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# **Modeling feed intake and feed efficiency along the lactation curve of Norwegian Red Dairy Cattle**

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European Master in Animal Breeding and Genetics

# EUROPEAN MASTER IN ANIMAL BREEDING AND GENETICS

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## Abstract

Including feed efficiency into breeding goals could be a key in ensuring sustainable dairy cattle production as selection could be based on how efficient a cow is in terms of what it consumes and produces all through the lactation period. Hence, prioritizing feed efficiency could aid profitability and reduced methane emission in dairy cow sector.

The objective of this study was to explore random regression models of varying order of Legendre polynomials to fit feed intake and feed efficiency records in Norwegian Red dairy cows. Data included 2632 daily dry matter intake and average daily milk yield records from 45 cows in 1 to 5 parities for 56 days of lactation. A random regression model with both random and fixed regressions fitted by Legendre polynomials of order 1 to 5 for fixed effects curve and 1 to 2 for random animal effect curve were compared while accounting for homogeneous and four heterogeneous classes of residual variance across the lactation. Models were evaluated by goodness of fit (LogL and  $-\frac{1}{2}$  AIC values), graphical inspection of variance functions for the random animal effect, while difference between the standard error and regression solution for the fixed effect curves.

The results showed improvement in goodness of fit moving from order 1 to order 2 but order 3 showed no convergence for the animal random effect in both feed intake and feed efficiency models. For feed intake analyses, order 1,2,4 and 5 was significant while for feed efficiency analysis only order 3 was significant for fixed effect curves. In general, the result showed that random regression models using fifth order Legendre polynomials (Mleg5) for fixed effect curve and first order Legendre polynomials (Aleg1) with heterogeneous residual variance was sufficient to fit feed intake records. While random regression models using third order Legendre polynomials (Mleg3) for fixed effect curve and second order Legendre polynomials (Aleg2) with homogeneous residual variance was sufficient to fit feed efficiency data.

In conclusion, random regression model with Legendre polynomial of order 3 for fixed effect curve and order 2 with homogeneous classes of residual variances is a good model for fitting feed efficiency records, Legendre polynomial of order 5 for fixed effect curve and order 1 with heterogeneous residual variances could be an appropriate model to consider while fitting feed intake records to avoid complexity of the models.

## Table of Contents

Abstract.....	2
INTRODUCTION.....	4
LITERATURE REVIEW .....	7
Overview of feed intake and feed efficiency in cattle .....	7
Genetics of feed intake .....	7
Genetics of feed efficiency.....	8
Modeling of feed intake and feed efficiency .....	8
The use of Legendre Polynomials in modelling longitudinal traits .....	9
Residual Variance(s).....	10
MATERIAL AND METHODS.....	11
Animal Management .....	11
Feed intake.....	11
Milk Yield.....	12
Data.....	12
Statistical analysis .....	12
RESULTS .....	16
Feed Intake.....	16
Comparison of models with Homogeneous and Heterogeneous variance(s) .....	16
Random regression analysis of feed intake .....	17
Feed Intake Models Comparison .....	21
Feed Efficiency .....	28
Comparison of models with Homogeneous and Heterogeneous variance(s) .....	28
Random regression analysis of feed efficiency.....	28
Feed Efficiency Models Comparison.....	31
DISCUSSION.....	36
References .....	40

## INTRODUCTION

Dairy cattle play an essential role in the world food production system because it provides milk and other products such as cheese, which serve as an efficient source of protein to man. As the global human population increases, so is the need for animal protein expected to increase. To meet up with dairy product's demand, the need to prioritize some of the factors that affect the continuous productivity and cost-efficiency of the dairy herd arises. Feed intake as an essential component of feed efficiency is crucial for livestock performance of which dairy cattle is no exception. Feed intake is an important factor of dairy breeding as it entails the largest share of the total production cost, however it is not so often considered since it is hard to record. Also, feed intake has a significant influence on dairy cattle health and milk production (Harder et al., 2019). It has a considerable effect on the cow's susceptibility to diseases especially during the first phase of the lactation (Httmann et al., 2009; Kramer et al., 2009).

The rapid increase in feed costs and concern for the reduction of methane emissions as well as nutrient losses to the environment makes feed efficiency an important factor in the dairy production system, thereby making it a benchmark for profitability and thus inclusion in the breeding goal (Guinguina et al., 2019). In dairy production systems, feed efficiency has been defined as the amount of milk produced per unit of feed intake (Olijhoek et al., 2020), but there are still some challenges to the acceptance of the definition especially during selection since there is no perfect term to define feed efficiency. It is good to have in mind that calculating feed efficiency involves comparing what an animal eats to what it produces. Traditionally, an efficient cow can be viewed in two ways: a cow that increases milk yield with the same dry matter intake, or a cow with decreased dry matter intake while it maintains the same milk yield (Pino et al., 2018). Therefore, identifying more efficient animals requires recording the feed consumed and the amount of milk produced. The most efficient animals produce the most milk per kg of feed.

Several measures can be used in expressing feed efficiency in the dairy production system. Feed efficiency can be expressed in terms of net feed efficiency or residual feed intake, which focuses on the difference between actual feed intake and predicted feed intake based on an animal's performance. Another way of expressing feed efficiency is in terms of feed conversion efficiency (FCE) or gross feed efficiency, defined as the amount of milk produced per unit of feed intake. But the limitation of FCE is that it does not account for mobilization of body condition, and consequently, animals losing body condition to support milk production may appear more efficient, particularly if the evaluation is done in early lactation (Coleman et al., 2010). These feed efficiency parameters are subject to change over time because the feed

efficiency of dairy cattle is influenced by factors such as age, diet type, environmental temperature, breeds, and other management and environmental variables (Lamb & Maddock, 2009).

Another reason why interest in feed intake and feed efficiency is justified is that the feed ingested by a cow influences several functions like maintenance, growth, reproduction other than milk production. There is a wide margin between the ingested food and the energy channeled into production in cows when compared to other livestock (Hurley et al., 2018). However, a decrease in feed intake during certain stages of lactations may be detrimental to the health of the cow. A negative energy balance is observed when the energy needed for milk production is above the energy ingested, thereby, resulting in the cow mobilizing its body reserves to balance the deficit/gap between food energy intake and milk energy production. A long period of negative energy balance exhibited by the cow can lead to body energy loss and other health-related problems and increased production cost (Banos et al., 2005). It has also been reported that carryover effects from the previous lactation period could contribute to a negative energy balance and also reducing feed efficiency (Banos et al., 2005; Coffey et al., 2001).

Studying the lactation curves aids in the evaluation of milk production by showing peak production and time of production. The lactation curve helps with the appropriate management of dairy cattle herd by maintaining the nutritional condition for each stage of lactation as well as the herd health. With the lactation curve, prediction of the total milk yield can be made and a good understanding of the curve helps dairy farms in deciding on selecting cows for breeding purposes as well as paying attention to the dietary need of the cows at each lactation stage (Cankaya et al., 2011; Gipson & Grossman, 1989). For the estimation of breeding values, the lactation curves need to be modeled at the genetic and the environmental level, in order to disentangle genetic from environmental effects.

Milk yield is phenotypically and genetically correlated with feed intake. Previous research has reported that the genetic correlation of milk yield and feed intake is in the range from 0.46 to 0.65 (Veerkamp, 1998). Cankaya et al. (2011) observed that “increasing portion of the curve depicts that the cows should be place on a high plane of nutrition, while a declining portion of the curve indicates a lower plane of nutrition”. The lactation curve will give the farmer an idea of what to expect from the herd during their lactation phase and the necessary dietary plan. According to Harder et al. (2019), high feed intake at the beginning of the lactation can solve the problem of a postpartum energy deficit by reducing susceptibility to metabolic diseases

since energy deficit is reported to depend on milk yield and feed intake diseases in the dairy cow during early lactation stages.

#### Aim

This study aims to model the feed intake, and feed efficiency curves along the lactation using longitudinal data modelling.



## LITERATURE REVIEW

### Overview of feed intake and feed efficiency in cattle

Feed intake being the most significant component of dairy production is still not found on the lists of breeding goals because of the cost associated with measuring this trait. The limited information makes it difficult for selection. The available information from several countries is based on a small amount of data used in research (Donagh P Berry et al., 2014).

The feed efficiency traits are still not found in the Nordic total merit (NTM) index (a document with attached economic weights to dairy breeds production and functional traits of Nordic countries) or any national dairy cow breeding index because of the limited access to phenotypic data of feed intake (McParland et al., 2015; Pedersen et al., 2008). For decades, longevity and udder health were the most important two traits being selected for in dairy cattle production. However, some studies have shown that feed efficiency has similar to equal economic weight as this two traits (Hardie., 2016; Hietala et al., 2014). Improving feed efficiency could play a significant role in reducing cost of production and reducing greenhouse gas emission, which is a result of high methane and manure from milk production (Hietala et al., 2014; Thoma et al., 2013).

### Genetics of feed intake

Previous studies have shown that feed intake in dairy cattle is a moderately heritable trait. Animals with high genetic merit for milk yield tend to have greater feed intakes when compared with those with low genetic merit. They also tend to use their body reserves during the early lactation thereby reducing negative energy balance. As described by Korver (1988), feed intake in dairy cows is influenced by several factors ranging from genetic to environmental. The author further stated that there is variation between breeds and within breeds for appetite, digestion and nutrient absorption, maintenance requirement, utilization of metabolizable energy for production, nutrient partitioning and output composition making it difficult to ascertain some reports. Despite the variation in feed intake, a mature cow requires 57% of energy intake for milk production (Coffey et al., 2001).

