Chapter 6: Genetic Determination of Individual Birth Weight and Sow Reproductive Performance of Mukota Pigs

Abstract

Genetic parameters for individual birth weight (IBWT), total number of pigs born (NBT), number of pigs born alive (NBA), number of pigs born dead (NBD) and total litter weight at birth (LBWT) were estimated using 1961 Mukota pigs kept at the University of Zimbabwe Farm, Harare, Zimbabwe. A direct-maternal effects model was fitted using the average information restricted maximum likelihood algorithm. The genetic relationships among NBT, NBA, NBD and LBWT were also assessed using a multi-trait direct effects model. The LBWT was obtained as an aggregate of the IBWT of pigs within a litter. The direct, maternal and common environmental litter proportions of phenotypic variances were 0.090, 0.033 and 0.009, respectively. After adjustment for NBT, the respective proportions were 0.091, 0.034 and 0.011 for direct, maternal and litter effects. The correlations between the direct and maternal genetic effects are –0.354 and –0.295, with and without adjustment for NBT, respectively. Heritabilities for NBT, NBA, NBD and LBWT were 0.013, 0.00, 0.103 and 0.178, respectively. Differences in the maternal heritability and the heritability for LBWT, a trait of the dam, emphasise the need to use individual birth weights in genetic selection for birth weight.

6.1 Introduction

Mukota pigs have been demonstrated to show adaptation traits to survive under tropical low input smallholder production conditions. For example, they are better able to utilise agricultural by-products (Kanengoni *et al*., 2002, 2004) and are less susceptible to parasites (Zanga *et al*., 2003) than exotic pigs. Currently, there are no formal genetic improvement programmes for Mukota pigs in Zimbabwe. Genetic improvement of pigs leads to efficient pork production. It is imperative that genetic parameters for reproductive traits in Mukota pigs are generated to design effective selection and genetic improvement programmes.

To date, selection for sow productivity in the Large White and Landrace has concentrated on litter size at birth (Mungate *et al*., 1999; Bolet *et al*., 2001; Holl and Robinson, 2003). Litter traits of economic importance include litter weight at birth (LBWT), total number of pigs born per litter (NBT), number of pigs born alive (NBA), average birth weight and number of pigs born dead (NBD). These traits are cumulative and do not refer to individual pigs. It has been repeatedly shown that the economics of sow productivity are also influenced by individual birth weight. Low birth weight results in higher mortality at birth as well as during the nursing period (Roehe, 1999; Milligan *et al*., 2002). Low birth weight also reduces postnatal growth (de Passille *et al*., 1993; Klemcke *et al*., 1993). Genetic analyses of individual birth weight are rare because of the additional labour, time and costs involved. Accurate estimates of the variance and covariance components for Mukota pigs have to be available to produce reliable predictions of breeding values of animals, particularly if genetic correlations exist between weight at birth and growth performance of pigs. The objectives of this study were, therefore, to:

1. Estimate direct and maternal additive genetic parameters for individual birth weight (IBWT);

2. Determine the effect of adjusting the weight of pigs at birth to the total number of pigs born per litter (NBT) and number of pigs born alive in a litter (NBA), and
3. Estimate genetic parameters for cumulative litter traits (LBWT, NBT, NBA and NBD) in Mukota pigs.

6.2 Materials and Methods

6.2.1 Description of study site

The study site was described in Section 3.2.1. Genetic determination of the crossbred pigs was not assessed due to low sample size (n = 640 litters).

6.2.2 Pig population structure

The pig population structure is described in Section 3.2.2.

6.2.3 Animal management

The management and feeding conditions of the pigs were described in Section 3.2.3.

6.2.4 Data preparation and statistical analyses

Out of a total of 2467 individual pig records kept between January 1998 to August 2003, 506 were deleted due to missing records on any one of the traits from birth to slaughter. A total of 1961 records were, therefore, used in the analyses.

6.2.4.1 Individual birth weight

The average information restricted maximum likelihood (AIREML) algorithm (Gilmour *et al.*, 1995) was used to generate (co) variance components for the animal model. Individual birth weight (IBWT) was regarded as a trait of each pig born alive. In the first basic model, a direct animal model, without maternal and common environmental effects, was fitted. In the second model, IBWT was regarded as a trait influenced by maternal genetic and litter effects during pregnancy. The model fitted for the second model was:

$$\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}_l\mathbf{u}_l + \mathbf{Z}_2\mathbf{u}_a + \mathbf{Z}_3\mathbf{u}_m + e$$

where $\mathbf{Y}$ is vector of n observations for individual birth weight, β is a vector of fixed effects and includes the year-season (four seasons per year), parity (8 parities) and sex (male and female) effects. Vectors of random effects consists of environmental effects ($\mathbf{u}_l$) common to all pigs within each litter, direct ($\mathbf{u}_a$) as well as maternal genetic effects ($\mathbf{u}_m$) of pigs, and residual environmental effects (e) peculiar to each pig. The incidence matrices $\mathbf{X}$ and $\mathbf{Z}_i$ (i = 1, 2, 3) link the fixed and random effects, respectively, with corresponding records in vector $\mathbf{Y}$.

All random effects were sampled from a normal distribution with a zero mean and variance-covariance structure of:

$$v\begin{bmatrix} u_l \\ u_a \\ u_m \\ u_e \end{bmatrix} = \begin{bmatrix} I\sigma_l^2 & 0 & 0 & 0 \\ 0 & A\sigma_a^2 & A\sigma_{am} & 0 \\ 0 & A\sigma_{am} & A\sigma_m^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

The **I** and **A** are the identity and numerator relationship matrices, respectively. The implied genetic model is known as an infinitesmal model, as described by Bulmer (1980). The base population is assumed to be unselected, non-inbred and unrelated.

The third model included litter size as a covariate to adjust IBWT. First, IBWT was linearly regressed on NBT. Preliminary analyses showed that the linear regression of IBW on NBT was significant ($P < 0.05$). An additional pig in the uterus resulted in an average decrease of 21 g per piglet. The regression of IBWT on NBA was not significant ($P > 0.05$). The relationship between IBWT and NBT may be expected from the biological point of view, because all pigs born compete for limited resources within the uterus, not only the pigs born alive.

6.2.4.2 Sow productivity

The LBWT was regarded as a trait of the sow giving birth. The other traits considered in a multivariate model were NBT, NBA and NBD. The NBT was defined as the number of fully formed pigs at birth, while NBA and NBD constituted the number of live and dead pigs at birth, respectively. The model used was:

$$\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{u}_{pe} + \mathbf{Z}_2\mathbf{u}_a + e;$$

where **Y** is vector of n observations of sows in each of the four traits and β is a vector of the fixed effects associated with each trait. The term $\mathbf{u}_{pe} \sim N(\mathbf{0}, \mathbf{P} \otimes \mathbf{I})$ represents the random permanent environmental effects common to all litters produced by each sow, $\mathbf{u}_a$

represents the additive genetic effect of the sows distributed as N ($\mathbf{0}$, $G_a \otimes \mathbf{A}$. The residual (environmental) effects, e, is distributed as N ($\mathbf{0}$, $\mathbf{R} \otimes \mathbf{I}$). The matrices **P**, G_a and **R** represent the variances and covariances among traits due to permanent environmental, additive genetic and residual environmental effects, respectively. Maternal genetic effects were not fitted as they have been reported to be insignificant on sow productivity traits (Chen *et al*., 2003).

An adjustment of LBWT for NBA was also included in the model, because there was a significant relationship of LBWT on NBA, whereas no such relationship existed between LBWT and NBT. These preliminary findings are expected, since only live pigs were weighed at birth. Stillbirths were, therefore, not included in the LBWT.

The models were run for five times, using estimates of each run as the inputs for the subsequent one, until the estimates stabilised.

6.3 Results

6.3.1 Summary statistics

The descriptive statistics for the traits analysed are presented in Table 6.1. The standard deviations for average and individual birth weights were 0.23 and 0.29, respectively. The minimum weights were, however, slightly higher for average birth weight.

Table 6.1: Summary statistics of total number of piglets born (NBT), number of live pigs born (NBA), number of piglets born dead (NBD), litter weight at birth (LBWT), average weight at birth (AVBWT) and individual birth weights (IBWT) in Mukota pigs

Variable	N	Mean	SD	Minimum	Maximum
NBT	434	8.70	1.82	4.00	13.0
NBA	434	8.17	1.68	2.00	12.0
NBD	434	0.53	0.32	0.00	4.00
LBWT (kg)	434	6.20	2.00	0.40	13.2
AVBWT (kg)	1961	0.78	0.23	0.39	1.47
IBWT (kg)	1961	0.74	0.29	0.30	1.70

N: sample size; SD: standard deviation

6.3.2 Individual weight at birth

Using the simple model that did not include maternal and common environmental litter effects, direct heritability for IBWT was 0.172 ± 0.050. The phenotypic standard deviation was 0.294. A marginal 0.2 percent reduction in the total phenotypic variance of IBWT was obtained after adjustment for NBT. Adjusted and unadjusted variances for IBWT, after including maternal and litter effects, are shown in Table 6.2. The additive genetic variance was 2.7 times larger than the maternal genetic variance. There was a significant negative correlation between direct and maternal genetic influences on IBWT. Genetic effects (both additive and maternal) accounted for 12.4 percent of the phenotypic variation. Common environmental litter effects accounted for 1.1 percent of the total phenotypic variation.

The adjustment of IBWT for NBT resulted in marginal increases in the estimates of additive and maternal genetic effects. Additive and maternal genetic influences increased by 0.1 and 2.6 percent, respectively. Adjusting IBWT for NBT, however, increased the common environmental litter effect by 17.5 percent. Table 6.3 presents the unadjusted and adjusted heritability estimates of the additive, maternal and litter effects for IBWT.

Table 6.2: Variance components due to additive (σ_a^2), maternal (σ_m^2) genetic effects, their genetic covariance (σ_{am}), common environmental litter (σ_l^2) and residual environmental (σ_e^2) effects for individual birth with and without adjustment for NBT in Mukota pigs

Component	Unadjusted	Adjusted for NBT
σ_a^2	7.659×10^{-3}	7.667×10^{-3}
σ_m^2	2.834×10^{-3}	2.909×10^{-3}
σ_{am}	-1.373×10^{-3}	-1.673×10^{-3}
σ_l^2	7.653×10^{-4}	9.277×10^{-4}
σ_e^2	7.497×10^{-2}	7.485×10^{-2}
σ_p^2	8.486×10^{-2}	8.468×10^{-2}

σ_p^2: Phenotypic variance

NBT: total number of pigs born

Table 6.3: Proportions of the variance components due to additive, maternal genetic effects, their genetic correlation between direct and maternal genetic effects (r_g) and common environmental litter effects for individual birth with and without adjustment for NBT to total phenotypic variation in Mukota pigs

	Unadjusted	Adjusted for NBT
Component	h^2 ± se	h^2 ± se
Additive	0.090 ± 0.045	0.091 ± 0.026
Maternal	0.033 ± 0.018	0.034 ± 0.009
r_g	-0.295 ± 0.052	-0.354 ± 0.016
Litter	0.009 ± 0.005	0.011 ± 0.003

h^2: heritability; se: standard error of the estimate

NBT: total number of pigs born

The correlation between direct and maternal genetic effects was negative and significantly different from zero ($P<0.05$). Adjusting IBWT for NBT increased the precision of the estimated genetic parameters since there were significant reductions in the standard errors. For example, the standard error for the correlation between direct and maternal genetic parameters dropped by 3.25 times from 0.052 to 0.016.

