"Pig farming is a wonderful mixture of scientific precision and massive ignorance"
C.Clark (1998) International Pig Letter **18** (3) : 13

THE EVALUATION OF THE GROWTH PARAMETERS OF SIX SOUTH AFRICAN COMMERCIAL CROSSBRED PIG GENOTYPES

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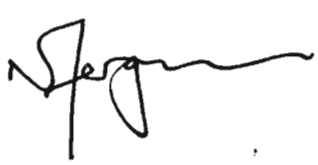
I HEREBY DECLARE THAT THE RESEARCH IN THIS THESIS IS OF MY OWN INVESTIGATION. WHERE USE WAS MADE OF THE WORK OF OTHER AUTHORS IT HAS BEEN DULY ACKNOWLEDGED IN THE TEXT.

S.T. KYRIAZIS

AS SUPERVISOR OF THIS THESIS, I HEREBY ENDORSE THIS WORK.



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ABSTRACT

Simulation modeling is an active part of animal nutrition. These complex programs rely on mathematical functions to predict the performance of an animal. The Gompertz equation is a simple, but accurate function that fits animal growth data well. In conjunction with allometry, the growth of a specific genotype can be predicted. Only three parameters are needed to sufficiently describe a genotype, *viz.* protein weight at maturity (P_m), the Gompertz growth rate parameter (B) and the lipid to protein ratio at maturity (LPR_m). These descriptors are lacking for commercial pig genotypes in South Africa, and this hinders the use of models in simulating nutrient requirements. It is the aim of this thesis to estimate these parameters in six South African pig genotypes. Thirty pigs from each of six commercial genotypes were analysed using a serial slaughter method in which pigs were slaughtered at 4 and 14 days of age, and at 30, 40, 70, 80, 90 and 100kg live weight. The animals were choice fed and were housed in conventional housing facilities. Analyses for protein, lipid, water, and ash contents of the empty body at the respective weights were performed. The results indicated that there were no significant differences between the six genotypes in terms of mature weights or B of the various body chemical components, or between the B values estimated for all components across genotypes. The mean of the estimated values for P_m, B and LPR_m were 38.8 ± 2.1 kg, 0.012 ± 0.004 day $^{-1}$, and 1.16 kg/kg respectively and can therefore be used to adequately describe all six genotypes. The assumption made that all body components have a similar B value is supported.

To investigate the possible effects of the environment on growth, a comparative trial was performed on 20 pigs each from genotypes 4, 5 and 6 using chambers in which the temperature could be controlled to within 1°C of the setting. All other experimental methodologies were similar to those adopted in the first experiment. No significant differences were found between the two housing facilities, in terms of the genetic parameters, within the respective genotypes supporting the findings of the previous trial. It may therefore be possible to estimate B using the live weight and estimating P_m and lipid at maturity using allometry, instead of going to the expense of a full serial slaughter trial. The allometric coefficients relating lipid, water and ash to protein were 1.18, 0.88 and 0.97 respectively.

CHAPTER 1

A REVIEW OF SOME MATHEMATICAL FUNCTIONS DESCRIBING GROWTH

1.1 Introduction

Growth has traditionally been quantified using body mass (live weight) over time or various linear body dimension measurements, such as height, hip width and girth (Brody, 1945), or, more recently, in terms of the chemical components of the body (Emmans, 1988). These measurements can be obtained directly from the animal, or alternatively can be estimated using growth models. A comprehensive theory of growth that can be defined in terms of a series of mathematical functions has been an area of speculation, postulation and research for quite some time (Parks, 1982). The advent of modeling animal growth has further underlined the importance of functions that quantify as accurately, and as simply as possible, the potential growth of an animal. The variables, or parameters, defined in these equations have a significant effect on the applicability of a particular model, as does the simplicity of these parameters (Emmans and Kyriazakis, 1999). Purely mathematical, or mathematically derived, parameters are difficult to calculate and, depending on the complexity of the equation, offer a daunting obstacle to anyone hoping to put a particular model into practice.

Many approaches to describe growth have been published, each using a different function. Older functions and approaches, such as those of Gompertz (1825), Brody

(1945) and von Bertalanffy (1938) were derived by collecting data experimentally, plotting the data, and then fitting a function statistically suitable to the data. Functions such as those of Robertson, (1923); Parks, (1982); Bridges et al., (1986), although much more accurate in describing the data, use mathematics, or statistics, to derive parameters that have little biological meaning. In the latter, data sets were re-analysed and manipulated to improve their fit. In older models, the method with which the parameters were derived meant that the equations were simple, and the parameters were meaningful and measurable.

A good statistical fit to the data is an obvious necessity when using functions to describe growth, because this will ensure the best possible description of growth, and an accurate estimation when incorporated into a model. Equations (Eq.) describing curves with a characteristic sigmoidal shape have been widely accepted as the ideal form to describe growth over time. The functions most commonly used to define the potential growth of an animal include the following:

1.2 Growth Functions

1.2.1 Gompertz (1825)

Function: $W_t = A \cdot e(-e[-k \cdot (t - t^1)])$ (1.1)

Where $t^1 = \{\ln(\ln W_0/A)\} \cdot (1 / k)$ (the point of inflection)

W_t = live weight at time t (days)

W_0 = birth weight (kg)

A = mature weight (kg)

k = exponential decay constant

The Gompertz function is probably one of the most well known equations describing growth. Originally developed for describing human growth, it has relatively recently been applied to the growth of animals. This function is sigmoidal in shape, simple and fits growth data well (Ferguson and Gous, 1994; Hancock et al., 1995). The parameters are of an empirical nature and therefore can be measured rather than derived. This allows the parameters to be comparable between animals.

1.2.2 Robertson (1923)

Function: $W_0 = A / \{ 1 + e[-k . (t - t^I)]\}$ (1.2)

Where $t^I = (1/k) . \ln[(A-W_0) / W_0]$

(all other parameters as for Gompertz function (Eq. 1.1))

Robertson (1923) drew a comparison between growth and autocatalytic chemical reactions based purely on the fact that the function describing these reactions seemed to fit growth data statistically well. He also suggested the concept of a "master reaction" of growth being the sum of a number of smaller reactions within the body. Although intuitively correct, the approach had some problems and was incomplete in terms of the nature of the reaction that took place, and the catalyst factor important in autocatalytic reactions. The theory was criticised by a number of authors, including Parks (1982), because of the simplistic approach adopted. It was also argued that a good statistical fit alone was not the only grounds to accept a model. The parameter "t^I" is similar to that of the Gompertz function, and can be derived using meaningful measurements.

1.2.3 von Bertalanffy (1938)

Function: $W_t = (N / n - e[- \{1-m\} . n . \{ t - t^I \}])^V$ (1.3)

Where N = anabolic efficiency

n = catabolic efficiency

v = metabolic index; v = 1/(1-m)

m = metabolic type (I, II, or III), $(2/3 < m < 1)$

Approaching the problem of describing growth through visualising it as the sum of anabolic and catabolic processes is conceptually sound; however, there are some shortcomings. Firstly, the measurement of these parameters is difficult and impractical. Secondly, the definition of the parameter "m" is somewhat subjective and is not determinable from growth data, yet the accuracy of the function depends on it.

1.2.4 Brody (1945)

Functions: $W_t = W_0 \,.\, e(c \,.\, t)$ where $0 < t < t^1$ (1.4)

$W_t = A \,.\, (1 - e[-k.(t-t^*)])$ where $t > t^1$

Where t^1 = time at point of maximum growth (days)

c = exponential growth constant

t^* = time taken to reach 63% mature mass (days)

Brody (1945) used two exponential functions to describe the growth of various farm animals. The problem with this description is that the latter function ignores the period of prenatal growth, which is described by the first function. Both functions are independent of each other. The fact that Brody (1945) needed two functions to describe the growth of animals supports the idea of a sigmoid shaped curve rather than a curvilinear shape. Brody (1945) worked on the principal that growth was defined as purely an increase in size (volumetric), and therefore made no allowance for the possibility that there might be physiological changes taking place during growth. Measurements were therefore

subjective in nature and not good indicators of growth, e.g. height at withers, hip width, girth. A possible conceptual problem with Brody's approach is the reasoning that puberty occurs at the point of maximum growth. Whittemore (1998) showed that in pigs, puberty occurs after this point. This however should not affect the usefulness of the function.

1.2.5 Parks (1982)

Function: $W_t = (A - W_0) \cdot \{1-e(-BC.[(t-t^*)(1-D/C)(1-e(-t/t^*))])\}$ (1.5)

Where B = efficiency of feed intake converted into body tissue

C = mature food intake (g/day)

D = food intake at birth (g/day)

(all other parameters as for Gompertz (Eq. 1.1))

The parameters used by Parks (1982) are simple and biological in nature, but the model has two shortcomings. Firstly, the function is complicated and difficult to conceptualise. Secondly, the model depends on an estimate of feed intake, and efficiency of food utilisation. Considering that a complete description of the growth potential of an animal is often required to predict food intake, then this approach is inappropriate for modeling food intake and growth. It makes little sense using a model that requires an estimate of mature and birth foo intake, in order to predict feed intake.