Accounting for the relationship between Dry matter intake (DMI) and milk yield and body weight could help in measuring feed efficiency especially if the goal is reduced DMI and increase in milk production (Hardie, 2016; Werf, 2004). Hardie (2016), described the danger of selecting for less feed intake while the animal maintain the same level of production, as this could lead to the cow's susceptibility to diseases which the author termed "unintentional correlated response to selection".

Genetic variation and Dry matter intake (DMI) heritability was recorded at various stages of lactation (Coffey et al., 2001). Generally, DMI heritability was reported to be between 0.02 and 0.52. High DMI heritability was reported to be a result of a high genetic correlation between DMI and milk yield (D P Berry & Crowley, 2013; Gonzalez-Recio et al., 2014). Heritability for feed intake between the 31 and 60 days of lactation was recorded to be 0.24 (Veerkamp, 1998). While some reported heritability estimates of 0.13 to 0.54 (Koenen & Veerkamp, 1998; Veerkamp, 1998; Veerkamp & Thompson, 1999). Berry et al. (2014) reported an average DMI heritability of 0.34. Also, the ability to estimate genetic component of the DMI was attributed to the large size of the dataset (7000 cows) used for the experiment.

### Genetics of feed efficiency

Selection for feed efficiency (FE) was reported to be feasible (Gonzalez-Recio et al., 2014). However, over the years the heritability estimate of feed efficiency in dairy lactating cows seems to vary based on the DIM or lactation stage, parity, numbers and ages of the cows under consideration. Several research papers have reported FE heritability in dairy cattle, but the estimates vary.

Van Arendonk et al. (1991) reported 0.37, 0.26 (Nieuwhof et al., 1992), and 0.14 to 0.21 (Vallimont et al., 2011). Van Arendonk et al. (1991) estimated a heritability of FE for 360 cows for the first lactation and first 105 days of 0.19, while Ngwerume & Mao (1992) reported a heritability of 0.02 for the whole lactation of 247 mixed-aged cows. Also, Svendsen et al. (1993) reported 0.00 for 353 mixed-age cows in weeks 2 to 12 of lactation while Svendsen et al. (1993) reported 0.02 for weeks 13 to 24 of lactation for the same cows. Veerkamp et al. (1995) estimated a heritability of 0.32 for 204 mixed aged cows for 26 weeks of lactation while Vallimont et al. (2011) reported 0.01 for 970 mixed age cows for a period of 6 months.

### Modeling of feed intake and feed efficiency

Modelling feed intake could help in evaluating differences in the feed efficiency and lactation curves in dairy cows. There are several models which could be used in modelling longitudinal traits like feed intake and, average daily milk data which are measured repeatedly in an individual. Random regression models (RRM) have been used in several countries to analyze some traits because of their high accuracy of predicting breeding values of dairy cows and accurately estimate environmental effects on the animals lactation at different stages (Brito et al., 2017; Englishby et al., 2016; Naserkheil et al., 2016; Strabel et al., 2004; Thepparat et

al., 2015). RMM is also known for its ease of estimating covariances directly from the datasets (Jakobsen et al., 2002; Kheirabadi et al., 2014).

Random regression model consists of several functions that could be used in modelling. These functions could be classified into parametric and non-parametric functions. Examples of the parametric function are the Ali and Schaeffer function, Wood function and Wilmink function. While an example of the non-parametric functions is the Legendre orthogonal polynomials. Legendre polynomial function is considered to be very flexible in addition to its ability to fit curves independently from the traits under consideration, and ability to properly model the peak of lactation curve (Bohmanova et al., 2008; Naserkheil et al., 2016; Schaeffer, 2004). These functions are used in modelling fixed and random curves. In random regression models, a fixed curve for the entire population under consideration is calculated and individual animal curves are fitted as deviation from the curve of the population (Brito et al., 2017).

The parametric functions fit data based on the components of curves and are recorded to be non-flexible especially when the data follow a path different from that of a typical curve. Despite the advantages of Legendre polynomials, some studies have used functions like B-splines in modelling the lactation curve because they give a similar fit or maybe better than the Legendre function. However, the report of Bouallegue et al. (2015) only agreed with the fact that a spline function should be considered when working on a dataset that involves various components of milk (fat, protein). But most studies still model milk yield and its various components using Legendre functions.

#### [The use of Legendre Polynomials in modelling longitudinal traits](#)

The ease of modelling Legendre polynomial functions makes it a widely used option in modelling covariance structures (Bignardi et al., 2009; Pereira et al., 2013). Several studies (Costa et al., 2008; Schaeffer, 2004) described it as the most appropriate function to model covariates in RRM. But the choice of order or degree to use in modelling fixed and random curves needs to be carefully chosen since there are no set rules on the highest or lowest order of fit (Li et al., 2020). Hence choices are based on the size and structure of the dataset. which is one of the constraints or difficulty of using this function while using RRM (Costa et al., 2008; Olori et al., 1999). Model selections are based on the goodness of fit measured by Logarithm of the Maximum Likelihood function (LogL), Akaike's information criterion (AIC), and Bayesian information criterion (BIC) output. As reported by previous studies (Li et al., 2020; Pereira et al., 2013), increasing the order of fit should give higher LogL values. However,

increasing the order of fit increases the complexity of the model, parameters and computational demands which are the factors to consider while selecting between orders of fit.

Li et al. (2020) suggested that the choice of order to fit random and fixed effects need to consider a balance between selection criterion (Goodness of fit) and model complexity. Pereira et al. (2013), reported that cubic Legendre polynomials for fixed and random effects were sufficient to fit lactation curves because the report assumed using a higher order does not significantly improve the order of fit. Based on the BIC values, López-Romero & Carabaño (2003) concluded that Legendre polynomial function of order 3 was sufficient to fit lactation but higher values could be considered for permanent environmental effects. Some studies (Li et al., 2020; Meyer, 2005) reported that higher order was not required in RRM using Legendre polynomial function as it can lead to estimating higher genetic variances at the beginning and end of lactation or oscillatory patterns along the lactation curve which is not biological or unrealistic.

#### Residual Variance(s)

The choice of residual variance classes also plays a significant role in the model. Residual variance is said to be influenced by stages of lactation (López-Romero et al., 2003). Therefore, understanding the residual variance structure along the days in milk or lactation stage is needed in order to avoid incorrect estimations. Some authors (López-Romero et al., 2003; Olori et al., 1999) found maintaining homogeneous residual variance in a random regression model could cause overestimation/underestimation of other components of variance in the analysis and create bias while estimating the residual variances. Pereira et al. (2013) found that 5 heterogeneous residual variance classes is sufficient for the analysis while comparing different number of residual variance classes. Li et al. (2020) and López-Romero & Carabaño (2003) reported that little or no improvement was found when increasing the order of fits of the polynomial (e.g order 3 to order 4 to order 5) under homogeneous class of residual variance in Chinese dairy cattle and Spanish Holstein population. While working on Chinese Holsteins Li et al. (2020), reported that residual variances vary according to the number of classes. Also, the estimated residual variances showed a higher value at the beginning of the lactation period. The author further recorded that orders Leg3 and Leg4 is sufficient to model and estimate variance components of milk yield especially when one considers factors such as balance between computational demand and goodness of fit.

## MATERIAL AND METHODS

### Animal Management

The experiment was carried out at the Animal Production Experimental Centre at the Norwegian University of Life Sciences following the laws and regulations controlling experiments on live animals in Norway under the Norwegian Animal Research Authority's surveillance. The cows were housed in a free-stall accommodation with concrete slatted floors and rubber mat beds with regularly applied sawdust in the resting areas. All cows had free access to drinking water and mineral blocks.

Forty-eight early to mid-lactation Norwegian Red Dairy cows were used in the experiment that lasted for 56 days. The cows were fed *ad libitum* during the 56 days of the investigation. These diets were in 2 forms (grass/clover) silages: the first, low in crude protein (112 g CP per kg dry matter (DM)) while the second one was a mixture of four different silages (142 g per kg DM). However, these basal diets were augmented with a fixed level of concentrate feed (160 g CP per kg DM).

At the start of the experiment, information such as the cows' mean days in milk ( $\text{DIM} \pm \text{SD}$ ) of  $126 \pm 60$  and milk yield (mean  $\pm$  SD) of  $27.8 \pm 5.4$  kg/day, and average dry matter intake for the three days of pretreatment/acclimatization (PretDMI) were recorded. The herd was composed of cows from 1st to 4th lactation in 21%, 46%, 21%, and 13%, respectively. Blocking was based on parity, pre-experimental milk yield and milk composition, and body weight at the start of the experiment. After that, cows within a block were assigned to one of the two groups of feed randomly. The cows in each group received *ad libitum* access to their respective grass/clover silages. The silages were fed from individual automatic feeders (BioControl AS, Rakkestad, Norway) equipped with vertically moving gates where electronic cow identification ensured each cow's access to the correct silage source.

