the only fixed effect while for subsequent body weights, an additional fixed effect of sex was added. In addition, EW was fitted as a covariate in the analysis of BW0 while for BW2 to BW10, EW was replaced with BW0 as a covariate.

The model used was: -

$$\mathbf{y_i = Xb_i + Zs_i + \varepsilon_i} \qquad [1]$$

where: y_i = vector of observations of the i^{th} observation; X and Z = incidence matrices relating observations to the respective fixed and random effects, respectively; b_i = vector of fixed effects on observations; s_i = vector of random sire effects; ε_i = vector of random residual effects.

Heritability estimates (h^2) were calculated as:

$$\mathbf{h^2 = \frac{4\,\sigma_s^2}{\sigma_s^2 + \sigma_\varepsilon^2}} \qquad [2]$$

where: σ_s^2 and σ_ε^2 = sire and residual variances, respectively.

The genetic and phenotypic correlations were estimated as:

$$\mathbf{r_{y(1,2)} = \frac{\sigma_{s(1,2)}}{\sqrt{\sigma_{y(1)}^2 \times \sigma_{y(2)}^2}}} \qquad [3]$$

where: $r_{y(1,2)}$ = genetic or phenotypic correlation between trait 1 and 2; $\sigma_{s(1,2)}$ = sire covariance between trait 1 and 2; $\sigma^2_{y(1)}$ and $\sigma^2_{y(2)}$ = sire or phenotypic variances of trait 1 and 2, respectively.

4.3 Results

4.3.1 Heritability estimates for egg and body weights

The single trait variance components and heritability estimates for EW and BW0 to BW30 are presented in Table 9. The heritability estimate for EW was high (0.95±0.27). The estimate for BW0 was close to zero (0.05±0.09), moderate (0.28±0.18 to 0.39±0.18) for BW2 to BW6, low (0.12±0.08 to 0.16±0.10) for BW8 to BW16 and close to zero (0.01±0.04 to 0.07±0.07) for BW18 to BW30. The sire variance was low and close to zero for BW0. However, the sire variances for all body weights fluctuated while both phenotypic and residual components increased with age.

Table 9. Single-trait estimates of sire (σ^2_s), residual (σ^2_ε) and phenotypic (σ^2_p) variances and heritability coefficients (h^2) with standard error (SE) for egg weight and biweekly body weights

	Phenotypic measurements			Variance components				
Trait[1]	Mean	Min	Max	σ^2_s	σ^2_ε	σ^2_p	h^2	SE
EW	47.5	36.0	58.0	3.17	10.17	13.34	0.95	0.27
BW0	32.7	24.0	43.0	0.04	3.22	3.26	0.05	0.09
BW2	77.9	42.0	135.0	9.39	123.47	132.85	0.28	0.18
BW4	172.5	85.0	263.0	78.75	732.06	810.81	0.39	0.18
BW6	309.5	147.0	504.0	225.75	2712.50	2938.25	0.31	0.18
BW8	438.9	212.0	766.0	173.49	4291.57	4465.06	0.16	0.10
BW10	558.9	250.0	988.0	216.96	7328.32	7545.28	0.12	0.09
BW12	668.8	315.0	1259.0	480.09	11568.20	12048.28	0.16	0.10
BW14	789.6	430.0	1558.0	521.59	17148.03	17669.62	0.12	0.09
BW16	956.1	503.0	1716.0	640.35	21618.21	22258.55	0.12	0.08
BW18	1112.6	571.0	1961.0	498.53	29861.00	30359.53	0.07	0.07
BW20	1330.2	616.0	2102.0	366.35	37749.92	38116.27	0.04	0.06
BW22	1419.9	705.0	2286.0	218.34	66622.14	66840.47	0.01	0.05
BW24	1525.7	621.0	2481.0	389.59	67602.35	67991.94	0.02	0.05
BW26	1629.0	824.0	2656.0	548.57	70029.53	70578.10	0.03	0.05
BW28	1692.8	830.0	2844.0	443.22	72119.00	72562.23	0.02	0.04
BW30	1741.0	836.0	3034.0	118.97	79422.39	79541.36	0.01	0.04

[1]EW- egg weight (g), BWt- body weight (g) at age t (weeks)

The heritability estimates changed with age (Figure 5). The estimates increased sharply from 0.05±0.09 at hatch to 0.39±0.18 at 4 weeks of age and thereafter, generally decreased to 0.01±0.04 at 30 weeks.

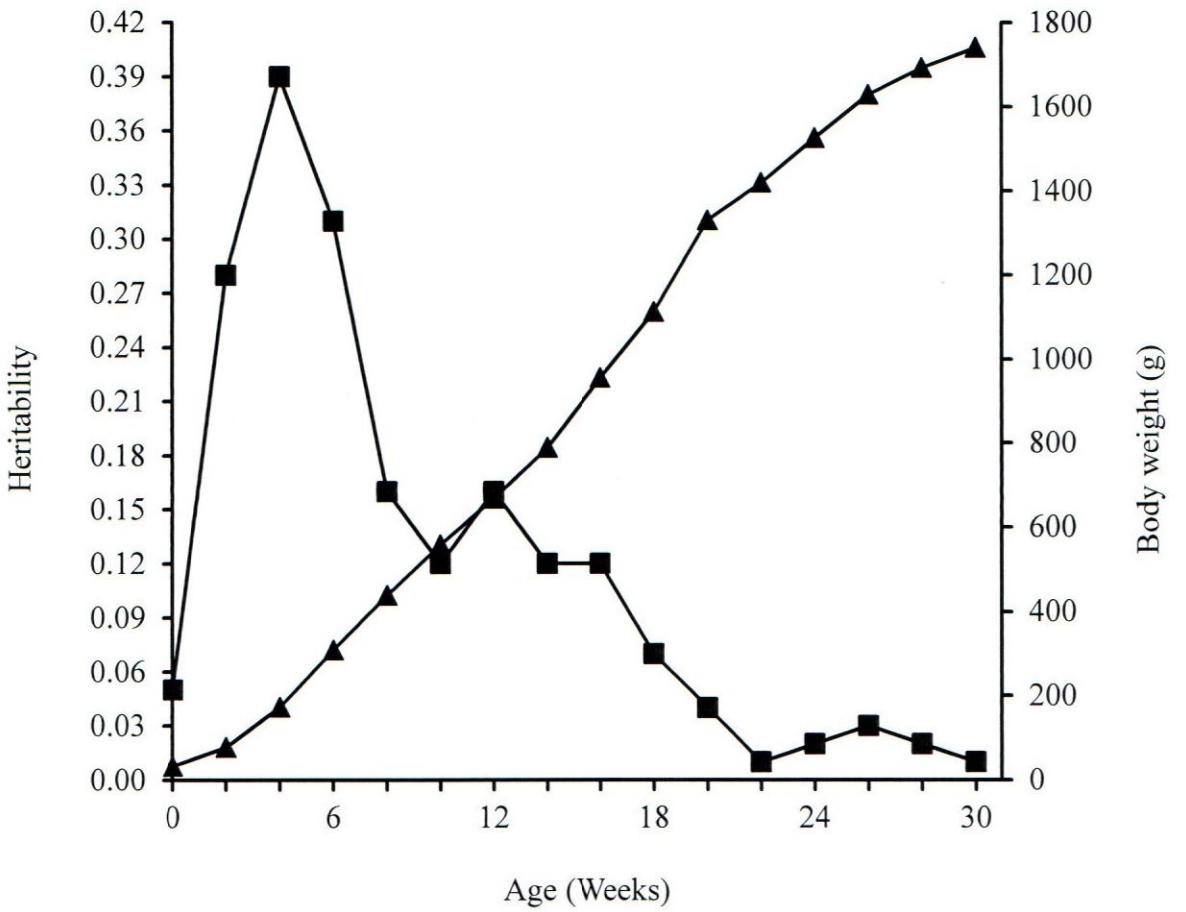


Figure 5. Changes in heritability coefficients (■) and body weights (▲) of indigenous chickens with age

The variance components and heritability estimates from multi-trait analysis are presented in Table 10. For each trait, the heritability estimate was higher than in single-trait analysis. The heritability estimates were high (0.51±0.22 to 0.65±0.24) for juvenile body weights (BW2 to BW6), intermediate (0.29±0.20 to 0.35±0.20) for grower weights (BW12 to BW16) and low 0.11±0.10) for the mature weight (BW26). Whereas all the variance components increased with age, the proportion of the sire variance for each trait increased while the residual variance reduced.

Table 10. Multi-trait estimates of sire (σ^2_S), residual (σ^2_ε) and phenotypic (σ^2_p) variances, and heritability coefficient (h^2) with standard error (SE) for egg weight and body weights at various ages

Traits[1]	σ^2_s	σ^2_ε	σ^2_p	h^2	SE
EW	3.31	10.15	13.47	0.98	0.26
BW2	17.47	119.54	137.01	0.51	0.22
BW4	136.61	706.55	843.16	0.65	0.24
BW6	385.16	2637.71	3022.86	0.51	0.22
BW12	1074.93	11219.12	12294.05	0.35	0.20
BW14	1385.91	16592.70	17978.61	0.31	0.23
BW16	1668.68	20964.47	22633.16	0.29	0.20
BW26	1875.50	69066.96	70942.46	0.11	0.10

[1]EW- egg weight, BWt- live body weight (g) at age t (weeks)

4.3.2 Correlation between egg and body weights

The genetic and phenotypic correlations are presented in Table 11. Whereas all phenotypic correlations between traits were low (0.01 to 0.14), genetic correlations ranged from low to near unity (0.05 to 0.99). Both phenotypic and genetic correlations between EW and juvenile body weights (at 2, 4 and 6 weeks of age) were negative while correlations with growing and adult body weights were positive. The genetic correlations between body weight traits were all positive and decreased with age from near unity to moderate (0.99 to 0.44).