1.2.6 Bridges et al. (1986)

Function: $W_t = a \,.\, \{1 - e(-k \,.\, t^z)\}$ (1.6)

Where W_t = same as for Parks (1982) (Eq. 1.5)

$a = A / \{e\,(1/k)\}$

k = same as for Parks (1982) (Eq. 1.5)

$z = 1 / \{\ln(1 - W_t/a) + 1\}$

Bridges et al. (1986) used a continuous function that was sigmoidal in shape and the parameters used were mathematically derived. However, when fitted against actual data, there was a high degree of variability between randomly measured weights and weights predicted by the model.

1.3 Comparisons

Figure 1.1 shows the functions of Gompertz (1825), Robertson (1923) and Brody (1945) plotted on the same axis and using the same growth data. The data is taken from trial work done by Young and Gous (1999, unpublished) on broilers. These plots show clearly that the functions fit the data appropriately. Curves that are sigmoidal in shape (Gompertz (1825) and Robertson (1923)) appear to fit the data accurately, as does the dual-curve, curvilinear approach of Brody (1945).

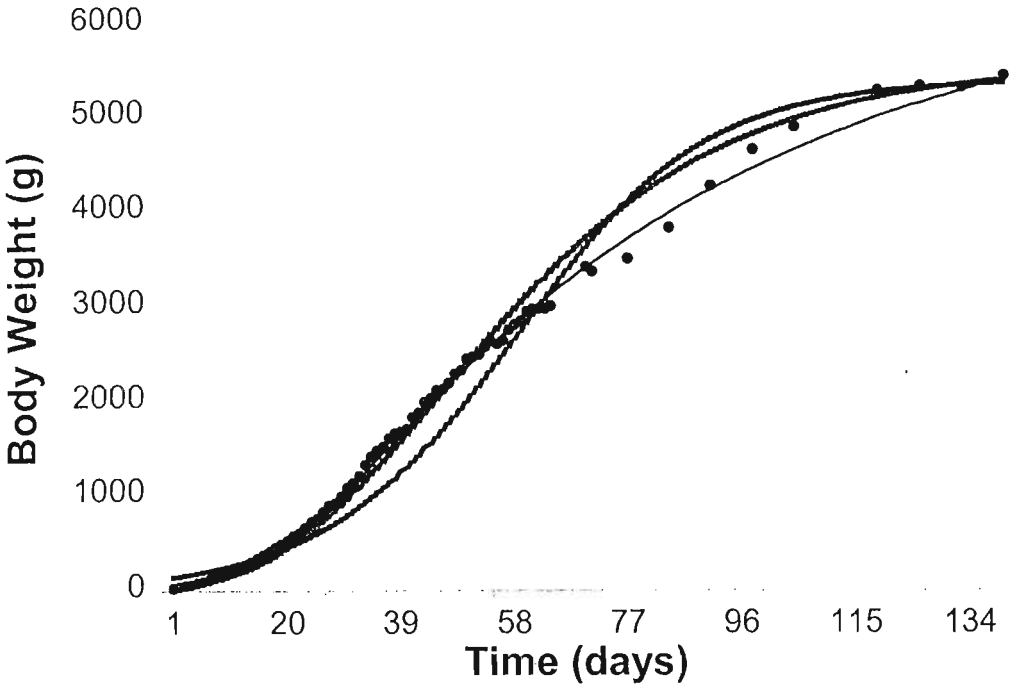

Figure 1.1: Change in body weight over time in broiler chickens using the growth functions of Gompertz (· · ·), Robertson (-----), and Brody (——), actual data (•).

The simplicity, determination of parameters and the ease of use are important factors to consider when selecting a growth function. Complicated functions with intricate parameters such as those of Parks (1982), von Bertalanffy (1938) and the dual-curve of Brody (1945), make experimental measurement tedious, and applications such as allometry difficult, if not impossible. Functions such as those of Gompertz (1825), Robertson (1923) and Brody (1945) are similar in that they use variables that have biological meaning and can be measured from the animal. On the above grounds, the Gompertz equation was selected as the function of choice for this research, and will therefore be discussed in more detail.

1.4 The Gompertz Function

The Gompertz equation (Eq. 1.1) adequately describes the more rapid increase in growth in the early stages of life, and the slower decline in growth in the later stages (Whittemore, 1998). This function can also be expressed in terms of degree of maturity (Eq. 1.7), which is the preferred form when applying the equation in allometry (to be discussed in section 1.4.1)

$$u = \exp\{-\exp[-B(t-t^{1})]\} \qquad (1.7)$$

(where $u = W_t/W_m$)

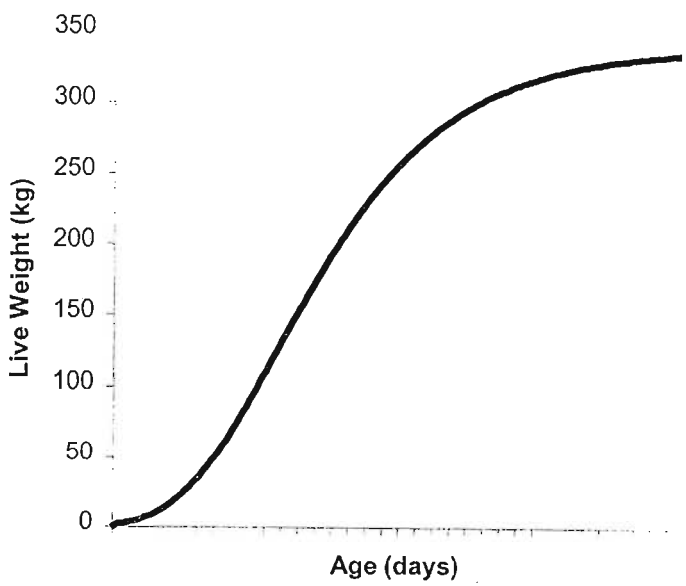

Figure 1.2 *The form of the Gompertz function of live weight vs. age of pigs (after* Emmans and Kyriazakis, 1999*)*

The Gompertz function is a fixed inflection-point curve (Figure 1.2) with the inflection point of the graph set at 0.368 (37%) of the mature age. Other functions, such as those of Parks (1982) and Bridges et al. (1986), have variable points of inflection and are thus said to be more flexible in describing the shape of protein accretion curves. These functions are, however, not suitable in that their parameters are unstable (Schinckel 1999), thus rendering the use of allometry almost impossible when using these functions to describe growth. Variable inflection point curves are also complicated, which would suggest that although they are good descriptors of data, they do not describe growth itself (Emmans and Kyriazakis, 1999).

The characteristic fixed inflection point of the Gompertz function has been one of the major sources of its criticism. It has been argued that the function is inflexible, or rigid, and might therefore not be descriptive of different species or genotypes (Schinckel, 1999). This is a valid argument. However, judging by the goodness of fit of the function, the fact that animals mature at different times, and the possible combination with allometry to predict individual body component growth, suggests that the "fixed" point of inflection is insignificant when evaluating the accuracy of the function as a whole.

The slope of the Gompertz curve (dW_t / dt) is also commonly referred to as the absolute growth rate at a given point in time. When absolute growth rate is plotted against W_t, the graph as shown in Figure 1.3 is attained:

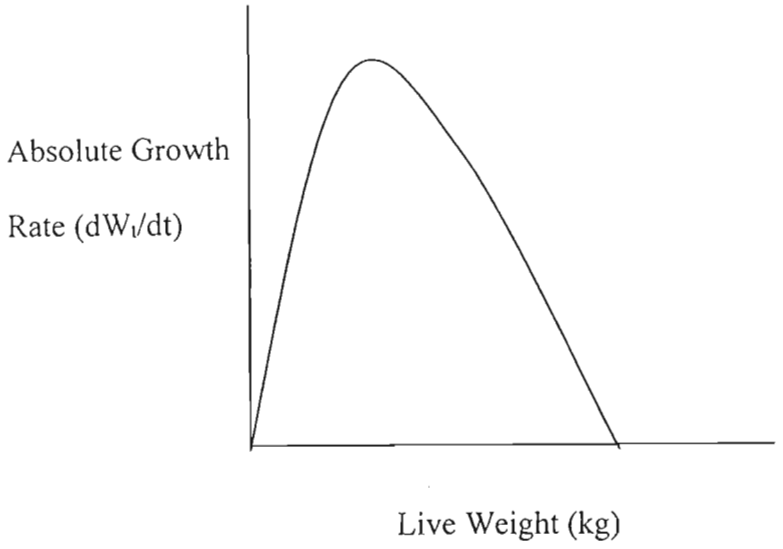

Figure 1.3 Absolute growth rate vs. live weight as derived from the function in Figure 1.2.