### Feed intake

For daily dry matter intake (DMI), the automatic feed troughs registered summed daily intakes from multiple feeding episodes during a day. Feed troughs were filled with fresh silages twice a day (during morning and afternoon milking) after moving the cows to a resting and milking area. A manually controlled gate separated the milking and silage feeding zones. Feed refusal was cleared every Monday and Friday each week.

Daily feed intakes of concentrate and silage were retrieved from the automated feeding system each morning starting from the second day of the experiment. Mean daily feed intake was reported as the sum of DMI from both concentrate and silages.

### Milk Yield

Cows were milked twice a day (between 06:15 and 08:15 a.m. and between 15:00 and 17:00 p.m.) using milking machines. During each milking, individual milk yield was registered for the a.m. and p.m. milking.

### Data

A total of 2632 daily milk yield (MY) records from 56 days of 48 Norwegian Red Dairy cows from a single herd owned by the Norwegian university of life sciences (NMBU) were used for this study. The data comprises: Cow identification number, Dry matter intake (DMI), Days in Milk (DIM), Parity. The data editing was performed using Microsoft Excel. 45 cows were kept for further studies. Feed efficiency was calculated as;

$$\text{Feed efficiency} = \text{Milk yield (kg)}/\text{Dry matter intake (kg)} \quad (\text{de Oliveira et al., 2014})$$

In order to strengthen the link between the feed eaten and milk produced, the above was calculated on a weekly basis, instead of on a daily basis. Next the log of the above feed efficiency was used for the statistical analysis described below.

### Statistical analysis

Single-trait Random Regression analyses were performed. Curves along the lactation (along DIM), i.e. lactation curves, were fitted by Legendre polynomials of varying degrees. The model included a fixed lactation curve for Days in Milk (DIM) reflecting the mean for all cows and a random deviation for each animal, i.e. an individual animal effect. The random individual animal effect was either constant across the entire lactation, or was also presented by a Legendre polynomial curve, whose degree of fit was generally smaller than that of the fixed lactation curve. The latter assumes that the curve of individual deviations from the fixed mean lactation curve are not as complex as the fixed mean curve itself.

In matrix notation, the RRM can be written as:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}$$

where  $\mathbf{y}$  is the vector containing average daily feed intake records,  $\mathbf{b}$  is the vector of fixed effects (Legendre polynomial coefficients for DIM and an environmental effect for week of the

experiment and parity);  $\mathbf{a}$  is the vector of random animal Legendre polynomial coefficients,  $\mathbf{e}$  is the vector of the residuals,  $\mathbf{X}$ ,  $\mathbf{Z}$  are the corresponding incidence matrices (containing the Legendre covariates) for fixed and animal random effects, respectively.

A Legendre polynomials regression on DIM was used to model the mean curve. The alternative models had a varying combinations of orders of fit for the polynomials for fixed and individual animal curves. In addition, the residual variance was assumed either homozygous or heterogeneous across the lactation and grouped into four classes based on days in milk (49 to 100, 101 to 150, 151 to 200, 201 to 233 DIM).

The first model evaluated order 3 for fixed and 1 for animal effect while considering homogeneity of variances. While in the subsequent steps, ten different models were assessed considering the heterogeneity of residual variance.

Table 1a: Models evaluated for feed intake with corresponding order of fixed and animal effect and classes of residual variances

Feed intake Model(s)	Fixed effect (Mleg)	Animal effect (Aleg)	Residual variance classes (H)
Mleg3Aleg1H1	3	1	1
Mleg1Aleg1H4	1	1	4
Mleg1Aleg2H4	1	2	4
Mleg2Aleg1H4	2	1	4
Mleg2Aleg2H4	2	2	4
Mleg3Aleg1H4	3	1	4
Mleg3Aleg2H4	3	2	4
Mleg4Aleg1H4	4	1	4
Mleg4Aleg2H4	4	2	4
Mleg5Aleg1H4	5	1	4
Mleg5Aleg2H4	5	2	4

Note: MlegxAlegxHx for feed intake models where Mlegx is the polynomial order for fixed curve and Alegx is the degree for animal effects. And Hx is the number of residual variance classes.

Table 1b: Models evaluated for feed efficiency with corresponding order of fixed and animal effect and classes of residual variances

Feed efficiency Model(s)	Fixed effect (Mleg)	Animal effect (Aleg)	Residual variance classes (H)
Mleg3Aleg1H4	3	1	4
Mleg1Aleg1H1	1	1	1
Mleg1Aleg2H1	1	2	1
Mleg2Aleg1H1	2	1	1
Mleg2Aleg2H1	2	2	1
Mleg3Aleg1H1	3	1	1
Mleg3Aleg2H1	3	2	1
Mleg4Aleg1H1	4	1	1
Mleg4Aleg2H1	4	2	1
Mleg5Aleg1H1	5	1	1
Mleg5Aleg2H1	5	2	1

MlegxAlegxHx for feed efficiency models, where Mlegx is the polynomial order for fixed curve and Alegx is the degree for animal effects. And Hx is the number of residual variance classes.

The variance and covariance components between random regression coefficients were estimated through the restricted maximum likelihood (REML) method using the WOMBAT software (Meyer, 2007).

The outputs obtained will be compared by change in the logarithm of the Maximum REML likelihood function ( $\log L$ ) and Akaike's information criterion (AIC). The information criterion AIC was calculated as follows:



$$\text{AIC} = -2\log L + 2p$$

Where  $p$  is number of variance components,  $N$  is total number of observations,  $r$  is rank of the fixed effect incidence matrix. In order to make a more direct comparison to  $\log L$ , we also compare  $-\frac{1}{2} \text{AIC} = \log L - p$ .

## RESULTS

### Feed Intake

Comparison of models with Homogeneous and Heterogeneous variance(s)

The estimated variances for model Mleg3Aleg1H1 (homogeneous variance) and model Mleg3Aleg1H4 with heterogeneous residual variances (Table 2) showed similar variation. The animal variances were similar, with the heterogeneous variances slightly lower than the value of the homogeneous residual variance. The residual and phenotypic variances were also similar for a heterogeneous and homogeneous group of residual variance except for the first group close to the beginning of lactation (DIM 49-100), which is slightly lower than other values.

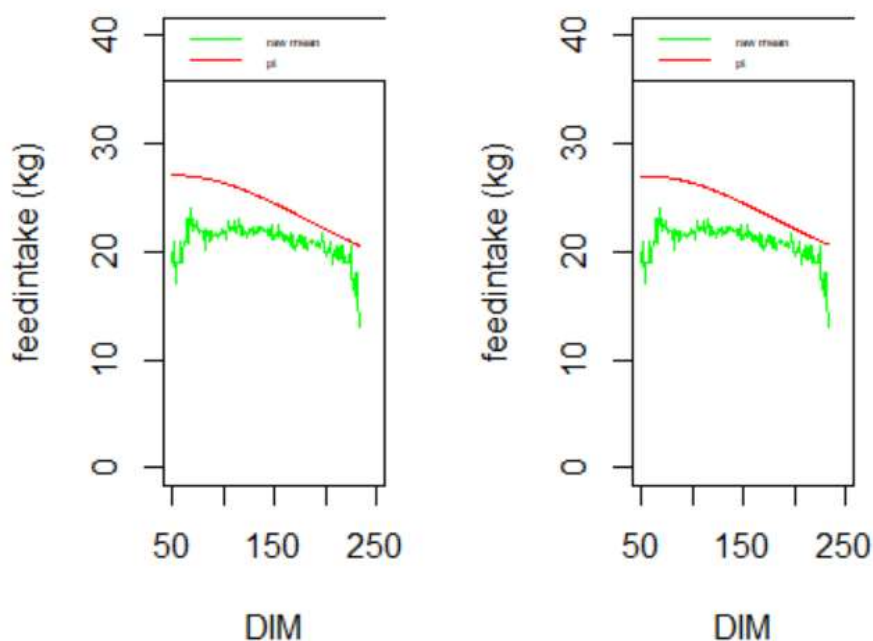
Generally, the models with heterogeneous variances shows similar residual variances. The first group (DIM 49-100) has the lowest value, which increased in the second group and shows a slight decrease again at DIM 151- 200 and DIM 201- 233.

Table 2: Comparison between Homogeneous and Heterogeneous animal, residual and phenotypic variances and standard error (Mleg3Aleg1H1 & Mleg3Aleg1H4) for feed intake.

Group (DIM)	Animal		Residual		Phenotypic	
	variance	±se	variance	±se	Variance	±se
Homogenous	4.0	0.99	3.32	0.09	7.21	0.99
Heterogenous						
49 – 100	3.94	0.98	2.44	0.19	6.38	1.00
101-150	3.94	0.98	3.41	0.15	7.35	0.99
151-200	3.94	0.98	3.26	0.15	7.20	0.98
201-233	3.94	0.98	3.40	0.37	7.35	1.04

Figure 1 shows that the homogeneous Mleg3Aleg1H1 and heterogeneous Mleg3Aleg1H4 displayed similar deviation from the mean. Both models showed a descending curve for the points fitted along the DIM. The points fitted on the fixed curve is higher than the raw mean. This could be a result of parity and week effect which are not accounted for in the displayed fitted curve.

Figure 1: Estimates of raw mean and point fitted on the curve of Mleg3Aleg1H1 and Mleg3Aleg1H4 for feed intake.