In all cases, adjusting IBWT for NBT increased the magnitude of the genetic parameters. Genetic effects (direct and maternal) accounted for 12.5 percent of the phenotypic variation. By using the model that accounted for maternal and common environmental effects, heritability dropped from 0.172 to 0.09. After adjusting IBWT for NBT, the correlation between direct and maternal genetic effects decreased by 17 percent. Adjustment for litter size did not influence the ratio between the residual and total phenotypic variances. Both genetic and litter variances accounted for 13.2 and 13.6 percent, with and without adjustment for NBT.

6.3.3 Sow productivity

The variances obtained using univariate analyses for the animal and permanent environmental effects on NBT, NBA, NBD and LBWT are shown in Table 6.4. The heritability for NBT, NBA and NBD was 2, 3 and 9 percent, respectively. To obtain LBWT, IBWT was aggregated for each litter and treated as a trait of the dam. The heritability for LBWT was 20 percent. The estimated permanent environmental effects for NBT, NBA and LBWT were 1, 2.4 and 3.9 percent, respectively. The permanent environmental effects on NBD were not different from zero. To generate both phenotypic

Table 6.4: Estimates of variance components and genetic parameters from univariate analyses for total number of pigs born (NBT), number of pigs born alive (NBA), number of piglets born dead (NBD) and litter weight at birth (LBWT) in Mukota sows

		Variances		
Trait	Additive (σ_a^2)	Permanent (σ_{pe}^2)	Residual (σ_e^2)	Total
NBT	7.347×10^{-2}	3.792×10^{-2}	3.573	3.684
NBA	6.175×10^{-5}	8.506×10^{-2}	3.428	3.513
NBD	6.846×10^{-2}	4.026×10^{-5}	7.125×10^{-1}	0.781
LBWT	1.030	2.059×10^{-1}	4.017	5.253
		Genetic parameters		
NBT	0.020 ± 0.015	0.010 ± 0.009	-	-
NBA	0.030 ± 0.001	0.024 ± 0.001	-	-
NBD	0.088 ± 0.002	0.000 ± 0.002	-	-
LBWT	0.196 ± 0.122	0.039 ± 0.018	-	-

and genetic covariances and correlations, multivariate analysis was used to estimate genetic parameters for LBWT, NBT, NBA and NBD. Phenotypic correlations among the four traits are depicted in Table 6.5. The correlation between NBT and NBA was high and positive. The NBA and NBD showed a significant negative phenotypic correlation. Genetic covariances are shown in Table 6.6.

The genetic correlations for the unadjusted and adjusted LBWT are presented in Table 6.7. There was a positive genetic correlation between NBT and NBA (0.870). Adjusting LBWT for NBA reduced the genetic correlation to 0.794. The genetic correlation between LBWT and NBT was 0.455, and was significantly different from zero ($P<0.05$). The correlation was, however, negative after adjusting for NBA (-0.118), although it was not significantly different from zero. The NBT and NBD were positively correlated, while NBA and NBD showed negative genetic correlations. Genetic correlation between NBA and LBWT was 0.263.

6.4 Discussion

There are few reports on the genetic determination of individual birth weight of pigs in the literature. Furthermore, the reports available give conflicting results (Roehe, 1999; Kaufmann *et al.*, 2000). The maternal heritability (0.034) was far lower than the estimates reported for Large White pigs (Roehe, 1999). Maternal genetic effects are, presumably, caused by genetically controlled components of uterine nutrition and uterine capacity. The additive genetic component, which is due to the genetic potential of the

Table 6.5: Unadjusted and adjusted phenotypic correlations of total number of pigs born (NBT), number of pigs born alive (NBA), number of piglets born dead (NBD) and litter weight at birth (LBWT) using multivariate analyses in Mukota sows

		Unadjusted		
Trait	NBT	NBA	NBD	LBWT
NBT		0.791 ± 0.013	0.276 ± 0.060	0.420 ± 0.065
NBA			-0.188 ± 0.063	0.560 ± 0.046
NBD				-0.241 ± 0.071
		Adjusted for NBA		
NBT		0.794 ± 0.013	0.279 ± 0.060	-0.025 ± 0.066
NBA			-0.188 ± 0.063	0.027 ± 0.067
NBD				-0.159 ± 0.076

Table 6.6: Adjusted and unadjusted genetic covariances of total number of pigs born (NBT), number of pigs born alive (NBA), number of piglets born dead (NBD) and litter weight at birth (LBWT) in Mukota sows

Unadjusted				
Trait	NBT	NBA	NBD	LBWT
NBT		0.080 ± 0.0324	0.051 ± 0.0318	0.269 ± 0.1215
NBA			-0.0129 ± 0.0042	0.00037 ± 0.00001
NBD				-0.2811 ± 0.1207
LBWT				
LBWT adjusted for NBA				
NBT		0.0060 ± 0.0026	0.0664 ± 0.0369	0.0255 ± 0.01005
NBA			-0.1121 ± 0.0605	0.0036 ± 0.0019
NBD				-0.0373 ± 0.01765
LBWT				

Table 6.7: Genetic correlations of total number of pigs born (NBT), number of pigs born alive (NBA), number of piglets born dead (NBD) and litter weight at birth (LBWT) using multivariate analyses in Mukota sows

		Unadjusted		
Trait	NBT	NBA	NBD	LBWT
NBT		-0.870 ± 0.013	0.697 ± 0.098	0.455 ± 0.606
NBA			0.981 ± 0.453	0.048 ± 0.041
NBD				-0.885 ± 0.233
LBWT				
		Adjusted for NBA		
NBT		0.794 ± 0.013	0.599 ± 0.099	-0.118 ± 0.119
NBA			-0.754 ± 0.344	0.263 ± 0.033
NBD				-0.892 ± 0.258
LBWT				

embryo or foetus for growth during gestation, was higher than the one reported in Kaufmann *et al*. (2000) for Large White pigs. These authors reported a direct heritability of 0.02. These findings suggest that there is reasonable variation that exists in the birth weight of Mukota pigs, reflecting the varied sub-populations from where the pigs were obtained.

The low maternal heritability observed in this study differs with previous reports (Roehe, 1999; Kaufmann *et al*., 2000). The observed low level of maternal heritability is, however, comparable to estimates for other reproductive traits, such as NBA (Roehe and Kennedy, 1995; Crump *et al*., 1997). These findings suggest that, with low litter sizes, the maternal environment is not as important in limiting foetal growth. These results could imply that, although Mukota pigs have low mature body sizes (Holness, 1972, 1991), they are as efficient as the improved breeds in maintaining successful gestation.

Common environmental litter effects were also lower than the 0.09 reported by Roehe (1999). Common environmental litter variation represents litter-specific effects, such as non-genetic components of uterine nutrition and uterus capacity and non-additive genetic effects, such as dominance. The low within-litter variation observed in this study could also be a reflection of less competition for nutrients by the embryos in the uterus, due, probably, to low litter sizes and birth weights in Mukota pigs (Ncube *et al*., 2003). than is found in other breeds, such as the Large White and Landrace (Mungate *et al*., 1999).

Although Roehe (1999) reported that adjustment of IBWT for NBT reduced additive and maternal genetic variances, our findings showed an increase in these estimates. In the same study, the common environmental litter effects were significantly influenced by the adjustment. The finding that adjustments for NBT had marginal influences on the variance components suggest that number of pigs in the litter had no substantial influence on the ability of the embryos or foetuses to grow. Though likely, it is not clear whether Mukota sows are able to comfortably carry litter sizes larger than was observed in this study, especially so under the relatively low energy diets they were fed on. Pigs in this study were fed on diets that contained 25 percent maize cob meal, to mimic the low energy density of diets encountered in smallholder production environments.

Total genetic effects for birth weight (summation of additive and maternal genetic effects) for Mukota pigs in this study accounted for 12.4 percent of the total phenotypic variation, which is less than half the genetic effects reported by Roehe (1999). Moreover, Kaufmann and co-workers (2000) reported a total genetic effect of 0.22. The total genetic effects were lower than the direct heritability of 17 percent obtained from the simple model. These findings indicate the role of the statistical model in influencing the genetic parameter estimates. In a study to identify appropriate models to use in pig data sets, Satoh and co-workers (2002) concluded that the largest biased estimates of additive genetic variance are observed when a simple model including only the additive genetic effects is fitted. Using a simpler model may be appropriate only in the absence of maternal and common litter effects or when their effects are negligible. The practical consequence is that it results in lower genetic gain than expected. The direct heritability using the simple model in this study, however, compares well with estimates obtained for average birth weight (Hermesch *et al*., 2000; Kerr and Cameron, 1995).

The negative genetic correlation between direct and maternal genetic effects for IBWT suggests an antagonistic association between direct and maternal genetic influence on growth. This is in agreement with Roehe (1999), but contradicts with Kaufmann and co-workers (2000) who reported a positive genetic correlation between direct and maternal effects. Roehe (1999) observed an increase in the genetic correlation from –0.41 to –0.22 by adjusting for NBT. In our study, however, adjusting IBWT for NBT further reduced the genetic correlation from –0.295 to –0.354. The explanation for the negative genetic correlation is not clear, although it can be due to different management factors (Van Vleck *et al*., 1996). It could, therefore, be possible that the genetic correlation reflects the different environmental conditions from where the base generation pigs originated. Unlike in Roehe (1999), adjusting IBWT for NBT further reduced the genetic correlation, ruling out the hypothesis that the main antagonism is related to environmental competition for limited resources within the uterus, as suggested by Christenson and co-workers (1987). Our findings suggest that litter size at birth did not reflect the competitive condition within the uterine environment.

The influence of the correlation between direct and maternal genetic effects can be a matter of concern in estimating breeding values. A negative correlation can result if an animal has a high direct estimated breeding value based on its own record. This could have been the case in our study. Schaeffer (2003), however, warns that a strongly negative correlation between direct and maternal effects could be due to few of the animals having progeny too, reflecting the assumed correlation amongst true breeding values.

The heritability for NBT obtained in this study was lower than those reported in literature (Haley *et al*., 1988; Hermesch *et al*., 2000). Heritability estimates for NBA were also smaller than those reported by Chen and co-workers (2003). Kaufmann and co-workers (2000) reported a heritability of 0.22 for litter size. The low heritability reported in our study probably reflects the large differences in the genetic pool of the breeding sows, rather than differences in the environmental management conditions, since they were reared in the same herd. The heritabilities for NBT and NBA agree with Holl and Robinson (2003) and Haley and Lee (1992) obtained using DFREML. Permanent environmental effects were lower than those estimated by Chen and co-workers (2003).

The heritability of 0.196 for LBWT obtained using multivariate analyses agrees with Hermesch *et al*. (2000) and Serenius *et al*. (2003). These authors established that the weight of pigs at birth for first and later parities should be considered as different traits. Parity effects for LBWT were not determined for this study, due to the relatively small sample size. The heritability for LBWT was thus far much higher than the maternal heritability of IBWT of 0.034, which shows the great difference between a complex trait and one of its components (Roehe, 1999). The maternal heritability of IBWT and the heritability of LBWT are both estimates for the maternal genetic potential of the sow. The expectation should thus be of a similarity of maternal heritability of IBW and heritability of LBWT. Our findings indicate that the aggregation of IBWT per litter to obtain LBWT reduced the residual variance in comparison to its additive genetic variance. This, consequently, increased the heritability for LBWT. In circumstances that aggregation of IBWT inflates the residual variances, adjustment of LBWT for NBA is extremely necessary. After adjusting for NBA, Roehe (1999) obtained an increase in heritability of LBWT from 0.08 to 0.43. Our findings tend to suggest that the differences in genetic make-up of Mukota pigs within a litter are smaller than is for other breeds, for example, the crossbred pigs used in the study of Roehe (1999).

The use of the direct maternal genetic effects model is the most accurate way for genetic determination for IBWT. The model allows for the pre-selection of pigs according to their direct genetic potential for growth, as well as their future maternal genetic ability to provide improved uterine conditions for growth of embryos or foetuses. In fact, the additional cost for determining individual pig weights is marginal, considering the care put in preparing sows for farrowing house. Most pig producers even record aggregate litter weights that it takes a little more effort to weigh the pigs individually.

