

**GENETIC EVALUATION OF GROWTH PERFORMANCE OF LARGE
WHITE PIGS REARED UNDER INTENSIVE MANAGEMENT SYSTEM IN
KENYA**

**BY
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DECLARATION

Declaration by the Candidate

This thesis is my original work and has not been presented for a degree in any other University. No part of this thesis may be reproduced without the prior written permission of the author and/or University of Eldoret.

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DEDICATION

I would like to dedicate this thesis to my family; Martin and Nancy Otieno and to my dear wife Faith Ntinyari. You selflessly gave all you had and worked beyond limit to make this journey a possibility. I will forever cherish.

ABSTRACT

Pig production in Kenya is characterized by lack of genetic performance parameters, crucial in setting up sustainable genetic improvement strategies. To partly address this situation, random regression (RR) models have been applied in a varied range of longitudinal data from pigs to other animals. The objective of this study was to undertake genetic evaluation of growth performance of large white pigs reared under intensive management systems in Kenya. Growth data was obtained from KALRO-Naivasha and consisted of body weight (BW) records from 1,398 pigs. The fixed effects of the model used, included dam parity, piglet sex and contemporary groups while litter size at birth was treated as a linear covariate. Random regressions for weight on Legendre polynomials (LP) were included for direct additive gene, maternal additive genetic and permanent environment. Residual effects were modeled to account for heterogeneity of variance by age. Estimates of phenotypic variance increased with age from 3.43 ± 0.28 (3rd week) to $2,449.28 \pm 392.07$ (36th week), while estimates of direct additive genetic heritability (h^2) ranged between 0.20 ± 0.04 and 0.52 ± 0.08 . Similarly, maternal additive genetic heritability (m^2) increased from 0.26 ± 0.05 to 0.79 ± 0.04 while the ratio of permanent environmental variance to phenotypic variance (e^2) ranged between 0 ± 0.01 and 0.15 ± 0.10 . Direct additive genetic correlations were greater than 0.48 between all measures of weight and decreased with increase in age interval. The first three eigenvalues of the coefficient matrix of the additive genetic covariance accounted for 98.62 % of the sum of all the eigenvalues. Growth was highly heritable at pre-weaning age and influenced by maternal and common environmental effect. This study found the highest heritability at the 8th week of growth and recommends selection for increased growth at the same age.

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LIST OF ABBREVIATIONS

AIC:	Akaike's Information Criterion
ASAL:	Arid and Semi-Arid Lands
BIC:	Schwarz's Bayesian Information Criterion
BW:	Body Weight
CF:	Covariance Functions
CV:	Covariance
e^2 :	Ratio of permanent environmental variance to phenotypic variance
h^2 :	Direct additive genetic heritability
KALRO:	Kenya Agricultural and Livestock Research Organization
LW:	Large White
m^2 :	Maternal additive heritability
MCMC:	Markov Chain Monte Carlo
MMGE:	Mixed Model for Genetic Evaluation
MTGE:	Multiple Trait Genetic Evaluation
RAM:	Reduced Animal Model
REML:	Restricted Maximum Likelihood
RR:	Random Regression
STA:	Single Trait Animal Model

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If the reader finds beneficial information in this work, I owe it to the persons named above, for the mistakes, I assume entire responsibility.

CHAPTER ONE

INTRODUCTION

1.1. Background of the Study

Animal production plays vital socio-economic roles in human societies. In Kenya, it contributes 45% of GDP in the agricultural sector, which is a major economic earner (IGAD, 2013). Pig production in Kenya is characterized by exotic breeds raised under confinement and free range systems in the high agricultural potential areas (Kagira *et al.*, 2009; FAO, 2012; Mbuthia *et al.*, 2015a). Figure 1 gives a comparison of pig production trends in selected East African countries, where Uganda is seen to record the highest production from the year 1975 to 2013.

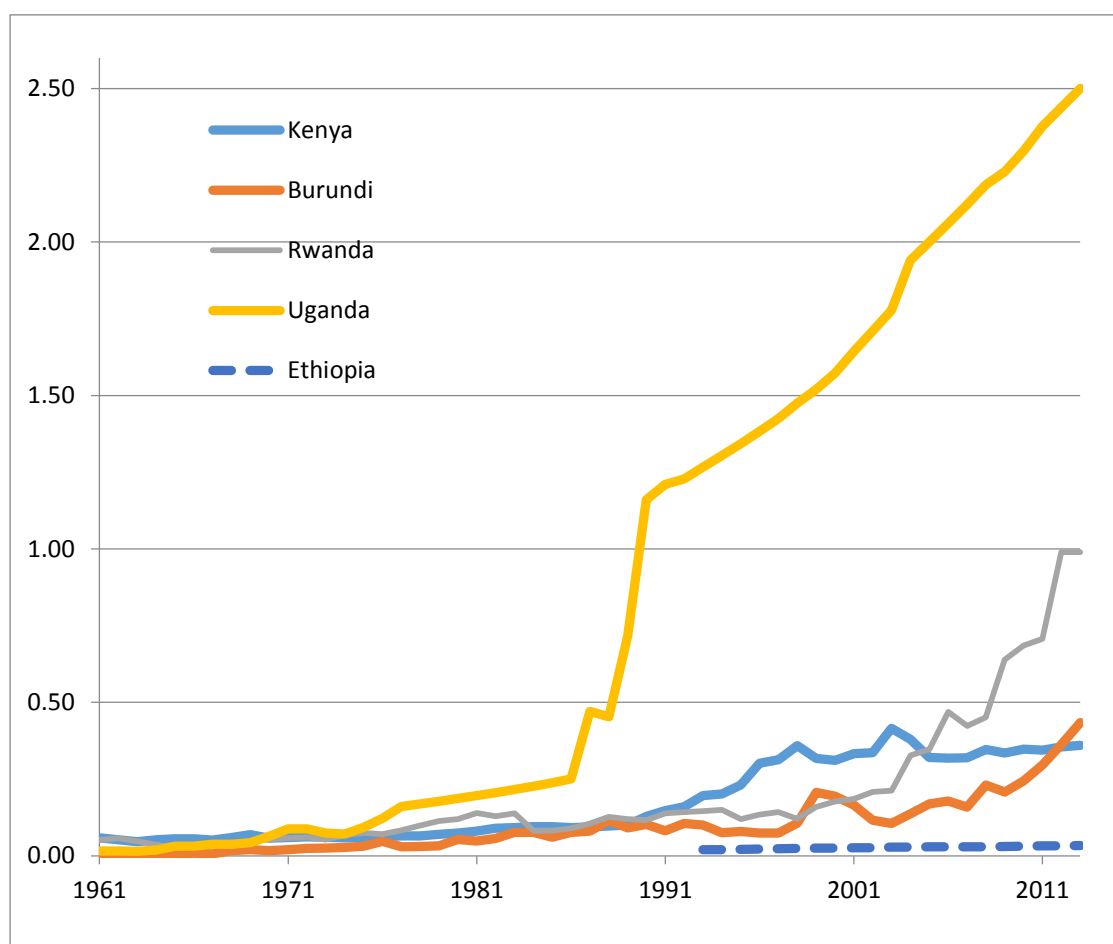


Figure 1: Pig production trends in Eastern African countries (FAOSTAT, 2014)

Breeding of pigs in Kenya is done by companies that produce, process and sell pork. Other breeding center include medium to large scale commercial farmers and some government owned entities (FAO, 2012). Smallholder pig farming has also evolved and remains a major source of white meat and supports the livelihood of both rural and urban households (Wabacha *et al.*, 2004; Kagira *et al.*, 2009; Mbuthia *et al.*, 2014). Despite the importance of pig industry in Kenya, implementation of a nationwide pig breeding program has been hampered by among other factors; lack of breeding objectives, poor performance and pedigree recording (Kagira *et al.*, 2009; Mbuthia *et al.*, 2014; 2015b). This scenario has started deliberate efforts aimed at initiating long term strategies to support the pig industry in the country. Mbuthia *et al.* (2014) and (2015b) recently conducted elaborate studies to understand the production systems, identify traits of economic importance and estimated their economic values for purposes of setting up selection strategies for pig breeding in the country. These studies (Mbuthia *et al.*, 2014; 2015b) made recommendations for setting up nucleus flock in both government and private farms where performance and pedigree recording could be concentrated as basis for selection and mating.

Setting up selection programs can only be implemented where pedigree and performance records are available for genetic evaluation and subsequently, ranking of candidates for selection. The Kenya Agricultural and Livestock Research Organization (KALRO) through the Non Ruminant Research Institute, has been managing a nucleus flock of large white (LW) pigs as a source of breeding animals for distribution to farmers. This nucleus farm has collected performance and pedigree data over the years on various growth and fertility traits. These performance data can only be useful when subjected to an evaluation process that would form the basis for supporting selection decisions and other husbandry practices.

When conducting performance evaluation for purposes of estimating genetic and phenotypic parameters, the desire should be the use models that best describe the data so as to obtain accurate parameter estimates. Genetic and phenotypic parameter estimates for growth of LW pigs based on univariate and bivariate animal models have been reported (Ilatsia *et al.*, 2008). However, random regression (RR) models have rapidly gained popularity (Dzomba *et al.*, 2010; Svitakova *et al.*, 2014) as the choice models for genetic evaluation of growth in many species due to their superiority over the conventional univariate and multivariate animal mixed models (Huisman *et al.*, 2002; Kariuki *et al.*, 2010).

1.2. Problem Statement

There have been efforts to conduct performance evaluation of growth data of pigs using conventional animal models (Ilatsia *et al.*, 2008). However, this approaches have been criticized because of inaccuracy in estimation of genetic parameters (Meyer, 2005). The fact that there exist poor record keeping among small scale farmers in the region, makes genetic evaluation using most conventional models impossible (Kagira *et al.*, 2009; Muasya *et al.*, 2014).

Multi-trait Models (MTM) which have been in consistent use are faced with several challenges, which include; assumption of homogenous temporal and spatial variance (Meyer, 2005), which is however, not the case in biological conditions. Secondly, they assume unstructured correlation matrix; implying that traits at an initial time or space are not related to later traits (Jakobsen *et al.*, 2002; Veerkamp & Thompson, 1998). Overallly, they tend to have large computational demands, due to their treatment of records at different points of the control variable as different traits (Arango *et al.*, 2004; Bohmanova *et al.*, 2005; Ghaderi-Zefrehei *et al.*, 2014; Huisman *et al.*, 2002).

The pig production industry in Kenya is coupled with numerous challenges, among them lack of sustainable breeding strategy that resulted in poorly coordinated breeding schemes, breeding organisation and performance evaluation (FAO, 2012; Mbuthia *et al.*, 2014; 2015b). Even in cases where there is some form of performance recording like in nucleus maintained pig breeding farms, the information has not been adequately utilized for purposes of supporting husbandry measures and objective selection of breeding candidates.

1.3. Justification

The limitations associated with conventional genetic evaluation methods necessitates the use of models with high degree of accuracy and capacity to work with the limited data, common in the Kenyan situation. Random regression models comes in handy to address this challenge. They also provide an elaborate method for evaluation of traits that vary in time and space; due to their ability to account for temporal variation, data interpolation, utilization and efficiency (Wasike *et al.*, 2007). There has been limited application of RR models in Kenya (Kariuki *et al.*, 2010); in as much as they have the capacity to enable better selection of LW pigs and other animals (Meyer, 2004; Lukovic *et al.*, 2007; Ilatsia *et al.*, 2008).

This study adds valuable information to LW pigs genetic evaluation in Kenya; a field that has received limited attention over a long time. Consequently, enabling the improvement of breeding strategies for enhanced production efficiency. According to FAO (2012), breeding information is currently confined to a few commercial farms in Kenya and not availed to the public. This study will therefore provide genetic information important to formulation of breeding strategies to both commercial farms and research institutions.

1.4. Objectives

1.4.1. General Objective

To undertake Genetic evaluation of growth performance of large white pigs reared under intensive management systems in Kenya.

1.4.2. Specific Objectives

- To estimate direct additive, maternal genetic and phenotypic parameters of Large white pigs' weight using random regression model.
- To predict Estimated Breeding Values (EBV) through the growth curve for LW pigs

1.5. Hypothesis

H₀1: Random regression models can not estimate direct additive, maternal genetic and phenotypic parameters of Large white pigs' weight.

H₀2: Random regression models can not predict Estimated Breeding Values (EBV) through the growth curve for LW pigs.

CHAPTER TWO

LITERATURE REVIEW

2.1. The Pigs Industry Kenya

2.1.1. Historical development of the pig industry in Kenya

Pigs were first introduced in Kenya by European settlers in the beginning of the twentieth century for subsistence farming. Commercial farming became active between 1900 and 1963 due to surplus production of cereals and other farm products as initiated by the colonial government. During this period, large black and Berkshire pigs were introduced in Kenya. With the popularization of pig production and consumption by the colonial government, the Uplands Bacon Factory was built in 1906, though it became a parastatal in 1959. In the 1940s, Pig Producers Association and Pig Industry Board were formed to facilitate marketing and scientific breeding of pigs in the country, though this was later taken up by Uplands Bacon Factory. After 1963, several African-owned commercial farms emerged in Central Kenya, including Farmer's Choice which caused the massive increase in pig production. In 1972, Uplands Bacon Factory became large scale with government support but later collapsed in 1982, giving way to monopoly by Farmer's Choice (FAO, 2012).

By the year 2008, most government farms including; National Animal Husbandry Research Station (NAHRS), Naivasha and Agricultural Development Corporation (ADC), had stopped breeding and production of pigs. This left Farmer's Choice and other privately owned commercial farms as the only breeders and producers of pigs in the country.