In Figure 1.3, the peak is defined as the live weight (W_t) at which the maximum growth rate is achieved, or the live weight at the inflection point on the original Gompertz curve (Figure 1.2). A measure of the relative growth rate of an animal in non-limiting circumstances holds more relevance than conventional growth rate in that one can express the rate of growth in terms of the physiological stage rather than chronological age (Ferguson and Gous, 1993a). This is achieved in expressing relative growth rate as $(dW_t / dt) / W_t$, or the growth rate at a certain live weight. If the relative growth rate ($dW_t / dt / W_t$) is expressed according to live weight, one gets an exponential curve as shown by Ferguson and Gous (1993(a)). Plotting the logarithm of relative growth rate over body weight will produce a straight line (Figure 1.4). The slope of this line represents the relative growth rate co-efficient of the original Gompertz growth curve. Extrapolation of

the straight line to intercept the x-axis will produce the logarithm of the mature mass (Log W_m, Figure 1.4), although theoretically this will not happen due to the asymptotic nature of the Gompertz curve.

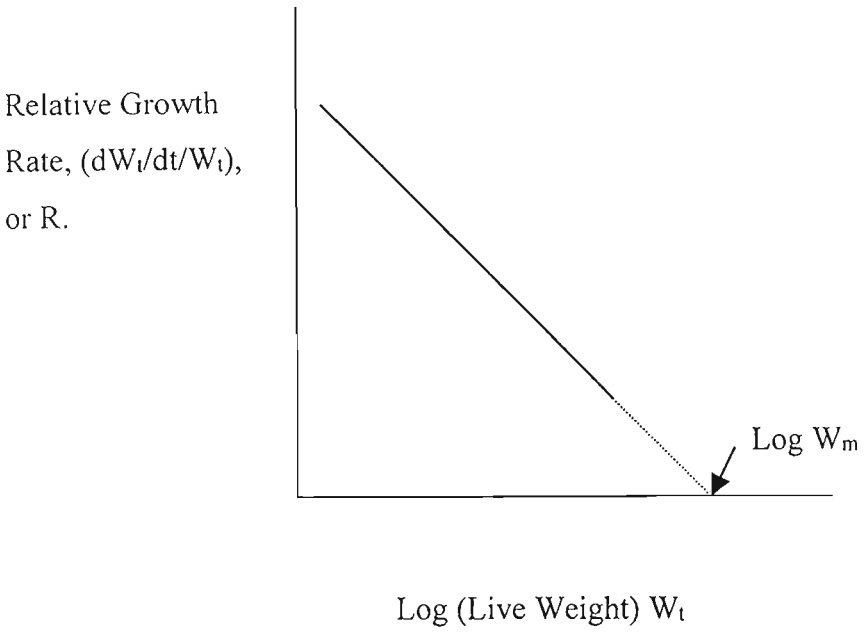

Figure 1.4 *Relative Growth Rate ($dW_t / dt / W_t$) vs. Log W_t as derived from the function of Figure 1.3*

1.4.1 Allometric Relationships between Chemical Components

Allometry is a process by which the change in one variable is mathematically predicted from the changes in another variable (Emmans and Kyriazakis 1999). For example, one could predict the growth of one body component mathematically using the growth of another as reference, provided certain mathematical relationships existed between the two

components. It would therefore not be necessary to measure the growth of the former component; it could be predicted through only measuring the latter.

Allometry has become a useful tool in the description of the growth of chemical components of the body, i.e. protein, lipid, ash and water (Emmans and Kyriazakis 1999). Its use relies on two assumptions; firstly, that the growth of the individual components follow a similar curve, and secondly that the Gompertz rate parameter (B) of the components are the same. If the latter assumptions hold, then the growth of one component will be a simple power function of the other (Eq. 1.8). For example, lipid weight can be expressed as a function of protein weight:

$$L = a \cdot P^b \qquad (1.8)$$

Where L = lipid weight

P = protein weight

a = constant

b = allometric co-efficient

Equation 1.8 proves useful when deriving parameters for allometric application. When the parameters are expressed using the Gompertz function, the degree of maturity of the different components can be mathematically related to each other through a simple power function (Emmans and Kyriazakis 1999). According to Schinckel (1999), the use of allometry also offers simple and stable derivatives, and this holds true when the Gompertz parameters are used. Equation 1.7 describes the degree of maturity (u), or

W_t/W_m, in terms of a rate parameter (B). This means that one could first describe the growth of the protein component of the body using the Gompertz parameters, i.e. initial (P_0) and mature mass (P_m) for protein, as well as relative growth rate, and then estimate the growth rates of the other chemical components using allometry. If allometry is not used, eight parameters in total need to be determined (Table 1.1).

Table 1.1 Chemical Components of the body and the applicable Gompertz parameters needed to predict their growth.

	PROTEIN	LIPID	WATER	ASH
RATE PARAMETER (Gompertz)	$\mathbf{B_p}$	$\mathbf{B_l}$	$\mathbf{B_{wa}}$	$\mathbf{B_{ash}}$
WEIGHT AT MATURITY	$\mathbf{P_m}$	$\mathbf{L_m}$	$\mathbf{WA_m}$	$\mathbf{ASH_m}$

Provided the allometric coefficients (a and b) are quantified and the growth of the various chemical components are Gompertz functions of time, with the same B value, the situation is simplified. Only B, an estimate of mature protein weight and an estimate of the pig's mature fatness, expressed as a ratio of mature protein (L_m/P_m, or LPR_m) are required to describe the growth of the chemical components of a certain genotype of pig in non-limiting conditions using allometry. In addition, three constants are required in order to quantify the growth of the various body components. These constants include the water to protein ratio at maturity, the allometric co-efficient linking water and protein, and the ash to protein ratio. Various estimates of these constants have been made

(Kyriazakis and Emmans, (1992a,b); Kyriazakis et al., 1994). There is evidence to suggest that the genotype of a pig will affect the scalar value in allometric functions relating water to body protein (Emmans and Kyriazakis 1995).

1.4.2 Quantification of Parameters

The quantification of the Gompertz parameters is a simple process as was shown by Hancock et al. (1995) and Gous et al. (1999). Body weights, or the weights of the various chemical components, can be fed into statistical software and, using a "fit non-linear" procedure, the Gompertz parameters of the applicable component are estimated. This process yields B-parameters and mature weights for whatever data is used. Calculating the lipid to protein ratio at maturity (LPR_m) becomes a simple task and is calculated by dividing the mature lipid weight with that of protein.

1.5 Conclusions

Many different approaches to modeling or describing the growth of animals exist; some of which are complex and some that are simpler. Complexity and statistical fit are not the only measures of accuracy and should therefore only be seen as part of the evidence supporting the choice of a particular function. The parameters that are used in a particular function need to be measurable and biologically meaningful. The function of Gompertz was shown to comply with these criteria and its parameters proved applicable when using

allometry to predict the growth of the chemical components of the body. It has also been shown that deriving these parameters from experimental data is relatively simple and does not require complex mathematics. All these factors bear testimony to the appropriateness of applying the Gompertz function when predicting, of quantifying the genotype of the animal.

CHAPTER 2

THE DETERMINATION OF THE GROWTH PARAMETERS OF SIX COMMERCIAL PIG GENOTYPES

2.1 Introduction

In order to model animal growth, and thereby calculate the optimum nutrient requirements of growing pigs, there needs to be an adequate description of the animal. If the Gompertz function is used to describe the growth then only three parameters are required to describe the genotype of the pig *viz.* the rate at which the animal can mature (B), mature protein weight (P_m) and a measure of the fatness at maturity (LPR_m). The objective of this experiment was to estimate these parameters for six commercial crossbred pig genotypes, by means of a serial slaughter technique, following the protocol proposed by Ferguson and Gous (1993a).

2.2 Materials and Methods

2.2.1 Animals and Housing

Thirty entire male pigs from each of six commercial pig genotypes were chosen for the purposes of this trial. All pigs were slaughtered at one of the following live weights or ages: 4 and 14 days, 30, 40, 70, 80, 90, and 100kg. These age and weight groups were chosen to facilitate the planned statistical analysis discussed below. There were three piglets slaughtered at four and 14 days of age, and four pigs at each of the subsequent weights. Due to insufficient facilities, the trial was divided into two

periods with three genotypes grown in each trial period. The genotypes can be described as follows:

Table 2.1 Genotype descriptions and the genotype label to be used in this thesis

Producer	Genotype	Label
Pro-pig	F1 Large White (LW) cross	1
P.I.C. (Kanhym)	(LW x LR) x Hamline	2
Hathaway Farms	LW/LR x Duroc (DC)	3
Dalland	LW x Pietran	4
Oakleigh	(LW x LR) X (LW x DC)	5
Rollands	LW x LR x DC x Hampshire	6

On arrival at Ukulinga Research Station, the piglets were approximately eight weeks of age (mean live weight of 19.2 ± 3.2 kg), and were dewormed with a treatment of macro-cyclic lactones (Dectomax^{TM}) before being individually and randomly placed into pens. The pens used were of two sizes, i.e. approximately $2m^2$ and $7m^2$. The buildings were open-sided to allow free airflow, but had an insulated ceiling, to minimise the fluctuation in temperature. Each pen was furnished with two feed bins (Big Dutchman®) in order to facilitate the choice-feeding regime.