Table 11. Genetic (above diagonal) and phenotypic (below diagonal) correlations between egg weight, juvenile body weights (BW2 to BW6), grower body weights (BW12 to BW16) and mature body weight (BW26)

Traits[1]	EW	BW2	BW4	BW6	BW12	BW14	BW16	BW26
EW	-	-0.13±0.28	-0.14±0.27	-0.15±0.28	0.05±0.32	0.17±0.32	0.25±0.30	0.58±0.36
BW2	-0.02	-	0.99±0.21	0.99±0.12	0.89±0.31	0.84±0.34	0.78±0.35	0.52±0.47
BW4	-0.03	0.14	-	0.99±0.26	0.85±0.25	0.80±0.38	0.74±0.30	0.47±0.47
BW6	-0.03	0.13	0.14	-	0.83±0.33	0.78±0.37	0.72±0.41	0.44±0.46
BW12	0.01	0.09	0.10	0.09	-	0.99±0.62	0.97±0.51	0.80±0.51
BW14	0.02	0.08	0.09	0.08	0.08	-	0.99±0.71	0.87±0.50
BW16	0.03	0.08	0.08	0.07	0.08	0.08	-	0.92±0.60
BW26	0.05	0.03	0.03	0.03	0.04	0.04	0.04	-

[1]EW- egg weight, BWt- live body weight (g) at age t (weeks)

4.4 Discussion

4.4.1 Heritability estimates for egg weight and body weights

Heritability for EW was high (0.95) and comparable to the value of 0.91 reported for chicken populations not selected or with a short selection history for EW (Wei and van der Werf, 1995; Poggenpoel et al., 1996). However, it was higher than the range of 0.26 to 0.64 reported for populations with long EW selection histories using either sire or animal models that accounted for maternal additive and maternal or common environmental effects (Koerhuis and Thompson, 1997; Hartmann et al., 2003; Nurgiartiningsih et al., 2004; Zhang et al., 2005; Kamali et al., 2007). Differences in genetic backgrounds and the estimation model used explain the very high heritability estimate for EW obtained in this study. Selection is expected to change variances of traits depending on the duration, intensity and direction of the selection (Hill et al., 2007). Although EW is a highly heritable trait, the chicken population in this study have not been subjected to any selection and therefore exhibited high additive genetic variation as expected (Iraqi et al., 2002). On the other hand, EW is determined by processes in the hen's reproductive tract. Non-additive, maternal additive and, maternal and common environmental effects highly contribute to variation in EW (Hartmann et al., 2002; Bunter and Cloete, 2004; Saatci et al., 2006). In the current study, maternal and common environmental influences were not accounted for in any way. Castillo and Segura-Correa (2004) showed that failure to separate these effects from the direct additive effects leads to overestimation of heritabilities. It is therefore concluded that both maternal additive and environmental variances may have been confounded with the sire variance, leading to overestimation of the heritability of EW. It is an established fact that EW accounts for between 86 to 97% of chick weight at hatch and hatching weight is therefore also considered a trait of the hen (Hartmann et al., 2003).

The sire component of variance in this study explained less the variation in BW0. This was in agreement with Koerhuis and Thompson (1997) who reported negligible sire variance for chick weight at hatch. The heritability estimate of BW0 was 0.05 and close to 0.01 reported by Hartmann et al. (2003) and Le Rouzic et al. (2008) using models that included maternal and environmental effects. Similar low hatching weight heritability estimates have been reported for Quails (Akbaş et al., 2004; Saatci et al., 2006). In contrast, Adeyinka et al. (2006), Norris and Ngambi (2006) and Dana et al. (2011) reported heritability estimates of 0.32, 0.36 and 0.40, respectively, despite including maternal and environmental effects in their estimation models. Castillo and Segura-Correa (2004) compared various models that included or excluded maternal and environmental effects and reported hatching

weight heritability estimates ranging from 0.13 to 0.99. They concluded that estimates of direct heritability decreased when the maternal or environmental effects were included in the model. The genes of the hen that determine EW have a large influence on chick weight, whereas the chick's own genes only explain a very small part of its weight at hatch (Hartmann et al., 2003). Hatching weight is therefore also treated as a trait of the hen. However, explicit estimation of maternal and environmental effects is generally difficult unless a very well designed data set is available (Satoh et al., 2002; Castillo and Segura-Correa, 2004). Nevertheless, Bunter and Cloete (2004) suggested that accounting for differences in egg and/or chick weight may reduce the need to model hen effects explicitly. In this study, fitting EW as a covariate appears to have indirectly accounted for maternal and environmental effects thus leading to unbiased direct BW0 heritability estimate.

The heritability estimates for BW2 (0.28), BW4 (0.39) and BW6 (0.31) were moderate and in agreement with Adeyinka et al. (2006) and Norris and Ngambi (2006). The low estimates for BW8 to BW16 are in agreement with Iraqi et al. (2002) who reported estimates of 0.15, 0.20 and 0.14 for body weights of Egyptian chickens at 8, 12 and 16 weeks, respectively. Dana et al. (2011) reported estimates of 0.16, 0.16 and 0.23 for Horro chicken at 8, 12 and 16 weeks, respectively. However, Norris and Ngambi (2006) found an estimate of 0.41 for body weights of Venda chickens at 10 weeks of age. The very low estimates ranging from 0.01 to 0.07 for BW18 to BW30 were at variance with several reports in literature (e.g. Kabir et al., 2006; Norris and Ngambi, 2006; Le Rouzic et al., 2008; Momoh and Nwosu, 2008). Heritability estimates are not only a property of a trait but also of a population and the environment in which the estimates are made (Falconer, 1989). The differences in estimates may be attributed to differences in genetic backgrounds, data structures and the estimation models used.

The general decrease in heritability with age may be due to gene effects and an increase in environmental effects that could not be accounted for. Growth is a complex process involving the basic genetics of metabolism, health and the general adaptation to a particular environment. The growth process involves large numbers of genes with some being activated or deactivated at different stages of development (Le Rouzic et al., 2008). Growth hormone (GH) and insulin-like growth factors (IGF) are involved in metabolism and body growth by regulating the synthesis and degradation of glycogen and proteins in animals (Zhou et al., 2005). In the avian species, the plasma concentration of GH and IGF has been shown to increase from hatch to between 5 and 7 weeks with the highest concentration being at 3 to 5 weeks (Baéza et al., 2001; Yun et al., 2005). Baéza et al. (2001) showed that GH and

IGF decrease with age. This phenomenon appears to agree with the changes in heritability estimates in the current study. An increased GH and IGF gene action probably leads to high additive genetic variances hence the increase in heritability from hatch to 4 weeks of age (Figure 5). Conversely, reduced gene action probably reduces the additive genetic variance leading to decreased heritability thereafter. However, the decreasing estimates may also be explained by increases in environmental effects as indicated by the sire variances fluctuations with age. Environmental (seasonal temperatures) and poor management conditions are known to increase the residual variance and decrease the heritability estimates (Prado-Gonzalez et al., 2003). Furthermore, the increase in phenotypic and residual variances with age is expected in time series growth data and is attributed to increased body weights and a corresponding increase in standard deviations (Nahashon et al., 2006a).

The variance components and heritability estimates from multi-trait analysis were higher than in single trait analysis. Although the estimates at various ages were within the ranges reported in literature (Chambers, 1990; Zhang et al., 2003; Le Rouzic et al., 2008; Momoh and Nwosu, 2008), high juvenile heritability estimates have been reported for various poultry species (Mignon-Grasteau et al., 2000a; Mielenz et al., 2006). The increase in heritability from week 2 to week 4 and subsequent decrease with age followed the same trend as in single trait analysis. Increases in heritability estimates as a result of analysing several traits or variates simultaneously have been reported in Ostriches (Bunter and Cloete, 2004) and cattle (Ramirez-Valverde et al., 2001; Ilatsia et al., 2007). The high heritability estimates are due to stabilizing effects that reduces environmental noise of correlated traits leading to increased additive and reduced residual variances (Ilatsia et al., 2007).

4.4.2 Correlation between egg weight and body weights

The phenotypic correlations for juvenile weight were low. Adeyinka et al. (2006) and Lwelamira et al. (2009) found medium to high phenotypic correlations for body weights between 2 and 8 weeks for broilers and between 12 and 20 weeks of age for IC ecotypes, respectively. The low to near zero phenotypic correlations indicate that environmental factors had a low overall effect on phenotypic expressions between the various traits. This apparently surprising phenomenon may be explained by the genetic background of the chicken.

Indigenous chicken in most regions of the country are non-descript crosses between the original chickens and exotic pure breeds and hybrids of differing genetic backgrounds (Nyange, 1995). As shown by the wide range of phenotypic measurements (Table 9), the population studied had both light and heavy individuals. Furthermore, the population

comprised of various genotypes whose body weight changes and deviations differed at various ages (Chapter 3). Therefore differing body weight's phenotypic deviations of the various genotypes at different ages may have caused the low phenotypic correlations (Falconer, 1989). In addition, correlation coefficients of less than unity are also indicators of presence of genotype by environment (G x E) interactions (Settar et al., 1999). The low phenotypic correlations in the current study may also be due to high interactions between the genotypes and the environment, especially in regard to environmental temperature fluctuations. During the brooding period, temperature fluctuations were minimal, leading to a reduction in the effects of G x E interactions.

The high genetic correlations between body weight traits, and their decrease with age, were in agreement with various authors for various poultry species (Danbaro et al., 1995; Kranis et al., 2006; Saatci et al., 2006; Lwelamira et al., 2009). Body weight traits in chickens are controlled by many interacting or pleiotropic genes, each exerting a small phenotypic effect (Deeb and Lamont, 2002; Zhou et al., 2006; Le Rouzic et al., 2008). The reduction in genetic correlations with age is explained by the gene interaction effects being higher in traits close to each other than in traits further apart.

The low negative genetic correlations between EW and juvenile body weights obtained were inconsistent with various findings for broilers (Koerhuis and McKay, 1996), quails (Mielenz et al., 2006) and IC ecotypes (Lwelamira et al., 2009). These apparently conflicting results may be explained by the genetic differences of the populations and probably the estimation model used in the current study. Whereas body weights at a given age are traits of an individual bird, egg and hatching weights are traits of the hen due to the high maternal influences that affects the traits. Interestingly, BW0 as a covariate appears to have accounted for maternal influences on body weights from 2 to 6 weeks of age. However, maternal influences on EW were not accounted for in any way thus leading to a probable confounding effect. Therefore, the genetic correlation between EW and juvenile body weights may probably be indicating, to a larger extent, correlations between EW maternal additive effects and the body weights direct additive effects. Comparable negative genetic correlations between direct and maternal additive genetic effects in chickens have been reported in literature (Koerhuis and Thompson, 1997; Prado-Gonzalez et al., 2003; Norris and Ngambi, 2006). The confounding effect may also explain the negative phenotypic correlations between EW and juvenile body weights. Furthermore, the positive and increasing genetic correlation between EW and body weights at 12, 14, 16 and 26 weeks of age appear

to support this argument. Lwelamira et al. (2009) obtained genetic correlations between body weights at 12, 16 and 20 weeks of age that ranged from 0.22 to 0.34.

4.5 Conclusions

This study has demonstrated that juvenile, growing and mature body weights can be improved through selection. Although improvement at an early age would be more appealing, possible antagonistic maternal relationships with EW would need to be considered and appropriate genetic evaluation models developed. The moderate heritability estimate of body weight at week 12, lack of maternal influences and high genetic correlation with both juvenile and mature weights suggests this to be a possible selection point.

Since one of the positive attributes of IC is their adaptation to harsh environmental conditions, it may be important to consider issues of G x E interactions and the general fitness when attempting to improve body weights of these IC. The estimates of heritabilities of, and correlation (genetic and phenotypic) between EW and body weights presented in this study are important as initial estimates, but would later be updated as more data is collected and analysed once a breeding programme is in place.

CHAPTER FIVE

GROWTH PATTERNS OF INDIGENOUS CHICKEN BODY PARTS AND THEIR RELATIONSHIPS WITH BODY MASS

5.1 Introduction

Development of higher carcass yielding IC must target market demand and consumer preferences. Consumers have preferences for various meat parts. The major parts include the shanks, drumsticks, thighs, breasts, backs, wings and necks (Cevger et al., 2004). In broilers, strong consumer demand for breast meat has increased its value to the industry and led breeders and producers to look for ways to optimize breast muscle growth (Zerehdaran et al., 2005). Basic information on growth patterns of these major body parts and their relationship with body weight are particularly important in orientating further investigations aimed at developing and improving IC carcass yield.