\*pt– point fitted on the curve

Random regression analysis of feed intake

Tables 3a to 3k shows the results of the regression analysis of the feed intake data. To select the best data to fit the fixed effects the difference between the standard error and regression solution are being considered. A model is considered being significant if the estimate of the coefficient of the highest degree (e.g. coefficient of degree 3 in Mleg3) is greater than twice the standard error value (estimate > 2\*SE).

Based on this criterion for selecting the models, the models in Tables 3a, 3f and 3g were not significant. While the Table 3b, 3c, 3d, 3e, 3h, 3i, 3j and 3k shows significance of the coefficient of the highest degree. Hence, models with Mleg3 (both homogenous and heterogenous variances) were not significant as their solution was less than twice the standard error. While Model Mleg1, Mleg2, Mleg4 and Mleg5 were all significant as their solution was

greater than twice the standard error. Our overall conclusion is that we need at least 5<sup>th</sup> order of fit to fit the fixed mean curve of feed intake along the DIM.

Table 3a, 3b, 3c, 3d, 3e, 3f, 3g, 3h, 3i, 3j, 3k: Estimates of the regression coefficients of the Legendre polynomials for the fixed mean feed intake curve and their standard errors

a) Model: Mleg3Aleg1H1

Covariable	Reg. coeff.	Solution	Std Error	Signif.
dim(-3,leg)	0	4.41	2.85	
dim(-3,leg)	1	-2.89	0.67	
dim(-3,leg)	2	-0.45	0.12	
dim(-3,leg)	3	0.116	0.09	No

b) Model: Mleg1Aleg1H4

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-1,leg)	0	4.772	2.79	
dim(-1,leg)	1	-2.94	0.66	**

\*\* - significant

c) Model: Mleg1Aleg2H4<sub>FI</sub>

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-1,leg)	1	-3.08	0.69	**

\*\* - significant

d) Model : Mleg2Aleg1H4

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-2,leg)	0	4.35	2.81	
dim(-2,leg)	1	-2.95	0.66	
dim(-2,leg)	2	-0.45	0.11	**

\*\* - significant

e) Model : Mleg2Aleg2H4

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-2,leg)	0	4.94	2.87	
dim(-2,leg)	1	-3.18	0.68	
dim(-2,leg)	2	-0.56	0.15	**

\*\* - significant

f) Model: Mleg3Aleg1H4

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-3,leg)	0	4.42	2.84	
dim(-3,leg)	1	-2.84	0.67	
dim(-3,leg)	2	-0.46	0.11	
dim(-3,leg)	3	0.18	0.097	No

g) Model: Mleg3Aleg2H4

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-3,leg)	0	4.88	2.88	
dim(-3,leg)	1	-3.06	0.70	
dim(-3,leg)	2	-0.56	0.15	
dim(-3,leg)	3	0.095	0.12	No

h) Model: Mleg4Aleg1H4

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-4,leg)	0	4.42	2.81	
dim(-4,leg)	1	-2.83	0.66	
dim(-4,leg)	2	-0.71	0.13	
dim(-4,leg)	3	0.17	0.096	
dim(-4,leg)	4	-0.32	0.090	**

\*\* - significant

i) Model: Mleg4Aleg2H4

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-4,leg)	0	5.01	2.87	
dim(-4,leg)	1	-2.97	0.68	
dim(-4,leg)	2	-0.75	0.16	
dim(-4,leg)	3	0.13	0.11	
dim(-4,leg)	4	-0.28	0.10	**

\*\* - significant

j) Model: Mleg5Aleg1H4

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-5,leg)	0	4.46	2.82	
dim(-5,leg)	1	-2.95	0.67	
dim(-5,leg)	2	-0.72	0.13	
dim(-5,leg)	3	0.015	0.12	
dim(-5,leg)	4	-0.31	0.09	
dim(-5,leg)	5	-0.22	0.08	**

\*\* - significant

k) Model: Mleg5Aleg2H4

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-5,leg)	0	4.87	2.87	
dim(-5,leg)	1	-3.04	0.68	
dim(-5,leg)	2	-0.75	0.15	
dim(-5,leg)	3	-0.021	0.12	
dim(-5,leg)	4	-0.28	0.09	
dim(-5,leg)	5	-0.19	0.08	**

\*\* - significant

### Feed Intake Models Comparison

Eleven analyses with different models using the Legendre polynomial function were performed to find the best model of fit for the feed intake data. Akaike information criterion (AIC), and LogL are reported in Table 4. These criteria were used to compare the models and to choose the best one to fit the data for the animal effect. Higher values obtained for  $-\frac{1}{2}$  AIC signify better goodness of fit of the model. This rule is also the same when high values are obtained for LogL.

Firstly, consider Model Mleg3Aleg1H1, in which all the animal effects only fitted the intercept, and contained a homogeneous residual variance. The model included the fixed effects of parity and week and an animal random effect. The REML Log L was significantly lower compared to all other models. But the  $-\frac{1}{2}$  AIC was lower when compared to the same model with heterogeneous residual variances. Since the AIC compares the quality of fit of the two models, and prefers Mleg3Aleg1H4, we will henceforth use the heterogeneous variance model.

In the models with heterogeneous variances, the goodness of fit (LogL and  $-\frac{1}{2}$  AIC) generally improved as the degree of fit of the animal effect changed from 1 to 2. Also  $-\frac{1}{2}$ AIC showed variability as the polynomial degree of the animal effect varied from 1 to 2. Looking at Table 4 model Mleg5Aleg1 gives a better  $-\frac{1}{2}$  AIC value than the other models. Hence, recommending order 5 (Mleg5) for fixed effect and order 1 (Aleg1) for animal effect.

Table 4. Model (with the effect of parity and week), number of parameters estimated (p), the logarithm of the Residual Maximum likelihood function (log L), and Akaike's information criterion (AIC)

Model	p	LogL	-½ AIC	Ani-Var	Res-Var			
Mleg3Aleg1H1	2	-2844.66	-2846.66	4.00	3.20			
Mleg1Aleg1H4	5	-2843.02	-2848.02	3.82	2.54	3.43	3.27	3.40
Mleg1Aleg2H4	7	-2835.56	-2842.56	3.90	2.42	3.40	3.22	3.26
Mleg2Aleg1H4	5	-2837.26	-2842.26	3.89	2.46	3.42	3.28	3.35
Mleg2Aleg2H4	7	-2831.49	-2838.49	4.10	2.40	3.40	3.22	3.23
Mleg3Aleg1H4	5	-2837.90	-2842.90	3.94	2.44	3.42	3.27	3.41
Mleg3Aleg2H4	7	-2833.33	-2840.33	4.10	2.40	3.40	3.20	3.30
Mleg4Aleg1H4	5	-2834.28	-2839.28	3.89	2.40	3.42	3.26	3.25
Mleg4Aleg2H4	7	-2832.22	-2839.22	4.00	2.41	3.40	3.23	3.20
Mleg5Aleg1H4	5	-2833.11	-2838.11	3.89	2.45	3.41	3.25	3.19
Mleg5Aleg2H4	7	-2832.22	-2839.22	4.00	2.42	3.40	3.23	3.17

Note: MlegxAlegxHx, where Mlegx is the polynomial order for fixed curve and Alegx is the degree for animal effects. And Hx is the number of residual variance classes.

The animal, phenotypic and residual variances (Figure 2a,b & c) were lower in early lactation and increased at the end of lactation. For the animal effect this may be a result of the smaller number of records at the end of the lactation. The animal variance estimates (Figure 2a) from models Mleg5Aleg1 and Mleg5Aleg2 differed. The animal variance for model Mleg5Aleg1



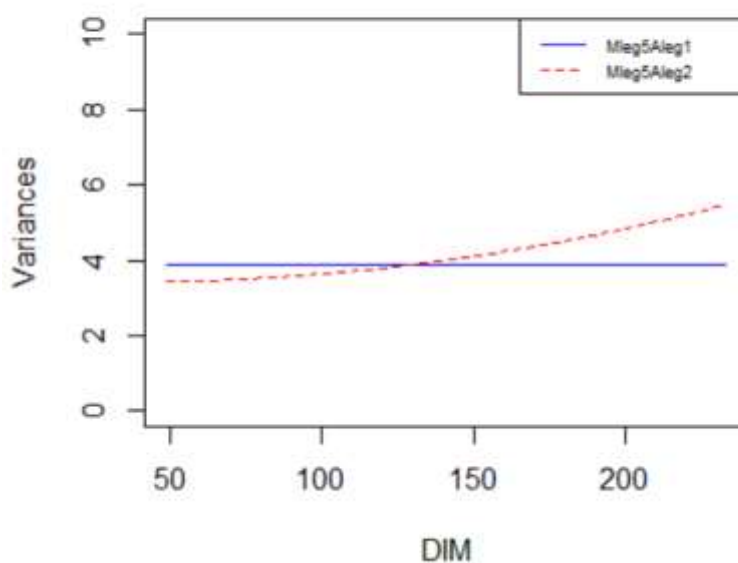
maintained a constant value all through the lactation period. While model Mleg5Aleg2 yielded a relatively, constant value until DIM ~ 100 and from this point on, it showed an increase.