2.2.2 Diets and Feeding

Animals were put on a choice feeding program. Two diets, isoenergetic but containing high and low levels of crude protein respectively (HP and LP), were fed at the same time, thus allowing the pigs to satisfy their crude protein requirements for maximum protein growth (Bradford and Gous, 1991a, b; Kyriazakis et al., 1991). Vitamins and minerals were included at 1.5 times the prescribed level recommended by the

suppliers to ensure they were not limiting. The amino acids were balanced according to the ideal protein balance (Wang and Fuller, 1985).

The feeding of the pigs was divided into two phases to more closely meet the nutrient requirements of the growing animal. The first phase was from arrival to 40kg live weight (W-40), and the second from 40 to 100kg (40-100). Over the two trial periods, a total of eight feeds were produced and pelleted by Meadow Feeds. Feed samples were analysed in duplicate (Table 2.2). Changes in formulation were made due to raw material availability and nutrient content, although this could have a significant effect on performance if the maximum inclusion levels of certain raw materials are exceeded. All feeds were offered on an *ad libitum* basis and each animal underwent a six-day training period as described by Bradford and Gous (1991a, b). Water was supplied by means of drinker nipples (one or two per pen depending on pen size).

2.2.3 Sampling and Sample Analysis

Piglets slaughtered at the beginning of the trial i.e. at 4 and 14 days, were randomly selected from their littermates in the farrowing house. Once the animals arrived at Ukulinga Research farm they were randomly divided into six slaughter groups. The animals were weighed on a weekly basis in order to determine average daily weight gain and proximity to respective slaughter weight targets. The animals that reached their slaughter weight were killed either by means of a lethal intra-cardial injection of sodium-pentobarbitone (Euthanase^{TM}) if they weighed 40kg or less, or by exsanguination at the local abattoir if over 40kg. The animals were subjected to no fasting, or any other special treatment, before slaughter.

Table 2.2: Ingredients and chemical composition of the experimental diets expressed as a percentage of the feed on an as fed basis.

Growth Phase	Period 1*				Period 2**			
	W-40		40-100		W-40		40-100	
	High Protein	Low Protein	High Protein	Low Protein	High Protein	Low Protein	High Protein	Low Protein
Ingredients								
Fine Maize	40.5	68.3	38.3	56.4	37.9	67.0	38.3	56.4
Full Fat Soya	25.0	25.0	16.0	10.1	21.0	21.0	16.0	10.1
Soya Oilcake	5.0	2.0	6.0	-	33.0	3.8	6.0	-
Sunflower Oilcake	6.6	-	4.8	-	-	-	4.8	-
Fish Meal	16.1	-	-	-	-	-	-	-
Wheat Middlings	4.0	-	15.0	13.8	-	-	15.0	13.8
Maize Germ	-	-	15.0	15.0	4.0	4.0	15.0	15.0
Vit. & Min. Premix	0.3	0.3	0.3	0.3	0.2	0.2	0.3	0.3
Lysine HCl	-	-	0.6	-	0.2	0.2	0.6	-
DL-Methionine	0.1	-	0.1	-	0.2	0.0	0.1	-
Limestone	-	0.9	1.4	1.3	1.6	1.6	1.4	1.3
Monocalciumphosphate	2.2	3.3	2.1	2.6	1.4	1.7	2.1	2.6
Salt (NaCl)	0.3	0.3	0.4	0.4	0.4	0.4	0.4	0.4
Chemical Analysis (%)								
Digestible Energy (MJ/kg)	14.2	14.5	13.4	13.4	15.1	14.7	13.1	13.4
Crude Protein	27.0	15.3	17.2	11.8	27.4	16.1	17.5	11.5
Lysine	1.8	0.9	1.0	0.5	1.8	1.0	1.1	0.5

* Genotypes 4, 5 and 6 tested

** Genotypes 1, 2 and 3 tested

Digestible Energy = 3.77 - (0.19 x NDF) + (0.75 x GE) (Whittemore, 1998)

The whole bodies of the animals killed by lethal injection were individually sealed in plastic bags to prevent moisture loss, and were cooled (10°C) overnight. Pigs selected for the 4 and 14 day group were sacrificed and analysed (following the methods described below) before the rest of the pigs arrived at the research station.

The gastro-intestinal tract (GIT) was removed, weighed and flushed in order to determine gut fill. The empty body and washed digestive tract was then minced twice before sampling.

When slaughtered at the abattoir, blood was collected and sealed in plastic buckets. The viscera was collected and sealed in large plastic bags. The GIT was weighed and flushed before being weighed again to determine gut fill. The viscera and blood were minced together and halved by weight. Unfortunately there was a 24-hour delay period in retrieving the half carcasses from the abattoir due to abattoir regulations. A correction of 2% of carcass weight was made for possible drip loss during this period. The half carcasses (defrosted completely) were cut up and minced twice, together with the blood-viscera mixture before sampling. The mincing machine was washed and dried with hot water and detergent between successive carcasses to negate any mixing, and/or carry-over effects of samples. Samples were placed in glass bottles, after which they were sealed and frozen. Proximate analyses were performed according to the methods of the Association of Official Analytical Chemists (AOAC, 1984).

Moisture content was determined by freeze-drying the samples for 48 hours. The dried samples were then subjected to bomb-calorimetry in order to determine gross energy (GE). Digestible energy (DE) content was calculated using the following equation:

$$DE = 3.77 - 0.19 \times NDF + 0.75 \times GE \quad \text{(Whittemore, 1998)}$$

Protein content was calculated as N x 6.25, where N content of the dry matter was determined using the Dumas Combustion method in a Leco Nitrogen Analyser. The ash content was determined after incineration of the sample at 550°C for 4 hours. Lipid content was calculated using an equation derived from previously analysed pig carcasses (Ferguson et al., 2000). After each sample was chemically analysed in triplicate, the results were pooled to give a single mean value per sample.

2.2.4 Statistical Analysis

The fit-non-linear procedure in Genstat 5 (1997) was used to fit the Gompertz function to component weight data collected on trial. The B-parameter and mature weights for live weight, protein, lipid, water and ash were predicted. To determine the relationship between body components the allometric function $Y = aX^b$ was used. The allometric constant (a) and coefficient (b) were calculated by regressing the logarithmic weights of lipid, water and ash (dependent variables; Y) against that of protein weight (independent variable; X). The intercept of this regression was then anti-logged to get the constant ("a") while the slope of (or x-coefficient) provided the estimate of the allometric exponent ("b"). Lipid, water and ash to protein ratios at maturity (LPR_m, $WAPR_m$, and APR_m respectively) were calculated by dividing the components weights at maturity with the protein weight at maturity (Emmans and Kyriazakis, 1995).

Further statistical analyses were performed to compare differences between, and within, genotypes. Comparisons between genotypes in terms of the various body components, as well as of the allometric constants, were done using pooled estimates of standard error to determine significant difference, and by means of the Student t-test. Gut fill data was analysed using linear regression in order to determine if the

proportion of gut fill changed with increasing live weight. Pigs that suffered from intestinal infections and/or injury were removed from the analyses because it is unlikely that they would have been able to attain their genetic potential.

2.3 Results

The estimates of the Gompertz parameters for the six genotypes are shown in Table 2.3. There were significant differences between the various parameters and B-values between breeds as indicated by the superscript notation. The B-values of the different parameters within breeds also differed significantly.

The allometric constants and exponents relating lipid, water and ash weights to that of protein are presented in Table 2.4. There were significant differences in the allometric exponents between genotypes. The estimates of gut-fill are represented in Table 2.6 as a proportion of live weight at slaughter. Genotype 4 had the highest mean value (0.11 ± 0.02), while Genotype 1 showed the lowest mean gut fill in relation to live weight (0.07 ± 0.01). Except for Genotype 2, there were no meaningful linear trends between gut fill capacity and live weight, as noted by the poor fit (R^2 very low).

Table 2.3: Estimates of the Gompertz parameters for live weight, protein, lipid, water, and ash in six commercial pig genotypes.