Whereas the Gompertz-Laird function is cited as the model of choice for modelling chicken growth, several functions, which include covariance, correlation and regression, are also used to measure relationships between variables (Fajemilehin, 2008). Regression analysis is indeed the single most important measure of association used to explain the amount of change in one variable as a result of a unit change in the value of other variables. Regression functions have been used to derive equations for predicting body weights from linear body measurements in chickens and ducks (Guèye et al., 1998; Téguia et al., 2008). Establishment of the relationships existing between traits is important in designing breeding programmes that optimize a combination of traits for maximum economic returns. This makes genetic improvement easier and faster as efforts can then be concentrated on traits that are easier to measure. Furthermore, prediction equations can be used to estimate body weights of IC in the absence of weighing scales (Latshaw and Bishop, 2001). This Chapter describes growth patterns of selected IC body parts, determines their relationship with body weight and derives equations for predicting live body weight at any age.

5.2 Materials and methods

5.2.1 Data collection

The source of data for the study is as described in Chapter 3. In addition to measuring body weight (BW) at hatch and bi-weekly thereafter to 30 weeks of age, the shank length (SL), drumstick length (DL), drumstick circumference (DC) and chest circumference (CC) of each bird were also measured using an ordinary measuring tape. For ease of measurement, SL

was taken from the base of the hallux (digit 1) to the hock joint, DL from the hock to the knee joint, DC around the widest part near the knee joint and CC under the wings anterior to the legs at the edge of the sternum. A total of 511 birds with records from hatch to 30 weeks of age were available for analysis.

5.2.2 Statistical analyses

Body mass and selected parts linear measurements

Analyses of variance (ANOVA) for the various body measurements (BM) at each age were performed using PROC GLM (SAS, 1998). A model that accounted for the fixed-effects of hatch, genotype, sex and genotype nested within sex was fitted. In the analysis of each BM at hatch (BM0), egg weight (EW) was fitted as a covariate, while in all other ages, the respective BM0 was fitted as a covariate. Least squares means were separated using the probability differences option. The model was:

$$\mathbf{Y_{ijkl} = \mu + H_i + G_j + S_k + G(S)_{jk} + \varepsilon_{ijkl}} \quad [1]$$

where: Y_{ijkl} = body measurement (BW, SL, DL, DC or CC) of the l^{th} bird at a particular age; μ= overall mean; H_i = effect of the i^{th} hatch (i = 1..., 7); G_j = effect of the j^{th} genotype (j = crested-head, frizzle-feather, naked-neck, normal-feather); S_k = effect of the k^{th} sex (k = male, female); $G(S)_{jk}$= effect of genotype nested within sex; ε_{ijkl} = error term associated with each measurement.

Specific growth patterns

The specific growth pattern of each body measurement (BW, SL, DL, DC and CC) was modelled using the Gompertz-Laird function described in Chapter 3 as:

$$\mathbf{BWt = BW0 \times exp\left((L/K) \times \left(1 - exp(-K \times t)\right)\right)} \quad [2]$$

where: BMt = body measurement at age t; BM0 = estimated body measurement at hatch; L = initial specific growth rate; K = exponential rate of decay of the initial specific growth rate; and t = age in days.

Recorded body measurements from hatch to 30 weeks of age were fitted into Eq. 2 and growth parameters BM0, L and K estimated for each bird using PROC NLIN (SAS, 1998). The estimated parameters were refitted into the function (Eq. 2) so as to model each

body measurement at a particular age for each bird. In addition, age at inflection (t_I) was computed for each bird as detailed in Chapter 3.

Analysis of variance for each modelled BM and its estimated parameters were performed according to Eq. 1 above. The least squares means for each BM were then plotted against age to obtain specific growth curve patterns.

Relationships between body weight and linear measurements

The phenotypic relationships between body measurements for each sex were estimated by Pearson correlation procedures of SAS (SAS, 1998). The correlation function fitted was:

$$\mathbf{r_{xy}} = \frac{\sum_i((\mathbf{x_i} - \bar{\mathbf{x}})(\mathbf{y_i} - \bar{\mathbf{y}}))}{\sqrt{\sum_i(\mathbf{x_i} - \bar{\mathbf{x}})^2 \sum_i(\mathbf{y_i} - \bar{\mathbf{y}})^2}} \quad [3]$$

where: r_{xy} = Pearson product-moment correlation between measurements x and y; x_i and y_i = measurement x and y, respectively, of the i^{th} bird (i = 1, 2, ..., 511); $\bar{x}$ and $\bar{y}$ = mean of measurement x and y, respectively.

The BW prediction equations were derived irrespective of age and sex. Usually under field conditions, it is difficult to determine sex before 8 weeks of age. Simple linear regression procedures (SAS, 1998) were used to derive equations describing the relationship between BW as the response variable and linear measurements (SL, DL, DC and CC) as the predictor variables. The best single, two, three and four variable prediction models were selected by MAXR option and compared using the coefficient of determination (R^2) and the Mallow's Cp test. The regression model fitted was:

$$\mathbf{Y = a + b_1X_1 + b_2X_2 + b_3X_3 + b_4X_4} \quad [4]$$

where: Y = body weight; X_1 to X_4 = linear measurements; a = intercept; b_1 to b_4 = partial regression coefficients of response variable on each predictor variable.

5.3 Results

5.3.1 Body mass and selected parts linear measurements

The overall least squares means of observed measurements are presented in Table 12 and for each sex in Table 13. The overall mean body weights at hatch, 6, 12, 18, 24 and 30 weeks of age are presented in Table 5 in Chapter 3. At the same ages, the overall mean SL were 1.86, 4.51, 6.11, 7.59, 8.50 and 8.73cm, respectively, while the mean DL were 3.19, 7.77, 10.86, 13.28, 14.39 and 14.88cm, respectively. The DC at the same ages were 2.33, 5.44, 7.09, 8.57, 9.97 and 10.60cm, respectively, while the mean CC were 6.36, 15.18, 21.00, 24.71, 26.97 and 28.51cm, respectively. Between weeks 28 and 30 of age, the linear measurements either stagnated or increased marginally.

Table 12. Least squares means (LSM±se) for overall observed body weight and linear measurements at various ages

Age	Body measurements[1]				
(weeks)	BW (g)	SL (cm)	DL (cm)	DC (cm)	CC (cm)
0	32.7±0.13	1.86±0.006	3.19±0.011	2.33±0.011	6.36±0.012
2	77.9±0.79	2.59±0.010	4.40±0.014	3.17±0.012	9.13±0.025
4	172.5±1.32	3.64±0.016	6.26±0.022	4.55±0.023	12.59±0.044
6	309.5±2.61	4.51±0.020	7.77±0.029	5.44±0.025	15.18±0.054
8	438.9±3.67	5.14±0.021	8.93±0.039	6.03±0.026	17.50±0.061
10	558.9±4.83	5.66±0.026	9.97±0.037	6.49±0.030	19.56±0.075
12	668.8±6.11	6.11±0.034	10.86±0.046	7.09±0.035	21.00±0.086
14	789.6±7.64	6.62±0.041	11.70±0.061	7.49±0.036	22.16±0.090
16	956.1±8.12	7.12±0.042	12.44±0.065	8.13±0.040	23.68±0.105
18	1112.6±8.87	7.59±0.042	13.28±0.073	8.57±0.036	24.71±0.115
20	1330.2±12.26	8.24±0.036	14.04±0.069	9.12±0.045	25.62±0.121
22	1419.9±13.28	8.39±0.039	14.30±0.073	9.40±0.048	26.23±0.123
24	1525.7±13.52	8.50±0.040	14.39±0.071	9.97±0.051	26.97±0.139
26	1629.0±13.67	8.68±0.044	14.70±0.074	10.54±0.061	28.45±0.122
28	1692.8±14.09	8.73±0.041	14.84±0.076	10.60±0.062	28.49±0.123
30	1741.0±14.49	8.73±0.041	14.88±0.077	10.60±0.062	28.51±0.124

[1]BW- body weight, SL- shank length, DL- drumstick length, DC- drumstick circumference, CC- chest circumference

Table 13. Least squares means (LSM±se) per sex for body weight (BW), shank length (SL), drumstick length (DL), drumstick circumference (DC) and chest circumference (CC) at various ages

Age	BW (g)		SL (cm)		DL (cm)		DC (cm)		CC (cm)	
(weeks)	Male	Female	Male	Female	Male	Female	Male	Female	Male	Female
0	32.7±0.14[a]	32.7±0.11[a]	1.87±0.010[a]	1.87±0.008[a]	3.19±0.015[a]	3.20±0.012[a]	2.39±0.017[a]	2.38±0.013[a]	6.37±0.017[a]	6.37±0.013[a]
2	79.3±0.89[a]	75.1±0.68[b]	2.64±0.015[a]	2.58±0.011[b]	4.43±0.022[a]	4.37±0.017[b]	3.24±0.018[a]	3.18±0.014[b]	9.24±0.040[a]	9.06±0.031[b]
4	180.5±2.21[a]	167.2±1.68[b]	3.73±0.024[a]	3.60±0.018[b]	6.38±0.037[a]	6.19±0.028[b]	4.63±0.033[a]	4.46±0.025[b]	12.82±0.068[a]	12.48±0.052[b]
6	326.3±4.10[a]	290.3±3.13[b]	4.66±0.031[a]	4.43±0.024[b]	7.97±0.047[a]	7.65±0.036[b]	5.66±0.040[a]	5.39±0.031[b]	15.68±0.081[a]	15.03±0.062[b]
8	478.7±5.32[a]	414.7±4.06[b]	5.36±0.031[a]	5.05±0.024[b]	9.19±0.063[a]	8.73±0.048[b]	6.34±0.038[a]	5.96±0.029[b]	18.12±0.090[a]	17.22±0.069[b]
10	622.3±6.91[a]	529.0±5.27[b]	6.00±0.034[a]	5.56±0.026[b]	10.36±0.058[a]	9.73±0.044[b]	6.87±0.041[a]	6.44±0.031[b]	20.28±0.121[a]	19.21±0.093[b]
12	747.7±8.86[a]	628.7±6.76[b]	6.49±0.040[a]	6.01±0.030[b]	11.28±0.063[a]	10.59±0.048[b]	7.45±0.050[a]	6.59±0.038[b]	21.79±0.134[a]	20.54±0.102[b]
14	882.9±10.25[a]	756.6±7.81[b]	7.08±0.047[a]	6.56±0.036[b]	12.27±0.076[a]	11.57±0.058[b]	8.00±0.052[a]	7.44±0.039[b]	23.09±0.134[a]	21.76±0.102[b]
16	1063.7±11.94[a]	907.8±9.10[b]	7.60±0.051[a]	7.02±0.039[b]	13.07±0.079[a]	12.24±0.060[b]	8.51±0.054[a]	7.98±0.041[b]	24.66±0.140[a]	23.29±0.107[b]
18	1227.4±13.40[a]	1042.4±10.21[b]	8.13±0.053[a]	7.41±0.040[b]	13.95±0.086[a]	12.94±0.066[b]	8.95±0.059[a]	8.42±0.045[b]	25.87±0.150[a]	24.37±0.114[b]
20	1423.1±16.81[a]	1215.1±12.81[b]	8.74±0.056[a]	7.91±0.043[b]	14.74±0.097[a]	13.59±0.074[b]	9.43±0.070[a]	8.89±0.053[b]	26.65±0.153[a]	25.19±0.117[b]
22	1542.9±18.78[a]	1310.0±14.32[b]	8.96±0.059[a]	8.01±0.045[b]	15.14±0.100[a]	13.77±0.076[b]	9.90±0.071[a]	9.25±0.054[b]	27.66±0.163[a]	25.80±0.124[b]
24	1655.0±20.43[a]	1403.9±15.58[b]	9.05±0.063[a]	8.14±0.048[b]	15.20±0.101[a]	13.90±0.077[b]	10.44±0.081[a]	9.72±0.062[b]	28.43±0.171[a]	26.58±0.131[b]
26	1760.5±20.86[a]	1495.3±15.90[b]	9.21±0.069[a]	8.28±0.053[b]	15.54±0.103[a]	14.17±0.079[b]	10.86±0.082[a]	10.20±0.063[b]	29.61±0.176[a]	27.73±0.134[b]
28	1829.2±21.32[a]	1559.2±16.26[b]	9.27±0.062[a]	8.32±0.047[b]	15.72±0.106[a]	14.30±0.081[b]	10.94±0.081[a]	10.24±0.062[b]	29.69±0.177[a]	27.74±0.134[b]
30	1882.2±22.34[a]	1611.6±17.03[b]	9.27±0.061[a]	8.32±0.046[b]	15.78±0.108[a]	14.36±0.082[b]	10.94±0.081[a]	10.24±0.062[b]	29.70±0.178[a]	27.75±0.135[b]