The phenotypic variance estimate for both models (Figure 2b) showed a similar trend; it was very small until the second phase of DIM group (101-150) and showed an increase from this point to the end of the test period. The phenotypic variances for Mleg5Aleg1 were of low magnitude at DIM 49-100 and increase until 150 days in milk, slightly decreased at 151 DIM and maintained this value to 233 DIM. In the model Mleg5Aleg2; the smallest phenotypic variances were observed initially and then showed an increase with the largest value at the end of the test period.

Residual variances estimated by both models were similar and showed, just like animal variance, the smallest values at the beginning of the lactation. When moving from 100 to 150 DIM the residual variance increased, and then slightly decreased from 151 DIM to the end of the test period.

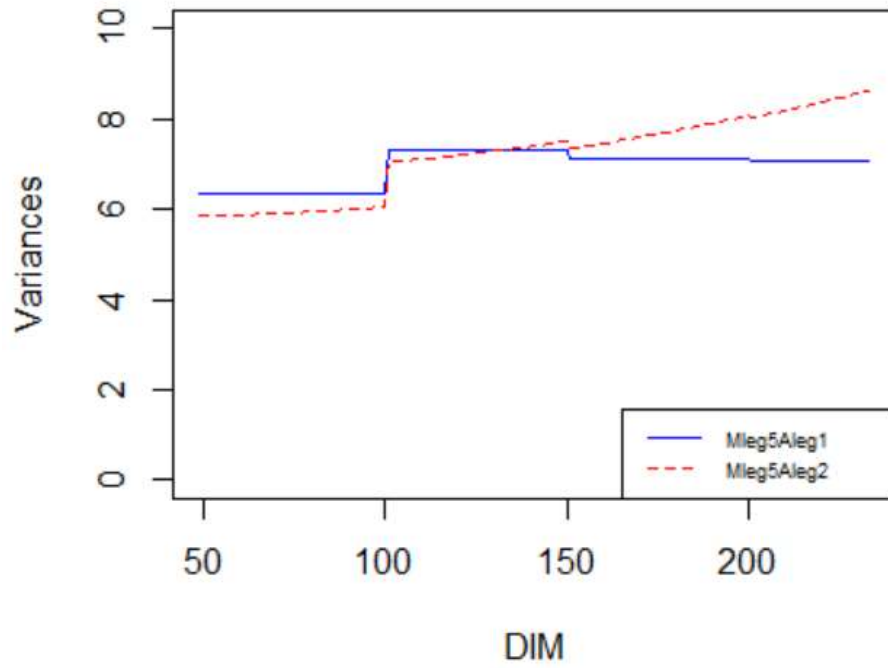
Figure 2: Animal (a), Phenotypic (b) and Residual (c) Variance of model Mleg5Aleg1H4 and Mleg5Aleg2H4 for feed intake

a) Animal variances



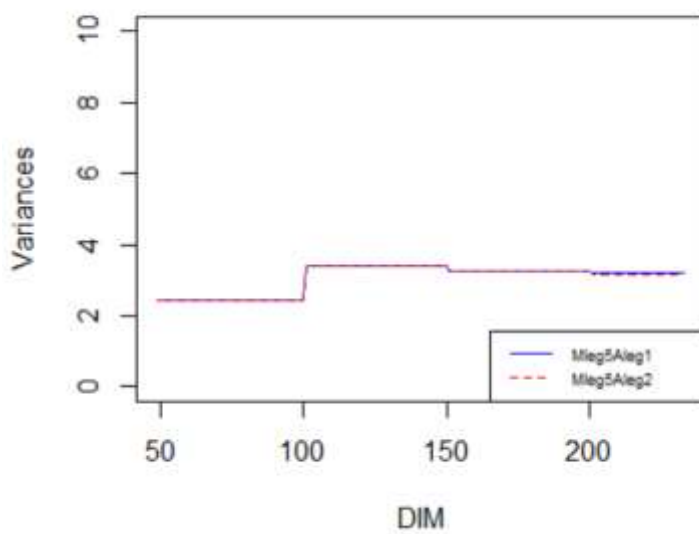
b) Phenotypic variances

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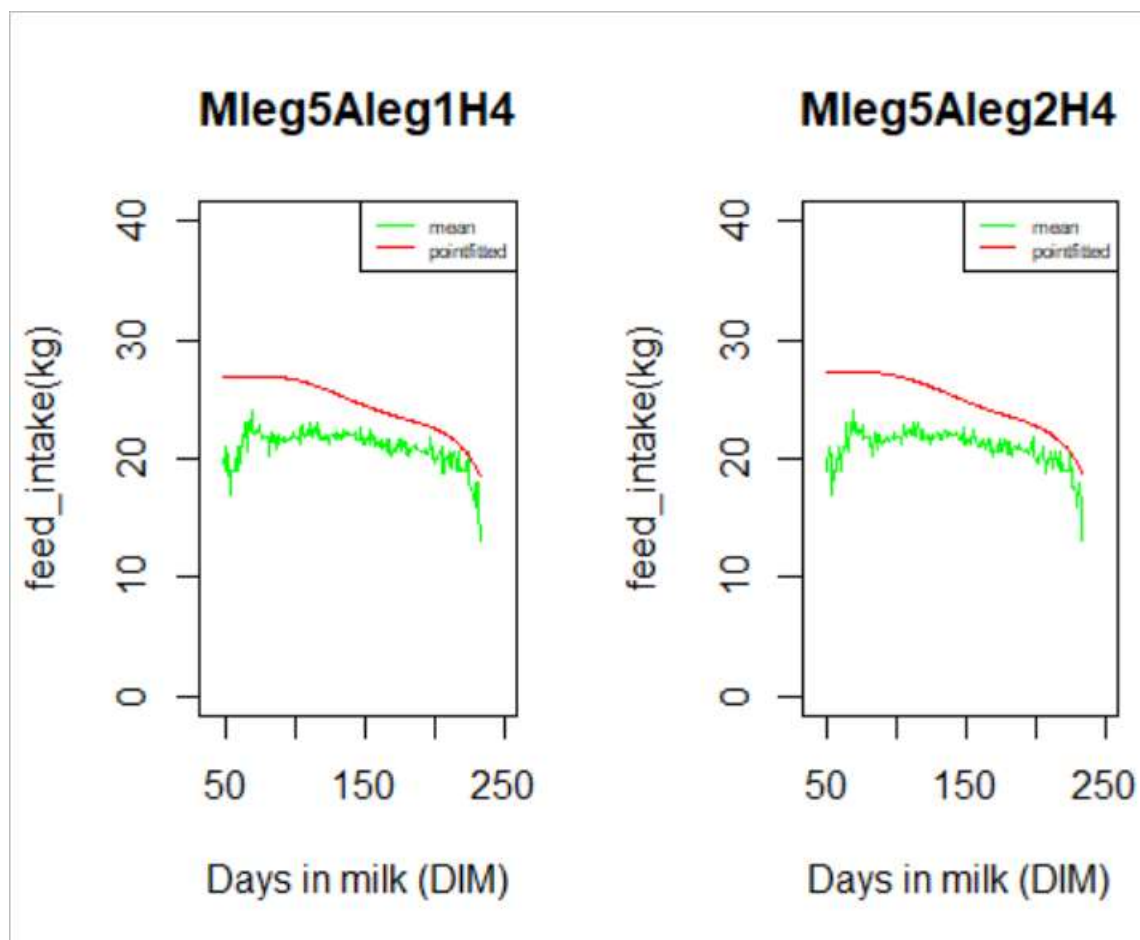
c) Residual variances

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Also the result of raw mean and point fitted on the curve estimate (Figure 3) of both models shows that Mleg5Aleg1H4 and Mleg5Aleg2H4 displayed similar deviation from the mean. Both models showed a curve similar to the lactation curve. From the figures, the raw mean was lower than the points fitted on the fixed effect curve. The predicted value is higher than the raw mean because of the fixed effect of parity and week. WOMBAT sets one of the fixed (week) to zero for the analysis. This could be a good week with high feed intake implying that the other weeks have negative estimates, i.e. a correction for the week effect is generally negative. The same holds for the parity effect: again a parity with relatively high feed intake may be set to 0, implying generally negative parity effects. Correcting for these generally negative parity and/or week effects will bring the fitted values closer to the raw means in Figure 3, which implies thus a generally negative correction.

Figure 3: Estimates of raw mean and point fitted on the curve of Homogenous and heterogeneous residuals with fixed effect of parity and week (Mleg5Aleg1H4 and Mleg5Aleg2H4) for feed intake



The histogram of the estimated residuals (figure 4) of Mleg5Aleg1H4 shows that it is normally distributed. It shows a bell shape, therefore indicating normality of the estimated residuals.

Figure 4: Histogram of residual distribution for Mleg5Aleg1H4 for feed intake.