	Live weight		Protein		Lipid		Water		Ash	
Genotype	Mature Weight	Rate Parameter (B)	Mature Weight	Rate Parameter (B)	Mature Weight	Rate Parameter (B)	Mature Weight	Rate Parameter (B)	Mature Weight	Rate Parameter (B)
1	236.4	0.0108	45.6^{a}	0.0107^{a}	58.7^{ad}	0.0101^{ac}	133.7	0.0107	8.2	0.0099^{ac}
2	247.4	0.0109	39.9^{ac}	0.0115^{ac}	94.5^{b}	0.0088^{b}	119.3	0.0115	8.6	0.0100^{ac}
3	234.3	0.0111	37.17^{bc}	0.0119^{bc}	66.7^{ad}	0.0098^{ac}	127.2	0.0111	7.6	0.0109^{a}
4	246.1	0.0115	44.7^{a}	0.0110^{ac}	55.3^{cd}	0.0119^{a}	133.1	0.0112	10.5	0.0096^{b}
5	201.8^{a}	0.0125^{a}	33.6^{bc}	0.0128^{b}	81.1^{a}	0.0097^{ac}	109.2^{a}	0.0126^{a}	8.4	0.0106^{ac}
6	236.7	0.0115	38.9^{ac}	0.0115^{bc}	58.3^{ad}	0.0115^{a}	134.6	0.0109	8.4	0.0109^{a}
Pooled se	**21.1**	**0.00061**	**5.86**	**0.000715**	**20**	**0.0019**	**18.2**	**0.00821**	**3.5**	**0.00093**
CV (%)[1]	**9.0**	**5.3**	**14.7**	**6.2**	**28.9**	**18.4**	**14.4**	**7.2**	**41**	**9**

[1] Co-efficients of variation (CV) are indicated as percentages [CV = Pooled se/mean X 100]

[a-d] Values within a column with no common superscript, differ significantly ($P < 0.05$)

The mature weight of lipid (LPR_m), water ($WAPR_m$) and ash (APR_m) relative to mature protein weight of the six genotypes are shown in Table 2.5. The APR_m ratios remained relatively constant across genotype at a mean value of 0.22 (± 0.024). Pigs from genotypes 2, 3 and 5 showed slightly higher $WAPR_m$ values as well as lower LPR_m values relative to the other genotypes.

Table 2.4: Estimates of the allometric constant (a) and exponent (b) for lipid, water and ash in relation to protein weight, calculated using log-linear regression.

	Lipid		Water		Ash	
Genotype	**a**	**b**	**a**	**b**	**a**	**b**
1	0.525	1.182	4.970[a]	0.872[a]	0.195	0.920[a]
2	0.525	1.171	5.189[b]	0.857[b]	0.197	0.930[a]
3	0.549	1.177	4.954[c]	0.874[a]	0.184	0.981
4	0.703[a]	1.178	5.259[d]	0.865[c]	0.172[a]	1.021[b]
5	0.640[b]	1.113[b]	4.903	0.890	0.188	0.976
6	0.556	1.270[a]	4.905	0.892	0.196	0.984
Pooled se	**0.1012**	**0.0482**	**0.0221**	**0.0106**	**0.0440**	**0.0209**
CV (%)[1]	**12.3**	**2.9**	**0.3**	**0.9**	**16.6**	**1.5**

[a-d] Values within a column with no common superscript differ significantly ($P < 0.05$)
[1] Co-efficients of variation (CV) are indicated as percentages [CV = Pooled se/mean X 100]

Table 2.5: Lipid (LPR_m), water ($WAPR_m$) and ash (APR_m) to protein ratios at maturity in six pig genotypes as calculated using the estimates of mature component weight from Table 2.3.[1]

	Genotypes					
Ratios	**1**	**2**	**3**	**4**	**5**	**6**
LPR_M	1.29	2.37	1.79	1.24	2.41	1.5
$WAPR_M$	2.93	2.99	3.42	2.98	3.25	3.46
APR_M	0.18	0.22	0.2	0.23	0.25	0.22

[1] Estimates of variation not provided as values in the table are calculated and not means

Table 2.6: The proportion of gut fill to Live weight across the six genotypes.

	Genotype					
Live weight	**1**	**2**	**3**	**4**	**5**	**6**
30kg	0.056	0.055	0.058	0.091	0.096	0.081
40kg	0.066	0.054	0.069	0.124	0.111	0.097
70kg	0.076	0.107	0.098	0.101	0.066	0.099
80kg	0.089	0.131	0.089	0.090	0.069	0.107
90kg	0.059	0.112	0.129	0.115	0.111	0.120
100kg	0.071	0.127	0.066	0.140	0.115	0.086
Slope (se)	0.00017 (0.0002)	0.00116 (0.0002)	0.00049 (0.0004)	0.00030 (0.00030)	0.00004 (0.00004)	0.00023 (0.00023)
Significance		**				
Intercept (se)	0.058^a (0.015)	$0.0182^{\#}$ (0.0159)	0.0513^a (0.0294)	0.0901^b (0.0236)	0.0923^b (0.029)	0.0828^b (0.0165)
R^2	0.16	0.85	0.27	0.17	0.002	0.20

[a-b] Values within a row with no common superscript differ significantly ($P < 0.05$)
[#] Genotype 2 excluded from comparisons because gut fill changed over time
** $P > 0.01$

2.4 Discussion

If one applies the Gompertz curve as illustrated in Figure 1.2, it becomes easy to understand and, therefore, classify the individual characteristics of the six genotypes tested here. Genotypes with higher live and protein weights, as well as lower lipid weights at maturity are those that, provided the correct supply of nutrients, would be of most economic benefit. Conversely, those that exhibit lower mature live and protein weights, and higher lipid weights at maturity, would be more challenging to the producer in terms of nutritional management. Placing the six genotypes tested here on some sort of performance scale is inappropriate as the genetic difference could be overcome through accurate management of the nutrients supplied. Comparisons with other authors are discussed later (Table 2.7)

The lipid fraction of the chemical body is the most variable as has been shown in previous work (Kyriazakis et al, 1991; Susenbeth and Keitel, 1988). There are three possible reasons for the variation in the lipid fraction of the body, including (1) Environment, specifically temperature, and its effect on energy intake; (2) Feeding method and the balance of nutrients provided; and (3) Genotype, in terms of maturity type and selection pressure exerted on growth rate and the inherent differences between individual animals within a certain genotype. In the experiments conducted in this thesis, the method of feeding, namely choice feeding does seem to affect the fatness of the carcasses. Choice feeding has the disadvantage of producing more variation between individually penned animals in terms of growth (Rose and Kyriazakis, 1991). With only four pigs per slaughter group, the effect of an incorrect choice and subsequent fattening can distort the final lipid weight. Choice feeding

affords a greater opportunity for individuals to express their genetic potential, and therefore if there are insufficient replications of a treatment, then there will be a higher degree of variation between individuals within the same treatment. It would therefore appear that the source of variability in lipid content was a result of the interaction between individuals, within certain genotypes, and the choice feeding method.

Emmans and Kyriazakis (1999) illustrate possible genetic parameters for different types of pigs (Table 2.7). According to these values, most of the genotypes tested in this thesis fall between the moderate and poor group. The genotypes tested by this thesis are all terminal (slaughter) stock and are therefore crosses of dams selected for breeding prowess and boars selected for growth. Some of the performance these sire-line boars are capable of is naturally lost as only half of the boars' genes are being passed on to the progeny. Hybrid vigour would play a significant role if the dams were also selected for their growth, but growth is negatively correlated with reproductive ability. No pure line-breeding stock was tested in this study, only commercial stock, which may explain why these genotypes did not deliver the low LPR_m, and high mature protein weight or growth rates presented as "Best of '98" in Table 2.7.

Table 2.7: Possible values for the growth parameters for different kinds of pig (Emmans and Kyriazakis, 1999)

Kind of Pig	Sex	P_m	LPR_m	B (day $^{-1}$)
Best of '98	Boar	50	2.0	0.0140
Moderate of '98	Boar	45	2.8	0.0125
Poor of '98	Boar	40	3.6	0.0100

Trait selection will, over time, change the mean values of the Gompertz parameters (Emmans and Kyriazakis, 1999). Mature protein weight (P_m), along with the B-parameter, is expected to increase, and LPR_m is expected to decrease through selection. This selection must be exercised on weights of protein and lipid at a certain body weight. According to Emmans and Kyriazakis, (1999) the age, or stage of growth, at which selection takes place will have differing effects on these parameters. Early selection will affect the B-parameter and later selection will affect the mature protein weight, whereas selection at any weight against fatness will decrease LPR_m. According to Emmans (1988) there exists no relationship between P_m and LPR_m, genotypes are either fat or lean. There is, however a relationship, or correlation between LPR_m and the B-parameter as animals are lean at birth and get fatter as they mature. There is a negative correlation between P_m and the B-parameter and this is an inherent characteristic of the Gompertz function (Emmans 1988). Knap (2000) investigated the time trends in the Gompertz parameters and reported that although pig genotypes in general have become leaner, the mature body weight, and thus P_m, have remained "practically unchanged" for growing pigs. This is most likely as a result of only selecting against lipid content, rather than for higher P_m at slaughter and is in agreement with the effects of selection outlined above.

The data showed that there was significant variation between the B-values across parameters within the breeds. This challenges the key assumption made when using the Gompertz to predict the growth of animals *viz.* that the rate of decay is the same for all body chemical components. This assumption therefore needs to be investigated more thoroughly because it impacts on the use of allometry to predict the growth of the other components from that of protein.