2.1.2. Distribution and Production Trends

Table 1 presents the distribution of pigs in Kenya where it is evident that production is distributed in all the regions apart from North Eastern and Coast, where the numbers are marginal. The traditional free range rearing system is commonly used in Western and Nyanza regions unlike the commercial intensive system widely used in Central Kenya (Kagira *et al.*, 2009). Production remained low until the early 1990's when initiatives were put in place, thereby generating an increase in production up to the year 2003 (FAO, 2012).

Table 1: Distribution of pig population in commercial and traditional sectors

Region	Pig population	Commercial Sector	Traditional/Backyard Sector
Western	87,838	3,512	84,325
Rift Valley	48,495	14,579	35,654
Nyanza	27,612	900	26,712
North Eastern	68	68	0
Eastern	43,480	35,654	7,826
Coast	5,243	5,243	0
Central	91,977	75,421	16,556
Nairobi	29,976	13,976	16,000
Total Kenya	335,301	149,965	18,7073

Source: FAO, 2012.

There lacks indigenous pig breeds in Kenya, with existing ones constituting of exotic breeds and their crosses (Wabacha *et al.*, 2004; Kagira *et al.*, 2009; FAO, 2012). These breeds include; Large white, Landrace and Duroc.

A comparison between production trends of livestock in Kenya by FAOSTAT (2014) has exhibited little preference of pigs (Figure 2); which could be attributed to cultural and religious beliefs and the large Arid and Semi Arid lands (ASAL) available, favouring cattle and goat production.

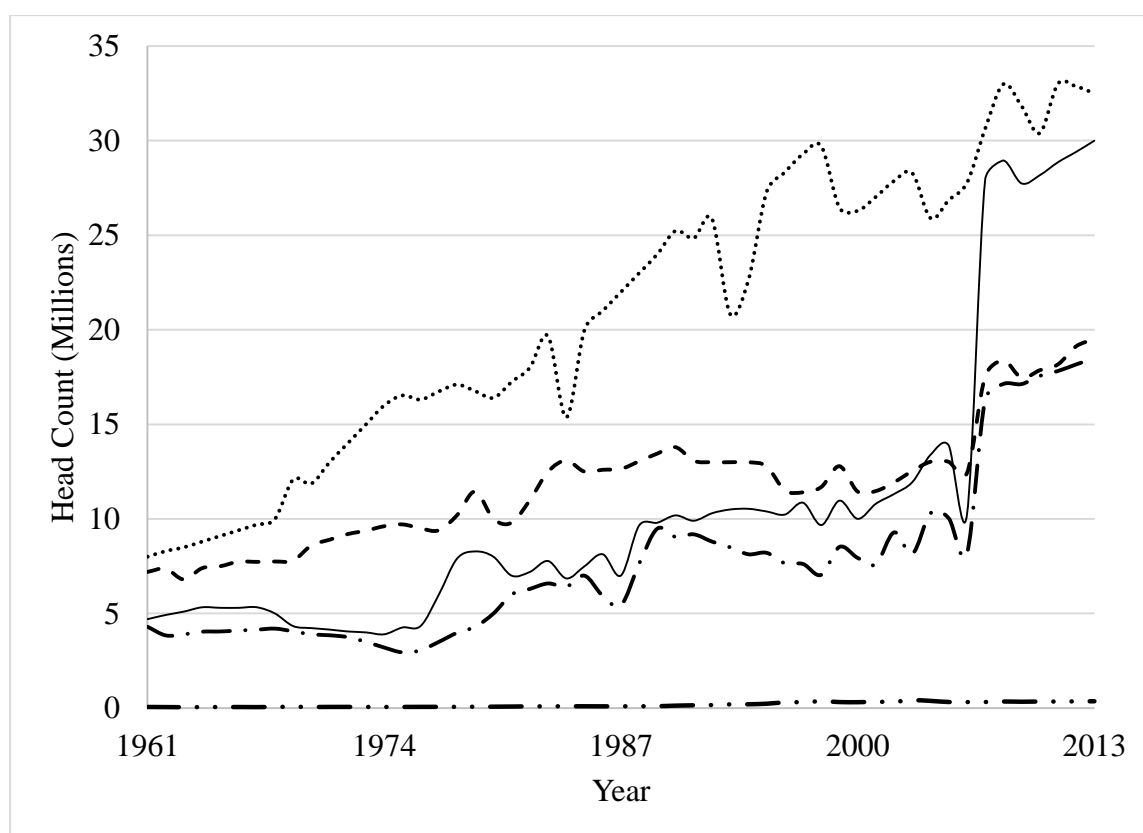


Figure 2: Production trends of cattle (- - -), sheep (- · -), goats (-), pigs (- · · -) and chicken (····) in Kenya.

Source: FAOSTAT, 2014.

2.2.Production systems

The greatest proportion of pig farmers in Kenya are the small holder who rely on breeds sourced from each other (FAO, 2012; Mbuthia *et al.*, 2015b). Even though allowing pigs to roam freely is illegal in Kenya, farmers still practice free range system in many parts of the country (Mutua *et al.*, 2010). In addition, pigs kept in the free range system are faced with many challenges including; high mortality rates, low reproductive rates, lack of proper housing, high levels of inbreeding, poor nutrition and disease (Kagira *et al.*, 2009; Wabacha *et al.*, 2004). The free-range system keeps one to ten pigs and has been reported mainly in the Western region including Kisumu, Busia, Kakamega and the suburban slum areas in the major cities (Kagira *et al.*, 2009; Mutua *et al.*, 2010; Nganga *et al.*, 2008).

Other small holder farmers have preference for the intensive system which is characterized by bigger flock size and ‘improved’ breeds due to the expected higher financial returns (Mbuthia *et al.*, 2015b; Wabacha *et al.*, 2004). This type of production is common within commercial farms around Nairobi, Nakuru, Kiambu, Eldoret and Kitale (FAO, 2012; Kagira *et al.*, 2009). Farmers involved in this system engage in farrow-to-finish production, rarely keeping a breeding boar, have organized disease control programs and keep between 10 and 100 pigs (Wabacha *et al.*, 2004). Pigs from this system are sold to local butcheries and Farmer’s Choice which is the major processor of pork in the country.

Commercial farms keeping between 5,000 and 30,000 pigs intensively, owned by Farmer’s Choice exist in major towns including; Nairobi (Karen and Kamiti), Kiambu (Uplands) and Eldoret (Oasis Farm) (FAO, 2012). Operations in these farms are highly mechanized all through the value chain where all technical and scientific operations including; breeding and medication, are handled by personnel on the

farms. Products from these farms are sold through Farmer's Choice butcheries in major towns and leading supermarkets.

2.3. Phenotypic and genetic parameter estimates

Small holder pig farmers in Kenya keep mostly Landrace, Large White and Duroc breeds and their crosses in the different production systems (FAO, 2012; Wabacha *et al.*, 2004). The Landrace has been used widely in the tropics for crossbreeding; because it is highly prolific and performs relatively better than other exotic breeds. On the other hand, Large White is bigger than the other two breeds and is preferred for a fast growth rate, high adaptability though with a late maturity. This breed is solely supplied by Farmer's Choice (FAO, 2012). The Duroc has a good mothering ability and is docile. Production and reproduction performance of some breeds found in the tropics are listed in Table 2.

Reproductive traits are negatively correlated with production traits (Arango *et al.*, 2004) and this is evident in Table 2 where moderate to high heritability are reported for weight, while low for litter size. High heritability were reported in LW and Landrace weight by Ilatsia *et al.* (2008), Iloeje (1987) and Mishra *et al.* (1989), contrasting with low values reported by Darfour-Oduro *et al.* (2009) and Dube *et al.* (2012) in Ashanti Black and LW breeds respectively. High heritability for weaning weight was reported by Ilatsia *et al.* (2008) and a low one for the same breed reported by Iloeje (1987) as illustrated in Table 2. Lakhani (1989) and Alves *et al.* (1987) reported moderate heritability for litter size, while Dube *et al.* (2012) reported lower values. It is evident that recent estimates are lower than older ones, implying better estimation due to improved computation power (Dzomba *et al.*, 2010).

Table 2: Estimates of some production and reproductive traits and heritability of different pig breeds in the tropics.

Trait ^a	Breed	Country	Mean	No of records	h^2	Source
BW (kg)	Ashanti Black	Ghana	1.00	3,058	0.06	Darfour-Oduro <i>et al.</i> , 2009
	Large White	India	1.29	987	0.18	Lakhani & Nema, 1989
	Large White	Kenya	1.5	11,902	0.38	Ilatsia <i>et al.</i> , 2008
	Large White	Nigeria	1.36	10,188	0.31	Iloeje, 1987
	Large White	South Africa	1.49	21,127	0.11	Dube <i>et al.</i> , 2012
	Large White	Zimbabwe	1.44	3,515		Mungate <i>et al.</i> , 1999
	Landrace	India	1.34	2,466	0.47	Mishra <i>et al.</i> , 1989
WW (kg)	Large White	India	11.33	987	0.30	Lakhani & Nema, 1989
	Large White	Nigeria	9.31	10,188	0.12	Iloeje, 1987
	Large White	Kenya	11.00	10,902	0.47	Ilatsia <i>et al.</i> , 2008
	Large White	Zimbabwe	8.02	3,340		Mungate <i>et al.</i> , 1999
	Ashanti Black	Ghana	5.68	3,058	0.14	Darfour-Oduro <i>et al.</i> , 2009
LS	Large White	India	5.91	47	0.31	Lakhani, 1989
	Large White	South Africa	10.46	21,127	0.07	Dube <i>et al.</i> , 2012
	Large White	Brazil	10.21	2,570	0.23	Alves <i>et al.</i> , 1987
	Duroc	Brazil	9.27	687		Alves <i>et al.</i> , 1987
	Landrace	Brazil	9.77	3,416	0.11	Alves <i>et al.</i> , 1987

^a BW, Birth weight; WW, Weaning weight; LS, Litter size; h^2 , Heritability.

2.4. Genetic evaluation of Pigs in Kenya

There has been little genetic evaluation and selection of pigs in Kenya (FAO, 2012; Mbuthia *et al.*, 2015a; 2015b) and consistent programs have only been carried out in a few large scale commercial farms. Molecular studies have focused on zoonotic concerns and not on genetic evaluation for selection purposes (Amimo *et al.*, 2014; Atuhaire *et al.*, 2014). This is despite the low production as indicated in Figure 2 together with its importance in the Country (Karanja *et al.*, 2005). Recent evaluation on pig production systems identified economic values of specified traits necessary for setting up selection strategies (Mbuthia *et al.*, 2014; 2015a; b; c). In a different scenario, Ilatsia *et al.*, (2008) found that early growth rates of Large White pigs was greatly variable and influenced by litter and maternal genetic effects.

2.5. Models for genetic evaluation

2.5.1. Univariate animal models

Univariate models analyze a single trait in space and time and have been used for analysis of pig weight giving a single value of genetic parameter like heritability as observed in the cases of Alves *et al.* (1987), Iloeje (1987) and Lakhani and Nema (1989). These models have been faced with challenges due to their limited accuracy (Meyer, 2005), thereby prompting the generation of advanced models with the capacity to analyze more than one trait. The challenges include, assumption of a unit correlation in traits separated spatially and temporally, which is not true in practical cases. The limitation in accuracy can be observed with the high values of heritability in Table 2 in comparison to those in Table 3.

The general formula for a univariate model is;

$$y = Xb + Zu + e, \quad (1)$$

where, y is the phenotypic observation, b and u are the vectors with fixed and random effects respectively, X and Z are the corresponding design matrices relating observations to fixed and random effects respectively, while e is the vector with residual error.

2.5.2. *Multivariate animal models*

Multivariate animal models are an extension of the univariate models, with the difference being that data on more than one trait is stored in y (Equation 1). The major advantage of multivariate animal model compared to the former is that it is less bias since it accounts for traits that are measured after successive rounds of selection, only the superior ones are evaluated. It is also more accurate since information from correlated traits are utilized (Meyer, 2005).

The same equation as given in the univariate model applies, with the only difference being that more traits are represented with y . An example with two traits will have each trait having equation 1 and combining them will result into;

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}, \quad (2)$$

where, y_1 represents the n^{th} phenotypic observation for trait one while y_2 represents the n^{th} observation for the trait two.

2.5.3. *Random Regression Models*

Random regression (RR) models are more robust and accurate than multivariate animal models, due to the ability to estimate breeding values through the entire growth trajectory. Currently, three studies (Kariuki *et al.*, 2010; Muasya *et al.*, 2014;

Wasike *et al.*, 2007) have worked with RR models to evaluate animal genetic resources in Kenya. The concept of using RR models in animal breeding was initiated by Henderson (1982) and was not put into practice until 1994 (Schaeffer & Dekkers, 1994). The late adoption of RR models was due to low computer power and lack of appropriate softwares in the 1980's and early 1990's (Ducos *et al.*, 1993; Mosharraf *et al.*, 2014). Initially, these models were used in genetic evaluation of dairy cows (Schaeffer & Dekkers, 1994), but have recently found application in virtually all traits in animal breeding (Laureano *et al.*, 2014; Mohammadi *et al.*, 2014; Naser *et al.*, 2012). A summary of the traits analyzed are presented in Table 3 and model given in equation 3.

Table 3: Heritability of some traits in different pig breeds estimated by RR models.