[ab] means with the same subscript within a body measurement are not significantly different ($P \geq 0.05$)

At hatch, all measurements were not significantly different ($P \geq 0.05$) between sexes (Table 13). Significant differences between sexes for all measurements began from week 2 onwards where males were superior to females. In both sexes, the linear measurements either stagnated or increased marginally between weeks 28 and 30 of age.

5.3.2 Specific growth patterns

The average estimated growth parameters are presented in Table 14. The shanks had an overall estimated length at hatch (SL0), initial specific growth rate (L), exponential rate of decay of the initial specific growth rate (K) and age at inflection (t_I) of 1.91 cm, 0.0283 cm/day, 0.0175 cm/day and 33.0 days, respectively. Whereas the drumsticks had an estimated overall length at hatch (DL0), L, K and $t_I$of 3.18 cm, 0.0303 cm/day, 0.0191 cm/day and 25.0 days, their estimated circumference at hatch (DC0), L, K and $t_I$were 2.66 cm, 0.0208 cm/day, 0.0138 cm/day and 45.0 days, respectively. The chests had an overall estimated circumference at hatch (CC0), L, K and t_I of 6.88 cm, 0.0263 cm/day, 0.0179 cm/day and 23.0 days, respectively. Each estimated parameter at hatch, parameter K and t_I for all body measurements were not significantly different ($P \geq 0.05$) between males and females. Whereas parameter L for BW, SL and DL were similar between sexes, they were significantly different for DC and CC with males growing at significantly higher initial rates than females.

The specific growth curve patterns of each body measurement for both males and females are presented in Figure 6. The whole body mass for both males and females displayed characteristic sigmoid patterns that reached maximum growth rate at week 13 and 14 for females and males, respectively (Table 14). In contrast, all linear measurements of both males and females displayed diminishing returns growth patterns that reached maximum growth at between 3 and 6 weeks.

Table 14. Least squares means (LSM±se) for growth parameters of each body measurement

Body measurements[1]	Sex	Parameters[2] BM0	L	K	t_I
BW (g)	Male	52.3±2.01[a]	0.0613±0.00176[a]	0.0154±0.00031[a]	95.0±2.1[a]
	Female	49.2±1.53[a]	0.0586±0.00134[a]	0.0151±0.00024[a]	94.0±1.6[a]
	Overall	49.8±1.16	0.0599±0.00099	0.0150±0.00018	97.0±1.2
SL (cm)	Male	1.91±0.016[a]	0.0295±0.00047[a]	0.0176±0.00030[a]	31.0±2.0[a]
	Female	1.89±0.012[a]	0.0287±0.00036[a]	0.0183±0.00023[a]	30.0±1.5[a]
	Overall	1.91±0.012	0.0283±0.00036	0.0175±0.00023	33.0±1.2
DL (cm)	Male	3.19±0.026[a]	0.0309±0.00052[a]	0.0188±0.00034[a]	28.0±0.1[a]
	Female	3.16±0.021[a]	0.0302±0.00039[a]	0.0193±0.00026[a]	26.0±0.1[a]
	Overall	3.18±0.018	0.0303±0.00032	0.0191±0.00020	27.0±0.4
DC (cm)	Male	2.60±0.023[a]	0.0225±0.00032[a]	0.0148±0.00031[a]	39.0±2.9[a]
	Female	2.63±0.018[a]	0.0213±0.00032[b]	0.0146±0.00024[a]	41.0±2.2[a]
	Overall	2.66±0.017	0.0208±0.00033	0.0138±0.00026	45.0±1.9
CC (cm)	Male	6.88±0.046[a]	0.0273±0.00039[a]	0.0180±0.00028[a]	24.0±0.6[a]
	Female	6.82±0.035[a]	0.0262±0.00030[b]	0.0180±0.00021[a]	22.0±0.5[a]
	Overall	6.88±0.035	0.0263±0.00029	0.0179±0.00019	23.0±0.4

[1]BW- body weight, SL- shank length, DL- drumstick length, DC- drumstick circumference, CC- chest circumference

[2]BM0- estimated body measurement at hatch, L- initial specific growth rate (g or cm/day, respectively), K- exponential rate of decay of the initial specific growth rate (g or cm/day, respectively), t_I- age at inflection (days)

[ab]means between sexes in the same body measurement with the same subscript are not significantly different ($P \geq 0.05$)

5.3.3 Relationships between body weights and linear measurements

The Pearson correlation coefficients between BW and each linear measurement at each age are presented in Table 15. Whereas all correlations between BW and each linear measurement were significant ($P<0.05$) at all ages, BW correlations with SL and DL in females at hatch were not significantly different from zero. All correlations ranged from low (-0.013) to high (0.879) and varied with age.

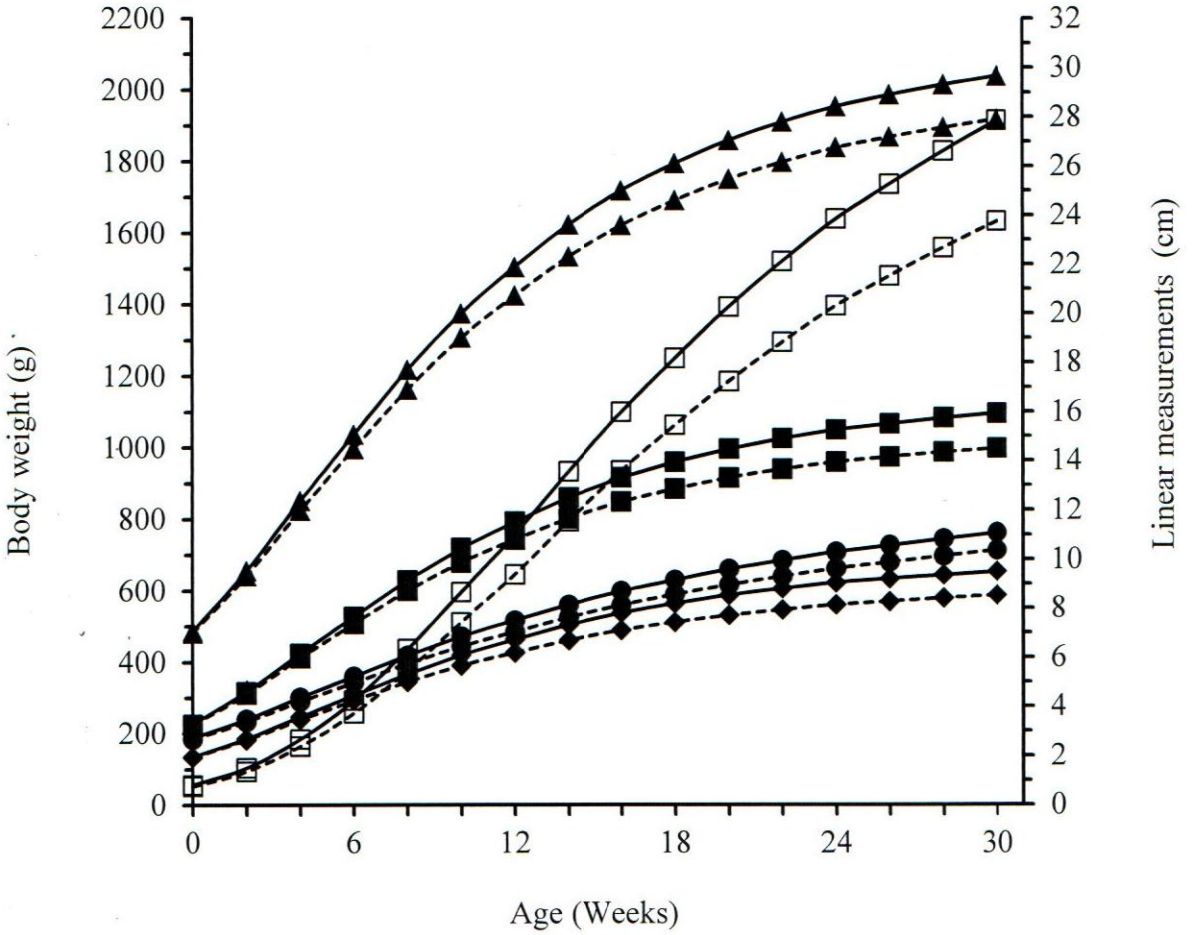


Figure 6. Growth patterns of whole body mass (□), shank length (♦), drumstick length (■), drumstick circumference (●) and chest circumference (▲) of male (solid lines) and female (dotted lines) indigenous chickens.

The variation patterns of the correlations between BW and each linear measurement for males and females are presented in Figure 7. In both sexes, all correlations were low at hatch and 2 weeks of age and increased to moderate at 4 weeks. Whereas BW correlations with SL and DC ranged from moderate (0.500) to high (0.788) from week 4 onwards in both males and females, the correlation with DL ranged from moderate (0.517) to high (0.831) between weeks 4 and 22 in males and between weeks 4 and 16 in females, and low thereafter, respectively. On the other hand, the correlations with CC ranged from moderate (0.509) to high (0.879) between weeks 4 and 26 in males and between weeks 4 and 20 in females, and low thereafter, respectively. Correlations with DL and CC were generally higher in males than females at all ages. However, the correlation with DC was higher in females than males from week 4 onwards. On the other hand, the correlations with SL were lower between weeks 4 and 8, higher between weeks 10 and 24, and lower thereafter in males than in females.