The theory of allometry states that the weight of one chemical component can be predicted by another, through the function $Y = aX^b$. This allometric relationship only holds if the logarithmic transformation of the variables follows a linear trend, such that the relative increase in X is followed by a similar relative increase in Y. The "b" value (also called the allometric exponent or coefficient) describes the proportional change between the two components. If this exponent is greater than one, for example in the case of lipid, then the response variate "Y" grows at a faster relative rate than that of "X". If the exponent is less than one, for example water, then the rates are reversed and "X" grows at a relatively faster rate than "Y".

In this thesis, there were no discernable patterns in the differences of the allometric constants and exponents between genotypes. The exponent for lipid (b-lipid) was significantly higher in Genotype 6, which suggests that it is a fatter genotype or at least has the predisposition to deposit more fat per unit of protein than the other genotypes. Conversely, Genotype 5 had the lowest value although it was still greater than 1.0. Genotype 5 will therefore have a lower relative lipid growth than the other genotypes but still deposit lipid at a greater relative rate than protein. All other genotypes had similar growth rates as protein. As lipid is the most variable factor and is influenced by many factors including diet and environment, comparisons between this study and others are not meaningful except to give an idea of the range of lipid variation. The mean value for b-lipid was 1.18 (se ± 0.05), which was lower than the values presented by Tullis (1981) (b = 1.84), and Doorenbal (1975) (b = 1.66).

The allometric coefficients for water (b-water) in this study were on average (0.875 ± 0.01) which was lower than the value determined by Moughan et al. (1990) (b =

0.925), but higher than that reported by Emmans and Kyriazakis (1995) (b = 0.855). Whether these differences are significant, or specific to South African breeds is difficult to ascertain, given the dangers of using a limited set of data to extrapolate to all genotypes. However the values are within an acceptable range (6%) of other published values.

Although there was some evidence in this thesis to suggest that there is a positive relationship between the gut fill and live-weight, the results are not convincing. There appears to be some differences in this relationship, between genotypes but it is inconclusive. For example, Genotypes 1 and 2 had a lower proportion of digesta in their alimentary tract than Genotypes 4 and 5, but these differences were not statistically significant. This could indicate differences in appetite between the various genotypes of pig.

2.5 Conclusions

As the evidence suggests the six genotypes are described by statistically different parameters making the use of a simulation model more complex in that one would have to ascertain which genotype's growth is being predicted. The variation in the B-values within a certain genotype is important to note because of the implications it has on the accuracy of the Gompertz as a growth describing function, as well as on the possible use of allometry to predict the growth of lipid, ash and water from that of protein.

CHAPTER 3

COMPARISON OF GROWTH PARAMETERS BETWEEN PIGS IN CONVENTIONAL VERSUS CONTROLLED ENVIRONMENT FACILITIES

3.1 Introduction

The possible adverse effects of the environment, especially temperature, on feed intake and subsequently growth are well known (Emmans and Oldham, 1988). To allow animals the opportunity to achieve their genetic potential they must be grown in an ideal environment and fed a non-limiting diet (Emmans and Oldham, 1988). The primary aim of this thesis was to quantify the Gompertz parameters of the various genotypes, and therefore preference should be given to eliminate or reduce the adverse affects of the environment, and particularly ambient temperature. It is most likely that the temperatures in a conventional facility are not ideal, given that the animals are exposed to variable ambient temperatures. This could prevent the attainement of potential growth and thereforethe the accuracy of predicting the Gompertz parameters (Ferguson et al., 1997). It was decided to duplicate part of the trial in an environment where temperature could be controlled in an attempt to compare the Gompertz parameters between animals grown in conventional, uncontrolled housing facilities with those exposed to temperatures that more closely match the animals' optimum for growth.

3.2 Materials and Methods

In addition to the pigs that were on trial in the conventional pigpens, as described in Chapter 2, 20 pigs from each of Genotypes 4, 5 and 6 were also housed in temperature controlled chambers; so as to minimise the potential adverse effects of temperature on growth. These chambers were 6 meters long, 3 meters wide and 3 meters high, which gave a floor space of close to $18m^2$. The chambers were tested beforehand and the air conditioning systems were able to maintain the temperature to within 1° Celsius above or below the setting. Ten pigs per genotype were randomly allocated to a chamber and were allowed to move freely within these chambers. The floors were covered with interlinking hard plastic matting that was perforated, thus allowing urine and faeces to pass through to the grooved steel floor underneath. Two fans per chamber were set to ventilate the chamber every minute, for one minute, thus providing sufficient fresh air but still maintaining the set temperature (Figure 3.1).

Four pigs were slaughtered per live weight group according to the methods described in section 2.2 of Chapter 2. The weight groups were 30, 40, 70, 80 and 90 kg live weight. As the genotypes used in the chambers were the same as those in described in Chapter 2, it was not necessary to slaughter additional pigs at 4 and 14 days, respectively. The same estimates of body composition at 4 and 14-days, as reported in the previous chapter were therefore used.

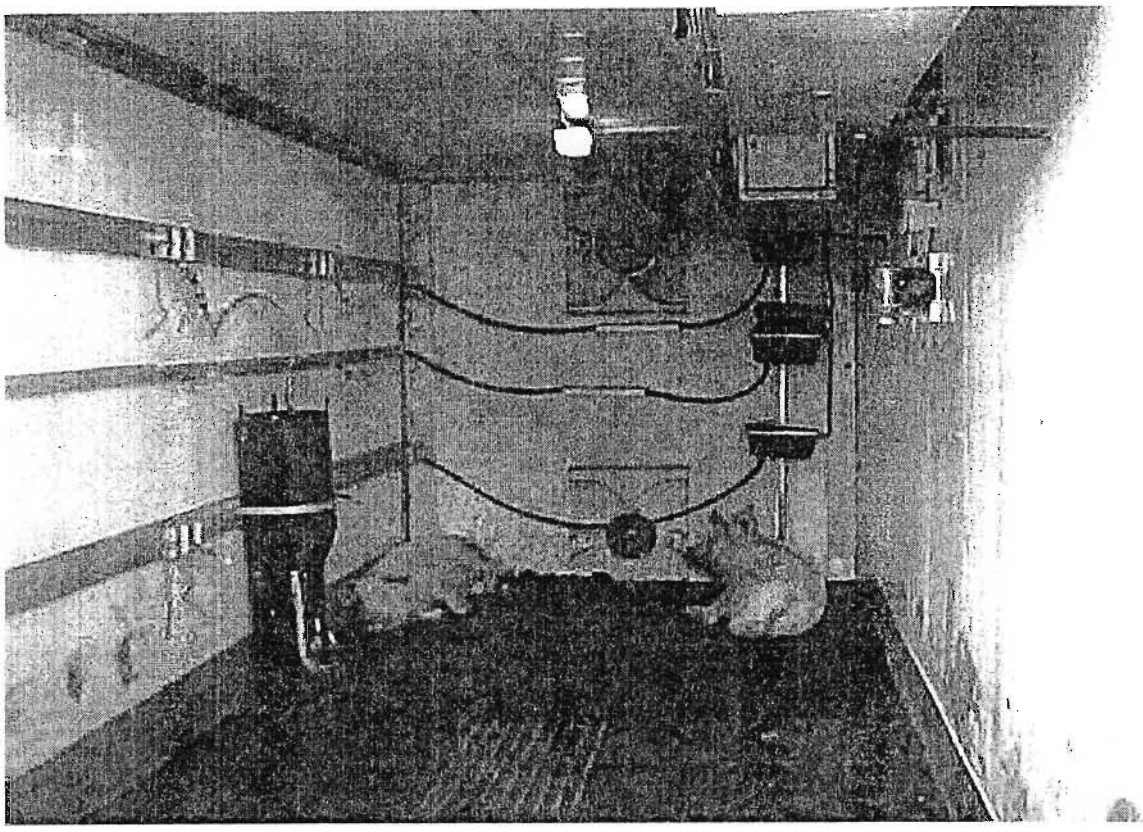

Figure 3.1: Illustration of the environmental chambers.

Slaughter methods, sampling and carcass composition analyses, as well as statistical analyses were performed using the same methodology as described in Chapter 2. The pigs were weighed weekly and the chambers were cleaned and serviced twice a week. The pigs were also fed a choice of the same diets as previously described for period 1 in Chapter 2. The only difference in the feeding system between the chambers and the conventional pens was that the two feed bins in the chambers were fitted for wet feeding by means of a nipple drinker at the side of the bowl. This was the only water source for the pigs.

The temperature was controlled according to a proposed optimum temperature scheme for growth (Whittemore, 1998). At the start of the trial, when the pigs weighed between 15 and 20kg, the temperatures of the chambers were set at 27°C. As the average weight of the pigs in each chamber reached 25kg, the temperature was dropped to 24°C. From 30kg body weight, the temperature was dropped one degree for every 10kg gain in average body weight per chamber, until the final temperature was 17°C for the pigs weighing 90kg (Table 3.1).

Table 3.1: Temperature settings in environmental chambers corresponding to the average pig live weight.