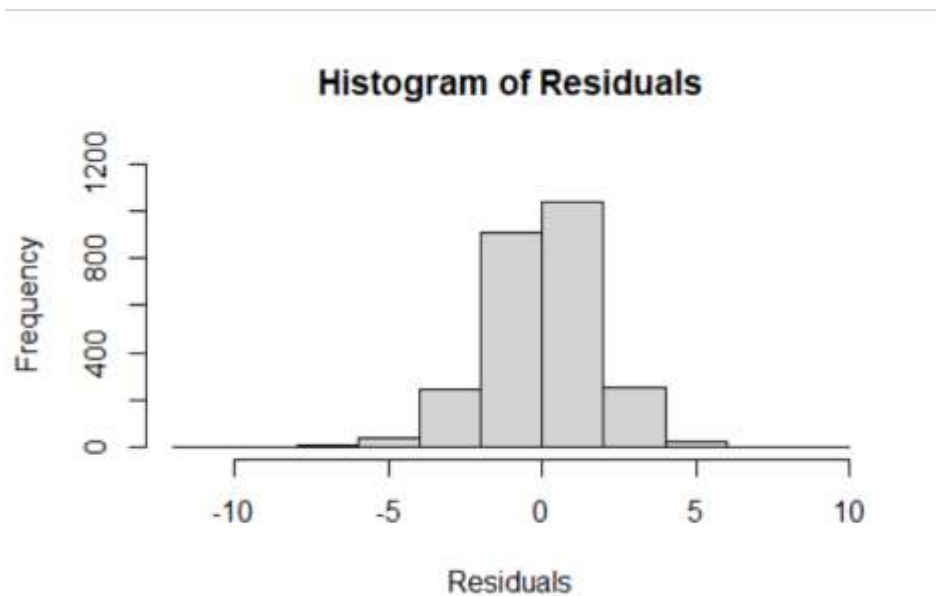
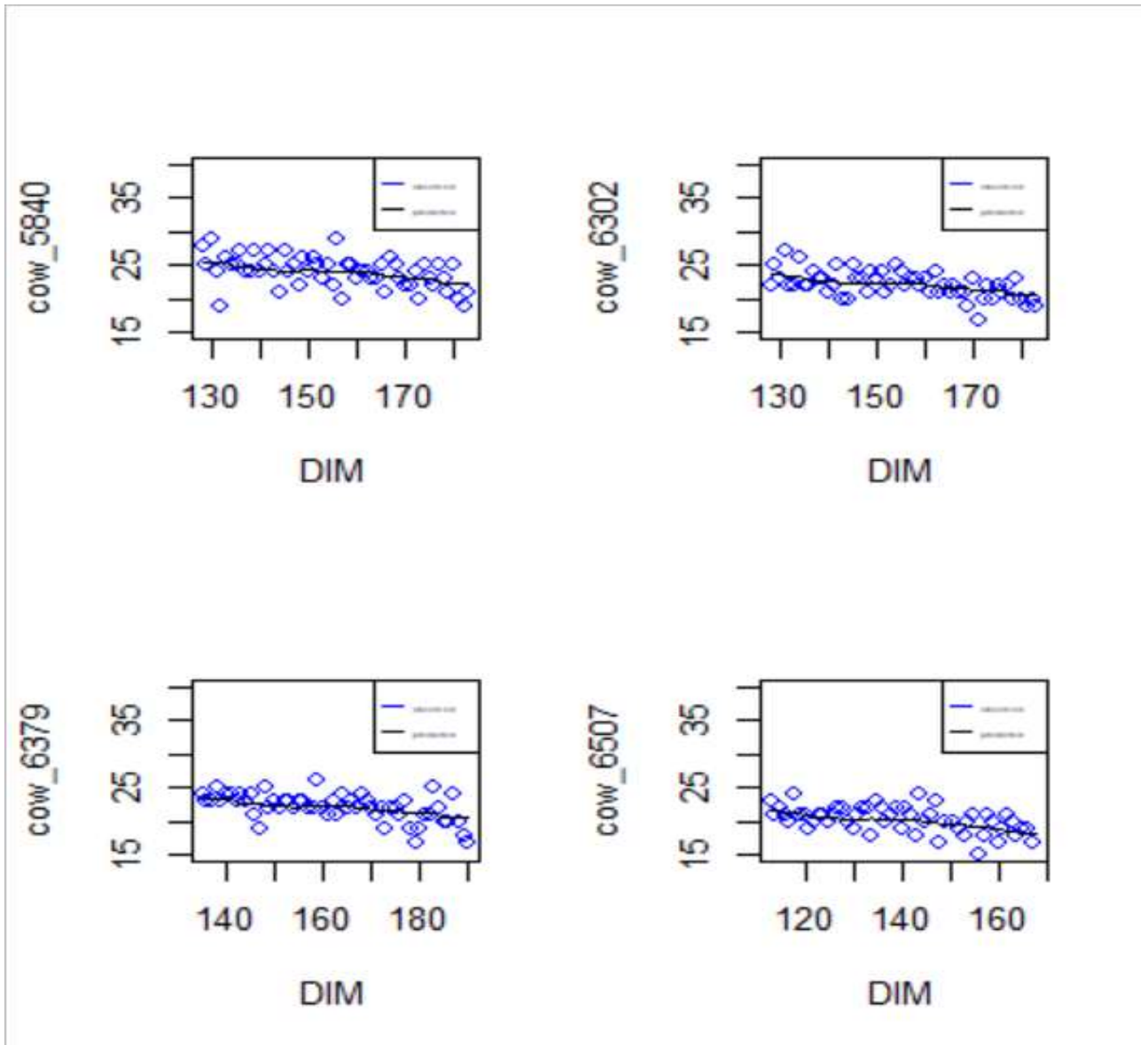


Figure 5 shows the variation between the observed and predicted feed intake values of some selected animals. These animals were not randomly chosen. Animal 5840 and 6302 records stretched over the same lactation period. This was also applicable with animals 6379 and 6507 which were in the same DIM at the beginning of the experiment. The values show that there are differences between the observed feed intake values and predicted values. Though the predicted didn't assume a straight line. Figure 5 also showed a declining feed intake over DIM.

Figure 5: Observed and predicted feed intake of model Mleg5Aleg1H4- animal 5840, 6302, 6379 and 6507



## Feed Efficiency

Comparison of models with Homogeneous and Heterogeneous variance(s)

The estimated variances for model Mleg3Aleg1H1 (homogeneous variance) and model Mleg3Aleg1H4 with heterogeneous residual variances (Table 5) showed similar variation. The animal variances for both models were the same. The residual and phenotypic variances were marginally different for the heterogeneous and homogeneous group of residual variance.

Generally, the models with heterogeneous variances shows similar residual variances. The third group (DIM 151-200) has the lowest value, which increased in the fourth group.

Table 5: Comparison between Homogeneous and Heterogeneous animal, residual and phenotypic variances and standard error (Mleg3Aleg1H1 & Mleg3Aleg1H4) for feed efficiency

Group (DIM)	Animal variance	±se	Residual variance	±se	Phenotypic Variance	±se
Homogenous	1.37	0.32	0.23	0.02	1.61	0.32
Heterogenous						
52 – 100	1.37	0.32	0.24	0.06	1.62	0.32
101 - 150	1.37	0.32	0.24	0.03	1.61	0.32
151 – 200	1.37	0.32	0.22	0.03	1.60	0.32
201 – 230	1.37	0.32	0.27	0.08	1.65	0.33

### Random regression analysis of feed efficiency

Based on this criterion for selecting the models, the models in Tables 6b, 6c, 6d, 6e, 6h, 6i, 6j and 6k were not significant. While the Table 6a, 6f, and 6g shows significance of the coefficient of the highest degree. Hence, models with Mleg3 (both homogenous and heterogenous variances) were significant as their solution was greater than twice the standard error. While Model Mleg1, Mleg2, Mleg4 and Mleg5 were all not significant as their solution was lesser than twice the standard error. Our overall conclusion is that 3<sup>rd</sup> order is sufficient to fit the fixed mean curve of feed efficiency along the DIM.

Table 6a, 6b, 6c, 6d, 6e, 6f, 6g, 6h, 6i, 6j, 6k: Estimates of the regression coefficients of the Legendre polynomials for the fixed mean feed efficiency curve and their standard errors

a) Model: Mleg3Aleg1H4

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-3,leg)	0	-0.32	1.68	
dim(-3,leg)	1	-0.66	0.44	
dim(-3,leg)	2	0.10	0.08	
dim(-3,leg)	3	-0.18	0.07	**

\*\* - significant

b) Model: Mleg1Aleg1H1

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-1,leg)	0	-0.34	1.69	
dim(-1,leg)	1	-0.51	0.44	NO

c) Model: Mleg1Aleg2H1

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-1,leg)	0	-0.52	1.65	
dim(-1,leg)	1	-0.35	0.46	NO

d) Model : Mleg2Aleg1H1

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-2,leg)	0	-0.27	1.68	
dim(-2,leg)	1	-0.51	0.44	
dim(-2,leg)	2	-0.08	0.08	NO

e) Model : Mleg2Aleg2H1

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-2,leg)	0	-0.47	1.65	
dim(-2,leg)	1	-0.34	0.45	
dim(-2,leg)	2	0.06	0.11	NO

f) Model: Mleg3Aleg1H1

Covariable	Reg. coeff.	Solution	Std Error	Signif.
dim(-3,leg)	0	-0.34	1.68	
dim(-3,leg)	1	-0.66	0.44	
dim(-3,leg)	2	0.10	0.08	
dim(-3,leg)	3	-0.18	0.06	**

\*\* - significant

g) Model: Mleg3Aleg2H1

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-3,leg)	0	-0.55	1.65	
dim(-3,leg)	1	-0.64	0.47	
dim(-3,leg)	2	0.08	0.11	
dim(-3,leg)	3	-0.17	0.08	**