Table 15. Correlation coefficients between body weight and each linear measurement per sex from hatch to 30 weeks of age

Age	Linear measurements[1]							
(weeks)	SL		DL		DC		CC	
	Male	Female	Male	Female	Male	Female	Male	Female
0	0.245	-0.013[ns]	0.307	0.099[ns]	0.480	0.262	0.292	0.148
2	0.341	0.232	0.412	0.270	0.496	0.422	0.430	0.386
4	0.539	0.617	0.571	0.540	0.555	0.604	0.658	0.683
6	0.715	0.761	0.735	0.726	0.635	0.690	0.816	0.810
8	0.772	0.788	0.820	0.807	0.690	0.722	0.876	0.848
10	0.786	0.750	0.831	0.796	0.707	0.732	0.879	0.834
12	0.778	0.695	0.821	0.735	0.714	0.733	0.869	0.794
14	0.771	0.635	0.790	0.633	0.727	0.742	0.845	0.729
16	0.757	0.594	0.745	0.517	0.726	0.742	0.811	0.653
18	0.731	0.580	0.688	0.411	0.698	0.736	0.766	0.577
20	0.702	0.583	0.620	0.329	0.657	0.701	0.711	0.509
22	0.669	0.601	0.549	0.272	0.608	0.662	0.652	0.457
24	0.636	0.610	0.474	0.230	0.567	0.620	0.592	0.418
26	0.601	0.612	0.410	0.209	0.535	0.579	0.541	0.391
28	0.568	0.608	0.349	0.193	0.518	0.539	0.492	0.370
30	0.527	0.593	0.292	0.183	0.508	0.500	0.450	0.352

[1]SL- shank length, DL- drumstick length, DC- drumstick circumference, CC- chest circumference

[ns]not significant from zero($P \geq 0.05$)

The best single, 2, 3 and 4 variable regression equations for predicting body weights at any age irrespective of sex are presented in Table 16. The coefficient of determination (R^2) for the single variable model was 0.896 while for each of the other models was 0.907. The DC was the best single variable for predicting BW of both males and females. However, its Mallows' Cp statistic was high (993.5). The best two variables were SL and DC with a Mallows' Cp statistic of 29.5. The best three variables were SL, DC and CC with a Mallows' Cp statistic of 13.7. The model with all the variables (SL, DL, DC and CC) had a Mallows' Cp statistic of 5.0.

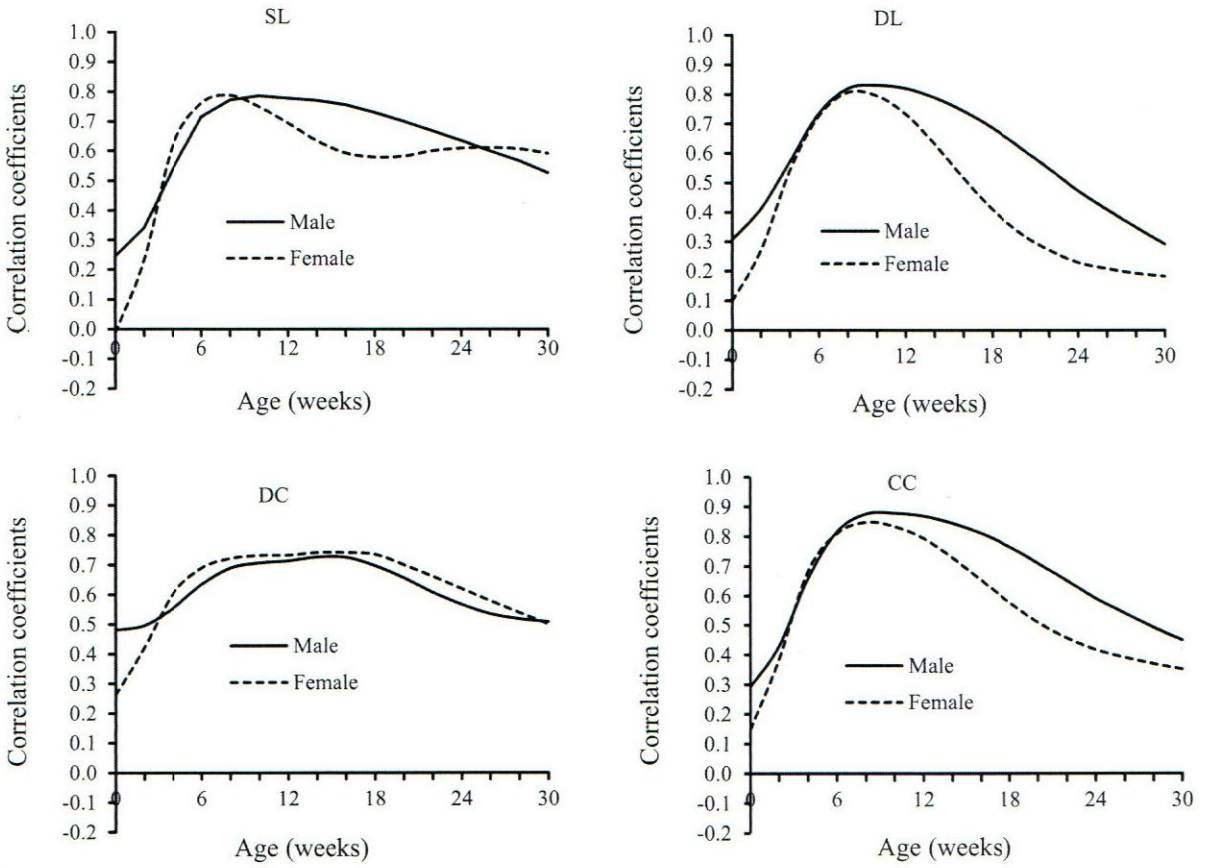


Figure 7. Changes in correlation coefficients between body weight and shank length (SL), drumstick length (DL), drumstick circumference (DC) and chest circumference (CC) of indigenous chickens with age

Table 16. Regression equations for predicting body weight (BW) of both males and females at any age

Variables[1]	Regression equation	R^2	C(p)
DC	BW = -737.2 + 219.6DC	0.896	993.5
SL + DC	BW = -752.3 + 96.6SL + 138.6DC	0.907	29.5
SL + DC + CC	BW = -742.1 + 109.1SL + 143.2DC – 5.9CC	0.907	13.7
SL + DL + DC + CC	BW = -739.1 + 103.8SL + 9.0DL + 145.7DC – 10.0CC	0.907	5.0

[1]SL- shank length, DL- drumstick length, DC- drumstick circumference, CC- chest circumference

5.4 Discussion

5.4.1 Body mass and selected parts linear measurements

The shank and drumstick are important organs that hold and physically support the whole body mass of the chicken. Whereas comparative studies for IC are either scarce or unavailable in literature, the overall SL at various ages obtained in this study were lower than reported for various improved chicken strains at similar ages (Robinson et al., 2007; Wolanski et al., 2007; Ajayi and Ejiofor, 2009; Chen et al., 2009). However, the overall

observed SL at 30 weeks of age (8.73 cm) was within the range of 8.2 to 13.9 cm reported for mature IC in Tanzania and Botswana (Msoffe et al., 2001; Badubi et al., 2006). The average DL at 6 weeks of age (7.77 cm) was lower than the range of 12.06 and 12.68 cm reported for broilers at the same age (Raji et al., 2010). At ages 8 to 16 weeks, overall DL was similar to those of local chickens in Uganda (Semakula et al., 2011). Whereas the average DL at 30 weeks of age (14.88 cm) was close to the range of 14.04 to 14.68 cm reported for local chickens in Nigeria (Ogah et al., 2010), it was higher than the range of 12.25 to 12.57 cm reported for unimproved Catalonian chicken breeds (Francesch et al., 2011).

Heavy-bodied birds at a particular age would be expected to have comparatively longer shanks and drumsticks than light ones so as to support the heavier body mass. Indigenous chicken in most developing countries have comparatively low body weights and hence shorter shanks and drumsticks at any particular age. Whereas there is the need to improve IC body weights at particular ages, this should be accompanied by corresponding improvements in shank and drumstick lengths, and their diameters in order to support increased body weight. This would avoid skeletal problems associated with broilers (Applegate and Lilburn, 2002).

The average DC and CC at various ages were lower than for broilers and similar to those of indigenous chickens (Momoh and Kershima, 2008; Yakubu and Salako, 2009; Raji et al., 2010; Adebambo et al., 2011; Semakula et al., 2011). Drumsticks, thighs and chests are some of the most valuable carcass parts of a chicken (Nikolova and Pavlovski, 2009). Both invasive (slaughtering and dissection) and non-invasive (linear measurements) methods have been used to measure their yields. Linear measurements have been shown to be good indicators of carcass yields in chickens (Larivière et al., 2009; Raji et al., 2010). The low DC and CC measurements in this study could therefore indicate that IC would be expected to have lower drumstick and chest carcass yields. The need to improve carcass yields of IC warrants further studies to set the benchmarks for improvements. Furthermore, linear measurements are used in breed characterization and description, and as breed type standards in addition to other morphological characteristics (Olawunmi et al., 2008; Francesch et al., 2011). The measurements in this study may therefore be used to describe IC in Kenya and develop IC standards in a breeding programme. They may also be used as criteria for selecting superior individuals especially under field conditions.

Lack of sexual dimorphism for BW at hatch agrees with the findings of Osei-Amponsah et al. (2012). Goto et al. (2011) also reported lack of sexual dimorphism for BW and SL at hatch. However, Msoffe et al. (2004) and Ajayi and Ejiofor (2009) reported sexual

dimorphism for BW at hatch. Differences between males and females for SL, DL, DC and CC at various ages have been reported in chickens (Momoh and Kershima, 2008; Ajayi and Ejiofor, 2009; Yakubu and Salako, 2009; Peters et al., 2010; Raji et al., 2010; Adebambo et al., 2011; Semakula et al., 2011).The differences between males and females increased with age. Osei-Amponsah et al. (2012) reported similar findings for BW of local chickens in Ghana. In the current study, males at week 2 of age were on average, 5.6% heavier, with 2.3% longer shanks, 1.4% longer and 1.9% wider drumsticks, and 2.0% wider chests than females, while at week 30 of age, they were 16.8% heavier, with 11.4% longer shanks, 9.9% longer and 6.8% wider drumsticks, and 7.0% wider chests than females. In agreement with the current study, male chickens are known to be about 15-20% heavier than females (Mignon-Grasteau et al., 1998). The superiority of males is attributed to growth and testosterone hormonal differences and their ability to dominate while feeding, thus resulting in faster bone and muscle growth. In addition, breed differences also affect the onset and magnitude of sexual dimorphism in chickens (Nie et al., 2005; Osei-Amponsah et al., 2012). Due to the problem of sexual dimorphism in commercial production especially where mechanized processing is applied, rearing of males and females separately has been recommended in chickens and ducks (Mignon-Grasteau et al., 1998; Baéza et al., 2001). Therefore, it may be postulated that for the current population of IC, rearing more males than females would be expected to be more profitable to small scale commercial meat producers. However, in the development of commercial meat type IC for the future, the magnitude of sexual dimorphism should be reduced or removed altogether through selective breeding.