For improvement of litter weight of pigs, the aggregate litter weights and average birth weights are of high interest under practical conditions. This is so not only because of the lower recording cost than individual birth weight, but for Mukota pigs also because LBWT showed higher heritability than individual birth weight. Variation in litter size is the major contributor to inflation of residual variances and, as such, adjusting for NBA is necessary to increase the accuracy and precision of heritability estimates. It is likely that the high heritability of LBWT compared to maternal heritability of IBWT is a function of the number of pigs in the litter, which increased the genetic variance as compared to residual variance. The high heritability for LBW than maternal heritability was, therefore, likely due to genetic covariance between full sibs and not due to genetic determination *per se*. The same disproportional change in variances is also expected for other derivatives of litter weight, such as average birth weight.

Developing an effective selection programme for litter size and birth weight requires the information about genetic association with the other traits in the breeding goal. The positive genetic correlation between LBWT and NBA agrees with Siewerdt and co-workers (1995), indicating that competition for nutrients and uterine capacity is not the major limiting factor in Mukota sow productivity. Our inference could be that there is room to increase litter size in Mukota pigs. In Zimbabwe's smallholder pig production, for example, litter size is not as economically important as litter vigour and ability to survive to weaning (Mashatise, 2002). Our finding also suggests that even piglets or foetuses with lower birth weight than average, do not unnecessarily have a high chance to die as widely reported (Hermesch *et al*., 2000; Milligan *et al*., 2002). In such scenarios, a negative relationship between NBA and LBWT is obtained. Fostering, which tends to produce negative genetic correlation between NBA and LBWT (Fraser, 1990), was not practised. The lack of genetic relationship between LBWT and NBT contradicts Hermesch and co-workers (2000) and Roehe (1999). These findings indicate that in the Mukota pig population used, no significant genetic antagonism exist between litter size and birth weight. Antagonisms are usually a result of the interaction among genetic components of ovulation rate, uterine capacity and uterine nutrition. These findings could be linked to the relatively low birth weights of Mukota pigs (mean = 0.74 kg) in comparison to 1.3 to 1.5 kg in Large White pigs.

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Chapter 7: Genetic Determination of Individual Pig Traits and their Association with Sow Performance Traits from Birth to Weaning in Mukota Pigs

Abstract

The objective of this study was to determine genetic parameters of individual and sow records on weights at 21 and 35 days in Mukota pigs. Data from 2467 pigs gathered from at the University of Zimbabwe Farm between January 1998 and August 2003 were used in this study. Individual pig traits analysed were the weight at 21 days of age (THRWT), weight at weaning (WWT) and average daily gain from birth to weaning (ADGWW). Sow performance traits considered were the litter weight after 21 days (LTHRWT), litter weight at weaning (LWWT), number of pigs weaned (NW) and mothering ability (MA). An animal model was used to estimate genetic parameters using the average information restricted maximum likelihood procedure. Individual pig records were analysed using models with or without litter effects and maternal genetic effects.

Incorporating the maternal genetic variance component drastically reduced the standard errors of the heritability estimates. The heritabilities for LTHRWT, LWWT, NW and MA were 0.18, 0.15, 0.00 and 0.05, respectively. The LWWT and NW were positively correlated. There were no genetic relationships between MA and LTHRWT and LWWT. No antagonisms should be expected when selecting for MA and increasing litter weights in Mukota pigs.

7.1 Introduction

A successful genetic improvement programme requires accurate genetic parameter estimates. Because recording weights is time intensive and costly, many breeding programmes focus on the litter size (at birth, after 21 days and at weaning), with the aim of increasing number of pigs weaned per sow per year (Chen *et al*., 2003). There is need to determine the genetic contribution of weight traits before weaning as they are negatively related to age at slaughter (Whittemore, 1993). For most commercial producers, litter size at weaning is crucial, since mortalities beyond weaning are negligible. Litter performance at weaning is also regarded as a trait of the sow. Under smallholder production systems, however, farmers do not place much importance on body weight, but survival. Survivability could be a factor of the nursing sow or the pig itself. Determining not only the magnitudes of the components, but also their relationships, therefore, becomes critical.

Apart from weaning, another critical stage in the growth of a pig is the performance at 21 days of age. This is the stage when a pig starts to develop active immunity against the diseases in its production environment (Whittemore, 1993). As such, performance at this stage has a huge bearing on the performance of the pig at weaning, and even during the post-weaning phase. High performance at 21 days reflects the ability of a pig to compete well during suckling. Performance at 21 days indicates the ability of the pig to consume dry feeds, apart from the mother's milk (Chen *et al*., 2003). Effective breeding programmes should also focus on genetic and phenotypic correlations that exist between or among traits (Hahenberg *et al*., 2001). Undesirable correlated responses in other litter traits, such as mortality, decreases the overall effectiveness of selection on litter size (Johnson *et al*., 1999; Hermesch *et al*., 2000). Furthermore, most smallholder farmers have no capacity to determine body weights for livestock, due to unavailability of weighing scales. It is important, therefore, to determine whether genetic relationships exist between weights and litter size in Mukota pigs. Genetic parameters for these traits are not available for Mukota pigs, making it difficult to conserve or genetically improve them. Specifically, the role of the maternal genetic effects in influencing these traits should be determined for accurate estimation of breeding values. The objectives of this study were, therefore, to:

1. Estimate the direct and maternal genetic effects for weight of pigs at 21 days, 35 days and growth rate from birth to weaning, and
2. Determine the genetic parameters for cumulative litter traits and mothering ability in Mukota sows

7.2 Materials and Methods

7.2.1 Study site

The site of the study is described in Section 3.2.1.

7.2.2 Animal management

The management of the pigs is as described in Sections 3.2.2 and 3.2.3. Weaning of pigs was practised by separating the sows from their piglets after 35 days of nursing.

7.2.3 Data preparation and traits analysed

Records of 2467 pigs, farrowed between January 1998 and August 2003, were used. A total of 506 records were omitted, therefore, a total of 1961 records were analysed. Weaning was done at 35 days of age (with a standard deviation of 2 days). Individual pig traits analysed in this study were the weight at 21 days of age (THRWT), weight at weaning (WWT) and average daily gain from birth to weaning (ADGWW). Sow performance traits considered were the litter weight after 21 days (LTHRWT), litter weight at weaning (LWWT), number of pigs weaned (NW) and mothering ability (MA). The weight traits (LTHRWT and LWWT), were cumulative, and were obtained by aggregating the weights for each individual pig in each litter. In this study, MA was defined as:

$MA = \frac{NBA - NW}{NBA}$, where; NBA is the number of pigs born alive and NW is the number of pigs weaned per litter.

7.2.4 Statistical analyses

7.2.4.1 Individual pig traits

The average information restricted maximum likelihood (AIREML) algorithm (Gilmour *et al*., 1995) was used to generate (co) variance components. An animal model was used to estimate the genetic parameters. For the individual pig traits (THRWT, WWT and ADGWW), three models were used to estimate the variance components. Model 1 contained the direct animal genetic effects only while Model 2 contained both the direct genetic and the common environmental litter effects. Model 3 contained the maternal genetic effect, in addition to the other two random components. In matrix form, the models are presented as:

Model 1: $\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{u}_a + e$;

Model 2: $\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{u}_a + \mathbf{Z}_2\mathbf{u}_l + e$;

Model 3: $\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{u}_a + \mathbf{Z}_2\mathbf{u}_l + \mathbf{Z}_3\mathbf{u}_m + e$;

where $\mathbf{Y}$ is vector of n observations for individual birth weight, β is a vector of fixed effects and includes the year-season (four seasons per year), parity (8 parities) and sex (male and female) effects. Vectors of random effects consists of environmental effects $\mathbf{u}_l \sim N_{q1}(\mathbf{0}, \mathbf{I}\sigma_l^2)$ common to all pigs within each of q_l litters, direct $\mathbf{u}_a$ as well as maternal genetic effects $\mathbf{u}_m$ of q_2 pigs, and residual environmental effects $e \sim N_n(\mathbf{0}, \mathbf{I}\sigma_e^2)$, peculiar to each pig.

The variance-covariance structure for Model 1 is assumed to be:

$$v\begin{bmatrix} u_a \\ u_e \end{bmatrix} = \begin{bmatrix} A\sigma_A^2 & 0 \\ 0 & I\sigma_e^2 \end{bmatrix}.$$

Model 2 assumed a variance-covariance structure of:

$$v\begin{bmatrix} u_l \\ u_a \\ u_e \end{bmatrix} = \begin{bmatrix} I\sigma_l^2 & 0 & 0 \\ 0 & A\sigma_A^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

For Model 3, all random effects were sampled from a normal distribution with a zero mean and variance-covariance structure of:

$$v\begin{bmatrix} u_l \\ u_a \\ u_m \\ u_e \end{bmatrix} = \begin{bmatrix} I\sigma_l^2 & 0 & 0 & 0 \\ 0 & A\sigma_a^2 & A\sigma_{am} & 0 \\ 0 & A\sigma_{am} & A\sigma_m^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

The implied genetic models are infinitesmal (Bulmer, 1980), where the base population is assumed to be unselected, non-inbred and unrelated.

Vectors of the direct and maternal genetic effects are assumed to be distributed as follows:

$$\begin{bmatrix} u_a \\ u_m \end{bmatrix} \sim \mathrm{N}(\mathbf{0}, \mathbf{G}_{am} \otimes \mathbf{A}), \text{ where } \mathbf{G}_{am} = \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix}$$

The **I** and **A** are the identity and numerator relationship matrices, respectively. The $\mathbf{G}_{am}$ is the genetic (co) variance matrix between the direct and maternal effects and $\otimes$ denotes the direct product of matrices. Permanent environmental effects were assumed to be uncorrelated with direct additive genetic effects. For Model 3, the incidence matrices **X** and $\mathbf{Z}_i$ (i = 1, 2, 3) link the fixed and random effects, respectively, with corresponding records in vector **Y**.

7.2.4.2 Sow or litter traits

Cumulative weights traits (LTHRWT and LWWT), NW and MA, regarded as traits of the sow nursing the pigs, were modelled as:

$\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{u}_{pe} + \mathbf{Z}_2\mathbf{u}_a + e$; where;

$\mathbf{Y}$ is vector of n observations of q_1 sows in each of the four traits and β is a vector of the fixed effects associated with each trait. The term $\mathbf{u}_{pe} \sim N_{2q1}(\mathbf{0}, \mathbf{P} \otimes \mathbf{I})$ represents the random permanent environmental (non-genetic) effects common to all litters produced by each sow, $\mathbf{u}_a$ represents the additive genetic effect of the q_1 sows distributed as $N_{3q1}(\mathbf{0}, G_a \otimes \mathbf{A}$. The residual (environmental) effects, e, is distributed as $N_{3n}(\mathbf{0}, \mathbf{R} \otimes \mathbf{I})$. Matrices $\mathbf{P}$, G_a and $\mathbf{R}$ represent the variances and covariances among traits due to permanent environmental, additive genetic and residual environmental effects, respectively.

Genetic and phenotypic covariances were estimated using a multivariate model in AIREML.

7.3 Results

7.3.1 Summary statistics

The summary statistics are shown in Table 7.1. The AVWWT tended to have a higher variation (standard deviation) than individual weight at weaning (WWT).

7.3.2 Variance components and genetic parameters for THRWT

Table 7.2 shows the variance components using the three separate models. Using models 1, 2 and 3, the heritability for THRWT was 0.121, 0.124 and 0.132, respectively. Of the three models, model 3 had the lowest residual error variance. Common environmental litter effects accounted for 0.022 of the total phenotypic variance. The genetic correlation between additive and maternal genetic effects was -0.029 and was significantly different from zero. Incorporating the maternal genetic effects reduced the standard errors substantially (Table 7.2).