Trait	Breed	h^2	Source
Muscle protein content	Landrace	0.40	Gjerlaug-Enger <i>et al.</i> , 2010
	Duroc	0.54	Gjerlaug-Enger <i>et al.</i> , 2010
Muscle fat content	Landrace	0.50	Gjerlaug-Enger <i>et al.</i> , 2010
	Duroc	0.62	Gjerlaug-Enger <i>et al.</i> , 2010
Weight	Landrace	0.18-0.24	Wetten <i>et al.</i> , 2012
	Duroc	0.33-0.35	Wetten <i>et al.</i> , 2012
	Landrace	0.17-0.25	Haraldsen <i>et al.</i> , 2009
	Duroc	0.32-0.35	Haraldsen <i>et al.</i> , 2009
Feed intake	Landrace	0.09-0.11	Wetten <i>et al.</i> , 2012
	Duroc	0.09-0.11	Wetten <i>et al.</i> , 2012
	Large White	0.03-0.32	Schnydera <i>et al.</i> , 2002
	Landrace	0.14-0.30	Schnydera <i>et al.</i> , 2002
Litter Size	Iberian	0.12-0.22	Fernandez <i>et al.</i> , 2008
	Slavonian	0.03-0.26	Skorput <i>et al.</i> , 2014

2.6. Approach and Advantages of Random Regression Models

Random regression models can be used when a trait is repeated on a temporal or spatial scale (Kohn *et al.*, 2007; Lukovic *et al.*, 2007) in an animal. The models estimates a different regression coefficient for each animal in the trajectory and the slope for each parameter. These parameters include additive genetic effect, maternal genetic effect, environmental factors among others, as deemed necessary (Dzomba *et al.*, 2010; Meyer, 2004). The basis function used can be linear or non-linear to account for the relationship between the control variable and the phenotype. The model has two sections, a fixed and a random part; making it a dynamic stochastic model (mixed model). The fixed part of the model describes the average shape of the trajectory, while the random part accounts for deviations from the fixed regression (Lewis & Brotherstone, 2002).

Random regression models have the advantage of using fewer parameters to describe data unlike multitrait models (Carlos *et al.*, 2012; Huisman *et al.*, 2002; Schnyder *et al.*, 2001), provide smoother covariance estimates (Kohn *et al.*, 2007) and regular periods of measurements are not necessary for estimation of genetic parameters (Lukovic *et al.*, 2004; 2007). Additionally, the models also have the capacity to estimate genetic parameters at any point along the trajectory (Nephawe, 2004;. Skorput *et al.*, 2014), model environmental effects with greater accuracy (Mostafa *et al.*, 2013) and do not require data adjustment, thereby avoiding data loss (Solomon *et al.*, 2010). Unlike multitrait models, each record in the population contributes to the overall genetic information, thereby increasing on the accuracy of estimation (Lundgren *et al.*, 2014; Oliveira *et al.*, 2010; Wolc *et al.*, 2013).

2.7. Basis functions of random regression models

Legendre Polynomials (LP) are the commonly used basis functions in RR models (Maria *et al.*, 2014; Misztal, 2006). Orthogonal polynomials are also used, though with the limitation of expected occasional poor fit at the extremes of trajectory and non-convergence in large data sets (Meyer, 2005). Other studies have used linear splines as an alternative to Legendre and orthogonal polynomials with increased accuracy of estimation (Huisman *et al.*, 2002; Laureano *et al.*, 2014; Misztal, 2006; Naser *et al.*, 2012). Meyer (2005) reported increased accuracy when working with B-splines in comparison to polynomials, while Bohmanova *et al.* (2005) found them to be the same. Additionally, fractional and smoothing polynomials are also commonly used (Dzomba *et al.*, 2010; Misztal, 2006).

Wilmlink and Ali-Schaefer polynomials have been used with varied accuracy from one study to another. The choice of basis function to use in a model leads to improved estimation of genetic parameters therein (Mohammadi *et al.*, 2014). Therefore, it is crucial to examine the basis functions with their capabilities before utilizing them in genetic analysis.

2.8. Genetic analysis software

A wide range of computer programs are available for genetic analysis using the animal model and they vary of flexibility and capacity handling different types of models. All available programs require command prompts for operation, thereby, it is necessary to learn the syntax required in whichever software one chooses (Wilson *et al.*, 2009). The commonly used include; WOMBAT (Meyer, 2007), ASReml and ASReml-R (Gilmore *et al.*, 2006), MCMCglmm, DFREML (Meyer, 1998), VCE-5 (Kovac *et al.*, 2002) and REMLF90 (Misztal *et al.*, 2002) among others. These programs also vary in cost and are readily available online as described by Wilson *et*

al. (2009). Table 4 illustrates the commonly used softwares and online links for further information.

Table 4: List of commonly used software for animal models in genetic analysis

Software	Free to download/use?	Inference ^a	Notes/Website
ASReml	No	REML	Owned and licensed by VSN International Ltd http://www.vsn.co.uk/software/asrem/
ASReml-R	No	REML	Commercially available R interface for ASReml http://www.vsn.co.uk/software/asrem/
DMU	Yes	REML or MCMC	http://www.dmu.agrsci.dk/
MCMCglmm	Yes	MCMC	R package http://cran.r-project.org/web/packages/MCMCglmm/index.html
WOMBAT	Yes	REML	Replaces DFREML http://agbu.une.edu.au/~kmeyer/wombat.html
VCE	Yes	REML or MCMC	http://vce.tzv.fal.de/software

^aREML: restricted maximum likelihood; MCMC: Markov Chain Monte Carlo

Source: Wilson *et al.*, 2009.

CHAPTER THREE

MATERIALS AND METHODS

3.1. Study Site

Data on body weights for LW pigs was obtained from the Non-ruminant Research Centre, KALRO-Naivasha, Kenya (Figure 3). Naivasha lies approximately 90 km North-West of Nairobi at an altitude of 1,829 – 2,330 meters above sea level. The region fall within agro-ecological zone IV and is defined as semi-arid. Temperatures range between 8 °C and 26 °C with an annual average rainfall of 680 mm (Ilatsia *et al.*, 2008).

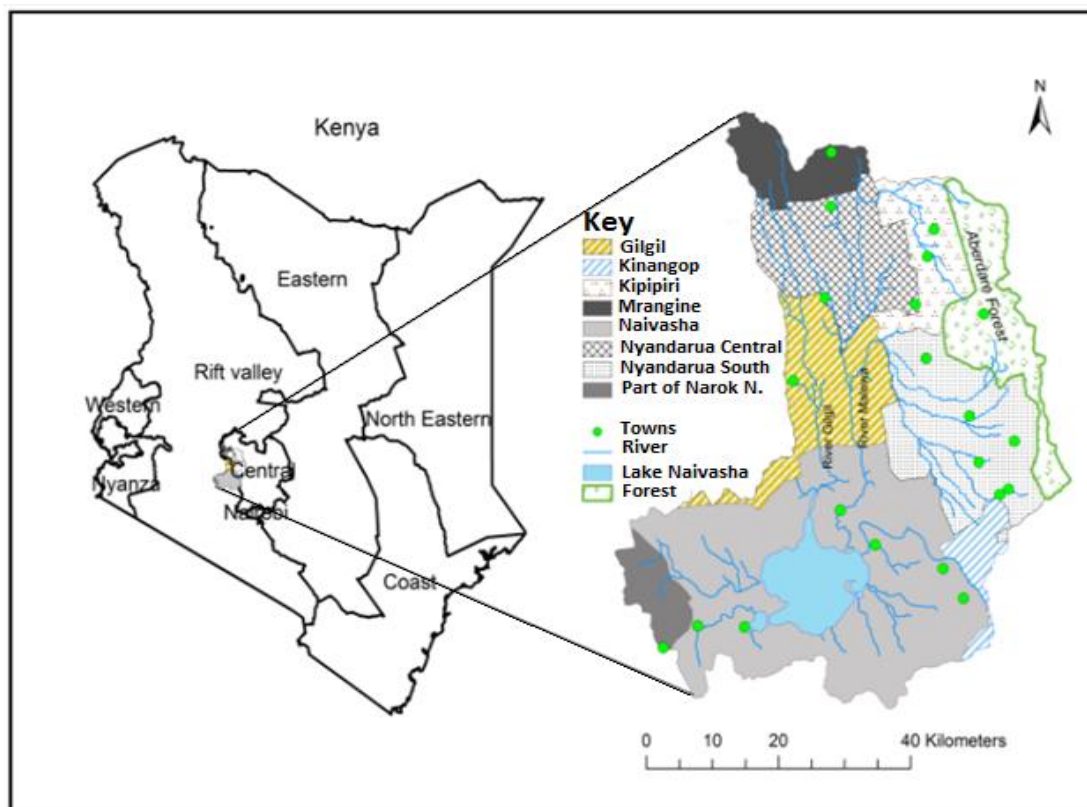


Figure 3: Naivasha region and its environs.

Source: GoK, 2012.

3.2. Data Description

Repeated weight records ($n = 13,678$) of LW pigs ($n = 2,108$) that furrowed between 1982 and 1996 were used in this study. Body weights in kg and pedigree structure are as indicated in Table 5. Data with inconsistencies, e.g. too high or negative, or not found in the pedigree were eliminated and this gave 10,428 records from 1,398 LW pigs. Fixed and random effects used herein were the same as those used by Ilatsia *et al.* (2008). Weight at birth was not included in the analysis to avoid implausible variance values as reported by Kohn *et al.* (2007)

Table 5: Data characteristics for LW pigs used in the study

Category	Measure (Number)
Total records	10,428
Pigs with records	1398
with 1-2 records	17
with 3 records	11
with 4 records	162
with 5 records	117
with 6 records	83
with 7-10 records	1008
Pigs in the analysis ^a	1476
Pigs without records	78
Sires ^b	16
Dams ^b	86
Mean live weight overall (kg)	33.03 (24.98)†
Mean live weight at weaning (8 weeks; kg)	11.00 (3.65)†
Mean live weight at the end of test (36 weeks; kg)	75.56 (16.00)†

^a Including parents without records; ^b with progeny in the data; † Standard deviation shown in parenthesis.

The discussion of the herd management is presented by Ilatsia *et al.* (2008). Briefly, pigs were reared intensively in concrete floored pigsties from birth to 36 weeks of age

when they were sold. The feeding regime was divided into two, depending on the amount of feed supplied. Between 1982 and 1989 sows were fed 3 kg of sow and weaner meal with 140 g CP/kg twice per day. Nursing of lactating sows were fed an extra 0.25 kg per piglet suckling. During this period, piglets were allowed to suckle thrice a day from birth to weaning. Between weaning and 18 weeks, piglets were fed on sow and weaner meal according to weight, and afterwards, fed on finisher meal up to marketing age. From 1990 onwards, sows were allowed only 2 kg of sow and weaner meal twice a day, in the morning and evening, with no extra feed provided for lactating sows. Piglets were allowed to suckle without restriction from birth to weaning. After weaning piglets were fed on sow and weaner meal according to weight up to marketing.

3.3. Statistics

Polynomials of order one to eight were used on random regression to model the mean growth curve by fitting weight as a function of age in weeks. Fixed effects were modelled as regression coefficients by fitting Polynomials at recording age (weeks).

The general RR model for LW pigs weight is:

$$Y_{ij} = F_{ij} + \sum_{m=0}^{K_A-1} \alpha_{im} \phi_m(t_{ij}) + \sum_{m=0}^{K_B-1} \gamma_{im} \phi_m(t_{ij}) + \sum_{m=0}^{K_C-1} \delta_{im} \phi_m(t_{ij}) + \epsilon_{ij} \quad (3)$$

Where: Y_{ij} is the j^{th} weight record for i^{th} pig taken at age t (weeks). $\phi_m(t_{ij})$ denotes the m^{th} Ordinary/Legendre polynomial at age t . ϵ_{ij} is the RR coefficient for residual error (temporary environmental effect) (Pirchner, 1981; Van Vleck *et al.*, 1987). $K_{A-1}, K_{B-1}, K_{C-1}, K_{D-1}$ are the Ordinary/Legendre polynomial orders of fit for each random effect, while α_{im}, γ_{im} and δ_{im} are the coefficient for direct additive gene, permanent environment and maternal additive gene effect (Cankaya *et al.*, 2014;

Kariuki *et al.*, 2010; Mohammadi *et al.*, 2014). F_{ij} represents the fixed effects used in the study; dam parity, piglet sex and contemporary groups.

In matrix form, RR model is given by:

$$Y = X\beta + Z_{\alpha}\alpha + Z_{\gamma}\gamma + Z_{\delta}\delta + e \quad (4)$$

Where Y denotes a vector containing weight records and β is a vector of unknown parameters for fixed effects. α , γ and δ are vectors with RR coefficients for direct additive gene effect, permanent environment and maternal effect. e is a vector representing random residual effects while X , Z_{α} , Z_{γ} and Z_{δ} are corresponding incidence matrices (Huisman *et al.*, 2002; Lukovic *et al.*, 2007). Assumptions in the analysis are given in the equations 5 to 8 below:

$$\alpha \sim N(0, A \otimes K_{0\alpha}) \quad (5)$$

$$\gamma \sim N(0, I_{\gamma} \otimes K_{0\gamma}) \quad (6)$$

$$\delta \sim N(0, I_{\delta} \otimes K_{0\delta}) \quad (7)$$

$$e \sim N(0, \Sigma^{\oplus} K_{0i}) \quad (8)$$

Where A is the numerator relationship matrix, $K_{0\alpha}$, $K_{0\gamma}$ and $K_{0\delta}$ are covariance matrices. I_{γ} and I_{δ} are corresponding identity matrices while K_{0i} is the residual matrix. \otimes and Σ^{\oplus} are Kronecker product and summation respectively.