\*\* - significant

h) Model: Mleg4Aleg1H1

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-4,leg)	0	-0.33	1.68	
dim(-4,leg)	1	-0.66	0.44	
dim(-4,leg)	2	0.07	0.09	
dim(-4,leg)	3	-0.18	0.07	
dim(-4,leg)	4	-0.04	0.06	NO

i) Model: Mleg4Aleg2H1

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-4,leg)	0	-0.48	1.43	
dim(-4,leg)	1	-0.64	0.42	
dim(-4,leg)	2	0.04	0.12	
dim(-4,leg)	3	-0.16	0.08	
dim(-4,leg)	4	-0.07	0.07	NO



j) Model: Mleg5Aleg1H1

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-5,leg)	0	-0.33	1.68	
dim(-5,leg)	1	-0.68	0.44	
dim(-5,leg)	2	0.07	0.09	
dim(-5,leg)	3	-0.21	0.08	
dim(-5,leg)	4	-0.04	0.06	
dim(-5,leg)	5	-0.04	0.05	NO

k) Model: Mleg5Aleg2H1

Covariable	Reg. coeff	Solution	Std Error	Signif.
dim(-5,leg)	0	-0.52	1.64	
dim(-5,leg)	1	-0.63	0.47	
dim(-5,leg)	2	0.04	0.12	
dim(-5,leg)	3	-0.19	0.09	
dim(-5,leg)	4	-0.05	0.07	
dim(-5,leg)	5	-0.05	0.06	NO

Feed Efficiency Models Comparison

Eleven analyses with different models using the Legendre polynomial function were performed to find the best model of fit for the feed efficiency data. Akaike information criterion (AIC), and LogL are reported in Table 7. These criteria were used to compare the models and to choose the best one to fit the data for the animal effect (higher values obtained for  $-\frac{1}{2}$  AIC signify better goodness of fit of the model. This rule is also the same when high values are obtained for LogL).

Firstly, considering Model Mleg3Aleg1H1 (in which all the animal effects only fitted the intercept, and contained a homogeneous residual variance). The REML Log L was marginally

lower than Model Mleg3Aleg1H4 (with heterogeneous residual variances). But the  $-\frac{1}{2}$  AIC was higher than the Model with heterogeneous classes of residual variances (Mleg3Aleg1H4).

In the models with homogeneous variances, the goodness of fit (LogL and  $-\frac{1}{2}$  AIC) generally improved as the degree of fit of the animal effect changed from 1 to 2. Also  $-\frac{1}{2}$ AIC showed an increase trend as the polynomial degree of the animal effect varied from 1 to 2. Furthermore, including 3<sup>rd</sup> degree of fit for the animal effect; Aleg3 (result unpublished), the analysis showed no convergence.

Hence, recommending order 3 (Mleg3) for fixed effect and order 2 (Aleg2) for animal effect. Since the AIC compares the quality of fit of the two models, and prefers Mleg3Aleg2H1, we will henceforth use the homogeneous variance models.

Table 7. Model (with the effect of parity and week), number of parameters estimated (p), the logarithm of the Residual Maximum likelihood function (log L), and Akaike's information criterion (AIC)

Model	p	LogL	$-\frac{1}{2}$ AIC	Ani-Var	Res-Var				
Mleg3Aleg1H4	5	-24.38	-29.38	1.38	<b>0.24</b>	<b>0.24</b>	<b>0.22</b>	<b>0.27</b>	
Mleg1Aleg1H1	2	-23.66	-25.66	1.39	0.24				
Mleg1Aleg2H1	4	-14.14	-18.14	1.30	0.20				
Mleg2Aleg1H1	2	-25.70	-27.70	1.38	0.24				
Mleg2Aleg2H1	4	-16.21	-20.21	1.31	0.20				
Mleg3Aleg1H1	2	-24.65	-26.65	1.37	0.23				
Mleg3Aleg2H1	4	-16.70	-20.70	1.32	0.23				
Mleg4Aleg1H1	2	-27.19	-29.19	1.36	0.23				

Mleg4Aleg2H1	4	-19.77	-23.77	0.97	0.20
Mleg5Aleg1H1	2	-29.84	-31.84	1.37	0.23
Mleg5Aleg2H1	4	-21.51	-25.51	1.29	0.20

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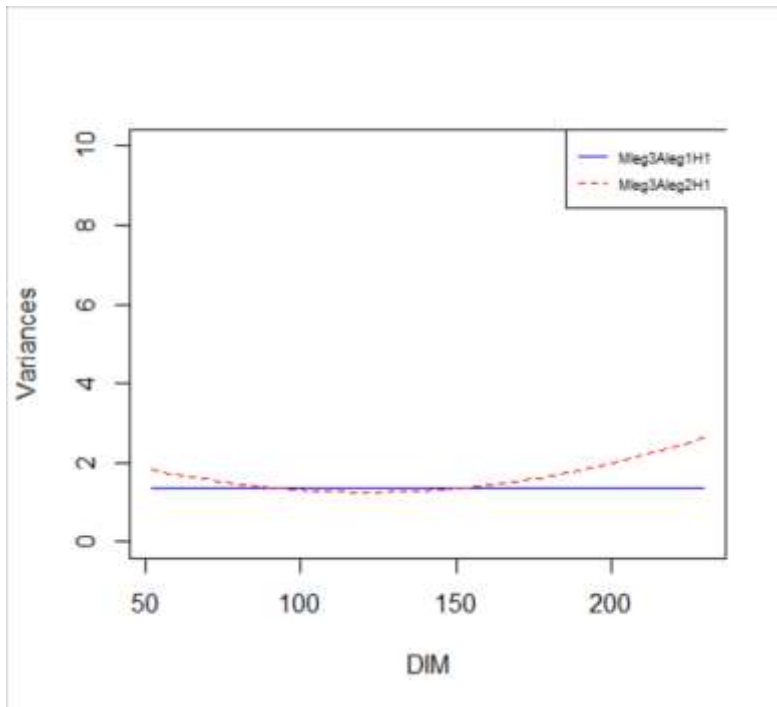
The animal variance estimates (Figure 6a) from models Mleg3Aleg1H1 and Mleg3Aleg2H1 differed in their trend. The animal variance for model Mleg3Aleg1H1 maintained a constant value all through the lactation period under study. While model Mleg3Aleg2H1 yielded a high value at the beginning of the lactation period, declined gradually until DIM ~ 150 and from this point on, it showed an increase.

The phenotypic variance estimate for both models (Figure 6b) showed a similar trend just like animal variance; the animal variance for model Mleg3Aleg1H1 maintained a constant value all through the lactation period. While model Mleg3Aleg2H1 yielded a high value at the beginning of the lactation period, declined gradually until DIM ~ 150 and from this point on, it showed an increase.

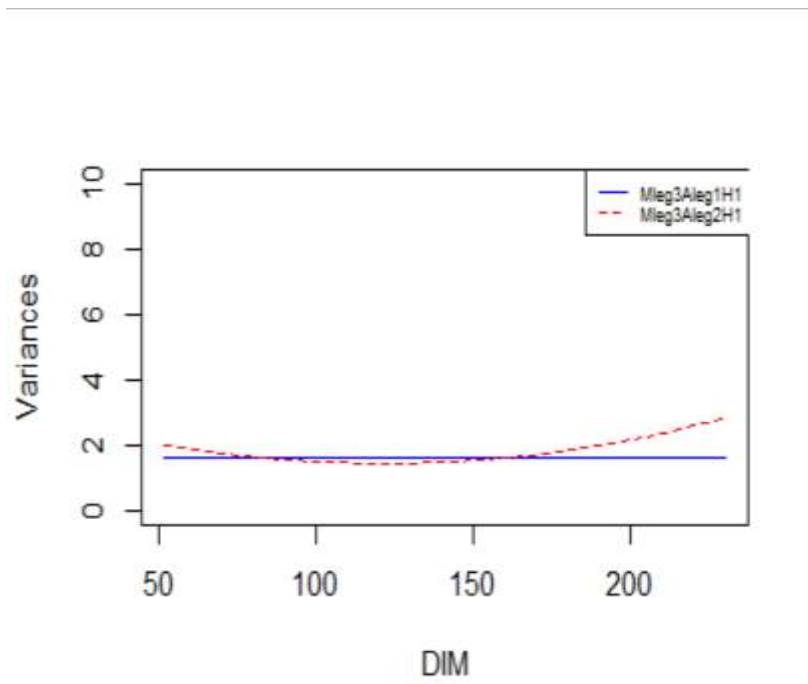
Residual variances estimated by both models were similar. Both models maintained a constant value all through the lactation period studied.