Table 7.1: Summary statistics for individual weight at three weeks (THRWT), litter weight (LTHRWT) at three weeks, number of pigs weaned (NW), litter weight at weaning (LWWT), average weight at weaning (AVWWT), individual weight at weaning (WWT), body weight gain from birth to weaning (ADGWW) and mothering ability (MA) in Mukota pigs

Trait	N	Mean	SD	Minimum	Maximum
LTHRWT	434	18.66	7.20	1.30	46.70
NW	434	7.85	1.71	2.00	12.00
LWWT	434	34.64	13.71	3.00	95.00
AVWWT	434	5.86	1.68	2.74	10.96
MA	434	0.13	0.02	0.00	0.80
THRWT	1961	2.20	0.98	0.50	9.00
WWT	1961	5.05	1.26	0.90	11.00
ADGWW	1961	0.18	0.12	0.08	0.26

N: sample size; SD: standard deviation.

Table 7.2: Genetic variances, residual variances and heritabilities for weight at 21 days of age (THRWT) using models with additive genetic effects only (Model 1), additive genetic effects and litter effects (Model 2) and additive genetic effects, litter effects and maternal genetic effects (Model 3) in Mukota pigs

Trait	Model 1	Model 2	Model 3
σ_a^2	0.116	0.119	0.126
σ_{am}			-0.028
σ_m^2			0.088
σ_l^2		0.021	0.021
σ_e^2	0.840	0.817	0.693
σ_p^2	0.956	0.956	0.956
h^2	0.121 ± 0.025	0.124 ± 0.016	0.132 ± 0.005
m^2			0.092 ± 0.004
l^2		0.022 ± 0.020	0.022 ± 0.002
r_{am}			-0.029 ± 0.009

σ_a^2: genetic variance, σ_m^2 : maternal genetic variance, σ_{am}: covariance between direct and maternal genetic effects, σ_l^2: litter variance, σ_e^2: residual variance, h^2: heritability, m^2 : maternal genetic effect, r_{am}: correlation between direct and maternal effect, l^2: litter effect, σ_p^2: phenotypic variance.

7.3.3 Variance components and genetic parameters for WWT

When compared to Model 1, the additive genetic effect for WWT increased by 1.5 and 10.5 percent when using Models 2 and 3, respectively (Table 7.3). The common environmental litter effect of 0.049 was significantly larger than for THRWT ($P<0.05$). Incorporating litter and maternal genetic effects reduced the residual error substantially. The heritability estimates were 0.144, 0.14 and 0.159 for Models 1, 2 and 3, respectively. Compared to THRWT (Table 7.2), the maternal genetic effect increased significantly from birth to three weeks. The maternal genetic effect was 0.232, and was larger ($P<0.05$) than the direct additive genetic effect.

7.3.4 Variance components and genetic parameters for ADGWW

The variance components and heritability estimates for average daily body weight gain from birth to weaning is shown in Table 7.4. The variances obtained were lower than those for THRWT and WWT (Tables 7.2 and 7.3). The heritability estimates, using Models 1, 2 and 3, were 0.116, 0.142 and 0.156, respectively. As was obtained with WWT, the ADGWW exhibited a significant maternal influence, which was higher than the direct heritability (0.197 versus 0.156). Incorporating the maternal genetic variance component drastically increased the precision of the heritability estimates. The common environmental litter effects for all the traits were generally low (less than 0.05).

Table 7.3: Genetic variances, residual variances and heritabilities for weight at weaning (WWT) using models with additive genetic effects only (Model 1), additive genetic effects and litter effects (Model 2) and additive genetic effects, litter effects and maternal genetic effects (Model 3) in Mukota pigs

Trait	Model 1	Model 2	Model 3
σ_a^2	0.400	0.406	0.442
σ_{am}			-0.590
σ_m^2			0.645
σ_l^2		0.136	0.135
σ_e^2	2.372	2.230	2.140
σ_p^2	2.772	2.772	2.772
h^2	0.144 ± 0.029	0.147 ± 0.072	0.159 ± 0.004
m^2			0.232 ± 0.004
l^2		0.049 ± 0.027	0.049 ± 0.004
r_{am}			-0.524 ± 0.326

σ_a^2: genetic variance, σ_m^2 : maternal genetic variance, σ_{am}: covariance between direct and maternal genetic effects, σ_l^2: litter variance, σ_e^2: residual variance, h^2: heritability, m^2 : maternal genetic effect, r_{am}: correlation between direct and maternal effect, l^2: litter effect, σ_p^2: phenotypic variance

Table 7.4: Genetic variances, residual variances and heritabilities for average body weight gain from birth to weaning (ADGWW) using models with additive genetic effects only (Model 1), additive genetic effects and litter effects (Model 2) and additive genetic effects, litter effects and maternal genetic effects (Model 3) in Mukota pigs

Trait	Model 1	Model 2	Model 3
σ_a^2	2.552×10^{-4}	3.170×10^{-4}	3.212×10^{-4}
σ_{am}			-3.893×10^{-4}
σ_m^2			4.376×10^{-4}
σ_l^2		1.092×10^{-4}	6.672×10^{-5}
σ_e^2	1.945×10^{-3}	1.803×10^{-3}	1.789×10^{-3}
σ_p^2	2.213×10^{-3}	2.213×10^{-3}	2.213×10^{-3}
h^2	0.116 ± 0.008	0.142 ± 0.071	0.146 ± 0.005
m^2			0.197 ± 0.005
l^2		0.049 ± 0.026	0.030 ± 0.006
r_{am}			-0.351 ± 0.361

σ_a^2 : genetic variance, σ_m^2 : maternal genetic variance, σ_{am} : covariance between direct and maternal genetic effects, σ_l^2 : litter variance, σ_e^2 : residual variance, h^2 : heritability, m^2 : maternal genetic effect, r_{am} : correlation between direct and maternal effect, l^2 : litter effect, σ_p^2 : phenotypic variance.

7.3.5 Variance components and heritability estimates for litter traits

Table 7.5 shows the variance components for the litter traits in Mukota sows. The heritability estimates for NW were not different from zero. The heritabilities for LTHRWT, LWWT and MA were 0.18, 0.15 and 0.05, respectively. For LTHRWT and MA, heritability estimates were bigger than the permanent environmental effects. No statistically significant differences, however, existed between heritability and permanent non-genetic effect for LWWT. The permanent environmental effects were higher than heritability for NW.

7.3.6 Genetic and residual (co)variances and correlations for litter traits

Table 7.6 gives the genetic and residual variances and covariances for litter traits. Estimates of genetic and phenotypic correlations from a multitrait analysis are shown in Table 7.7. All the phenotypic correlations among the four traits were different from zero. Weight traits (LTHRWT and LWWT) showed a high positive correlation (0.756). As expected, LWWT and NW were also positively correlated. Mothering ability was negatively correlated to NW, LTHRWT and LWWT. The MA was positively correlated to NW. The negative correlations of MA to both LTHRWT and LWWT were not statistically different from zero (-0.103 ± 0.288; -0.211 ± 0.301, respectively).

Table 7.5: Variances and genetic parameters for litter weight after 21 days (LTHRWT), litter weight at weaning (LWWT), number of pigs weaned (NW) and mothering ability (MA) in a univariate analysis in Mukota pigs

	Trait			
Variances	LTHRWT	LWWT	NW	MA
σ_a^2	9.3	29.9	4.117×10^{-5}	4.436×10^{-4}
σ_{pe}^2	3.7	32.7	2.073×10^{-2}	1.656×10^{-4}
σ_e^2	40.1	137.6	3.283	7.942×10^{-3}
σ_p^2	53.1	200.3	3.305	8.461×10^{-3}
h^2	0.175 ± 0.119	0.149 ± 0.118	0.000 ± 0.001	0.052 ± 0.013
pe^2	0.069 ± 0.028	0.163 ± 0.028	0.006 ± 0.001	0.019 ± 0.011

σ_a^2 : genetic variance, σ_{pe}^2 : permanent environmental variance, σ_e^2 : residual variance, σ_p^2 : phenotypic variance, h^2 : heritability, pe^2 : permanent environmental effect.

Table 7.6: Genetic and residual variances (on diagonal) and covariances (on off-diagonal) for litter weight after 21 days (LTHRWT), litter weight at weaning (LWWT), number of pigs weaned (NW) and mothering ability (MA) using multivariate analysis in Mukota pigs

	LTHRWT	LWWT	NW	MA
Genetic (co)variances				
LTHRWT	13.9 ± 5.90	18.2 ± 8.47	0.78 ± 1.017	-0.014 ± 0.0408
LWWT		55.1 ± 19.01	2.02 ± 2.019	-0.056 ± 0.0860
NW			0.18 ± 0.200	0.009 ± 0.0071
MA				0.001 ± 0.0008
Residual (co)variances				
LTHRWT	39.0 ± 5.58	58.5 ± 8.68	6.35 ± 1.168	-0.115 ± 0.0476
LWWT		139.6 ± 18.59	10.38 ± 2.262	-0.274 ± 0.0952
NW			3.16 ± 0.3341	-0.067 ± 0.0122
MA				0.007 ± 0.0009

Table 7.7: Phenotypic and genetic correlations [a] for litter weight after 21 days (LTHRWT), litter weight at weaning (LWWT), number of pigs weaned (NW) and mothering ability (MA) using multivariate analysis in Mukota pigs

	Phenotypic correlations			
	LTHRWT	LWWT	NW	MA
LTHRWT	-	0.76 ± 0.029	0.54 ± 0.047	-0.19 ± 0.063
LWWT		-	0.49 ± 0.050	-0.26 ± 0.062
NW			-	-0.34 ± 0.058

	Genotypic correlations			
	LTHRWT	LWWT	NW	MA
LTHRWT	0.18 ± 0.119	0.66 ± 0.123	0.49 ± 0.459	-0.10 ± 0.288
LWWT		0.15 ± 0.118	0.63 ± 0.423	-0.21 ± 0.301
NW			0.00 ± 0.001	0.62 ± 0.538
				0.05 ± 0.013

[a] Values on the diagonals under genetic correlations are the heritability estimates.

7.4 Discussion

Few reports exist on individual animal weight measurements before weaning, which is largely caused by the high cost and labour involved. Interpreting differences in variance components from literature is difficult because these estimates depend on the population and the data collected. The estimates obtained in this study, however, tend to be smaller than those reported in literature (Crump *et al*., 1997; Kaufmann *et al*., 2000). Estimates of animal additive genetic variances for LTHRWT are in agreement with the values reported by Ferraz and Johnson (1993) and Chen *et al*. (2003). This study confirms that using a simplified model (Model 1) tends to underestimate the heritability of a trait, as some non-additive and common environmental litter effects inflate the residual error variance. Maternal and litter influences should, therefore, be accounted for in estimating heritabilities in pigs. The observation that the THRWT had lower heritability than WWT suggests that more genetic gain can be attained by selecting for WWT.

More importantly, the maternal genetic influence in this study tended to increase as the pig grew. In fact, the maternal genetic effect for WWT was higher than the additive direct animal effect. These findings suggest that Mukota pigs possess superior genetically controlled effects on milk production and caring for their piglets. Kaufmann *et al*. (2000), however, reported a decrease in maternal genetic influence from birth to weaning in Large White pigs. The Mukota sows in this study were managed in a conventional commercial pig setting (brick housing with concrete floors under asbestos roofs), conditions which are not commonly used under smallholder farming conditions. It is, therefore, important that the maternal influence is genetically controlled, which makes them suitable for smallholder production, where the maternal influence plays a bigger role than in large-scale commercial pig production. In herds where the maternal influence is substantial, accounting for these random factors has also been shown to increase the precision and most likely accuracy, of heritability estimates (Chen *et al.*, 2003). It is, therefore, crucial to account for these maternal genetic effects in designing Mukota pig improvement programmes, as these effects are not transmitted to the next generation (i.e. are not additive).