3.3.1. Covariance functions

Equation 3 produces (co)variance matrices of RR, K. (Co)variance functions of RR (\hat{G}_0) were obtained by pre and post multiplying the K matrix with a matrix containing Ordinary/Legendre polynomial (Equation 9) (Kariuki *et al.*, 2010). Equation 9 illustrates (co)variances for additive gene effect (α). The same procedure was applied for the other random effects (Huisman *et al.*, 2002; Meyer, 2005).

$$\hat{G}_0 = \Phi K_\alpha \Phi' \quad (9)$$

3.3.2. Model selection

The different models fitted were evaluated based on Akaike's Information Criterion (AIC), Schwarz's Bayesian Information Criterion (BIC) and logarithm of the likelihood function ($\log L$) (Muasya *et al.*, 2014).

$$BIC = -2\log L + k\log(\lambda) \quad (10)$$

$$AIC = -2\log L + 2k \quad (11)$$

$$\text{Log of } L \text{ function} = -2\log L \quad (12)$$

Where k is the number of parameters in the model, λ is the sample size and $\log L$ is the Restricted Maximum log likelihood. Model with the lowest of the criteria was selected as the best model (Arango *et al.*, 2004; Cankaya *et al.*, 2014; Ghaderi-Zefrehei *et al.*, 2014). All estimates were obtained using the WOMBAT program (Meyer, 2007).

CHAPTER FOUR

RESULTS

Weight records used were distributed as illustrated in Table 5. A decline in the data counts with age (weeks) was evident and is attributed to culling and mortalities due to environmental and management constraints. The average weight increased from 1.50 kg at birth to 75.60 kg at the 36th week with a mean of 33.03 ± 24.98 . Similarly, standard deviation for live BW increased from the first weighing to the last. There were also observed overlaps in the records at different ages; with similar records represented at different points.

4.1. Model Selection

Wide-ranging models with unique order of polynomials were fitted on the data as illustrated in Table 6. This was to enable the modeling of additive genetic, permanent environment and maternal genetic effects. Eight measurement error classes were included. The order of fit for the fixed effects and covariate were similar for all the models, therefore, only the order of fit for the random effects differed. It was found that, Legendre polynomials generated significantly ($p < 0.01$) better models than ordinary polynomials (Appendix 1); based on the used selection criteria. Subsequently, (co)variance estimates were obtained from the Legendre polynomial models only.

There was observed improvement in fit by increasing the order or polynomial from 1 to 8. This resulted in a decrease in log L, AIC and BIC as indicated in **Error! eference source not found..** Thereby, results are provided for where polynomials of the 7th and 8th order were used to model direct additive genetic effect. Log L and the criteria used in model selection for some of the models are listed in Table 6. For

presentation purposes, the selection criteria are presented as a factor of a half. Log L ranged between; -35231.22 and -15488.49, AIC; 15540.49 and 35272.22 and BIC; 15729.04 and 35426.23.

Table 6: Log Likelihood (Log L), Akake's Information Criterion (AIC) and Bayesian Information Criterion (BIC) for analyses with different orders of polynomial fit (k) and rank (r) of the estimated coefficient matrices for analyses using Legendre polynomial as the basis functions for LW pigs.

Model ^a	Rank ^b	Par ^c	Log L	½ AIC	½ BIC
732	732	45	-17091.21	17136.21	17299.38
733	733	48	-17350.25	17398.25	17572.30
734	734	52	-15488.49	15540.49	15729.04
735	735	57	-16845.77	16902.77	17109.45
743	743	52	-17001.53	17053.53	17242.07
744	744	56	-17320.01	17376.01	17579.06
746	746	67	-16775.71	16842.71	17085.64
754	754	61	-18350.37	18098.76	18319.94
756	756	72	-17872.01	17944.01	18205.07
761	761	58	-16838.80	16896.80	17107.11
762	762	60	-16515.17	16575.17	16792.73
763	763	63	-17018.58	17081.58	17310.02
764	764	67	-17033.13	17100.13	17343.06
765	765	72	-17096.51	17168.51	17429.57
774	774	74	-17743.38	17817.38	18085.70
827	827	75	-16897.46	16972.46	17244.40

832	832	53	-15806.23	15859.23	16051.40
834	834	60	-16625.14	16685.14	16902.69
835	835	65	-16160.92	16225.92	16461.60
837	837	78	-16551.79	16629.79	16912.61
842	842	57	-17541.89	17598.89	17805.57
844	844	64	-17272.07	17336.07	17568.13
845	845	69	-17063.48	17063.48	17382.67
846	846	75	-17053.59	17128.59	17400.53
852	852	62	-17129.71	17191.71	17416.51
857	857	87	-17641.59	17728.59	18044.04
861	861	66	-18945.18	18064.32	18303.63
883	883	86	-17620.70	17706.70	18018.53
884	884	90	-17578.56	17668.56	17994.89
885	885	95	-17688.54	17783.54	18128.00

^a Models were labelled α , γ and δ ; where α , γ and δ are order of fit for direct additive genetic, direct permanent and maternal additive genetic factors respectively.

^b Rank of estimated coefficient matrices.

^c Number of parameters in the model.

4.2. Covariance Components

There was a consistent change in phenotypic variance in the model as illustrated in Figure 4. A general increase was observed from the 3rd week up to the 36th week and direct additive genetic variances during the growth period took a similar trend as phenotypic variance with a minimum at the 3rd week and a maximum at the 36th week. Variances due to maternal additive genetic effect took a trend similar to those of

phenotypic effect and ranged between 0.90 and 1930.00. Permanent environment reduced from a peak of 0.50 in the 3rd week, then reduced to a minimum of about naught in the 24th week, then increased steadily to 0.25 in the 36th week.

The models generated produced (co)variances that can be accurately used to estimate contributions of various random effects at different ages in the growth curve. It is also possible to analyze them and estimate genetic and environmental (co)variances at any points between points of recording.

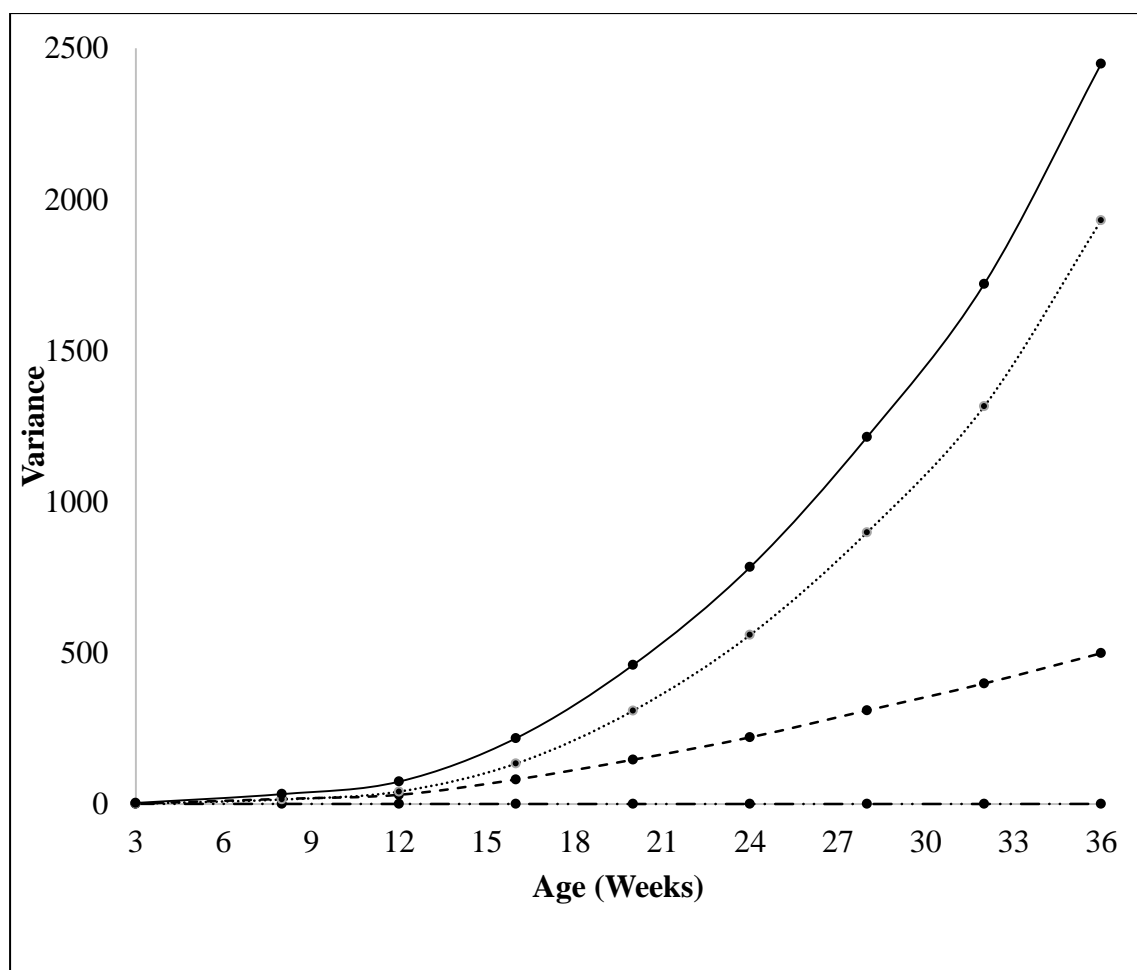


Figure 4: Comparison of variance estimates due to direct additive (---), permanent environmental (-·-), maternal (....) and phenotype (—) for the “best” model.

4.3. Genetic Parameters

Figure 5 presents the estimates of direct genetic and maternal genetic heritability and ratio of permanent environment variances to phenotypic variance. Direct genetic heritability increased from 0.37 in the 3rd week to a climax of 0.52 in the 8th week (age at weaning). It then declined gradually to 0.20 in the 36th week. Maternal genetic heritability increased from 0.26 in the 3rd week to 0.79 in the 36th week. Direct genetic and maternal genetic heritability were equal at around the 10th week. Permanent environmental variances as proportions of phenotypic variance decreased sharply from 0.42 in the 3rd week to naught in the 8th week.

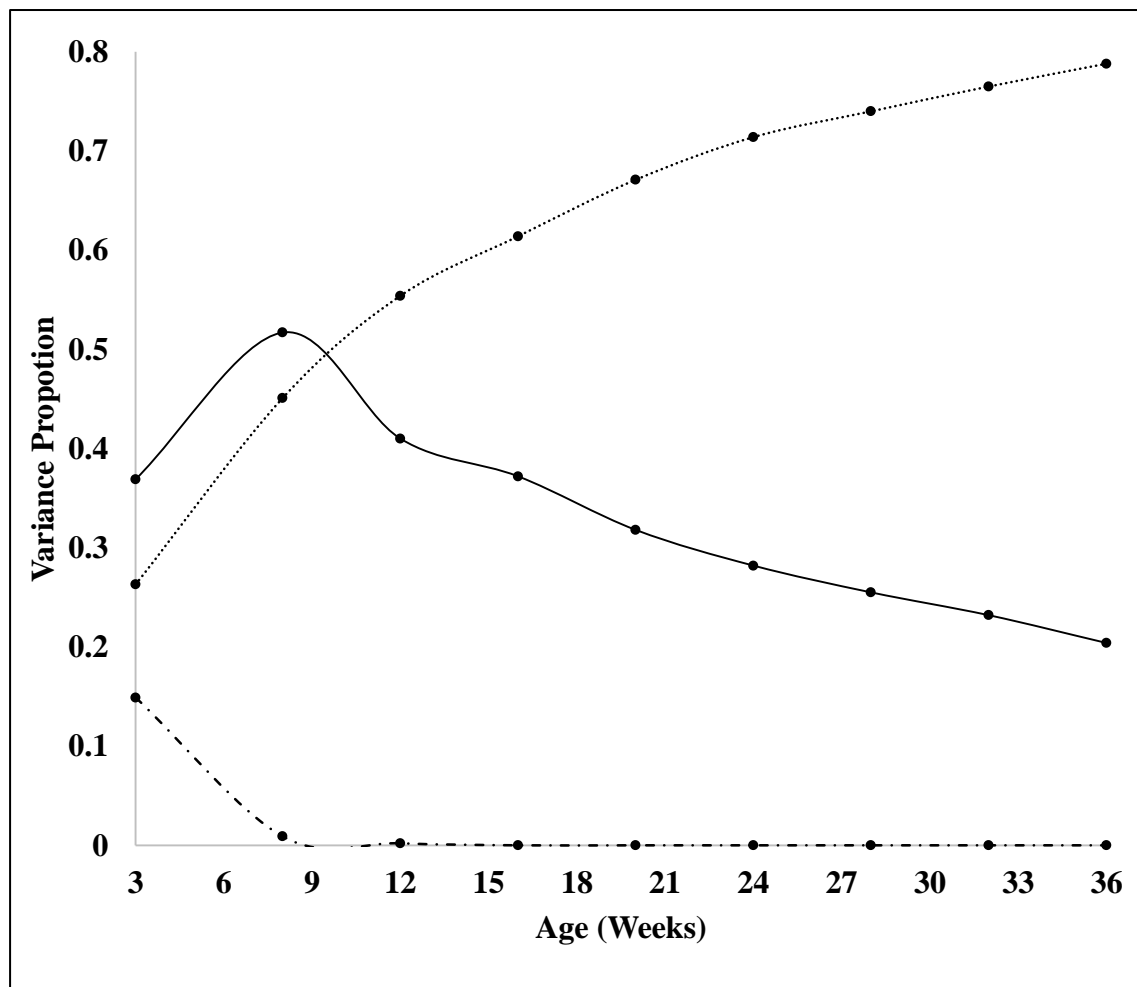


Figure 5: Direct (—) and maternal (....) heritability and permanent environmental variance as a proportion of the total variance (---) for LW pigs.