5.4.2 Specific growth patterns

The estimated growth parameters for BW are discussed in Chapter 3. Unlike parameter BW0, the estimated parameters SL0, DL0, DC0 and CC0 (Table 14) were close to the observed overall means (Table 12). Whereas the Gompertz-Laird growth function usually overestimates or underestimates BW0, it would appear that the function is able to accurately estimate linear measurements (SL0, DL0, DC0 and CC0). Apparently, this unexpected phenomenon may require further investigations.

Whereas BW measurements with age indicate growth of the entire body mass, SL and DL may indicate growth of long bones (tarsometatarsus and tibiotarsus, respectively), DC the growth of drumstick feathers and muscles, and CC the growth of feathers, short bones (keel and ribs), chest muscles and internal organs (heart, lungs, liver and spleen) contained within the chest cavity. The initial specific growth rate (L) and the maturation rate (K) for SL

(0.0283 and 0.0175 cm/day, respectively) and DL (0.0303 and0.0191 cm/day, respectively) appear to suggest a slower initial growth and maturation of the tarsometatarsus bone compared to the tibiotarsus. Although these results disagree with the classical centripal growth theory which suggests that bones most distal from the body are expected to mature first (Kwakkel et al., 1998), it agrees with the hypothesis that patterns of bone growth follows behavioral needs of the growing organism (Muir and Chu, 2002; Hayward et al., 2009). Indigenous chickens have an inherent scavenging and predator evasion behavior (Besbes, 2009). Within hours post hatch, IC chicks are able to walk and run, and within a few days are able to scratch the ground in search of food (Muir and Chu, 2002). It is well known that limb muscles control the movement of locomotor bones. Whereas the tarsometatarsus has no muscles attached, the tibiotarsus has several muscle attachments. These muscles need to be well attached to the bone at an early age to provide the necessary force for walking, running and scratching (Muir and Chu, 2002; Hayward et al., 2009). This may explain the faster growth and maturation of the DL relative to the SL.

In the same context, it is perhaps logical to expect the muscles to grow and mature at a slower rate than the bones. This may explain the low L and K for DC (0.0208 and 0.0138 cm/day, respectively). However, whereas L for CC (0.0263 cm/day) was higher than for DC and lower than for both SL and DL, its K (0.0179 cm/day) was higher than for DC and lower than for DL. The intermediate growth and maturation of the CC may be due to a fast growth and maturation of the short bones (keel and rib bones) and the internal organs, and a much slower growth and maturation of the chest muscles. This agrees with the entire spectrum of body growth whereby growth of the nervous system takes place first, followed by growth of internal organs, skeletal growth, muscle growth and finally the adipose tissue growth (Trenkle and Marple, 1983; Maruyama et al., 2001).

Although the units of measure for body mass (g) and linear measurements (cm) were different, the L and K for the entire body mass (0.0599 g/day and 0.0150 g/day) suggest that the entire body mass grows at a higher initial rate than the shank, drumstick and chest organs, and generally matures at a slower rate. In the precocial chicken, the bones of locomotion, the muscles and internal organs (gastro intestinal track, heart, lungs, liver and spleen) already constitute a large proportion of BW at hatch (Trenkle and Marple, 1983). These essential organs growth spurt occurs at the embryonic stage and would therefore be expected to grow at a much slower initial rate and mature faster than other organs and tissues that constitute the entire body mass (Kwakkel et al., 1998). This is clearly confirmed by the growth curve patterns (Figure 6). The typical sigmoid curve of the whole body mass denotes a slow initial

growth as opposed to the diminishing returns curves of the SL, DL, DC and CC. These curves indicate that the body parts were in the process of maturing after the initial growth spurt at the embryonic stage.

Whereas the whole body mass reached age at inflection (t_I) when maximum growth is attained in 97 days (about 14 weeks), the linear measurements (SL, DL, DC and CC) took between 23 days (about 3 weeks) and 45 days (about 6 weeks) to reach maximum growth. Age at inflection of the whole body mass or its component parts can be used to assess their respective maturation (Maruyama et al., 2001). Indeed, the linear measurements either stagnated or changed minimally after 28 weeks of age, thus indicating that they had reached maturity. Therefore it may be concluded that the chest, shank and drumstick organs of IC matures earlier than the entire body mass. This diphasic growth agrees with the findings of Goto et al. (2011) and has very critical implications to IC nutritional requirements and genetic improvement. On the one hand, there is need to formulate nutrient requirements and feeding regimes that would achieve maximum growth within the stipulated time. On the other hand, because growth parameters are known to be heritable (Mignon-Grasteau et al., 2000b), there is need to formulate breeding strategies that would improve t_I of the whole body mass and each component part.

Lack of sexual dimorphism for all estimated parameters at hatch (BW0, SL0, DL0, DC and CC0) agrees with Koncagul and Cadirci (2010) and Goto et al. (2011) who reported similar findings for estimated BW at hatch, and BW and SL at hatch, respectively. This suggests that neither males nor females can be differentiated at hatch by their body weights or body frame measurements, whether observed or estimated. In agreement with the current study, Koncagul and Cadirci (2010) also reported lack of sexual dimorphism for L and K parameters of BW in broilers. However, presence of sexual dimorphism for L of the DC and CC only, appear to indicate that whereas the entire body mass and the long bones in males and females grow at the same rate, the muscles and internal organs grow initially faster in males than in females, probably starting from the growth spurt at the embryonic stage. Sexual dimorphism of muscle growth at the embryonic stage has been demonstrated in chickens (Henry and Burke, 1998). Therefore, the higher L of DC and CC in males may probably account for their higher BW at later ages.

Parameters K for each respective measurement showed no sexual dimorphism, indicating that the entire body mass and each of the respective organs in males and in females matures at the same rate. Similar findings for BW and SL have been reported (Koncagul and Cadirci, 2010; Goto et al., 2011). However, different body weight K values for males and

females have also been reported (Mignon-Grasteau et al., 1999; Aggrey, 2002). The different findings may be attributed to genetic (breed and genotype) and environmental (temperatures and nutritional levels) differences. These differences are known to affect growth parameters between sexes in chicken (Aggrey, 2004; Santos et al., 2005; Koncagul and Cadirci, 2010).

Lack of sexual dimorphism for t_I of each measurement implies that both males and females reach maximum growth of the entire body mass and each organ, respectively, at similar ages. This would be expected given the lack of dimorphism for K (maturation rate) of each respective measurement. It is generally expected that individuals with higher L would reach t_I later and show a lower K than individuals with lower L (Aggrey, 2002). However, the significantly higher L of DC and CC in males did not lead to sexual differences in K and t_I, respectively, as expected. This implies that the general expectation does not necessarily hold, and that perhaps K is the factor that affects t_I as reported by Koncagul and Cadirci (2010). To improve the growth of IC, genetic improvement of K may therefore be necessary.

5.4.3 Relationships between body weights and linear measurements

Significant correlations between BW and various linear body measurements at various ages have been reported in chickens (Guèye et al., 1998; Semakula et al., 2011; Ojedapo et al., 2012). These studies also reported low, medium and high correlations between BW and the linear body measurements at different ages. In agreement with the findings of the current study, Ojedapo et al. (2012) reported low, negative and insignificant correlation between BW and SL as well as between BW and CC of commercial layer chickens at hatch. The significant and positive correlations between BW and each linear measurement in the current study imply that each of the linear measurement is related to BW. However, the lack of significance would appear to suggest that in females, BW is not related to SL and DL at hatch.

The increase in correlation coefficients between BW and each linear measurement from low at hatch to medium at 4 weeks is in agreement with the findings of Adeleke et al. (2011) and Ojedapo et al. (2012). The low correlations indicate weak relationships between BW and each of the linear measurement in both sexes. The different growth patterns of the whole body mass and each linear measurement (Figure 6) may explain the changes in correlation coefficients with age. The slow growth of the whole body mass from hatch to 2 weeks of age as opposed to the exponential growth of the SL, DL, DC and CC may perhaps result to the weak relationship between BW and the linear measurements at these ages. Subsequently, exponential growth of the body mass and all linear measurements from week 4

onwards may explain the high relationships at these ages. Linear measurements reflect structure growth. Although structural organs reach maturity at different ages, they are expected to mature earlier than the entire body mass (Trenkle and Marple, 1983; Goliomytis et al., 2003). After maturity is attained, they are not expected to change much unlike the immature entire body mass. Therefore, their relationships with body mass would be expected to reduce and at varying rates with age after maturity. Similar changes in correlations between body weight and various linear measurements with age have been reported in rock partridges (Çağlayan et al., 2011)

Different correlations in males and females between similar variables have been reported in chickens (Semakula et al., 2011) and ducks (Téguia et al., 2008). The high correlations between BW and CC between week 4 and week 26 of age in males and between week 4 and week 20 in females agrees with the findings of Guèye et al. (1998) and Semakula et al. (2011) who reported high BW and CC correlation coefficients in mature male and female IC. High correlation between BW and thoracic perimeter has also been reported in both male and female Muscovy ducks at 12 weeks of age (Téguia et al., 2008). However, the CC correlations variation patterns (Figure 7) in the current study indicate weak relationships beyond 20 and 26 weeks of age in females and males, respectively. Similarly, the low correlations between BW and DL beyond 16 and 22 weeks of age in females and males, respectively, also indicate weak relationships. In contrast, SL and DC showed strong relationships with BW from 4 weeks of age onwards. Strong relationships between BW and any linear measurement imply that the linear measurement can reliably be used to predict BW (Téguia et al., 2008). It may therefore be concluded that all linear measurements in this study would be poor predictors of BW at hatch and 2 weeks of age. On the other hand, SL and DC would be good predictors of BW in both males and females from week 4 of age onwards, with DC being more reliable than SL.

The coefficient of determination (R^2) obtained for the best single, 2, 3 and 4 variable prediction models were within the range of 0.85 and 0.99 reported by Ojedapo et al. (2012). However, they were higher than reported by Guèye et al. (1998) and Semakula et al. (2011) for mature IC. The DC was the best single variable predictor of BW. However, the high Mallow's Cp value (993.5) indicated poor fit of the linear function as a predictor of BW. A better fit may probably be achieved using a polynomial function (Ojedapo et al., 2012).

Although BW can easily be predicted from any given linear body measurements in birds, inclusion of more than one measurement improves the quality of fit (Latshaw and Bishop, 2001). This agrees with the improvement of R^2 and Cp values of the best 2, 3 and 4

variable predictors in this study. However, inclusion of CC, and both DL and CC in the models did not improve R^2, although Cp improved slightly. It may therefore be concluded that, in the absence of weighing scales, any of the models could be used to estimate BW of IC. However, due to improved fit and the ease of measuring SL and DC, it is suggested that these variables may be used to predict BW especially under field conditions, with high accuracy.