Individual animal records and cumulative traits have been shown to produce different genetic parameter estimates (Roehe, 1999). Since LTHRWT and LWWT are traits of the sow, the heritabilities of these traits, should, intuitively, be similar to the maternal genetic effects of the respective THRWT and WWT. The patterns obtained in this study were conflicting; the heritability for LTHRWT (0.18) being higher than the maternal genetic effect for THRWT (0.05) and the heritability of LWWT (0.15) being smaller than the maternal genetic effect for WWT (0.232). These findings indicate that the use of individual animal records is more reliable in estimating genetic parameters than using cumulative traits (Roehe, 1999), especially in small populations, as was in this case. The estimates for individual animals were far more precise (low standard errors) than for litter traits. In large populations, there might be a need to include other variables in the models, such as maternal and service sire effects to increase precision and accuracy (Chen *et al.*, 2003). The negative correlations between direct additive and maternal genetic effects agree with previous reports (Haley and Lee, 1992; Crump *et al.*, 1997; Chen *et al.*, 2003).

Permanent environmental effects are significant in litter traits (Crump *et al*., 1997). These are non-genetic effects that influence all the pigs produced by the same sow. The estimates of the permanent environmental effects for LTHRWT are similar to those obtained by Chen *et al*. (2003). Literature values for permanent environmental effects for WWT are scarce. However, the observation that the permanent environmental effects were higher than the additive genetic effects signifies the crucial role played by environmental factors, such as housing, in Mukota pigs.

Mukota pigs have traditionally been reported to possess superior mothering ability as compared to breeds exotic to the tropical and smallholder production conditions (Holness, 1991). Mothering ability, however, is a trait that is difficult to define, as it has received little attention in pig improvement programmes. In intensive production systems, there are facilities and equipment, such as farrowing crates that reduce the importance of mothering ability in a sow. In this study, as is the case in smallholder production systems, mothering ability relates to the number of pigs that survive to weaning. It is, thus a combination of real mothering ability and piglet survival. The heritability for mothering ability was higher than values reported in Dutch Landrace pigs (Hahenberg *et al*., 2001). The heritability for MA in this study is likely to differ substantially with estimates obtained from typical smallholder production environments. The finding that its heritability is comparable or even higher than reproductive traits indicates that MA should be incorporated in pig improvement programmes for Mukota pigs.

The positive correlation between NW and weight traits (LTHRWT and LWWT) was expected and is desirable. Both phenotypic and genotypic correlations in these traits were positive, suggesting that there is scope in using phenotypic correlation in smallholder areas, where pedigree records are largely unavailable. The negative genetic relationships between MA and the other traits were not different from zero, suggesting that the significant negative phenotypic correlation between MA and weight traits (LTHRWT and LWWT) is largely environmental. No antagonisms, therefore, exists when selecting for MA and increasing litter weights in Mukota pigs. The difference in the directions of the phenotypic and genetic correlation between MA and NW is, however, difficult to interpret.

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Chapter 8: Estimation of genetic parameters for growth performance and carcass traits in Mukota pigs

Abstract

The objective of the study was to determine genetic parameters for growth and carcass traits in Mukota pigs, maintained on a fibrous diet, using average information restricted maximum likelihood. Records (n = 1961) were obtained from a satellite population kept at the University of Zimbabwe Farm between January 1998 and August 2003. Backfat thickness was measured at 50 and 75 mm (K5 and K7.5), respectively. Variance components were estimated using Model 1 that had direct and residual random effects, Model 2 (direct, litter and residual effects) and Model 3 (with direct, litter and maternal genetic effects). The heritability for the average daily gain from weaning to 12 weeks (ADG1) was 0.27 using Model 3. The heritability for maternal genetic effects was 0.026 ± 0.003. The heritability for average daily gain from 12 weeks to slaughter (ADG2) were lower than for ADG1 ($P<0.05$). Common environmental litter effects accounted for 18 percent for cold dressed mass (CDM). The heritability estimates were 0.25, 0.23 and 0.32 for Models 1, 2 and 3, respectively. The heritability estimates for carcass length (CL) was 0.165, 0.343 and 0.621 for Models 1, 2 and 3, respectively. Maternal effects accounted for 10.5 percent of the variance in CL. The heritability estimates for K5 and K7.5 were 0.64 and 0.40, respectively. The CDM was positively correlated to K5, but negative to K7.5. The K5 and K7.5 were highly correlated (r_g = 0.88).

8.1 Introduction

One sustainable way to conserve a breed at risk is to develop niche markets for the products (Anderson, 2003). Meat from Mukota pigs has been described as tastier and is organoleptically more acceptable to the rural people than meat from European breeds (Ndiweni and Dzama, 1995). One possible reason could be the low amount of intramuscular fat in Mukota pig meat. Intramuscular fat is only important for flavour and to aid slow dehydration during curing. For the local market, however, the weight of the carcass is the trait of importance. Fat deposition in Mukota is largely subcutaneous (Holness, 1991; Kanengoni *et al*., 2004) and can easily be trimmed off and used as lard for cooking purposes. It is, therefore, essential to evaluate the genetic determination of these traits to develop selection indices that reduce or avoid the loss of sweetness and to predict genetic responses to selection and pig improvement programmes.

Estimation of genetic correlations is necessary for genetic evaluation procedures, determination of optimum selection indices or in modelling breeding schemes. It is important to determine relationships among traits to develop a sound genetic improvement programme for Mukota pigs. Genetic correlations are often difficult (require large sample sizes of individuals of known relatedness) or impossible (rare, endangered or extinct species) to obtain. On the contrary, phenotypic correlations are easily and accurately estimated requiring only moderately small sample sizes and no knowledge of relatedness among animals (Kominakis, 2003). Phenotypic correlations are more useful in smallholder areas where numerator relationship matrices are difficult, if ever possible, to construct. There is, therefore a need to determine both genetic and phenotypic correlations for carcass traits in Mukota pigs. The objective of the study was, therefore, to determine genetic parameters for growth and carcass traits in Mukota pigs and to determine appropriate models for estimating such parameters.

8.2 Materials and Methods

8.2.1 Study site

The study site is described in Section 3.2.1.

8.2.2 Animal management

The management of the breeding and growing pigs are described in Section 3.2.3.

8.2.3 Traits

Data from Mukota pigs farrowed between January 1998 and August 2003 were used. Pigs with missing records were deleted. A total of 506 records were deleted and, therefore not used in the genetic analyses. A total of 1961 records were used in the analyses. Weight related traits analysed in this study were the average daily gain from weaning to 12 weeks (ADG1), average daily gain from 12 weeks to slaughter (ADG2) and the weight of the dressed carcass after chilling at 4°C for 24 hours (CDM). Thickness of backfat was also recorded at three points along the last rib (50 and 75 mm), and denoted as K5 and K7.5, respectively. The length of the carcass (CL) was also analysed.

8.2.4 Statistical analyses

Variance-covariance components were estimated using AIREML (Gilmour *et al.*, 1995) for an animal model. Three models were used to estimate the variance components. Model 1 contained the direct animal genetic effects only while Model 2 contained both the direct genetic and the common environmental litter effects. Model 3 contained three random effects, direct animal, litter and the maternal genetic effects. In matrix form, the models are presented as:

Model 1: $\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{u}_a + e$;

Model 2: $\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{u}_a + \mathbf{Z}_2\mathbf{u}_l + e$;

Model 3: $\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{u}_a + \mathbf{Z}_2\mathbf{u}_l + \mathbf{Z}_3\mathbf{u}_m + e$;

where $\mathbf{Y}$ is vector of n observations for individual birth weight, β is a vector of fixed effects and includes the year-season (four seasons per year), parity (8 parities) and sex (male and female) effects. Vectors of random effects consists of environmental effects $\mathbf{u}_l \sim N_{q1}(\mathbf{0}, \mathbf{I}\sigma_l^2)$ common to all pigs within each of q_l litters, direct $\mathbf{u}_a$ as well as maternal genetic effects $\mathbf{u}_m$ of q_2 pigs, and residual environmental effects $e \sim N_n(\mathbf{0}, \mathbf{I}\sigma_e^2)$, peculiar to each pig.

The variance-covariance structure for Model 1 is assumed to be:

$$v\begin{bmatrix} u_a \\ u_e \end{bmatrix} = \begin{bmatrix} A\sigma_A^2 & 0 \\ 0 & I\sigma_e^2 \end{bmatrix}.$$

Model 2 assumed a variance-covariance structure of:

$$v\begin{bmatrix} u_l \\ u_a \\ u_e \end{bmatrix} = \begin{bmatrix} I\sigma_l^2 & 0 & 0 \\ 0 & A\sigma_A^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

For Model 3, all random effects were sampled from a normal distribution with a zero mean and variance-covariance structure of:

$$v\begin{bmatrix} u_l \\ u_a \\ u_m \\ u_e \end{bmatrix} = \begin{bmatrix} I\sigma_l^2 & 0 & 0 & 0 \\ 0 & A\sigma_a^2 & A\sigma_{am} & 0 \\ 0 & A\sigma_{am} & A\sigma_m^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

The implied genetic models are infitesimal (Bulmer, 1980), where the base population is assumed to be unselected, non-inbred and unrelated. Vectors of the direct and maternal genetic effects are assumed to be distributed as:

$$\begin{bmatrix} u_a \\ u_m \end{bmatrix} \sim N(\mathbf{0}, \mathbf{G}_{am} \otimes \mathbf{A}), \text{ where } \mathbf{G}_{am} = \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix}$$

The **I** and **A** are the identity and numerator relationship matrices, respectively. The $\mathbf{G}_{am}$ is the genetic (co) variance matrix between the direct and maternal effects and ⊗ denotes the direct product of matrices. Permanent environmental effects were assumed to be uncorrelated with direct additive genetic effects. For Model 3, the incidence matrices **X** and $\mathbf{Z}_i$ (i = 1, 2, 3) link the fixed and random effects, respectively, with corresponding records in vector **Y**. Genetic and phenotypic correlations were estimated using a multitrait model.

8.3 Results

8.3.1 Summary statistics and levels of significance for the fixed factors

Table 8.1 shows the summary statistics for the post-weaning growth performance and carcass traits of Mukota pigs. The levels of significance for the fixed factors are shown in Table 8.2. Sex of pig affected ($P<0.05$) ADG2, but not ADG1 ($P>0.05$). The weight at weaning, incorporated as a covariate, significantly affected ($P<0.05$) both ADG1 and ADG2. There was a significant interaction ($P<0.05$) between genotype and month on backfat thickness.

8.3.2 Variance components and genetic parameters for growth performance (ADG1 and ADG2)

Table 8.3 depicts the variance components and genetic parameter estimates for ADG1 and ADG2. The direct heritabilities for ADG1 were 0.25, 0.23 and 0.27 using Models 1, 2 and 3, respectively. Litter effects accounted for only 3.3 percent of the phenotypic variance. Residual error variances were 0.069, 0.068 and 0.068, respectively. Maternal genetic effects were 0.026 ± 0.003. The genetic correlation between direct and maternal genetic effects was -0.417 ± 0.071 and was significantly different from zero.

As shown in Table 8.3, the litter effect for ADG2 was low. The residual error variances were 0.074, 0.075 and 0.071 for Models 1, 2 and 3, respectively. The direct heritability for the respective models was 0.21, 0.19 and 0.20. Maternal genetic effects (Model 3) accounted for 3.1 percent of the phenotypic variance. As for ADG1, there was a negative correlation between direct and maternal genetic effects.