4.4. Correlations

Table 7 gives phenotypic and genetic correlations between weights at selected test ages. Direct additive genetic correlations were highest between adjacent ages (0.86 to 0.88) and decreased with increase with age interval. Phenotypic correlations were lower than genetic correlation and did not exhibit a clear pattern. On the other hand, genetic correlations were lower than unity and decreased as the distance between the weights increased. The low genetic correlation between pre-weaning weights and post-weaning weights indicates that they are not exactly under the same genetic control. Phenotypic correlations were generally lower than genetic correlations.

Table 7: Estimates of direct and phenotypic correlations^a and heritability^b of body weight measures for LW pigs.

Age (Weeks)	3	8	16	24	36
3	0.37	0.77	0.67	0.59	0.51
8	0.38	0.52	0.77	0.62	0.48
16	0.24	0.84	0.37	0.88	0.70
24	0.08	0.03	0.01	0.28	0.86
36	0.10	0.73	0.87	0.95	0.20

^a Genetic (above diagonal) and phenotypic (below diagonal) correlations; ^b Heritability (on diagonal).

4.5. Estimated Breeding Values

The heritability in Table 7 was used to estimate breeding values of twenty randomly selected pigs (Figure 6). The curve for most of the animals increased at the first part of the trajectory, until weaning. Pigs with high estimated breeding value at the 8th week were observed to maintain the same through the trajectory. This was despite the dip seen at the 12th week (due to weaning stress from week 8) and other fluctuations along the growth curve. It is evident that there exist variations throughout the growth curves of the pigs in the study, a central aspect for purposes of selection.

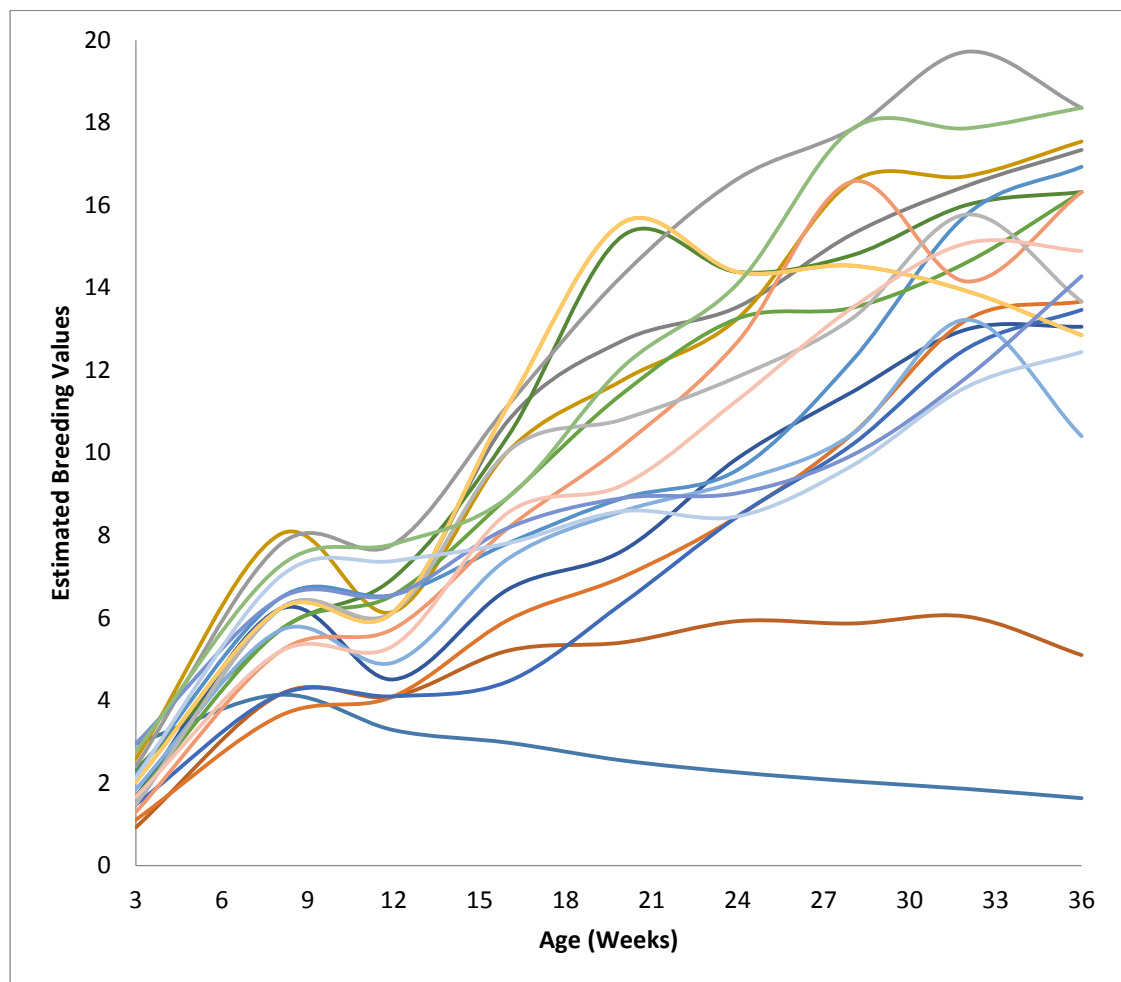


Figure 6: Estimates of breeding values for twenty randomly selected LW pigs' weight

CHAPTER FIVE

DISCUSSION

5.1. Model Selection and Variance Components

5.1.1. Model Selection

Log L, AIC and BIC used in model selection for some of the models are presented in Table 6. There was observed improvement in fit with increasing order of polynomial. Similar observations were made by Peixoto *et al.* (2014) and Lewis & Brotherstone (2002). In contrast, ordinary polynomial functions did not model the data adequately as compared to Legendre polynomial ($p < 0.01$). Covariance Functions (CF) and genetic parameters were thereby estimated by models with Legendre polynomial as the basis function.

It is advisable to use different orders of fit in modeling genetic and other effects in animal genetic evaluation (Cobuci & Claudio, 2012). With this regard, this study examined orders of fit ranging from 1-8 to model the growth trajectory. Lower levels of fit (1-4) were found to poorly describe the data unlike higher orders of fit (6-8). Contrary to that, Meyer (2005) suggested that the use of high order polynomials might result in inaccuracies in genetic estimations due to oscillations at the extremes of the curve. Despite this, several studies have worked with high polynomial orders with accuracy in estimation of genetic information (Tonhati *et al.*, 2011; Muasya *et al.*, 2014; Peixoto *et al.*, 2014).

5.1.2. Variance Components

Phenotypic variances increased progressively throughout the trajectory from the 3rd week up to 36th week as presented in Figure 4. This was due to cumulative increase in variances associated with the fitted random effects, indicating the change in

resemblance between the piglets with age. Similarity in weight early in life and the variation with age is due to genetic and gene-environment interactions. In the same way, continuous variation generated by the genotype at fertilization, determines the range of weight which an individual pig will fall in. The final weight expression is however, influenced by the environment the pig is exposed to. This trend observed in phenotypic variance is the most common in weight and has been observed in pigs (Abegaz *et al.*, 2010) and sheep (Kariuki *et al.*, 2010).

Phenotypic variance is an accumulation of genotypic variance (including additive, dominance and interaction) and environmental variance (Legarra *et al.*, 2004). Its partitioning to its components allow for the estimation of the important determinants of phenotype, specifically the role of heredity and environment. The most important component for animal breeding is heritability which is a ratio of additive genetic variance to the pigs' phenotypic variance.

Direct additive genetic variance during the growth period took a similar trend to phenotypic variance, with increment from a minimum at the 3rd week to a maximum in the 36th week. Other studies modeling growth using RR models have reported similar increase of variance with age in pigs (Huisman *et al.*, 2002 and Kohn *et al.*, 2007) and various sheep breeds (Kariuki *et al.*, 2010 and Somayeh *et al.* 2013). Lower variance estimates were reported in a study that used the same data set but fitting multivariate fixed regression models (Ilatsia *et al.*, 2008).

Additive variance is the measure of breeding value and of the greatest importance for breeding purposes, since it is the chief source of resemblance between relatives (Falconer, 1989). It is also a measure of response to selection and is the only component that can be estimated directly from the phenotypic observations in the

population. In practical pig breeding, the important partition is additive genetic variance against all the rest (non-additive genetic and environmental variance). This division provides the ratio, heritability (Benjamin, 2005; Leland *et al.*, 2008).

Other components of genetic variance (dominance and interaction) are always insufficient to account for the expression of LW pig's weight (Pirchner, 1981). It is also important to note that epistatic/interaction variance is due to interaction between genes at different loci and can not be estimated in practice (Crow, 1986).

Variance due to permanent environment reduced from the 3rd week to the 24th week, then increased steadily to the 36th week. Similar results have been recorded by Jakobsen *et al.* (2002), Mohammad *et al.* (2010) and Silvestre *et al.* (2005). This source of variation is due to factors which affect all observations made on an individual pig and is a typical case of genotype-environment interaction. In many cases, this variance is always small as observed in Figure 4 with respect to the other sources of variation. The small magnitude indicates that the studied pigs could perform just as well in a slightly different environment. In opposition, its existence is proof that the same environment has different effects on genotype. Therefore, it is not justifiable to associate a certain environment with a specific genetic response.

Variances due to maternal additive genetic effect increased throughout the trajectory similar to other studies (Silva *et al.*, 2013; Oliveira *et al.*, 2010; Kohn *et al.*, 2007). Omission of this source of variation in a model may lead to inaccuracy in genetic prediction (Falconer & McKay, 1996). In this regard, full-sibs sharing the same maternal environment tend to have higher covariances among themselves and the dam than their contemporaries. The reason for the increased similarity in full-sibs may be due to cytoplasmic inheritance or nutrition either via pre and post-natal supplies. It

could also be due to pathogen and antibodies transmission through pre-natal blood supply or by post-natal feeding, imitative behavior and interaction between sibs either directly with one another or with the dam (Mather, 1982). The increasing dam effect observed in this study, implies that test daughters should be prioritized in weight improvement programs.

5.2. Genetic Parameters

Estimates of direct genetic heritability and maternal genetic heritability and permanent environmental variance ratio are presented in Figure 5. Allowing maternal effect to vary along the growth trajectory instead of fitting it as a fixed effect, provided for a more accurate prediction of direct genetic and permanent environment heritability. Maternal heritability increased gradually throughout the trajectory. This trend accounts for both pre-natal environment (uterine nutrition and capacity) and the rearing dam's condition (milk production). The increasing maternal heritability indicates that piglets from superior parents tend to perform better throughout the growth trajectory. It is therefore important to include maternal genetic effect when modeling growth in LW pigs when weaning is done at the 8th week. This was also observed in similar studies in Boran beef cattle (Wasike *et al.*, 2007) and sheep populations (Kariuki *et al.*, 2010). Kohn *et al.* (2007) observed that when pigs are weaned in less than four weeks, then maternal genetic effect can be ignored when estimating (co)variance components. In a related study that used the same data set and fitting fixed regression multiple trait model, Ilatsia *et al.* (2008) reported lower maternal heritability with significance for early ages of growth.

Post-weaning ages experienced a constant reduction in direct genetic heritability, while the highest value was at the 8th week. The extreme ends of the trajectory had low heritability and this could be associated with the relatively large error variances

occasioned also by limited data; this should ordinarily not be of concern given that practical selection would not necessarily be based on this extreme age points (Scalez *et al.*, 2014). High heritability at the 8th weeks were reported by Ilatsia *et al.* (2008) who fitted a univariate model based on the same data set, while fitting a multi trait animal model (Darfour-Oduro *et al.* (2009) and sire model (Huisman *et al.*, 2002) reported lower heritability at the same age point. These variations in estimate would be expected given the differences in models of choice, data structure, breeds and husbandry support systems. It is worthwhile to acknowledge that the pedigree and data structure (Table 6) used in this study was somehow limited as compared to the aforementioned studies; an aspect that would affect estimates. However, performance and pedigree data has widely been acknowledged to be a major limiting factor in performance evaluation of livestock breeding programs in developing countries; and any effort towards utilizing the available data is substantial. The reduction of direct genetic heritability after the 8th week indicates that performance recording and selection for weight after this age may not be necessary under the studied condition.

Heritability is the proportion of phenotypic variance that is due to genetic variance, and should not be taken for the degree to which genes describe weight in pigs (Benjamin, 2005; Leland *et al.*, 2008). It is a measure relevant only to a population and makes no practical application on individual animals (Robert, 2009). Therefore, it is inaccurate to say that since h^2 in the 8th week is 0.52, 52% of weight is affected by genes at that age. This however means that, 52% of any pig's body weight in the 8th week is due to additive genes. It should be noted that, there is no universal h^2 for LW pig's body weight and the estimates in this study are specific to the population analyzed in the specified environment (intensive production system). These estimates

would thereby differ with the same breed reared in a free-range system or in a different ecological zone.