5.5 Conclusions

This study has demonstrated that IC have small body stature at all ages. They would therefore be expected to yield small carcasses and carcass parts. Whereas there is the need to improve IC body weights at particular ages, this should be accompanied by corresponding improvements in shank and drumstick lengths, and their diameters in order to support increased body weight. The average linear measurements obtained in this study can be used as benchmarks in the description of the Kenyan IC and in setting IC breed standards during the process of improved breed development. Furthermore, sexual dimorphism for BW and linear measurements from 2 weeks of age onwards in favour of males has been demonstrated in this study. It is concluded that sexual dimorphism may not be desirable in the development of IC for meat production.

The growth patterns of the entire body mass and each body part were demonstrated in this study. Whereas the body mass displayed the characteristic sigmoid pattern and reached age at inflection between 13 and 14 weeks of age for females and males, respectively, the body parts in both males and females displayed diminishing returns patterns and reached maximum growth between 3 and 6 weeks of age. This implies that the body parts mature earlier than the entire body mass. Through appropriate genetic and environmental intervention strategies, these patterns can be used to improve IC growth.

The magnitude and strength of relationships between BW and some body parts linear measurements were demonstrated in this study. The correlations between BW and each linear measurement ranged from low to high and varied with age. In both males and females, the SL and DC had the highest and most persistent correlations with BW from 4 weeks of age onwards. This implies that SL and DC relate better with BW than DL and CC from 4 weeks of age onwards. The BW prediction equations indicated DC as the best single predictor and SL combined with DC as the most reliable predictors of BW especially from 4 weeks of age onwards. The derived equations can be used reliably to predict BW of IC in the absence of weighing scales.

CHAPTER SIX
GENERAL DISCUSSION AND CONCLUSIONS

6.1 Aim of the study

This study was motivated by the observed low production performance of IC despite several improvement efforts that have been attempted in the past. Although the improvement efforts have focussed on both genetic, through cross breeding with exotic pure breeds and hybrids, and environmental, through improved nutrition, management and disease control measures, little gains in the overall productivity and economic performance of IC have been achieved (Juma and Ondwasy, 2002). Nevertheless, the demand for IC products has continued to increase, indicating that the potential for IC to supply animal protein and improve the economic welfare of producers is immense (Mack et al., 2005). To exploit this potential, there is the need to explore other available strategies for improving IC productivity.

Crossbreeding has not successfully resulted in improved productivity due to poor survival of the unadapted pure breeds, hybrids and their progenies in the harsh tropical free-range environment (Safalaoh, 2001). Environmental improvements have also not resulted in improved productivity mainly due to poor adoption of the strategies by producers arising from the high costs of inputs relative to the potential incomes derived from the resultant outputs (Juma and Ondwasy, 2002; Menge et al., 2005). Despite the overall low productivity, several genotypes possessing major genes exist in the IC population (Maina, 2000). These genotypes can be exploited to improve IC productivity.

The naked-neck and frizzle genotypes possess major genes for feather reduction, and feather reduction and curling, respectively, known to confer adaptive advantages to individuals possessing them either singly or in combinations (Horst, 1988). Utilizing these genotypes that are well adapted to hot and humid environments would be expected to increase productivity without additional costs. Furthermore, genetic improvement through selection of superior individuals would be expected to improve productivity without compromising on adaptability. However, genetic improvement through selection is dependent on the presence of sufficient genetic variation for a given trait in a population (Hill et al., 2007). The study was therefore undertaken to: - i) determine the influence of morphologically expressed major genes on body weights and to describe growth patterns of four IC genotypes, ii) estimate heritabilities of and correlations between egg weight and body weights of IC and iii) determine the relationship between growth patterns of IC whole body mass and selected body parts at various ages and derive linear equations for predicting live BW.

In line with the objectives, this study provided the answers as to i) how the morphologically expressed major genes influence body weights and growth patterns of IC, ii) the magnitude of the estimate of heritabilities of and correlations between egg weight and body weights of IC, and iii) how the growth patterns of IC whole body mass and selected body parts at various ages are related.

6.1.1 Study methodology

The study population was produced from an IC base population assumed to be random mating as there was no deliberate selection criterion used in allocating mates. The base population had individual birds possessing major genes distinguishable by the respective phenotypic appearance (Bartels, 2003). The phenotypic appearances were: - i) bare neck with a tuft of feather at the ventral side of the neck that indicates presence of the naked-neck (Na) gene, ii) curled feathers with their tips pointing towards the anterior that indicates presence of the frizzle-feather (Fr) gene, iii) presence of a tuft of feathers on top of the head that indicates presence of the crested-head (Cr) gene, and iv) normal feather with no distinguishable morphological appearance that indicates presence of normal-feather (na) gene.

To produce the study population, 7 naked-neck, 6 frizzle-feather, 6 crested-head and 14 normal-feather cocks were each allocated between 5 and 10 unrelated normal-feather hens and housed together in labeled deep litter pens. In total 87 naked-neck, 35 frizzle-feather, 100 crested-head and 289 normal-feather birds produced in seven hatches and with records from hatch to 30 weeks of age were available for analysis. All the birds were reared intensively. Because the genes disaggregate in Mendelian fashion, the mating plan produced heterozygous genotypes, with each genotype indicating the presence of the corresponding major gene (Falconer, 1989). Therefore, the average performance of each genotype was due to each individual bird possessing the corresponding major gene. This enabled the influence of each gene to be determined.

Due to large differences in the genotype sample sizes, a post hoc power statistical analysis was conducted to determine the achieved power to reject the null hypothesis of no differences given the sample sizes, small to large genotype effect sizes and a constant alpha (Faul et al. 2007). The effect sizes (f) considered were small (f=0.1), moderate (f=0.25) and large (f=0.4) while alpha (α) was 0.05. The power analysis showed the F-statistic had a low power (0.45) to detect small effect sizes and very high powers (0.99 to 1.00) to detect moderate and high effect sizes between genotypes.

6.2 The influence of major genes on body weights and growth patterns of indigenous chickens

Under the prevailing climatic conditions and the intensive management applied, the differences in body weights between genotypes indicate the influence of each respective gene. The results showed no influence on both body weights and growth patterns from hatch to 6 weeks of age (Chapter 3). The influence began from week 8 onwards, with each gene influencing body weights and growth patterns at various ages either positively or negatively.

6.2.1 Body weights

Lack of major gene influence from hatch to 6 weeks of age can be attributed to the relatively stable and unchallenging environmental temperatures during the brooding stage. This implies that under ideal environmental conditions (temperature, nutrition and disease), indirect gene actions (Table 2) exert no advantage or disadvantage on body weights or growth patterns. In addition, growth involves probably hundreds or thousands of genes being active at different stages of development (Le Rouzic et al., 2008). In challenging environments, genes are switched on and off in the course of an organism growth (Kraublich, 2000). It is therefore possible that other growth controlling genes, linked or interacting with the major genes are perhaps inactive at these ages. However, more in-depth studies are warranted

From week 8 onwards, the results showed that the normal-feather (na) gene had a positive influence on body weights while the naked-neck (Na) gene had a negative influence leading to reduced body weights. This implies that the naked-neck genotypes are disadvantaged in environments that are cool as is the case at the experimental station in Naivasha (NAHRC, 2000). This disadvantage is expected to be more severe in colder environments. The naked-neck genotype is therefore not ideal in cool to cold environments (N'dri et al., 2007b).

From week 8 to week 16, the Cr gene influenced body weights positively while from week 18 onwards, the influence was negative. Given that both crested-head and normal-feather genotypes had similar body weights up to 16 weeks of age, it appears that the indirect and direct effects the Cr gene (Table 2) had no influence, either positive or negative, on body weights at these ages. The positive influence can be attributed to the na gene. However, from week 18 onwards, presence of the Cr gene influenced body weights negatively. This phenomenon appears to indicate the switching on of BW reducing genes that may be linked or interacting with the Cr gene. The negative genetic correlations between body weights and egg production (Sang et al., 2006; Lwelamira et al., 2009), imply that the Cr gene could

influence egg production positively. Therefore the crested-head may perhaps be a better egg-laying genotype. However, comparative studies are warranted to ascertain this assertion.

From week 8 to week 16, the Fr gene influenced body weights negatively while from week 18 onwards the influence was positive. Similar to the Na gene, the negative influence can be attributed to the indirect heat loss effects due to reduced feather insulation. However, the positive influences indicate increased feather insulation that can be attributed to increased feather coverage with age. This implies that although the Fr gene is thermoregulatory, the frizzle-feather genotype would not be disadvantaged in cool environments, but may be severely affected in cold environments.

6.2.2 Growth parameters

Growth models summarize time series data into a few parameters that enable objective comparison of growth efficiencies. The Gompertz-Laird function was able to estimate BW0, L and K for each bird, thus enabling computation of BW_I and t_I. However, the function overestimated BW0, implying that BW0 should be measured rather than estimated (Aggrey, 2002).

This study demonstrated that IC have slow growth and low maturation rates, and that they achieve maximum growth at between week 12 and 14 of age. The results indicated that although the genes did not influence BW0, BW_I and t_I they influenced parameters L and K. Growth parameters are known to be heritable (Mignon-Grasteau et al., 2000b). It is therefore recommended that selection programmes be set up to genetically improve growth parameters of IC. To support productivity, highly nutritious feeds should be availed during the period of maximum growth. Feed requirements of each genotype should also be established.

6.2.3 Growth patterns

Growth modeling has many advantages. When expressed graphically, irregular fluctuations in weight caused by random environmental effects are usually eliminated, thus enabling clear growth patterns to be established (Nahashon et al., 2006b). Whereas the specific growth (SG) expressed a sigmoid growth pattern (Figure 2), the absolute growth rate (AGR) expressed a bell-shape pattern (Figure 3) and the relative growth rate (RGR) a diminishing pattern (Figure 4).

The patterns indicated that the asymptotic body weights of each genotype had not been reached at the age of 30 weeks, the highest maximum absolute growth rates (between 10.37 and 11.48 grams/day) were reached at the age of 12 to 14 weeks and the highest growth

efficiencies were from hatch to 16 weeks of age. This confirms that IC reach mature body weights late, affirms the need to genetically improve their growth and maturation rates and suggests that improvement by selection should be done before the age of 16 weeks when growth efficiencies are higher.

6.3 Estimation of genetic and phenotypic parameters

The understanding and application of quantitative genetics in chicken breeding has resulted in tremendous genetic improvement in production and production efficiency. The acceptance of quantitative concepts involving additive and non-additive genetic variation and the correlations (both genetic and phenotypic) between growth and reproduction traits has resulted in the development of the chicken for meat production and the chicken for egg production (Siegel et al., 2006). The results of this study have demonstrated the existence of sufficient variances and covariances within and between traits, which enables estimation of genetic and phenotypic parameters for the IC population (Chapter 4).

The sire model was used in this study. In this model, only the genetic effects of the sires are taken into account. The sire model assumes that all sires are mated to an average group of dams and that all dams are unrelated. In addition, it also assumes that all progeny of a sire are half sibs with an average relationship of one-fourth. These assumptions are often not true especially where selection has been practiced. In this study, the dams were average because they had not been subjected to selection and were unrelated. This is expected to change when selection programmes are implemented. Moreover, some progenies were fullsibs due to high reproductive rate of chickens and, consequently, animals had more genetic covariances than only through their sires. This requires the use of animal models to include the genetic relationships between all animals and account for selection. However, an animal model can only be applicable in situations where pedigree information from both paternal and maternal sides is available (Kim et al., 2006). In this study, only paternal pedigree information was available, hence the use of a sire model.