Table 8.1: Summary statistics for the average daily gain from weaning to 12 weeks (ADG1), average daily gain from 12 weeks to slaughter (ADG2), cold dressed mass after (CDM), thickness of backfat at 50 (K5) and 75 (K7.5) positions and carcass length (CL) in Mukota pigs

Trait	N	Mean	SD	Minimum	Maximum
ADG1 (kg)	1961	0.3	0.09	0.11	0.54
ADG2 (kg)	1961	0.4	0.16	0.15	0.59
CDM (kg)	1961	21.8	4.23	12.12	37.86
K5 (mm)	1961	11.4	1.69	6.00	20.40
K7.5 (mm)	1961	14.9	1.79	6.00	23.00
CL (mm)	1961	508.1	43.28	402.00	621.00

N: sample size; SD: standard deviation.

Table 8.2: Significant levels of the factors and covariates included in the analyses

	Main effects			Interactions			Covariates	
Trait	G	M	S	G × S	G × M	G × S × M	β_1	β_2
ADG1 (kg/day)	*		*	*	**	*	*	
ADG2 (kg/day)	**	**		*	**	*		
CDM (kg)	**	**		*	*	*		*
CL (mm)	***			*				
K5 (mm)	*		*	*	**			
K7.5 (mm)	**		*	*	*			

Abbreviations: ADG1: average daily gain before 12 weeks of age, ADG2: average daily gain after 12 weeks of age, CDM: cold dressed mass, CL: carcass length, K5: backfat at 50 mm from the midline along the last rib, K7.5: backfat thickness at 75 mm.

G: breed of sire, M: sex of pig, S: month of slaughter, β_1: weight at weaning, β_2: weight at slaughter.

*$P<0.05$, **$P<0.01$ ***$P<0.001$

Table 8.3: Variance components and heritabilities for ADG1 and ADG2, in Mukota pigs, using Models 1, 2 and 3

	ADG1 (kg/day)			ADG2 (kg/day)		
Component	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
σ_a^2	0.023	0.021	0.025	0.020	0.018	0.019
σ_{am}			-0.008			-0.008
σ_m^2			0.002			0.003
σ_l^2		0.003	0.003		0.001	0.003
σ_e^2	0.069	0.068	0.068	0.074	0.075	0.071
σ_p^2	0.092	0.092	0.092	0.094	0.094	0.094
h^2	0.25	0.23	0.271	0.21	0.19	0.20
m^2			0.026			0.031
l^2		0.033	0.033		0.011	0.032
r_g			-0.417			-0.499
se for m^2			0.003			0.001
se for l^2		0.015	0.003		0.014	0.001
se for r_g			0.071			0.026
se for h^2	0.033	0.031	0.003	0.036	0.042	0.001

Additive (σ_a^2), maternal (σ_m^2), covariance between direct and maternal (σ_{am}), litter (σ_l^2), residual (σ_e^2) and (σ_p^2) variances. h^2: heritability, m^2 : maternal effect, r_g: correlation between direct and maternal effect, l^2: litter effect, ADG1: average daily gain from weaning to 12 weeks, ADG2: average daily gain from 12 weeks to slaughter. Model 1 contained additive genetic effects only, Model 2 contained additive and litter effects while Model 3 had additive, litter and maternal genetic effects; se: standard error.

8.3.3 Variance components and genetic parameters for cold dressed mass and carcass length

The additive genetic variances for CDM were 4.492, 4.175 and 5.722 for Models 1, 2 and 3, respectively (Table 8.4). Common environmental litter effects accounted for 14 and 18 percent with Models 2 and 3, respectively. There was a 17 percent reduction in residual error variance from using the simple model to the one that incorporated direct, litter and maternal genetic effects. The heritability estimates were 0.249, 0.231 and 0.317 for Models 1, 2 and 3, respectively. Maternal genetic effects were 2.7 percent, and there was a negative correlation between direct and maternal genetic effects (r_g = -0.281).

The heritability estimates for CL were 0.165, 0.343 and 0.621 for Models 1, 2 and 3, respectively. The additive genetic variance increased four-fold after incorporating maternal genetic effects (Table 8.4). The error variance was 16.6, 19.9 and 9.6 for Models 1, 2 and 3, respectively. Litter effects were only four percent of the phenotypic variance. The maternal genetic influence accounted for 10.5 percent of the variance. In addition, there was a negative genetic correlation between direct and maternal effects (r_g = -0.482).

Table 8.4: Variance components and heritabilities for CDM and CL, in Mukota pigs, using Model 1, 2 and 3

	CDM			CL		
Component	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
σ_a^2	4.492	4.175	5.722	3.273	6.638	12.164
σ_{am}			-2.039			-4.995
σ_m^2			0.485			2.053
σ_l^2		2.484	3.199		0.7816	0.794
σ_e^2	13.541	11.341	11.25	16.623	11.905	9.569
σ_p^2	18.037	18.037	18.039	19.892	19.325	19.581
h^2	0.249	0.231	0.317	0.165	0.343	0.621
m^2			0.027			0.105
l^2		0.138	0.177		0.040	0.041
r_g			-0.281			-0.482
se for m^2			0.002			0.001
se for l^2		0.015	0.002		0.017	0.001
se for r_g			0.047			0.009
se for h^2	0.033	0.041	0.002	0.051	0.030	0.001

Additive (σ_a^2), maternal (σ_m^2), covariance between direct and maternal (σ_{am}), litter (σ_l^2), residual (σ_e^2) and (σ_p^2) variances. h^2: heritability, m^2 : maternal effect, r_g: correlation between direct and maternal effect, l^2: litter effect. Model 1 contained additive genetic effects only, Model 2 contained additive and litter effects while Model 3 had additive, litter and maternal genetic effects. CDM: cold dressed mass, CL: carcass length; se: standard error.

8.3.4 Variance components and genetic parameters for backfat thickness

Table 8.5 shows the variance components and genetic parameter estimates for backfat thickness in growing Mukota pigs. Common environmental litter effects were marginal for both K5 and K7.5 measurements. The residual error variance components were 1.69, 1.06 and 1.04 for Models 1, 2 and 3, respectively. The respective heritability estimates for K5 were 0.407, 0.622 and 0.635. The maternal influence was 12.3 percent. The additive genetic variance components for K7.5 were 1.0, 1.3 and 1.5, respectively using Models 1, 2 and 3, respectively. As shown in Table 8.5, the heritability estimates were 0.279, 0.344 and 0.404 for the three respective models.

8.3.5 Genetic and phenotypic correlations

Table 8.6 shows the genetic covariances among the post-weaning growth performance and carcass traits. The genetic and phenotypic correlations are shown in Table 8.7. The correlation between ADG1 versus K5 and K7.5 were negative, but weak. The ADG2 was also negatively correlated with both K5 and K7.5 (r_g = -0.29 and –0.34, respectively). Both growth traits were positively correlated with CL (Table 8.7). The CDM had a positive genetic correlation with K5 backfat measurement. The genetic correlation between CDM and K7.5 was, however, negative. Phenotypic correlations between CDM and backfat traits were all positive. The CDM and CL showed positive genetic correlations. The genetic correlations between CL and backfat measurements were positive. The K5 and K7.5 were highly correlated (r_g = 0.88; Table 8.6). All the phenotypic correlations among carcass traits were positive, except CDM and CL, which were not correlated.

Table 8.5: Variance components and heritabilities for backfat thickness (K5 and K7.5) using Model 1, 2 and 3

	K5			K7.5		
Component	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
σ_a^2	1.160	1.744	1.819	1.006	1.254	1.495
σ_{am}			-0.800			-0.452
σ_m^2			0.352			0.631
σ_l^2		0.001	0.002		0.001	0.001
σ_e^2	1.689	1.058	1.044	2.598	2.390	2.201
σ_p^2	2.849	2.802	2.863	3.604	3.644	3.696
h^2	0.407	0.622	0.635	0.279	0.344	0.404
m^2			0.123			0.171
l^2		0.000	0.001		0.000	0.000
r_g			-0.311			-0.245
se for m^2			0.001			0.001
se for l^2		0.002	0.001		0.001	0.001
se for r_g			0.007			0.005
se for h^2	0.025	0.002	0.001	0.034	0.001	0.001

Additive (σ_a^2), maternal (σ_m^2), covariance between direct and maternal (σ_{am}), litter (σ_l^2), residual (σ_e^2) and (σ_p^2) variances. h^2: heritability, m^2 : maternal effect, r_g: correlation between direct and maternal effect, l^2: litter effect. Model 1 contained additive genetic effects only, Model 2 contained additive and litter effects while Model 3 had additive, litter and maternal genetic effects. K5 and K7.5 are thicknesses of backfat at 50 and 75 mm from the midline, respectively; se: standard error.

Table 8.6: Genetic covariances among post-weaning growth performance and carcass traits from a multitrait analysis

	ADG1	ADG2	CDM	K5	K7.5	CL
ADG1		0.0102	0.1528	-0.0123	-0.0249	0.1459
ADG2			0.2144	0.0160	0.0258	0.1175
CDM				-0.8541	-0.3682	0.8914
K5					0.1887	0.3034
K7.5						0.4142

Abbreviations: ADG1: average daily gain before 12 weeks of age, ADG2: average daily gain after 12 weeks of age, CDM: cold dressed mass, CL: carcass length, K5: backfat at 50 mm from the midline along the last rib, K7.5: backfat thickness at 75 mm.

Table 8.7: Genetic correlations (above diagonal) and phenotypic correlations (below diagonal) between post-weaning performance and carcass traits from a multitrait analysis

	ADG1	ADG2	CDM	K5	K7.5	CL
ADG1		0.35 ± 0.015	0.45 ± 0.001	-0.21 ± 0.249	-0.32 ± 0.214	0.55 ± 0.143
ADG2	0.32 ± 0.002		0.68 ± 0.018	0.29 ± 0.053	0.34 ± 0.213	0.47 ± 0.160
CDM	0.62 ± 0.001	0.74 ± 0.002		0.23 ± 0.248	-0.34 ± 0.213	0.53 ± 0.146
K5	0.35 ± 0.024	0.34 ± 0.024	0.35 ± 0.024		0.88 ± 0.076	0.41 ± 0.222
K7.5	0.23 ± 0.026	0.23 ± 0.026	0.23 ± 0.026	0.79 ± 0.009		0.43 ± 0.202
CL	0.67 ± 0.017	0.65 ± 0.017	0.66 ± 0.017	0.35 ± 0.022	0.26 ± 0.024	

Abbreviations: ADG1: average daily gain before 12 weeks of age, ADG2: average daily gain after 12 weeks of age, CDM: cold dressed mass, K5: backfat at 50 mm from the midline along the last rib, K7.5: backfat thickness at 75 mm, CL: carcass length.

8.4 Discussion

Mukota pigs, which have been demonstrated to adapt to survive under smallholder extensive production systems, have been shown to exhibit low growth rates (Kanengoni *et al*., 2004). The low growth rates, however, could be an advantage in that they do not require high amounts of concentrated feeds. This study aimed at estimating the genetic contribution of growth rate and carcass traits in these pigs. There is controversy on the appropriate models to use in estimating genetic parameters for growth and carcass traits for pigs. For example, Hermesch *et al*. (2000) incorporated litter effects only, while Bryner *et al*. (1992) incorporated maternal effects (but no litter effects) to estimate genetic parameters for growth and carcass traits. More recently, Chen *et al*. (2002) incorporated direct, litter and maternal effects. This paper applied three models and evaluates how the genetic parameters compare with each other for a Mukota pig herd.