Average live weight in Chambers (kg)	Temperature Setting(°C)
15-20	27
25	24
30	23
40	22
50	21
60	20
70	19
80	18
90	17

3.3 Results

Table 3.2 shows the mature protein weights and the B values of the Gompertz function as fitted to the data. There were no significant differences found within genotypes between

the two housing treatments. The coefficient of variation of the mature weight of lipid was high (CV = 31.4%). Component weights as a proportion of protein weight were calculated by dividing the predicted mature component weight by that of protein and are represented in Table 3.3. Table 3.4 shows the predicted allometric constants and coefficients for the three genotypes tested. There were significant ($P < 0.05$) differences between the two housing types in both the "a" and "b" values of water accretion for Genotypes 5 and 6, and the "a" value of lipid accretion for Genotype 6.

3.4 Discussion

The results indicate that there were no significant differences in all estimated parameters, between the pigs housed in the chambers and those housed in the conventional pens (Table 3.2). The purpose of chambers was to provide an ideal temperature so that the pigs could achieve a growth rate closer to their inherent genetic potential. The similarities between the pigs of each genotype grown in these different housing facilities, however, suggest that the either the conventional facilities were not as limiting as expected (Ferguson and Gous, 1993a). There could have been social constraints, and even air quality effects, that may have impacted negatively on the performance of the pigs in the chambers, thus negating any possible advantage offered by controlled temperature. The trials described in this study were carried out during the late summer and autumn months of 2000/01 in South Africa and during this time there were no periods of sustained heat, or extreme cold. Maximum temperatures in the open air seldom exceeded 28°C,

Table 3.2: Comparison of Gompertz parameters for protein, lipid, water, and ash across housing treatments.

Genotypes	Protein		Lipid		Water		Ash	
Mature Weights	Pens	Chamb.	Pens	Chamb.	Pens	Chamb.	Pens	Chamb.
4	44.7	48.6	55.3	56.2	133.1	130.2	10.5	11.5
5	33.6	36.5	81.1	62.0	109.2	132.5	8.4	9.9
6	38.9	38.5	58.3	60.1	134.6	158.6	8.4	7.4
CV (%)	23.7		31.4		19.5		44.9	
B-Values	Pens	Chamb.	Pens	Chamb.	Pens	Chamb.	Pens	Chamb.
4	0.0110	0.0110	0.0119	0.0116	0.0112	0.0116	0.0096	0.0101
5	0.0128	0.0123	0.0097	0.0106	0.0126	0.0115	0.0106	0.0101
6	0.0115	0.0118	0.0115	0.0115	0.0109	0.0102	0.0109	0.0112
CV (%)	10.2		11.6		9.9		10.6	

Table 3.3: Comparison between pens and chambers of calculated lipid, water and ash to protein ratios.[1]

	Genotype 4		Genotype 5		Genotype 6	
	Pens	Chambers	Pens	Chambers	Pens	Chambers
LPR_m	1.24	1.16	2.41	1.70	1.50	1.56
$WAPR_m$	2.98	2.68	3.25	3.63	3.46	4.12
APR_m	0.23	0.24	0.25	0.27	0.22	0.19

[1] No significance test due to values being calculated

Table 3.4: Estimates of allometric constants for Lipid, Water and Ash in relation to protein weight calculated using log linear regression between pens and chambers.

Genotype	a-Lipid	b-Lipid	a-Water	b-Water	a-Ash	b-Ash
Chambers						
4	0.705	1.139	5.286	0.856	0.174	1.033
5	0.697	1.101	5.197[a]	0.860[a]	0.174	1.020
6	0.713	1.128[a]	5.189[c]	0.858[c]	0.175	1.019
Pens						
4	0.703	1.178	5.259	0.865	0.172	1.021
5	0.640	1.113	4.903[b]	0.890[b]	0.188	0.976
6	0.556	1.270[b]	4.905[d]	0.892[d]	0.196	0.984
Pooled se	0.100	0.050	0.026	0.013	0.046	0.023

[a-d] Values within a genotype and column with different superscripts differ significantly ($P < 0.05$)

and with insulated ceilings provided in the conventional housing facilities, the fluctuations in temperature were decreased and therefore could have exercised less of an effect on the performance of the pigs. Yet another factor, and source of variation, that

could have affected the performance of the pigs was the wet feeding system used in the chambers.

The lack of improved performance shown by the pigs kept in the chambers could also be due to the fact that only commercial genotypes were tested. An improved performance could possibly have been expected from genotypes with parameters closer to the "best of '98" values quoted by Emmans and Kyriazakis (1999) (Table 2.7). Animals such as these have high potential protein growth rates and thus produce more heat than the animals tested. The leaner genotypes would therefore, in striving to achieve these growth rates, place greater strain on the environment to dissipate this heat and would therefore have benefited through temperature control. If the growth of the high lean-growth genotypes was compared between conventional housing and environmentally controlled housing, it is expected that there would have been a more pronounced and significant difference in growth between the two housing treatments.

There were no significant ($P > 0.05$) differences between mature component weights, or B values as estimated for each genotype between the two housing facilities (Table 3.2). The high variability of the lipid fraction, as was shown in Chapter 2, was still present between genotypes grown in the chambers (CV = 31%). With environmental temperature controlled, it was expected that the effect of temperature on the lipid fraction would be minimised. This was, however not the case, and this supports the idea that the interaction between the genotypes and the choice feeding strategy was responsible for the variation in lipid. The similarities in growth and carcass composition between the pigs subjected to

the two different environments suggest that temperature did not significantly affect the quantification of the Gompertz parameters in this experiment.

The estimate of B for live weight of the genotypes grown in the pens did not differ from those grown in the chambers, which is consistent with the evidence given in Chapter 2. This supports the proposal made in Chapter 2 that in the future a reasonable estimate of B for all components could be estimated by measuring only changes in live weight over time.

The LPR_m of Genotype 5 is considerably lower in the chambers than in the pens due to a lower estimate of mature lipid weight (L_m). This supports the data in Chapter 2 that indicated that the L_m estimated for Genotype 5 in the pens was too high (although not significantly so), causing the B (for lipid) of Genotype 5 to be perhaps lower than it should (Table 2.3). In the chambers, the estimate of B (for lipid) of Genotype 5 did not differ significantly from B estimated for the other components of that genotype, thus supporting the fundamental assumption made in simulation modeling that B is constant across all body components (Emmans, 1981).

The WPR_m of Genotypes 5 and 6 were higher in the chambers than in the pens (Table 3.5). This trend was supported by the allometric constant values (a-values) which were also higher in the chambers than in the pens (Table 3.4). The allometric co-efficients, however, followed a contradictory trend given that lower allometric exponents will result in a lower growth rate of the water fraction, relative to protein, and *vice versa*. Thus, the

difference between water and protein weights at maturity would be less, thereby decreasing the WPR_m. This discrepancy could underline the differences in the two procedures used to describe the growth of the chemical components, namely allometry and fitting non-linear functions. This difference is clearly illustrated when mature weights for water are estimated using allometry and compared with those in Table 3.2. The mature protein weight of the respective genotypes was substituted into the allometric equation along with the "a" and "b" values calculated for these genotypes in the chambers. The resultant mature water weights for Genotypes 5 and 6, in the chambers are 114.6 and 119.0 kg respectively. These weights are well below the mature water weights predicted by the non-linear method in Table 3.2. Regarding the other component ratios to protein at maturity and their allometric constants, there were no such trends observed.

3.5 Conclusions

The aim of this comparison between pigs grown in controlled temperature environments and those in conventional facilities was to provide insight into the some of the factors, such as the constraints of excess temperature on feed intake, that could possibly prevent the pigs from reaching their genetic potential in terms of growth. The results support the notion that, in these trials and in terms of the genotypes tested, there were no environmental constraints on the growth of the animals. It follows that pigs tested using specialised environmental control equipment or pigs grown in a conventional manner would give statistically similar results and therefore exercise no effect on the resultant

Gompertz parameters quantified. Only Genotype 5 showed an improvement in LPR_m when subjected to a change in environmental conditions. Temperature control could affect the allometric constants and coefficients but the effect is limited only to water relative to protein.

CHAPTER 4

GENERAL DISCUSSION

As shown by Ferguson and Gous (1993a), and Emmans and Kyriazakis (1999) three parameters, namely protein weight at maturity (P_m), the Gompertz rate of maturing (B) and the lipid:protein ratio at maturity (LPR_m), are needed to accurately predict the potential growth of a pig. The results of both experiments conducted in this study have shown few statistical similarities in the Gompertz parameters between genotypes, as well as between the various body components, within a genotype. It therefore appears that only a reasonably accurate estimate of the Gompertz parameters for a particular genotype can be used when modelling the growth of that particular pig genotype.