This study involved the analysis of IC growth from hatch to 30 weeks of age which follows a prescribed trajectory. Performance was measured by repeatedly recording weights as the chicken grew. This constitutes longitudinal data and random regression models based on covariance functions methodology present a more flexible means of estimating (co) variances between the ages (Meyer, 2004). The models provide an efficient method of evaluating traits that change with time due to their ability to account for temporal variations in addition to allowing for efficient data utilization and interpolation, thereby minimizing

errors due to approximations and providing estimates for the particular ages when the measurements were taken (Kirkpatrick and Heckman, 1989). In this study, random regression models were not used because of the high imbalance in the data structure. This would have meant foregoing some advantages of random regression models thus leading to lower accuracy of the estimates (Wasike et al., 2007). However, random regression models should be exploited as recording infrastructures improve and more records become available.

6.3.1 Heritability estimates

The heritability estimate for EW in both single and multiple trait analyses (0.95 and 0.98, respectively) were overestimated due to the failure of the models to account for maternal influences on EW (Hartmann et al., 2003). To obtain unbiased estimates for EW, maternal influences must be accounted for by identifying the dams and fitting appropriate models. This was not possible in this study.

The single trait heritability estimates for body weights increased from hatch (0.05) to 4 weeks (0.39), and then generally reduced with age (Table 9 and Figure 5). The moderate to low single trait heritabilities obtained at 2 to 16 weeks suggest that selection at these ages would result in substantial genetic progress, while the very low heritabilities at hatch and after 18 weeks would result in slow genetic progress. However, the multiple trait heritabilities for juvenile body weights at 2, 4 and 6 weeks were high (0.51, 0.65 and 0.51, respectively), moderate for grower body weights at 12, 14 and 16 weeks (0.35, 0.31 and 0.29, respectively) and low for the mature body weight at 26 weeks (0.11) (Table 10). This implies that selection at juvenile and grower stages would be effective while selection at mature stage would yield slow progress.

6.3.2 Genetic and phenotypic correlations

Egg weight is a trait of the hen. Therefore, the negative genetic correlations between EW and juvenile body weights indicated correlations between maternal effects on EW and direct additive effects on body weights. This was because of the confounding effects of the maternal influences on EW (Chapter 4). This implies that selection for juvenile body weights would result in reduced EW, unless maternal effects can be partitioned and accounted for. The low to moderate positive correlation between EW and BW at 12, 14, 16 and 26 weeks (Table 11) indicated lack of maternal influences at these ages (Norris and Ngambi, 2006). Selection at these ages would hence be expected to yield marginal to moderate EW improvement.

The high positive genetic correlations between juvenile and grower body weights (0.72 to 0.99) and the moderate positive correlations with mature BW implies that selection at any juvenile age would result in rapid genetic improvement in grower weights and moderate improvement in mature BW. Further, the high positive genetic correlations within and between grower stage and mature body weights (0.80 to 0.99), respectively, imply that selection at any grower stage would be associated with a rapid improvement in mature BW. Therefore, to improve both EW and body weights at various ages in a breeding programme where maternal influences cannot be accounted, it is suggested that selection be done on body weights at 12 weeks of age. Dana et al. (2011) suggested 16 weeks as an ideal age for selecting Horro chickens in Ethiopia. Apart from lack of maternal influences, culling poor performers at 12 weeks of age would also reduce feeding costs thus reducing the overall costs of such an improvement programme.

6.4 Growth patterns of indigenous chicken body parts and their relationships with body weight

Development of higher carcass yielding IC must target market demand and consumer preferences. The major parts preferred by most consumers include the shanks, drumsticks, thighs, breasts, backs, wings and necks (Cevger et al., 2004). To improve their productivity, breeders and producers have to look for ways to optimize their growth. For instance, the strong consumer demand for breast meat has resulted in broilers with fast breast muscle growth (Zerehdaran et al., 2005).

Although consumer preference in Kenya has not been determined, this study has demonstrated that various IC body parts have different growth patterns. The study has also demonstrated existence of sexual dimorphism in the growth of IC whole body mass and the various body parts. In addition, the study has showed that linear measurements are related to the whole body mass (Chapter 5). This information will enable development of IC breeding and management strategies to optimize growth of the various body parts. Furthermore, it has been demonstrated that in the absence of weighing scales, BW can be reliably estimated by measuring one or several body parts using an ordinary tape measure.

6.4.1 Body mass and selected parts linear measurements

Zoometrical measurements are used to characterise and compare livestock breeds (Francesch et al., 2011). Although IC in Kenya have not been conclusively characterised, the average body mass and linear measurements from hatch to 30 weeks of age clearly showed

that the birds are small in stature and light than selected exotic breeds and hybrids. In as much as inadequate feeds have been cited as the main challenge to IC growth, the average measurements in this study suggests that the small stature may also be due to genetic factors. The small stature is essential for survival in the scavenging system due to scarcity and uncertainty surrounding feed supply (Semakula et al., 2011).These average measurements can therefore be used to set standards for development of IC breeds in Kenya. In addition, body measurements are heritable and can therefore be genetically improved (Adeleke et al., 2011). However, genetic improvement of BW should be accompanied by a corresponding improvement in both shank and drumstick length and width so as to support the extra body mass.

Sexual dimorphism is particularly marked in poultry. In this study, males were superior to females in all body measurements at all ages except at hatch (Table 13). The study confirmed that female IC are lighter and smaller in size than their male counterparts at all ages except at hatch. Sexual dimorphism is disadvantageous especially in commercial meat production systems. It is therefore recommended that in the development of meat type IC, the magnitude of sexual dimorphism should be reduced.

6.4.2 Specific growth patterns

Growth patterns are an important and prominent characteristic of a species' life history. Growth patterns define the change in size of either the whole body mass or specific body parts, organs and tissues with time (Karkach, 2006). In this study, the growth patterns of the entire body mass, the shank, drumstick and chest were defined. These patterns will be important in the design of IC improvement strategies. Such growth patterns have been used to develop fast growing broiler chickens, ducks, turkeys and quails, among other livestock species, through appropriate selection and environmental improvement strategies.

Although the units of measure for the entire body mass (g) and the linear measurements of the body parts (cm) were different, the magnitudes of the estimated growth parameters indicated differences in growth between the entire body mass and the specific body parts for both males and females (Table 14). All the linear measurements had lower L values than the entire body mass. On the other hand, apart from the DC that had a lower K than the entire body mass, all the other linear measurements had higher K values than the entire body mass. Furthermore, the linear measurements displayed lower t_I than the entire body mass.

The modeled measurements plotted against age displayed two patterns of growth (Figure 6). Whereas the body parts displayed a diminishing returns pattern, the entire body mass had a sigmoid growth pattern. These patterns indicated that the body parts mature earlier than the entire body mass and was in agreement with various studies in literature (Trenkle and Marple, 1983; Kwakkel et al., 1998; Goto et al., 2011).

To improve IC body mass and the body parts, these growth patterns need to be manipulated through genetic and environmental intervention strategies. Given that growth parameters are heritable (Mignon-Grasteau et al., 2000b) for instance, selection strategies aimed at increasing L and K and reducing t_I should be designed. The conclusion that K perhaps is the factor that affects growth patterns may be used to reduce sexual dimorphism during the selection process. Furthermore, feed rations that optimize growth at the various stages of the growth patterns should be formulated.

6.4.3 Relationships between body weights and linear measurements

The relationships between body weights and linear body parts measurements are of importance to both producers and scientists. The correlation coefficients indicated the existence of weak to strong relationships between BW and each of the linear measurements (Table 15). However, these relationships vary not only with age but also between linear measurements and sex within linear measurements (Figure 7). The changes in correlation coefficients with age showed that the DC had a better and more persistent relationship with BW from 4 weeks of age onwards in both males and females.

Although various body parts linear measurements may be used to predict body weights at different ages, this study showed that the DC and the SL were better predictors of BW in both males and females than the other linear measurements (Table 16). It can therefore be concluded that the derived equation combining DC and SL can reliably be used to predict BW of IC in the absence of weighing scales. Nevertheless, the use of a single linear measurement that is easy to measure in the prediction of BW would be more desirable under field conditions. However, given that the single variable equation with the DC as the predictor had a poor fit as shown by the high Cp value, it may be necessary to explore polynomial functions of each linear measurement as a single predictor of BW.

6.4.4 Conclusions

This study demonstrates how the morphologically expressed major genes for feather reduction, feather reduction and curling, and crested-head influence body weights and growth

patterns of IC. It also demonstrates the magnitude of genetic parameters estimates and their variation patterns with age. Further, it demonstrates the growth patterns of the whole body mass and selected body parts, in addition to the relationships between BW and linear measurements of the selected body parts.

The overall mean body weights across the ages in this study indicated that the IC from most regions of the country may not strictly be indigenous but are non-descript crosses. The body weights and growth patterns of the genotypes studied revealed that major genes exert their influence at different ages starting from week 8 of age. At moderate to low environmental temperatures, the frizzle-feather and naked-neck genes depress growth performance. Genotypes possessing these genes are therefore not ideal for cool environments even in the tropics. Although the crested-head gene also depresses growth, the crested genotype should be investigated further as it may be a candidate for egg production.

The study demonstrated that IC specific growth displays a characteristic sigmoid pattern. They grow and mature slowly although wide variations exist between genotypes and individuals within genotypes. The highest absolute growth rates for all genotypes occur between weeks 8 and 18 of age. This implies that there is need to formulate feed rations and feeding strategies that would optimize growth at these ages. Growth efficiencies occur between hatch and 16 weeks of age suggesting that selection strategies aimed at improving growth patterns in a breeding programme should be done within these ages.

The moderate heritability estimates suggest that juvenile, growing and mature body weights of IC can be improved through selection. Although improvement at an early age would be more appealing, possible antagonistic maternal relationships with EW would need to be considered and appropriate genetic evaluation models developed. The moderate heritability estimate of BW at week 12, lack of maternal influences and high genetic correlation with both juvenile and mature weights suggests this to be an ideal selection point.

The small body statures suggest that IC would be expected to yield small carcasses and carcass parts. However, further studies on carcass yields of IC are warranted. The specific growth patterns of the entire body mass and each of the selected body parts suggest that improvement of BW should be accompanied by improvement in body parts especially the shank and drumstick in both males and females. These can be achieved through appropriate genetic and environmental intervention strategies.

The SL and DC linear measurements relate better with BW from week 4 of age onwards than DL and CC. The BW prediction equations indicated DC as the best single predictor and SL combined with DC as the most reliable predictors especially from 4 weeks

of age onwards. However, the effects of using polynomial functions on each linear measurement as a single predictor of BW at various ages should be further investigated. Nevertheless, the derived linear equations can be used to reliably predict BW of IC in the absence of weighing scales.

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