The similar heritability of ADG1 and ADG2 could suggest that genetic improvement of either trait have the same genetic gain. The heritability estimate obtained in this study is similar to that reported for Australian pigs (Hermesch *et al*., 2000). These authors used a model with animal, litter and residual components as the random factors. The common environmental litter effects represent a non-genetic likeness between sibs caused by the sibs sharing a common environment. Littermates have a common mother whose milking ability and mothering ability contributes to all of her progeny in that litter. The environmental likeness reduces the accuracy of estimating breeding value because some of the similarity between records is due to non-genetic factors. Litter effects obtained in this study were, however, lower than literature values (Hermesch *et al*., 2000;

Perskovicova *et al*., 2002). Perskovicova *et al*. (2002) also reported differences in the heritability estimates using records for pigs kept by producers and those kept on-station. The heritability estimates for these two production systems in the Czech were 0.18 and 0.36, respectively. These heritability estimates compare well with values obtained for ADG2.

Heritability estimates obtained in this study were influenced more by the inclusion of the maternal than litter effects. Litter effects were lower than those reported in literature. Ferraz and Johnson (1993) reported that approximately five and seven percent of the variation in backfat and ADG were due to common environmental effects in Landrace and Large White pigs. Chen and co-workers (2002) reported estimates of eight to 12 percent in backfat across breeds. Crump and co-workers (1997) reported estimates of five and six percent in backfat and ADG, respectively, while Johnson and co-workers (1999) reported litter effects of 0.13 in Large White boars. Only litter effects for CDM were substantial.

Additive maternal genetic effects were large sources of variation in this study, especially for backfat thickness. The maternal genetic effect contribution to ADG was similar to findings of Chen *et al*. (2002). The negative genetic correlation between direct and maternal genetic effects also agrees with literature (Chen *et al*., 2002; Crump *et al*., 1997; Ferraz and Johnson, 1993). Ignoring maternal genetic effects, as was common in several models used before, has the consequence of producing biased heritability estimates with large standard errors or reduced precision. The influence of the maternal genetic variance component was quite pronounced in the carcass length of the Mukota pigs. The heritability of CL was 0.17 using both Models 1 and 2. Incorporating the maternal genetic component raised the heritability to 0.53, which agrees with earlier reports (e.g. 4-H Member Manual, 1997; Lopez-Serrano *et al*., 2000). The sharp rise in the additive genetic variance after incorporating maternal genetic effects may, however, indicate some degree of confounding in the litter and maternal effects, since cross fostering was rare and pigs of the same litter would be raised together until slaughter.

The increase in the heritability estimate for carcass trait measurements after adjusting for litter and maternal effects reduced the residual error variance, and increased the additive variance component. The heritabilities obtained after incorporating litter effects are similar to those in literature, which were based on even larger data sets than was used in this study (de Vries *et al*., 1994; Li and Kennedy, 1994; Hermesch *et al*., 2000). Backfat thickness in large framed pigs is usually measured at the P2 position, a position 65 mm from the midline along the last rib. The heritability of the P2 position seems to correspond well with the K5 position in Mukota pigs (0.48). The heritability for K5 was higher than for K7.5, suggesting that more gain in leanness is achieved for selecting Mukota pigs using the former. Chen *et al*. (2002) reported a heritability of 0.48 for the Yorkshire, Duroc, Hampshire and Landrace, while Perskovicova and co-workers (2002) also reported a similar value in the Czech Landrace. The K7.5 value was of low heritability. Kanengoni *et al*. (2004), in a growth performance and carcass trial, also indicated that the P2 or the K7.5 positions for backfat measurement seem inappropriate. In Zimbabwe, pigs are graded by measuring fat depth at the K7.5 position, which is thought to correspond well with the amount of lean in the carcass. There is need to determine the appropriate position for estimating the value of carcass, so as to avoid jeopardising Mukota pig producers. This calls for the development of appropriate grading systems to suit small breeds and genotypes, which in turn, would promote their utilisation and conservation.

The magnitude of the standard errors obtained for growth traits are similar to those reported earlier (Kemm *et al*., 1995; Hermesch *et al*., 2000). The results obtained in this study suggest the need to determine the appropriate age and weight of slaughter for Mukota pigs. Feed intake was not monitored in this study, since all the growing pigs were fed in groups. It was, therefore, not possible to determine the genetic relationships of growth rate and feed conversion efficiency. The pigs in this study were fed on a fibrous diet containing 20 percent maize cob meal, and as such, feed conversion efficiency was not a critical factor. Feed efficiency tends to be critical when the cost and quality of the feed is expensive, unlike when the feed resources are found in abundance and not much value is attached to them.

The finding that both genetic and phenotypic correlation coefficients were of the same sign and magnitude suggest that the genetic and environmental (residual) correlations share the same pattern and developmental basis (Roff, 1996). The residual correlations observed in this study were low to moderate in comparison to the genetic correlations, which agree with de Vries *et al*. (1994). As such, the environmental correlations are not discussed explicitly in this study.

The genetic correlations among backfat measurements were lower than those reported for Australian pigs (Hermesch *et al*., 2000), who obtained correlations that were not different from unity. When genetic correlations are not significantly different from unity, it suggests that the traits can be considered as one trait. In other words, a decrease or increase in one of the traits results in a similar change in the other. The high genetic correlation between K5 and K7.5, therefore, indicates the need to indicate that either position could be used in pig grading. The negative genetic correlation between CDM and K7.5 is difficult to explain. It is, however, generally accepted that high CDM are associated with high backfat thickness, as pigs tend to deposit more fat after reaching the plateau phase of growth (Whittemore, 1993). By that argument, the K7.5 position might not be an appropriate site to determine backfat thickness in Mukota pigs. The findings in this study, however, indicates the need to determine appropriate positions for taking backfat thickness that corresponds well with the meat or lean content in the carcasses.

The negative genetic correlation between ADG1 and backfat measurements agrees with Hermesch *et al*. (2000). In this study, the growing pigs were fed *ad libitum*. The genetic correlations obtained in this study are in good agreement with literature values that are based on *ad libitum* feeding systems (Lo *et al*., 1992; Ducos *et al*., 1993; Mrode and Kennedy, 1993; Cameron and Curran, 1994). The similarity of these estimates with those for Mukota pigs that were raised on a fibrous diets, tend to suggest the need to develop appropriate diets for the Mukota, as their slow growth rate is not ideal to feed them on the conventional feeds with high energy and protein concentrations. Such diets are likely to make them grow fat early and they become uneconomic to keep.

8.5 References

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Chapter 9: Genetic relationships among pre-weaning growth performance, post-weaning growth rate and carcass traits in Mukota pigs

Abstract

The objective of the study was to estimate genetic correlations for growth and carcass traits in Mukota pigs using AIREML. Weight traits determined before weaning showed positive genetic correlations with birth weight. Cold dressed mass (CDM) had a positive genetic correlation with backfat thickness at 50 mm along the midline (K5). The K5 and backfat thickness at 75 mm (K7.5) were highly correlated (r_g = 0.88). Weight at birth (BWT) was positively correlated with average daily gain from birth to weaning (ADGWW), whereas the relationships of BWT versus weight gain from 12 weeks to slaughter (ADG2) and BWT versus weight at slaughter were negative and, therefore, unfavourable. The correlations of BWT versus ADGWW and ADG4 were 0.71 and 0.17, respectively. The correlation between ADGWW versus K5, K7.5 and carcass length were 0.30, 0.05 and 0.35, respectively. The ADG2 was positively correlated with K5 and K7.5 (r_g = 0.29 and 0.34, respectively). The presence of the genetic correlations demonstrates the need to use multitrait analyses in evaluating genetic worthiness of pigs.

9.1 Introduction

It has been demonstrated that Mukota pigs are able to tolerate internal parasites and utilise fibrous feeds better than European breeds (Ndindana *et al*., 2002; Zanga *et al*., 2003; Kanengoni *et al*., 2004). These attributes make them suitable to keep under smallholder production systems to improve livelihoods of the poor (Anderson, 2003). In addition, meat from Mukota pigs has been described as being organoleptically more acceptable to the rural people than meat from European breeds (Ndiweni and Dzama, 1995), probably due to the low amount of intramuscular fat in the meat. Mukota pigs, however, have poor growth rates and readily deposit body fat, especially when they are fed on conventional high energy density diets. Commercial utilisation of the Mukota, which are indigenous to the tropical and sub-tropical environmental conditions, depends on determining genetic relationships among traits, especially when they are raised on fibrous diets.

Estimation of genetic correlations is necessary for genetic evaluation procedures, determination of optimum selection indices or in modelling breeding schemes. Many reports, for example have suggested a positive relationship between birth weight and growth rate, arguing that weaker pigs at birth lack the competitive advantage over heavier pigs in accessing milk and feeds (Whittemore, 1993). Generally, birth weight is negatively related to litter size at birth (Crump *et al*., 1997; Mungate *et al*., 1999; Hermesch *et al*., 2000a). It is important to determine the relationship among growth performance and carcass traits, to establish whether reproductive, growth and carcass traits should be incorporated and evaluated in a multitrait analysis. Besides knowing the genetic correlations among traits, phenotypic correlations are also useful, especially in smallholder areas where numerator relationship matrices are difficult, if ever possible, to construct. There is, therefore, need to generate genetic and phenotypic correlations among traits for Mukota pigs. The objective of this study was to estimate genetic parameters in Mukota pigs.

9.2 Materials and Methods

9.2.1 Study site

The study site is described in Section 3.2.1.

9.2.2 Pig management

Details on the management of the pigs are provided in Section 3.2.3.

9.2.3 Data preparation

Data from pigs farrowed between January 1998 and August 2003 were used. Pigs with missing records were deleted. A total of 506 records were deleted. A total of 1961 records were used in the analyses. Individual pig traits used in this study were the weight at birth (BWT) and average daily gain from birth to weaning (ADGWW). The other weight related traits analysed in this study were the average daily gain from weaning to 12 weeks from weaning (ADG1), average daily gain from 12 weeks slaughter (ADG2) and the weight of the dressed carcass after chilling at 4°C for 24 hours (CDM). Thickness of backfat was also recorded at three points along the last rib (50, 75 and 100 mm), and denoted as K5, K7.5 and K10, respectively. Length of carcasses (CL), measured from the anterior edge of the first rib to the pubic bone using a measuring tape, were also analysed.

9.2.4 Statistical analyses

All the fixed factors were analysed using the PROC GLM procedure of SAS (2000). The average information restricted maximum likelihood (AIREML) algorithm (Gilmour *et al*., 1995) was used to generate variance-covariance components in an animal model, which provides approximations of standard errors for heritabilities and correlations. Heritability estimates were generated using a model that contained direct, litter and maternal genetic effects. In matrix form, the models are presented as:

$\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{u}_a + \mathbf{Z}_2\mathbf{u}_l + \mathbf{Z}_3\mathbf{u}_m + e$;

where **Y** is vector of *n* observations for individual birth weight, β is a vector of fixed effects and includes the year-season (four seasons per year), parity (8 parities) and sex (male and female) effects. Vectors of random effects consists of environmental effects $\mathbf{u}_l \sim N_{q1}(\mathbf{0}, \mathbf{I}\sigma_l^2)$ common to all pigs within each of q_l litters, direct $\mathbf{u}_a$ as well as maternal genetic effects $\mathbf{u}_m$ of q_2 pigs, and residual environmental effects $e \sim N_n(\mathbf{0}, \mathbf{I}\sigma_e^2)$, peculiar to each pig. All random effects were assumed to be sampled from a normal distribution with a zero mean and variance-covariance structure of:

$$v\begin{bmatrix} u_a \\ u_m \\ u_l \\ u_e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I\sigma_l^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

The implied genetic models are infitesimal (Bulmer, 1980), where the base population is assumed to be unselected, non-inbred and unrelated. Vectors of the direct and maternal genetic effects are assumed to be distributed as follows:

$$\begin{bmatrix} u_a \\ u_m \end{bmatrix} \sim \mathrm{N}(\mathbf{0}, \mathbf{G}_{am} \otimes \mathbf{A}), \text{ where } \mathbf{G}_{am} = \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix}$$

The **I** and **A** are the identity and numerator relationship matrices, respectively. The $\mathbf{G}_{am}$ is the genetic (co) variance matrix between the direct and maternal effects and ⊗ denotes the direct product of matrices. Incidence matrices $\mathbf{X}$ and $\mathbf{Z}_i$ (i = 1, 2, 3) link the fixed and random effects, respectively, with corresponding records in vector $\mathbf{Y}$.