If statistical similarities in the Gompertz parameters were shown by the experiments presented here, a new possibility of quantifying these parameters would present itself. One could then predict the mature protein weight (P_m) from the live weight using allometry. It follows that if the protein weight at maturity (P_m) could be estimated using live weight, then the three parameters required to predict growth could be quantified without the expense of conducting a serial slaughter experiment and carcass analyses. This possible method would entail using allometry to estimate P_m from live weight, and then relate lipid to protein using the allometric constants and coefficients. The determination of LPR_m then becomes a relatively simple arithmetic task. There is evidence from this study to suggest that there may be differences in the allometric coefficients relating lipid to protein between genotypes, but these differences are

sufficiently small to allow the use of constant estimates, without compromising the accuracy of the predictions of growth (Emmans and Kyriazakis, 1995). A worked example of this approach is discussed below.

If there was a lack of significant differences between the three parameters within a range of commercial crossbred pig breeds, the data of the six genotypes could be combined and the Gompertz curve refitted to obtain mean estimates of B and the mature component and live weights. Allometric constants and exponents were also re-estimated for lipid, water and ash relative to protein, as well as protein to live weight (Table 4.1).

Table 4.1: Average mature weights (kg) and B (day^{-1}) of Live weight, Protein, Lipid, Water and Ash estimated across all genotypes and treatments, as well as allometric constants (a) and coefficients (b) for the growth of protein relative to live weight and lipid, water and ash relative to protein.

Average Estimates	Live weight	Protein[1]	Lipid[2]	Water[2]	Ash[2]
Mature weight (kg)	210.4	38.8	44.9	120.3	7.3
(se)	(11.5)	(2.1)	(7.0)	(6.7)	(0.8)
B values (day^{-1})	0.0120	0.0117	0.0120	0.0116	0.0111
(se)	(0.0004)	(0.0003)	(0.0008)	(0.0004)	(0.0006)
Allometric Constant (a)		0.123	0.602	5.01	0.191
Allometric Exponent (b)		1.07	1.18	0.88	0.97
R^2 of Regression[3]		0.998	0.987	0.999	0.996

[1] Relating protein to Live weight
[2] Relating Component to Protein weight
[3] R^2 of linear regression used to estimate "a" and "b".

An alternative approach to determining LPR_m involves firstly using Equation 4.1 to predict mature protein weight from live weight, and then substituting for P_m in Equation 4.2 to predict L_m. Lipid at maturity (L_m) is then divided by protein at maturity (P_m) to calculate LPR_m (Eq. 4.3).

$$P_m = 0.123 \times \text{Liveweight}^{1.07} \quad (4.1)$$

$$L_m = 0.602 \times P_m^{1.18} \quad (4.2)$$

$$LPR_m = L_m / P_m \quad (4.3)$$

The results of using Equations 4.1-4.3 to predict the growth parameters, compared to the non-linear method described in the previous chapters, are contrasted in Table 4.2.

Table 4.2: Mature protein weight (P_m) as predicted using the allometric relationship with live-weigh compared with mature protein and lipid weights (L_m), and the lipid:protein ratio at maturity (LPR_m), estimated using the serial slaughter method and carcass analyses.

Method of estimation	P_m	L_m	LPR_m	B
Allometric Prediction	37.6	43.5	1.12	0.0120
Fitting the Gompertz Function[1]	38.8	44.9	1.16	0.0120

[1] Data obtained from serial slaughter of pigs and carcass analysis

The L_m and LPR_m values were similar between methods and support the predictions for parameter values by the year 2005, made by Knap (2000) (Table 4.4). The LPR_m is, however, lower than that proposed by Emmans and Kyriazakis (1999) in Table 4.4. According to Knap (2000) the trend of LPR_m over time, would be for the ratio to decrease

towards unity because of intense selection pressure against fat. The most recent estimate of LPR_m quoted by Knap (2000) was 1.09 ± 0.16, which is similar to the results presented here.

The use of allometry and an estimate of B from live weight data only, to estimate the three parameters (B, P_m and LPR_m) would be useful when serial slaughter trials are not possible, or too expensive to run. This method does, however, place greater emphasis on the accuracy and appropriateness of the allometric constants and coefficients that relate the growth of protein to live weight, and the rest of the body chemical components to protein across all commercial genotypes.

Table 4.3:Estimates of the allometric constants (a) and coefficients (b) by various authors for lipid, water and ash relative to protein weight

	Lipid		Water		Ash	
Author(s)	**a**	**b**	**a**	**b**	**a**	**b**
Moughan et al. (1990)	-	-	4.076	0.924	0.229	0.927
Emmans and Kyriazakis (1995)	-	-	4.69-5.36	0.855	-	-
Tullis (1981)	-	1.84	-	-	-	-
Doorenbal (1972)	-	1.66	-	-	-	-

The values presented in Table 4.3 show some differences when compared to those given in Table 4.1. The b_{lipid} values calculated are lower than those shown by both Tullis (1981) and Doorenbal (1972) suggesting that, although lipid is still growing relatively faster than protein in the pig genotypes tested in this study, they are leaner than the pigs of Tullis

(1981) and Doorenbal (1972). This supports the proposal by Knap (2000) that pig genotypes are getting leaner with time. The exponent for water, b_{water}, is less than that of Moughan et al. (1990) but greater than that of Emmans and Kyriazakis (1995). It must, however, be stressed that the values reported in Table 4.1 are applicable to conditions and genotypes in South Africa.

The Gompertz parameters as estimated for the commercial crossbred pigs in South Africa, and estimates of the parameters made in the literature for the three parameters are presented in Table 4.4 for comparison. The estimates of Knap (2000) show a higher B-parameter and lower P_m values in comparison to the other estimates. Bearing in mind that the values given by Knap (2000) are predictions of expected values for 2005, they contradict the prediction of Emmans and Kyriazakis (1999) that there is expected to be an increase in P_m over time. The value of B predicted by Knap (2000), however, shows an increase over time and would therefore imply higher protein growth rates and leaner pigs in the future.

Traditionally, selection for a leaner carcass has been the standard selection criterion in the pig industry. Improvement in the fat distribution of a carcass has been achieved and modern pigs have, to a certain extent, improved in terms of growth rates and feed conversion as compared to pigs of some decades ago (Knap, 2000; Whittemore, 1998). According to Emmans and Kyriazakis (1999), selection for weight at a certain time, or age, is likely to increase both the mature weight and rate parameter (B). However, Knap (2000) has shown that only the B has shown a response to selection over time and that

mature weight has remained constant. Selection against fatter animals at a given age will decrease LPR_m, as well as possibly increase the P_m but to a lesser extent

Table 4.4: Comparison of the relative rate of growth (B), mature protein weight (P_m) and the lipid:protein ratio (LPR_m) at maturity as estimated by three different authors and by two different approaches in this study.

Source of Estimates	B (day^{-1})	P_m (kg)	LPR_m (kg/kg)
Using live weight and allometry	0.012	37.6	1.12
Serial slaughter and fitting Gompertz	0.012	38.8	1.16
Emmans and Kyriazakis (1999)	0.010 – 0.125	40.0 – 45.0	3.6 – 2.8
Knap (2000)[1]	0.019	33.0	1.0
Ferguson and Gous (1993b)	0.0107	38.7	2.6

[1] Prediction for 2005

The response of the parameters to selection is dependant on the intensity of selection and the various correlations between the parameters. A positive correlation is expected between both P_m and LPR_m, and B due to overall live weight, and thus the change in live weight, being dependant on P_m and LPR_m. Also, due to LPR_m tending to approach unity, there will be a relatively small change in mature body weight as L_m decreases and P_m increases (Knap, 2000). The timing of selection is also important because selection at an early age will tend to increase the B, whereas selection at a later stage will tend to increase P_m (Emmans and Kyriazakis, 1999).

The results presented in chapters 2 and 3, however, show that the individual Gompertz parameters, as quantified by serial slaughter, are the most accurate but are still subject to experimental variation. There were a number of possible sources of variation and error inherent within the experimental methodology used in the experiments. Firstly, only four animals were used per slaughter group, which could have led to increased variation and possibly skewed means. Unfortunately due to the capacity of the facilities, no more than four pigs per slaughter group could be accommodated. The limited space also caused the trials to be split into two periods, where only three genotypes could be tested at a time. This could have led to possible period effects between the two parts of the experiment.

Secondly, the choice feeding strategy could have led to higher variation within genotypes, as highlighted by Rose and Kyriazakis (1991). More replications per treatment, in this case more animals per slaughter group, could have lessened the errors caused by using choice feeding. Thirdly, no slaughters were performed at heavier weights (>120kg). This could have exercised an effect on the estimated B and mature component weights because the more points on the curve, the more accurate the estimates. There would also be more points closer to the predicted asymptote of the curve, which is the estimate of mature weight. Knap (2000) suggested that slaughter trials should continue up to a weight of at least 175kg.

The fact that one group of pigs on a particular farm performs better, or worse, than another group of the same genotype on another farm could be due to general husbandry, housing facilities and management, as well as possible feed constraints and feed quality. These also play a significant role in commercial pig production, as well as in trial

conditions, today. Management of these sources of variation is critical when ensuring the performance of ones stock, no matter what the genotype. Simulation modelling is therefore a useful tool when trying to address these challenges.

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