Permanent environmental variance ratio declined sharply from the 3rd week to weaning age (Figure 5), implying that most of the variation in pre-weaning weight was influenced by the maternal environment. It is therefore evident that dams with better body score tend to have heavier piglets and provision of enhanced conditions for the dam could improve the weight of the piglets. Post-weaning permanent environmental variance ratio was zero implying the absence of dam environmental influence to the piglets. It is therefore important to model permanent environmental variance ratio for pre-weaning weights in LW pigs.

5.3. Correlations and Eigenvalues

Direct additive genetic correlations (Table 7) were highest between adjacent ages and decreased with increase in age measurement intervals. This could be a case of correlated traits where similar genes are responsible for weight gain at adjacent ages, as has been previously reported in pigs (Ilatsia *et al.*, 2008; Abegaz *et al.*, 2010) and sheep (Kohn *et al.*, 2007). This implies that selection can be intensified at earlier ages to bring about desired high sale weight; a situation with high economic returns to pig enterprises since less labor would be required to measure repeated weights up to mature weight. Early selection for growth performance based on the high genetic correlation of extreme age point measures has been recommended for pigs (Ilatsia *et al.*, 2008; Haraldsen *et al.*, 2009). Similar observations have also been made by Arango *et al.* (2004) and Cankaya *et al.* (2014) in beef and dairy cattle respectively. Therefore, live weight early in a LW pig's life is a different trait to live weight later in life.

The fact that phenotypic correlations were lower than genetic correlations implies that performance of an individual is partly dependent on their ability to tolerate stressful conditions in the production system. These conditions include; confinement, ear tagging, crowding, heat stress, disease and medication among others. Therefore, breeding programs should consider adaptability traits for different production systems, though it was not possible to include such in this study due to unavailability of relevant data.

The genetic basis of correlated responses is either gametic disequilibrium at genes affecting two traits or the pleiotropic effects of particular genes (Leland *et al.*, 2008). The degree of correlation arising from pleiotropy expresses the extent to which two traits are influenced by the same genes. But the correlation resulting from pleiotropy is the overall or net effect of all the segregating genes that affect both traits. Some genes may increase both traits, while others increase one and reduce the other (Benjamin, 2005). The environment also causes correlation in as far as two traits are influenced by the same differences of environmental conditions. Again, the correlation resulting from environmental causes is the overall effect of all the environmental factors that vary; some cause positive correlation, others a negative one.

The first eigenvalue explained 90.21% of variation for additive genetic effect while the first three eigenvalues explained 98.71% of the total variation. This illustrates that fast genetic response is expected from selection at this point. It also implies positive genetic correlation at all ages and selection at an age point would result in a positive response at all other ages (Abegaz *et al.*, 2010; Akbas *et al.*, 2004; Kirkpatrick *et al.*, 1990).

5.4. Estimated Breeding Values

The heritability values indicated in Figure 5 were used to estimate breeding values of twenty randomly selected pigs (Figure 6). The curve for most of the animals increased at the first part of the trajectory, until weaning. Pigs with high estimated breeding value at the 8th week were observed to maintain the same at the end of the curve due to the positive genetic correlation between pre and post-weaning weights. It is evident that there exist variations in the growth curves of the pigs, which is an important aspect for selection based on performance records. Estimated breeding values (EBV) in the dataset had a mean of 5.69 ± 1.89 with pigs having high values at the 8th week, observed to have a high mature weight as indicated in Figure 6. Based on the EBV, pigs can be ranked for comparison and those with high EBV selected as parents for the next generation. The variation in the EBV indicates different patterns of growth in the flock which is as a result of little or no selection therein. The EBV obtained from this study provides a possibility of selection for high finishing weights at early ages given the positive correlation between pre and post-weaning weights.

Accurate prediction of breeding value is the most critical factor for any breeder with an intention of having rapid genetic improvement (Van Vleck *et al.*, 1987). This enables a breeder to rank all the animals in the farm, cull the poor ones and replace them with superior ones. It is described as a pig's expected progeny performance in relation to the population mean and like heritability; it is specific to the studied population. The importance of this concept is that the parents pass on their genes and not their genotypes to their offspring. It is therefore the average effects of the parents' gene that determine the mean genotypic value of its progeny.

5.5. Implication for a Breeding Program

Pig breeding programs in Kenya were initially in government owned entities such as Agricultural Development Corporation (ADC), research institutes and institutions of higher learning (FAO, 2012). The collapse of government owned uplands bacon factory in 1987 and ADC in the 1990's caused a major disturbance in both their breeding and marketing. This discouraged many farmers from the venture, thereby leaving a few multinationals and other privately owned commercial farms as the major players in the pig value chain and breeding in the Country (Kagira *et al.*, 2009). The aforementioned developments coupled with the emergent demand of white meat and reduced farming space for larger ruminants in the country has created renewed interest to invest in pig farming. In addition, the fast growth, high parity and large litter size associated with pigs, makes their farming an attractive venture with the capacity to improve on food security.

The nascent interest in pig farming should be coupled with elaborate breeding strategies to provide quality boars and gilts for sustainability of the venture as recommended by Mbuthia *et al.* (2015b). One of the initiatives necessary to achieve this, is by setting up performance evaluation programs that will enable ranking of pigs in existing populations using available data and resources. This study has contributed to the imminent venture by providing adequate genetic information, which would form the basis of ranking and selection of LW pig in Kenya.

CHAPTER SIX

CONCLUSION AND RECOMMENDATIONS

6.1. Conclusion

The covariance components for BW estimated increased along the trajectory while pre-weaning and post-weaning BW were found to be different traits due to a low correlation between them. Additionally, the heritability estimates were higher than those reported in literature by MTM, suggesting an improvement in modelling.

The estimated heritability provides an opportunity for selection of pigs at the 8th week. It is also evident that pig weights reduced after weaning due to post-weaning stress and recovery thereafter was due to additive genetic effect and ability to adapt to the new environment. The variation in EBV indicated little or no selection having been done on the flock

Pre-weaning pig weight was highly heritable and influenced with maternal and permanent environment effect. However, genetic parameters and breeding values were estimated with limited accuracy due to the narrow pedigree structure.

6.2. Recommendations

The major challenge in this study was the narrow pedigree structure used. Future studies should utilize larger record sizes with better pedigree structure. It would also be worthwhile to study how other basis functions would model the same data.

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APPENDICES

Appendix I: Log Likelihood (Log L), Akake's Information Criterion (AIC) and Bayesian Information Criterion (BIC) of the models on LW pigs run in the study

Model	Basis	Parameters	Log L	AIC	BIC
112	Leg	15	-27596.434	27611.434	27667.779
113	Leg	18	-24729.452	24747.452	24815.066
114	Leg	22	-24376.429	24398.429	24481.069
115	Leg	27	-23805.845	23832.845	23934.266
121	Leg	15	-27635.080	27650.080	27706.425
122	Leg	17	-25388.222	25405.222	25469.080
123	Leg	20	-22993.679	23013.679	23088.805
124	Leg	24	-22621.647	22645.647	22735.799
125	Leg	29	-22050.386	22079.386	22188.320
131	Leg	18	-26268.039	26286.039	26353.653
132	Leg	20	-22897.751	22917.751	22992.878
133	Leg	23	-22367.313	22390.313	22476.708
134	Leg	27	-21877.221	21904.221	22005.642
135	Leg	32	-21604.495	21636.495	21756.698
141	Leg	22	-26063.224	26085.224	26167.863
142	Leg	24	-22574.113	22598.113	22688.265
143	Leg	27	-22052.913	22079.913	22181.334
144	Leg	31	-21723.866	21754.866	21871.312
145	Leg	36	-21392.284	21428.284	21563.512
151	Leg	27	-25628.596	25655.596	25757.017
152	Leg	29	-22260.122	22289.122	22398.056
153	Leg	32	-21479.306	21511.306	21631.509
154	Leg	36	-19530.205	19566.205	19701.433
155	Leg	41	-23170.795	23211.795	23365.804
211	Leg	15	-25409.780	25424.781	25481.126
212	Leg	17	-26265.173	26282.173	26346.030
213	Leg	20	-23326.622	23346.622	23421.749
214	Leg	24	-22561.302	22585.302	22675.454
215	Leg	29	-22081.026	22110.026	22218.960
221	Leg	17	-25305.374	25322.374	25386.231
222	Leg	19	-25305.399	25324.399	25395.770
223	Leg	22	-22917.142	22939.142	23021.781
224	Leg	26	-22472.566	22498.566	22596.231
225	Leg	31	-22959.376	22990.376	23106.823
231	Leg	20	-22848.057	22868.057	22943.184
232	Leg	22	-24666.761	24688.761	24771.401
233	Leg	25	-22368.441	22393.441	22487.349
234	Leg	29	-21933.701	21962.701	22071.635
235	Leg	34	-23131.504	23165.504	23293.220
241	Leg	24	-22520.630	22544.630	22634.782
242	Leg	26	-22622.239	22648.239	22745.903

243	Leg	29	-21993.239	22022.239	22131.172
244	Leg	33	-24011.567	24044.567	24168.526
245	Leg	38	-23742.093	23780.093	23922.833
251	Leg	29	-22033.873	22062.873	22171.807
252	Leg	31	-22033.143	22064.143	22180.589
253	Leg	34	-21561.792	21595.792	21723.507
254	Leg	38	-21077.805	21115.805	21258.546
255	Leg	43	-20976.921	21019.921	21181.443
311	Leg	18	-22414.322	22432.322	22499.936
312	Leg	20	-22204.793	22224.793	22299.920
313	Leg	23	-23601.629	23624.629	23711.025
314	Leg	27	-23150.133	23177.133	23278.554
315	Leg	32	-21626.373	21658.373	21778.576
321	Leg	20	-22313.226	22333.226	22408.353
322	Leg	22	-22727.157	22749.157	22831.796
323	Leg	25	-23605.200	23630.200	23724.108
324	Leg	29	-22546.639	22575.639	22684.573
325	Leg	34	-21527.573	21561.573	21689.288
331	Leg	23	-22290.713	22313.713	22400.108
332	Leg	25	-22299.642	22324.642	22418.551
333	Leg	28	-22714.969	22742.969	22848.146
334	Leg	32	-23206.479	23238.479	23358.681
335	Leg	37	-21483.816	21520.816	21659.800
341	Leg	27	-21921.034	21948.034	22049.455
342	Leg	29	-22046.519	22075.519	22184.453
343	Leg	32	-22214.955	22246.955	22367.157
344	Leg	36	-21980.238	22016.238	22151.466
345	Leg	41	-21504.960	21545.960	21699.969
351	Leg	32	-21399.583	21431.583	21551.785
352	Leg	34	-21406.790	21440.790	21568.505
353	Leg	37	-21383.676	21420.676	21559.661
354	Leg	41	-18749.308	18790.308	18944.317
355	Leg	46	-20952.898	20998.898	21171.690
411	Leg	22	-21864.248	21886.248	21968.887
412	Leg	24	-21858.829	21882.829	21972.981
413	Leg	27	-21639.120	21666.120	21767.541
414	Leg	31	-23713.517	23744.517	23860.964
415	Leg	36	-23826.972	23862.972	23998.200
421	Leg	24	-21738.430	21762.430	21852.582
422	Leg	26	-23057.403	23083.403	23181.067
423	Leg	29	-21725.294	21754.294	21863.228
424	Leg	33	-24569.862	24602.862	24726.821
425	Leg	38	-20239.756	20277.756	20420.497
431	Leg	27	-21698.771	21725.771	21827.192
432	Leg	29	-21698.770	21727.770	21836.703
433	Leg	32	-23295.706	23327.706	23447.908

434	Leg	36	-24479.568	24515.568	24650.796
435	Leg	41	-20959.250	21000.250	21154.260
441	Leg	31	-21661.535	21692.535	21808.981
442	Leg	33	-21661.534	21694.534	21818.493
443	Leg	36	-17404.009	17440.009	17575.237
444	Leg	40	-22055.472	22095.472	22245.725
445	Leg	45	-21306.468	21351.468	21520.503
451	Leg	36	-21035.011	21071.011	21206.238
452	Leg	38	-21068.229	21106.229	21248.970
453	Leg	41	-21048.524	21089.524	21243.534
454	Leg	45	-18722.630	18767.630	18936.665
455	Leg	50	-24743.345	24793.345	24981.162
511	Leg	27	-21247.518	21274.518	21375.939
512	Leg	29	-21241.137	21270.137	21379.071
513	Leg	32	-21369.337	21401.337	21521.539
514	Leg	36	-21175.750	21211.750	21346.978
515	Leg	41	-32349.245	32390.245	32544.255
521	Leg	29	-21122.048	21151.048	21259.982
522	Leg	31	-30199.510	30230.510	30346.957
523	Leg	34	-21101.399	21135.399	21263.114
524	Leg	38	-22845.251	22883.251	23025.991
525	Leg	43	-22278.522	22321.522	22483.045
531	Leg	32	-21074.310	21106.310	21226.513
532	Leg	34	-32188.247	32222.247	32349.962
533	Leg	37	-21054.520	21091.520	21230.505
534	Leg	41	-32498.486	32539.486	32693.496
535	Leg	46	-21028.168	21074.168	21246.959
541	Leg	36	-30250.142	30286.142	30421.370
542	Leg	38	-32490.949	32528.949	32671.690
543	Leg	41	-21015.945	21056.945	21210.955
544	Leg	45	-31130.826	31175.826	31344.861
545	Leg	50	-23668.375	23718.375	23906.191
551	Leg	41	-35231.224	35272.224	35426.234
552	Leg	43	-27132.844	27175.844	27337.366
553	Leg	46	-20969.455	21015.455	21188.246
554	Leg	50	-30800.300	30850.300	31038.117
555	Leg	55	-23637.423	23692.423	23899.022
711	Leg	38	-18836.196	18874.196	19011.979
712	Leg	40	-18759.261	18799.261	18944.297
713	Leg	43	-18944.297	18762.562	18918.476
714	Leg	47	-18705.145	18752.145	18922.561
715	Leg	52	-18689.006	18741.006	18929.552
716	Leg	58	-18673.807	18731.807	18942.108
717	Leg	65	-18649.742	18714.742	18950.424
721	Leg	40	-18831.713	18871.713	19016.749
722	Leg	42	-18759.166	18801.166	18953.453