Figure 6: Animal (a), Phenotypic (b) and Residual (c) Variance of model Mleg3Aleg1H1 and Mleg3Aleg2H1 for feed efficiency

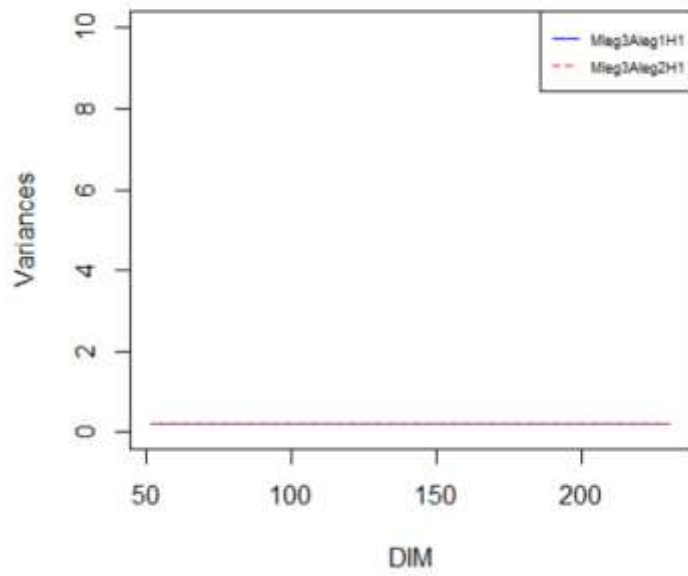
6a) Animal variances



6b) Phenotypic variances



### 6c) Residual variances



## DISCUSSION

The feed intake results of comparison between Mleg3Aleg1H1 Homogeneous and Mleg3Aleg1H4 heterogeneous residual variances models shown in table1 indicated that the model with the homogeneous residual variance showed worst fit, irrespective of the degree used in modelling the random effect. This is in agreement with the studies of Bignardi et al. (2011), in Brazilian Holstein cows. Similar results were obtained from studies carried out on dairy goats (Assis et al., 2006; Breda et al., 2006; Brito et al., 2017; Menezes et al., 2011; Silva et al., 2013). The current finding indicates the need for heterogeneous residual variances, where residual variances differ at different stages of the lactation (Bignardi et al., 2011). Also, Aspilcueta-Borquis et al. (2012) reported that assuming homogenous residual variances in a random regression test day model may not be adequate in the study for Brazilian dairy buffalo. Therefore, heterogeneous residual variances are generally found to be the preferred option in random regression test-day models.

Amongst the polynomials fitted to model the fixed feed intake curve in this study, the Mleg5 was found to be most suitable. However, higher order polynomials than Mleg5 were not studied here. This result agrees with the studies of Sesana et al. (2010) and Costa et al. (2008) who concluded that Legendre polynomial of order five was suitable to model dairy data. Although these authors recorded no difference between homogeneous and heterogeneous residual variances across the lactation because they considered animal genetic and permanent environmental effects in their RRM. The current findings differs from Kramer et al. (2009) and Flores & van der Werf, (2015) who analyzed dairy data on buffaloes, suggesting lower orders of fit for the mean lactation curve. The analysis of Kramer et al. (2009), considered both feed intake and water intake along the lactation period.

Aleg1 was found here sufficient for the degree of fit for the animal effect on feed intake data along the lactation. Increasing the order of fit from 1 to 2 showed improvement in the goodness of fit, which is similar to results achieved in other findings (Li et al., 2020). However, increasing the order of fit increased the number of parameters (p), which makes the model more complex, which decreases the AIC information criterion. In addition, a more complex model may be more computationally demanding. The result clearly showed that with a more sophisticated fixed effect model, Aleg2 (degree of animal effect) might not be needed to fit the animal effect (Table 4). Selecting a suitable test-day model requires a balance between goodness of fit and model complexity, and our data suggested a polynomial of degree 1 for the animal effect in our data. However, our data stretched only over 50 days in milk for individual

cows, and higher orders of fit may be needed for feed intake data that stretch over longer periods of the lactation.

The differences between Aleg1 and Aleg2 are shown in Fig2a, 2b and 2c, which shows a summary of the variance components. Generally, the animal, phenotypic and residual variances (were lower in early lactation and increased towards the end of lactation) This general trend was similar in the studies of Brito et al. (2017), who studied variance components of lactation models in dairy goats. It may be due to the limited size of our data set and thus limited information that our results suggest a Aleg1 fit for the animal effect, which suggests a constant animal variance throughout the lactation period. Though a lower variance at the beginning and a higher variance at the end of the lactation was suggested by the Aleg2 fit of the animal effect.

The residual variances for both Aleg1 and Aleg2 assumed the same trend along the lactation period. Fig 2c, shows that the residual variance was low at the beginning of the lactation stage then increased at DIM 101-150, which could be immediately after peak lactation stage, then gradually decreased till the end of the lactation stage. This finding differs from Li et al. (2020), who reported small differences in residual variances when fitting higher order of fit and that residual variances were larger in the early stage of lactation. It is important to note that residual variances are affected by the lactation stage and scale effects of the production level.

Comparing the phenotypic variances estimated by Aleg1 and Aleg2, large differences were found in their variances (Figure 2b). This pattern may be due to the complexity of the model. Also, genetic and non-genetic factors may have significant impact on feed intake during the lactation period. The non-genetic factors could be a result of weather and other environmental conditions which may have large effects on the level of feed intake. The high value of the phenotypic variance towards the end of the lactation period could also be explained by the fact that the cows compensate for the negative energy balance after the peak lactation period (Bignardi et al., 2009).

The studies of Pereira et al. (2013) showed that random regression model can be used in estimating genetic parameters such as heritabilities along the lactation, but large datasets are required in estimating these genetic parameters (Druet et al., 2003). Given the size of our dataset, it was not possible to separate genetic from environmental effects. Though RRM may accept incomplete data for the analysis, but the period of feed intake for the cows studied was short (56days). So it may not be sufficient to depict the trend of feed intake along the whole lactation curve of the cows. The effect of parity might have a significant impact on the shape

of the curves, which was not accounted for. Due to the small size of our data, we did not estimate a different curve for the different parities (1,2,3,4,5).

The results of comparison between feed efficiency Mleg3Aleg1H1 Homogeneous and Mleg3Aleg1H4 heterogeneous residual variances models shown in table5 indicated that the model with the homogeneous residual variance showed similar range of fit with the model with heterogeneous variances. This result agrees with the findings of Sesana et al. (2010) and Costa et al. (2008) who recorded no difference between homogeneous and heterogeneous residual variances across the lactation in their model. This disagreed with other studies which found models with heterogeneous variances best fit for milk yield data (Assis et al., 2006; Breda et al., 2006; Brito et al., 2017; Menezes et al., 2011; Silva et al., 2013). In this research, comparison of feed efficiency models were made in terms of random effect using homogeneous classes of residual variances. However, according to this findings homogeneous residual variances and heterogeneous residual in a RRM are sufficient to fit feed efficiency data.

Amongst the polynomials fitted to model the fixed feed intake curve in this study, the Mleg3 was found to be most suitable. However, higher order polynomials such as Mleg4 and Mleg5 were also studied. This current finding is similar to the studies of Li et al. (2019) who found that Legendre polynomial of order 3 sufficient to fit milk yield data in Chinese Holstein population.

Aleg2 was found sufficient for the degree of fit for the animal effect on feed efficiency data along the lactation in this current finding. Increasing the order of fit from 1 to 2 showed improvement in the goodness of fit, which is similar to results achieved in other findings (Li et al., 2020). However, increasing the order of fit from 2 to 3 (Aleg3 result which is unpublished) showed no convergence. This differs from the results Bohmanova et al.(2008) where the authors found better and high convergence rate in higher order of fit for random effect (for example: 4) while comparing Legendre polynomial model with linear spline models.

The differences between Aleg1 and Aleg2 are shown in Fig6a, 6b and 6c, which shows a summary of the variance components. Generally, the animal and phenotypic variances estimated followed a similar trend during mid-lactation, with higher estimates obtained at the beginning and at the end of lactation period of this study. This trend was similar in the studies of Bignardi et al. (2009). Aleg1 fit for the animal variance assumed a constant value throughout the lactation period. However, a higher variance at the beginning and at the end of the lactation was suggested by the Aleg2 fit of the animal effect.



The residual variances for both Aleg1 and Aleg2 assumed the same trend along the lactation period. Fig 6c, shows that the residual variance assumed a constant value all through the lactation stages. This finding differs from Li et al. (2020), who reported small differences in residual variances when fitting higher order of fit and that residual variances were larger in the early stage of lactation.

Comparing the phenotypic variances estimated by Aleg1 and Aleg2, large differences were found in their variances (Figure 6b). This pattern may be due to the complexity of the model. Also, factors such as animal's health condition, energy balance, environmental temperature, (Lamb & Maddock, 2009) could have significant effect on feed efficiency. At peak lactation, feed intake may be very low resulting into low phenotypic variance estimate at mid lactation, but an animal might compensate for this using stored fat in its adipose tissue (Hardie, 2016). The high value of the phenotypic variance towards the end of the lactation period could also be explained by the fact that the cows compensate for the negative energy balance after the peak lactation period (Bignardi et al., 2009).

In conclusion, random regression models using Legendre polynomials functions of varying order for the fixed mean curve and for the random animal effects were able to model the average feed intake, feed efficiency and individual deviations during the lactation period. For the mean lactation curve seemed well modelled by 5<sup>th</sup> order Legendre polynomials, whereas individual deviations were well modelled by a 1<sup>st</sup> order Legendre polynomial in the current data set for feed intake data. Whereas, mean lactation curve seemed well modelled by 3<sup>rd</sup> order Legendre polynomials, whereas individual deviations were well modelled by a 2<sup>nd</sup> order Legendre polynomial in the current data set for feed efficiency data. Although, it remains important to obtain larger data sets in order to get a more precise estimates over the entire 305-day lactation period, on individual differences and to distinguish genetic from environmental effects.

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