723	Leg	45	-18718.628	18763.628	18926.793
724	Leg	49	-18704.657	18753.657	18931.325
725	Leg	54	-18688.848	18742.848	18938.645
726	Leg	60	-18673.803	18733.803	18951.356
727	Leg	67	-18649.698	18716.698	18959.632
731	Leg	43	-18820.277	18863.277	19019.190
732	Leg	45	-17091.213	17136.213	17299.378
733	Leg	48	-17350.253	17398.253	17572.295
734	Leg	52	-15488.493	15540.493	15729.039
735	Leg	57	-16845.773	16902.773	17109.448
736	Leg	63	-17109.448	18727.069	18955.499
737	Leg	70	-18638.678	18708.678	18962.490
741	Leg	47	-18802.049	18849.049	19019.465
742	Leg	49	-18727.265	18776.265	18953.934
743	Leg	52	-17001.526	17053.526	17242.072
744	Leg	56	-17320.006	17376.006	17579.056
745	Leg	61	-18211.517	18272.517	18493.696
746	Leg	67	-16775.709	16842.709	17085.643
747	Leg	74	-18631.984	18705.984	18974.299
751	Leg	52	-18796.760	18848.760	19037.306
752	Leg	54	-18721.628	18775.628	18971.426
753	Leg	57	-18086.697	18143.697	18350.372
754	Leg	61	-18350.372	18098.760	18319.939
755	Leg	66	-18656.809	18722.809	18962.118
756	Leg	72	-17872.007	17944.007	18205.071
757	Leg	79	-18621.976	18700.976	18987.421
761	Leg	58	-16838.804	16896.804	17107.105
762	Leg	60	-16515.174	16575.174	16792.727
763	Leg	63	-17018.584	17081.584	17310.015
764	Leg	67	-17033.126	17100.126	17343.060
765	Leg	72	-17096.505	17168.505	17429.568
766	Leg	78	-18651.999	18729.999	19012.818
767	Leg	85	-18612.136	18697.136	19005.336
771	Leg	65	-19405.288	19470.288	19705.970
772	Leg	67	-18510.840	18577.840	18820.775
773	Leg	70	-19089.827	19159.827	19413.639
774	Leg	74	-17743.383	17817.383	18085.699
775	Leg	79	-17987.269	18066.269	18352.714
776	Leg	85	-18655.573	18740.573	19048.773
777	Leg	92	-18365.873	18457.873	18791.454
811	Leg	46	-18791.454	18776.218	18943.009
812	Leg	48	-18654.296	18702.296	18876.338
813	Leg	51	-18616.194	18667.194	18852.114
814	Leg	55	-18603.331	18658.331	18857.755
815	Leg	60	-18857.755	18646.336	18863.889
816	Leg	66	-18573.057	18639.057	18878.366

817	Leg	73	-18552.473	18625.473	18890.163
818	Leg	81	-18534.455	18615.455	18909.152
821	Leg	48	-18724.916	18772.916	18946.958
822	Leg	50	-18654.054	18704.054	18885.348
823	Leg	53	-18614.824	18667.824	18859.996
824	Leg	57	-18602.454	18659.454	18866.129
825	Leg	62	-18585.956	18647.956	18872.761
826	Leg	68	-18572.919	18640.919	18887.479
827	Leg	75	-16897.457	16972.457	17244.398
828	Leg	83	-18534.252	18617.252	18918.200
831	Leg	51	-18714.150	18765.150	18950.070
832	Leg	53	-15806.226	15859.226	16051.398
833	Leg	56	-18374.832	18430.832	18633.882
834	Leg	60	-16625.141	16685.141	16902.694
835	Leg	65	-16160.921	16225.921	16461.604
836	Leg	71	-18566.042	18637.042	18894.479
837	Leg	78	-16551.792	16629.792	16912.611
838	Leg	86	-18085.683	18171.683	18483.509
841	Leg	55	-18696.004	18751.004	18950.428
842	Leg	57	-17541.894	17598.894	17805.569
843	Leg	60	-18441.215	18501.215	18718.768
844	Leg	64	-17272.069	17336.069	17568.126
845	Leg	69	-17063.479	17063.479	17382.666
846	Leg	75	-17053.588	17128.588	17400.530
847	Leg	82	-18581.203	18663.203	18960.525
848	Leg	90	-18517.979	18607.979	18934.309
851	Leg	60	-18934.309	18750.211	18967.764
852	Leg	62	-17129.706	17191.706	17416.511
853	Leg	65	-18585.136	18650.136	18885.819
854	Leg	69	-18576.903	18645.903	18896.089
855	Leg	74	-18554.296	18628.296	18896.612
856	Leg	80	-18896.612	18137.735	18427.806
857	Leg	87	-17641.589	17728.589	18044.041
858	Leg	95	-18044.041	18600.720	18945.179
861	Leg	66	-18945.179	18064.319	18303.628
862	Leg	68	-18601.763	18669.763	18916.323
863	Leg	71	-18571.004	18642.004	18899.441
864	Leg	75	-18565.116	18640.116	18912.057
865	Leg	80	-18545.883	18625.883	18915.954
866	Leg	86	-18537.286	18623.286	18935.112
867	Leg	93	-18508.609	18601.609	18938.817
868	Leg	101	-18492.040	18593.040	18959.254
871	Leg	73	-18237.102	18310.102	18574.791
872	Leg	75	-19374.783	19449.783	19721.725
873	Leg	78	-18567.395	18645.395	18928.214
874	Leg	82	-18560.420	18642.420	18939.743

875	Leg	87	-17924.675	18011.675	18327.127
876	Leg	93	-18550.293	18643.293	18980.501
877	Leg	100	-18503.912	18603.912	18966.500
878	Leg	108	-18486.625	18594.625	18986.221
881	Leg	81	-19459.632	19540.632	19834.329
882	Leg	83	-19865.497	19948.497	20249.445
883	Leg	86	-17620.701	17706.701	18018.527
884	Leg	90	-17578.559	17668.559	17994.889
885	Leg	95	-17688.543	17783.543	18128.002
886	Leg	101	-18227.816	18328.816	18695.030
887	Leg	108	-18352.257	18460.257	18851.852
888	Leg	116	-19670.281	19786.281	20206.884
112	Pol	15	-27527.732	55085.464	55198.154
113	Pol	18	-23282.347	46564.694	46735.922
114	Pol	22	-25899.600	51843.200	52008.480
115	Pol	27	-31702.927	63459.854	63662.696
121	Pol	15	-27537.383	55104.766	55217.456
122	Pol	17	-25954.285	51942.570	52070.284
123	Pol	20	-22992.623	46025.246	46175.498
124	Pol	24	-23112.852	46273.704	46454.008
125	Pol	29	-33289.728	66637.456	66855.322
131	Pol	18	-26266.974	52569.948	52705.176
132	Pol	20	-22896.823	45833.646	45983.900
133	Pol	23	-22366.246	44778.492	44951.284
134	Pol	27	-22902.090	45858.180	46061.022
135	Pol	32	-33402.267	66868.534	67108.938
141	Pol	22	-26196.647	52437.294	52602.574
142	Pol	24	-23898.729	47845.458	48025.762
143	Pol	27	-22098.586	44251.172	44454.014
144	Pol	31	-22823.291	45708.582	45941.474
145	Pol	36	-31156.008	62384.016	62654.472
151	Pol	27	-31327.236	53975.746	54178.588
152	Pol	29	-23189.882	46437.764	46655.632
153	Pol	32	-22063.742	44191.484	44431.888
154	Pol	36	-24302.330	48676.660	48947.116
155	Pol	41	-31506.945	63095.890	63403.910
211	Pol	15	-25408.716	50847.432	50960.122
212	Pol	17	-25502.757	51039.514	51167.230
213	Pol	20	-22993.494	46026.988	46177.242
214	Pol	24	-23133.209	46314.418	46494.722
215	Pol	29	-33717.197	67492.394	67710.262
221	Pol	17	-25304.265	50642.530	50770.246
222	Pol	19	-25234.602	50507.204	50649.946
223	Pol	22	-22916.173	45876.346	46041.624
224	Pol	26	-23228.801	46509.602	46704.932
225	Pol	31	-33419.828	66901.656	67134.548

231	Pol	20	-22847.207	45734.414	45884.666
232	Pol	22	-23434.189	46912.378	47077.656
233	Pol	25	-22314.790	44679.580	44867.396
234	Pol	29	-23468.037	46994.074	47211.942
235	Pol	34	-34229.762	68527.524	68782.954
241	Pol	24	-22705.468	45458.936	45639.240
242	Pol	26	-22678.865	45409.730	45605.060
243	Pol	29	-23293.950	46645.900	46863.768
244	Pol	33	-22618.434	45302.868	45550.786
245	Pol	38	-32030.839	64137.678	64423.158
251	Pol	29	-32535.414	65128.828	65346.694
252	Pol	31	-22615.749	45293.498	45526.392
253	Pol	34	-21947.098	43962.196	44217.628
254	Pol	38	-22997.826	46071.652	46357.132
255	Pol	43	-33470.328	67026.656	67349.702
311	Pol	18	-22413.258	44862.516	44997.744
312	Pol	20	-22947.356	45934.712	46084.966
313	Pol	23	-22385.061	44816.122	44988.912
314	Pol	27	-23065.892	46185.784	46388.626
315	Pol	32	-33404.571	66873.142	67113.548
321	Pol	20	-22312.234	44664.468	44814.722
322	Pol	22	-23506.350	47056.700	47221.980
323	Pol	25	-22296.196	44642.392	44830.208
324	Pol	29	-23020.150	46098.300	46316.168
325	Pol	34	-31925.202	63918.404	64173.834
331	Pol	23	-22291.086	44628.172	44800.964
332	Pol	25	-22289.689	44629.378	44817.194
333	Pol	28	-22302.416	44660.832	44871.186
334	Pol	32	-23209.208	46482.416	46722.822
335	Pol	37	-31123.639	62321.278	62599.246
341	Pol	27	-22996.020	46046.040	46248.882
342	Pol	29	-22101.730	44261.460	44479.328
343	Pol	32	-22214.955	44493.910	44734.314
344	Pol	36	-23820.284	47712.568	47983.024
345	Pol	41	-36134.617	72351.234	72659.254
351	Pol	32	-22628.881	45321.762	45562.168
352	Pol	34	-22003.200	44074.400	44329.830
353	Pol	37	-22227.200	44528.400	44806.368
354	Pol	41	-23733.491	47548.982	47857.002
355	Pol	46	-33153.490	66398.980	66744.562
411	Pol	22	-23769.826	47583.652	47748.930
412	Pol	24	-22652.627	45353.254	45533.558
413	Pol	27	-22900.598	45855.196	46058.038
414	Pol	31	-23360.874	46783.748	47016.640
415	Pol	36	-35830.335	71732.670	72003.126
421	Pol	24	-22465.549	44979.098	45159.402

422	Pol	26	-22472.059	44996.118	45191.446
423	Pol	29	-22485.283	45028.566	45246.434
424	Pol	33	-24635.764	49337.528	49585.446
425	Pol	38	-34934.074	69944.148	70229.630
431	Pol	27	-22440.776	44935.552	45138.394
432	Pol	29	-22530.323	45118.646	45336.514
433	Pol	32	-23977.842	48019.684	48260.088
434	Pol	36	-23104.002	46280.004	46550.460
435	Pol	41	-35060.384	70202.768	70510.788
441	Pol	31	-22543.702	45149.404	45382.296
442	Pol	33	-22965.104	45996.208	46244.126
443	Pol	36	-23080.145	46232.290	46502.746
444	Pol	40	-27679.556	55439.112	55739.618
445	Pol	45	-33087.703	66265.406	66603.476
451	Pol	36	-22575.040	45222.080	45492.536
452	Pol	38	-22540.462	45156.924	45442.404
453	Pol	41	-24451.987	48985.974	49293.994
454	Pol	45	-25174.224	50438.448	50776.518
455	Pol	50	-33493.704	67087.408	67463.042
511	Pol	27	-44176.033	88406.066	88608.908
512	Pol	29	-38690.238	77438.476	77656.342
513	Pol	32	-44547.565	89159.130	89399.534
514	Pol	36	-44699.767	98851.910	99122.366
515	Pol	41	-33046.416	66174.832	66482.852
521	Pol	29	-30545.067	61148.134	61366.002
522	Pol	31	-38242.790	76547.580	76780.472
523	Pol	34	-45116.310	90300.620	90556.050
524	Pol	38	-49032.601	98141.202	98426.684
525	Pol	43	-32956.981	65999.962	66323.008
531	Pol	32	-47236.935	94537.870	94778.274
532	Pol	34	-39658.760	79385.520	79640.950
533	Pol	37	-44136.591	88347.182	88625.150
534	Pol	41	-34078.170	68238.340	68546.360
535	Pol	46	-32533.886	65159.772	65505.354
541	Pol	36	-44536.461	89144.922	89415.378
542	Pol	38	-38209.949	76495.898	76781.378
543	Pol	41	-47129.671	94341.342	94649.360
544	Pol	45	-52787.270	105664.540	106002.610
545	Pol	50	-35745.780	71591.560	71967.194
551	Pol	41	-44233.504	88549.008	88857.028
552	Pol	43	-36848.342	73782.684	74105.728
553	Pol	46	-48110.794	96313.588	96659.170
554	Pol	50	-50652.980	101405.960	101781.594
555	Pol	55	-39891.886	79893.772	80306.968

Appendix II: Variance components and approximate sampling errors from the best model for LW pig weight.

Value	Animal	Subject	Dam	Phenotypic				
3	1.267	0.4023	0.510028	0.33	0.9	0.206	3.43	0.278
8	16.875	2.1279	0.28119	0.9945	14.72	3.436	32.63	3.47
12	30.376	4.6946	0.146814	2.3084	41.03	9.199	74.02	8.918
16	81.003	9.1939	0.055724	4.2494	133.69	29.002	217.68	28.265
20	146.485	15.0116	0.007918	6.821	308.51	65.751	459.99	64.166
24	220.585	22.3213	0.003397	10.0262	559.26	118.281	783.54	115.451
28	309.626	31.2991	0.04216	13.8667	898.58	189.317	1214.17	184.978
32	398.646	41.0114	0.124209	18.3433	1315.31	276.479	1720.34	270.518
36	498.752	54.0225	0.249542	23.4565	1930.85	401.258	2449.28	392.071

Appendix III: Correlations and approximate sampling errors from the calculated variances

Correlations and approximate sampling errors for value 3								
	Animal	Subject	Dam	Phenotypic				
3	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000
8	0.768	0.098	1.000	1.024	0.021	0.184	0.379	0.072
12	0.730	0.108	1.000	6.352	-	0.072	0.179	0.274
16	0.670	0.104	1.000	34.917	-	0.034	0.180	0.241
20	0.631	0.108	0.999	420.025	-	0.053	0.180	0.196
24	0.590	0.114	-0.998	-0.071	-	0.180	0.159	0.084
28	0.559	0.117	-1.000	170.650	-	0.063	0.180	0.141
32	0.518	0.123	-1.000	77.951	-	0.061	0.180	0.121
36	0.509	0.126	-1.000	50.243	-	0.075	0.180	0.101
Correlations & approximate sampling errors for value 8								
	Animal	Subject	Dam	Phenotypic				
3	0.768	0.098	1.000	1.024	0.021	0.184	0.379	0.072
8	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000
12	0.888	0.024	1.000	2.276	0.931	0.023	0.879	0.016
16	0.765	0.031	1.000	23.984	0.949	0.019	0.836	0.020
20	0.684	0.037	1.000	379.587	0.962	0.016	0.807	0.023
24	0.621	0.043	-0.998	0.963	0.016	0.783	0.027	*
28	0.582	0.047	-1.000	198.104	0.960	0.017	0.766	0.029
32	0.511	0.055	-1.000	96.839	0.965	0.016	0.743	0.032
36	0.477	0.059	-1.000	65.609	0.962	0.017	0.728	0.034

Correlations & approximate sampling errors for value 16								
	Animal		Subject		Dam		Phenotypic	
					-			
3	0.670	0.104	1.000	34.917	0.034	0.180	0.241	0.079
8	0.765	0.031	1.000	23.984	0.949	0.019	0.836	0.019
12	0.909	0.017	1.000	11.484	0.978	0.008	0.927	0.011
16	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000
20	0.964	0.005	1.000	212.766	0.998	0.001	0.972	0.004
24	0.882	0.015	-0.998	0.994	0.003	0.944	0.008	*
28	0.822	0.020	-1.000	359.918	0.989	0.005	0.920	0.012
32	0.736	0.030	-1.000	217.196	0.976	0.009	0.885	0.017
36	0.695	0.035	-1.000	168.921	0.975	0.010	0.869	0.020
Correlations & approximate sampling errors for value 24								
	Animal		Subject		Dam		Phenotypic	
3	0.590	0.114	-0.998	-0.071	0.180	0.159	0.084	*
8	0.621	0.043	-0.998	0.963	0.016	0.783	0.026	*
12	0.748	0.033	-0.998	0.972	0.011	0.865	0.019	*
16	0.882	0.015	-0.998	0.994	0.003	0.944	0.008	*
20	0.970	0.004	-0.996	0.999	0.001	0.981	0.003	*
24	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000
28	0.978	0.003	0.999	654.012	0.998	0.001	0.988	0.002
32	0.902	0.012	0.999	888.417	0.992	0.003	0.963	0.005
36	0.860	0.017	0.999	995.159	0.991	0.003	0.949	0.010
Correlations & approximate sampling errors for value 36								
	Animal		Subject		Dam		Phenotypic	
					-			
3	0.509	0.126	-1.000	50.243	0.075	0.180	0.101	0.087
8	0.477	0.059	-1.000	65.609	0.962	0.017	0.728	0.034
12	0.589	0.054	-1.000	92.323	0.947	0.019	0.796	0.030
16	0.695	0.035	-1.000	168.921	0.975	0.010	0.869	0.020
20	0.785	0.025	-0.999	760.673	0.985	0.006	0.916	0.014
24	0.860	0.017	0.999	995.159	0.991	0.003	0.949	0.009
28	0.932	0.011	1.000	35.706	0.996	0.002	0.973	0.006
32	0.990	0.004	1.000	3.030	0.999	0.000	0.991	0.002
36	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000

Appendix IV: WOMBAT Parameter file for running a random regression model for the estimation of genetic parameters for LW pigs' weight.

```

COM Large White Pig Data
ANAL RR
PEDS ./pigped.d
DATA ./pigdat.d
    Animal
    Subject 2100
    Sire
    Dam 95
    Cgroup 2
    Parity 3
    Sex 2
    Littersize 15
    Weight 445
    Age 411
END DATA
MODEL
    FIX Cgroup
    FIX Sex 12 16 20 24 28 32 36
    COV Littersize(2) 3 8 12 16 20 24 28 32 36
    RRC Age
    RAN Animal(8,leg) nrm
    RAN Subject(3,leg)1 3 8
    RAN Dam(2,leg)
    trait Weight
END MOD
VAR Animal 8 8
    48.14 52.12 52.65 53.01 53.94 54.91 55.12 55.98
    61.12 62.23 62.12 63.32 64.21 64.99 65.12
    72.31 73.23 74.12 74.32 75.21 76.43
    80.12 81.12 82.33 83.23 84.23
    90.21 91.23 92.54 93.32
    101.21 102.21 103.23
    111.21 112.32
    120.21
VAR Subject 3 3
    89.63 91.12 92.43
    102.12 103.32
    111.21
VAR Dam 2 2
    22.2 23.43
    31.32
VAR residual 1 HET 8
    3      8      0.51082
    9      12      2.1001
    13     16      3.0229
    17     20      4.5599
    21     24      3.8594

```

25	28	4.1540
29	32	9.4683
33	36	10.898

Appendix V: WOMBAT SumEstimates file (output) from the Parameter file in Appendix IV for analysis of LW pig weight.

```
===== Version 01-11-2011 =====
**KM** =====
```

Program WOMBAT : Estimates of covariance components

Large White Pig Data

```
Analysis type      : "RR"
Data file          : "../pigdat.d"
Pedigree file      : "ReducedPedFile.dat"
Parameter file     : "wombat.par"
```

```
No. of traits      = 1          Weight
No. of records     = 10428      10428
No. of parameters  = 53
Maximum log L      = -15806.226
-1/2 AIC & AICC    = -15859.226  -15859.502
-1/2 BIC           = -16051.398  "Penalty factor" = 4.626
```

Parameter estimates

```
1 COVS Z 1 1 1      0.555746
2 COVS Z 1 1 2      1.20056
3 COVS Z 1 1 3      1.87599
4 COVS Z 1 1 4      2.12986
5 COVS Z 1 1 5      2.05349
6 COVS Z 1 1 6      2.23641
7 COVS Z 1 1 7      2.68964
8 COVS Z 1 1 8      4.06128
9 CHOL A 1 1        3.14536
10 CHOL A 1 2       10.7301
11 CHOL A 1 3       -1.52402
12 CHOL A 1 4        1.00143
13 CHOL A 1 5        0.135317
14 CHOL A 1 6       -0.418793
15 CHOL A 1 7        0.325800
16 CHOL A 1 8        0.247399
17 CHOL A 2 2        1.02412
18 CHOL A 2 3        0.375854
19 CHOL A 2 4        2.09200
```

20	CHOL A 2 5	-0.475737
21	CHOL A 2 6	0.471886
22	CHOL A 2 7	-0.494231
23	CHOL A 2 8	-0.151488
24	CHOL A 3 3	0.726734
25	CHOL A 3 4	1.30529
26	CHOL A 3 5	-0.103048
27	CHOL A 3 6	-0.397688E-01
28	CHOL A 3 7	-0.502113
29	CHOL A 3 8	-0.585270
30	CHOL A 4 4	1.01780
31	CHOL A 4 5	-0.433961
32	CHOL A 4 6	-0.525167
33	CHOL A 4 7	0.448842
34	CHOL A 4 8	0.594519E-01
35	CHOL A 5 5	0.204135
36	CHOL A 5 6	-0.669747
37	CHOL A 5 7	0.298411
38	CHOL A 5 8	0.533125E-02
39	CHOL A 6 6	-1.44491
40	CHOL A 6 7	0.213259E-01
41	CHOL A 6 8	0.219228
42	CHOL A 7 7	-0.482762
43	CHOL A 7 8	-0.619266
44	CHOL A 8 8	-1.01943
45	CHOL B 1 1	-0.354419
46	CHOL B 1 2	-2.57374
47	CHOL B 1 3	-0.565172
48	CHOL B 2 2	-8.95492
49	CHOL B 2 3	-0.523398
50	CHOL B 3 3	-1.80248
51	CHOL C 1 1	4.16003
52	CHOL C 1 2	8.58517
53	CHOL C 2 2	1.16980

Convergence criteria for last 3 iterates

Change in log likelihood	=	0.000675	0.001809	0.000483
Change in parameter vector	=	0.013143	0.012776	0.012535
Norm of gradient vector	=	12.6606	11.8538	11.5352
Newton decrement	=	-0.0499	-0.0509	-0.0438

***** Estimates of residual covariances

Order of fit = 1

No. of measurement error variance classes = 8

Class no. 1 Range 3 8

(Co)Variance components

1 0.30885

Class no. 2 Range 9 12

(Co)Variance components

```

1 1.4414
Class no. 3 Range 13 16
(Co)Variance components
1 3.5193
Class no. 4 Range 17 20
(Co)Variance components
1 4.5363
Class no. 5 Range 21 24
(Co)Variance components
1 4.2168
Class no. 6 Range 25 28
(Co)Variance components
1 5.0015
Class no. 7 Range 29 32
(Co)Variance components
1 7.2341
Class no. 8 Range 33 36
(Co)Variance components
1 16.494

```

***** Estimates for RE 1 "Animal"

```

No. of levels = 1475
Covariance structure = NRM
Order of fit = 8

```

Covariance matrix

```

1 539.54
2 249.24 122.89
3 23.261 16.571 14.740
4 -35.400 -15.306 1.9598 6.7418
5 3.1431 0.12722 -2.1951 -0.59817 1.9478
6 5.7466 2.2328 -0.66860 -1.6445 0.14660 0.99199
7 -9.7277 -3.1797 -0.93731 0.73335 -0.87058 -0.13492
1.1796
8 7.5677 2.1196 -0.12108 -1.7208 0.50216 0.10016
-0.78024 1.2743

```

Eigenvalues of covariance matrix

```

Value 659.86 17.98 4.75 3.94 1.86 0.81
0.10 0.02
(%) 95.73 2.61 0.69 0.57 0.27 0.12
0.01 0.00

```

Trace 689.30

Correlation matrix

```

1 1.0000
2 0.9679 1.0000
3 0.2608 0.3893 1.0000
4 -0.5870 -0.5318 0.1966 1.0000
5 0.0970 0.0082 -0.4097 -0.1651 1.0000
6 0.2484 0.2022 -0.1748 -0.6359 0.1055 1.0000
7 -0.3856 -0.2641 -0.2248 0.2601 -0.5743 -0.1247

```

```

      1.0000
  8   0.2886  0.1694 -0.0279 -0.5871  0.3187  0.0891
      -0.6364  1.0000

```

```
***** Estimates for RE 2 "Subject"
```

```
*****
```

```

      No. of levels      = 1398
      Covariance structure = IDE
      Order of fit       = 3
Covariance matrix
  1  0.49222
  2 -1.8057  6.6242
  3 -0.39651  1.4545  0.62055
Eigenvalues of covariance matrix
Value   7.45   0.29   0.00
(%)    96.28  3.72   0.00
Trace   7.74
Correlation matrix
  1  1.0000
  2 -1.0000  1.0000
  3 -0.7174  0.7174  1.0000

```

```
***** Estimates for RE 3 "Dam"
```

```
*****
```

```

      No. of levels      = 86
      Covariance structure = IDE
      Order of fit       = 2
Covariance matrix
  1  75.073
  2  35.715  17.306
Eigenvalues of covariance matrix
Value   92.12   0.26
(%)    99.72  0.28
Trace   92.38
Correlation matrix
  1  1.0000
  2  0.9908  1.0000

```

```
===== end of file =====26-01-015=====15:41=====
```


Appendix VI: Similarity Report

Document Viewer

Turnitin Originality Report

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