Genetic and phenotypic correlations were estimated using a multitrait model.

9.3 Results

9.3.1 Summary statistics and levels of significance for fixed factors

The descriptive statistics for the traits studied are shown in Table 9.1. The range for birth weight was 1.4 kg. The variance for ADG1 was bigger than for ADG2. Similarly, K7.5 measurements were twice more variable than K5 measurements. The levels of significance for the fixed factors from a linear model with first-order interactions are shown in Table 9.2. The sex of the pig influenced birth weight, ADG2 and CDM. Month of the year affected ADG1 and both backfat measurements. Significant month × sex interactions were existed on ADG1, ADG2 and CDM (Table 9.2).

9.3.2 Heritability estimates

As shown in Table 9.3, the heritability estimate for BWT was 0.09. The ADG1 had a higher heritability than ADG2. The heritability estimate for K5 was also higher than for K7.5 (0.64 versus 0.40). The heritability for ADGWW, CDM and CL were 0.15 ± 0.005, 0.32 ± 0.002 and 0.62 ± 0.001, respectively (Table 9.3).

Table 9.1: Summary statistics for birth weight (BWT), average daily gain from birth to weaning (ADGWW), body weight gain from weaning to 12 weeks (ADG1), gain from 12 weeks to slaughter (ADG2), cold dressed mass (CDM), carcass length (CL) and backfat thickness at K5 and K7.5 positions in Mukota pigs

Trait	Mean	SD	Minimum	Maximum
BWT (kg)	0.7	0.29	0.3	1.7
ADGWW (kg)	0.2	0.12	0.1	0.3
ADG1 (kg)	0.4	0.09	0.2	0.6
ADG2 (kg)	0.3	0.155	0.2	0.6
CDM (kg)	37.5	7.86	11.5	51.4
CL (mm)	581.4	51.28	468.0	793.0
K5 (mm)	11.2	1.77	6.0	13.0
K7.5 (mm)	14.9	3.90	9.0	17.0

N: sample size = 1961; SD: standard deviation.

Table 9.2: Significant levels of the fixed factors and covariates included in the analyses

	Main factors			Interactions			Covariates		
Trait	M	S	P	M × S	S × P	S × P × M	β_1	β_2	β_3
BWT	*		*		**				
ADGWW							*		
ADG1 (kg)		*	*	*	**	*		*	
ADG2 (kg)	**			*	**	*			
CDM (kg)	**			*	*	*			*
CL (mm)				*					
K5 (mm)		*		*	**				
K7.5 (mm)		*		*	*				

Abbreviations: BWT: weight of pigs at birth, ADGWW: average daily gain from birth to weaning, ADG1: ADG before 12 weeks of age, ADG2: ADG after 12 weeks of age, DP: dressing percentage, CDM: cold dressed mass, CL: carcass length, K5: backfat at 50 mm from the midline along the last rib, K7.5: backfat thickness at 75 mm.

M: sex of pig, S: month, β_1: AVBWT, β_2: weight at weaning, β_3: weight at slaughter.

*P<0.05, **P<0.01 ***P<0.001

Table 9.3: Heritability estimates for birth weight (BWT), average daily gain from birth to weaning (ADGWW), body weight gain from weaning to 12 weeks (ADG1), gain from 12 weeks to slaughter (ADG2), cold dressed mass (CDM), carcass length (CL) and backfat thickness at K5 and K7.5 in Mukota pigs

Trait	Heritability	Standard error
BWT (kg)	0.09	0.026
ADGWW (kg/day)	0.15	0.005
ADG1 (kg)	0.27	0.003
ADG2 (kg)	0.20	0.001
CDM (kg)	0.32	0.002
CL (mm)	0.62	0.001
K5 (mm)	0.64	0.001
K7.5 (mm)	0.40	0.001

9.3.3 Correlations between pre-weaning and post-weaning growth performance

Table 9.4 shows the genetic covariances among traits from a multitrait analysis. The genetic and phenotypic correlation coefficients are shown in Tables 9.5 and 9.6, respectively. There were positive phenotypic and genetic correlations between BWT and ADGWW. The genetic correlation coefficient was, however, higher than the phenotypic correlation (0.71 versus 0.42). Birth weight was also positively correlated to ADG1. No genetic relationship existed between BWT and ADG2. There was a significant ($P<0.05$) genetic relationship between pre-weaning growth rate andADG1. The genetic relationship between ADGWW and ADG2 was, however, negative. The ADG1 and ADG2 were positively correlated, both phenotypically (r_p = 0.32) and genetically (r_g = 0.35). Generally, the standard errors for genetic correlations for growth traits tended to be larger than for their phenotypic counterparts.

9.3.4 Correlations among carcass traits

The CDM had a positive genetic correlation with the K5 backfat measurement (r_g = 0.23; Table 9.6). The phenotypic correlation was also positive. Although CDM was phenotypically correlated with K7.5 (r_p = 0.23; Table 9.5), the genetic correlation was negative (r_g = -0.34; Table 9.6). Both the genetic and phenotypic correlations between CDM and CL were positive and high (r_g = 0.53; r_p = 0.66). The correlations between CL and backfat measurements were positive. Genetic correlations between these traits were higher than their phenotypic counterparts. The K5 and K7.5 were highly correlated (r_g = 0.88; r_p = 0.79), but the correlation coefficients were less than unity.

Table 9.4: Genetic covariances among pre-weaning growth performance, post-weaning growth rate and carcass traits from a multitrait analysis in Mukota pigs

	Trait						
Trait	ADGWW	ADG1	ADG2	CDM	K5	K7.5	CL
BWT	0.002	0.006	-0.006	0.001	-0.016	-0.028	-0.072
ADGWW		-0.017	-0.001	0.102	0.003	0.001	0.018
ADG1			0.010	0.153	-0.013	-0.025	0.146
ADG2				0.214	-0.016	-0.026	0.118
CDM					-0.854	-0.368	0.892
K5						0.189	0.303
K7.5							0.414

Abbreviations: BWT: weight of pig at birth, ADGWW: average daily gain from birth to weaning, ADG1: body weight gain from weaning to 12 weeks of age, ADG2: body weight gain from 12 weeks to slaughter, CDM: cold dressed mass, CL: length of carcass from the anterior edge of the first rib to the pubic bone, K5: backfat thickness 50 mm from the midline along the last rib, K7.5: backfat thickness 75 mm from the midline along the last rib.

Table 9.5: Phenotypic correlations (± standard errors) among pre-weaning growth performance, post-weaning growth rate and carcass traits from a multitrait analysis in Mukota pigs

	Trait						
Trait	ADGWW	ADG1	ADG2	CDM	K5	K7.5	CL
BWT	0.42 ± 0.024	0.46 ± 0.025	-0.13 ± 0.025	0.11 ± 0.005	-0.00 ± 0.025	-0.01 ± 0.026	-0.04 ± 0.028
ADGWW		0.04 ± 0.026	-0.21 ± 0.026	0.01 ± 0.003	0.03 ± 0.026	-0.01 ± 0.028	0.04 ± 0.032
ADG1			0.32 ± 0.002	0.62 ± 0.001	0.35 ± 0.024	0.23 ± 0.026	0.67 ± 0.017
ADG2				0.74 ± 0.002	0.34 ± 0.024	0.23 ± 0.026	0.65 ± 0.017
CDM					0.35 ± 0.024	0.23 ± 0.026	0.66 ± 0.017
K5						0.79 ± 0.009	0.35 ± 0.022
K7.5							0.26 ± 0.024

Abbreviations: BWT: weight of pig at birth, ADGWW: average daily gain from birth to weaning, ADG1: body weight gain from weaning to 12 weeks of age, ADG2: body weight gain from 12 weeks to slaughter, CDM: cold dressed mass, CL: length of carcass from the anterior edge of the first rib to the pubic bone, K5: backfat thickness 50 mm from the midline along the last rib, K7.5: backfat thickness 75 mm from the midline along the last rib.

Table 9.6: Genetic correlations (± standard errors) among pre-weaning growth performance, post-weaning growth rate and carcass traits from a multitrait analysis in Mukota pigs

	Trait						
Trait	ADGWW	ADG1	ADG2	CDM	K5	K7.5	CL
BWT	0.71 ± 0.111	0.17 ± 0.095	-0.08 ± 0.082	0.12 ± 0.021	-0.32 ± 0.050	-0.44 ± 0.009	-0.33 ± 0.009
ADGWW		0.58 ± 0.121	-0.29 ± 0.124	0.08 ± 0.005	0.30 ± 0.028	0.05 ± 0.021	0.35 ± 0.085
ADG1			0.35 ± 0.015	0.45 ± 0.001	-0.21 ± 0.049	-0.32 ± 0.014	0.55 ± 0.043
ADG2				0.68 ± 0.018	0.29 ± 0.053	0.34 ± 0.013	0.47 ± 0.060
CDM					0.23 ± 0.048	-0.34 ± 0.013	0.53 ± 0.046
K5						0.88 ± 0.026	0.41 ± 0.022
K7.5							0.43 ± 0.002

Abbreviations: BWT: weight of pig at birth, ADGWW: average daily gain from birth to weaning, ADG1: body weight gain from weaning to 12 weeks of age, ADG2: body weight gain from 12 weeks to slaughter, CDM: cold dressed mass, CL: length of carcass from the anterior edge of the first rib to the pubic bone, K5: backfat thickness 50 mm from the midline along the last rib, K7.5: backfat thickness 75 mm from the midline along the last rib.

9.3.5 Relationship between pre-weaning growth rate and carcass traits

Phenotypic correlations between pre-weaning growth performance and carcass traits were weak and ranged from 0.00 to 0.04. Birth weight was however, significantly (P<0.05) correlated with CDM (r_p = 0.11; Table 9.5). As shown in Table 9.6, there was a low, but significant (P<0.05) genetic correlation between BWT and CDM. Birth weight was genetically negatively correlated with backfat thickness. Carcass length and BWT were also negatively correlated (P<0.05). The magnitude of the genetic correlation between ADGWW and K5 was larger than the correlation between ADGWW and K7.5 (0.30 versus 0.05). Although BWT was negatively correlated to CL (r_g = -0.33), the correlation between CL and ADGWW was positive (r_g = 0.35).

9.3.6 Relationship between post-weaning growth performance and carcass traits

The phenotypic relationships between ADG1 and backfat thickness measurements were positive, whereas the genetic correlations were negative. The genetic correlation between ADG2 and backfat measurements (both K5 and K7.5), was positive. The phenotypic correlations between ADG2 and backfat thickness was also positive. Post-weaning growth rates had genetic positive correlations with CL. The phenotypic correlations were, in both cases, higher than genetic correlations. Both post-weaning growth rate measurements were positively related to CDM. Like CL, the phenotypic correlations were of a higher magnitude than their genetic counterparts.

9.4 Discussion

The direct heritability for birth weight, which is due to the genetic potential of the embryo or foetus for growth during gestation, was higher than the one reported in Kaufmann *et al*. (2000) for Large White pigs. These authors reported a direct heritability of 0.02. These findings suggest that there is reasonable variation that exists in the birth weight of Mukota pigs. Backfat thickness in large framed pigs is usually measured at the P2 position, a position 65 mm from the midline along the last rib. The heritability of the P2 position seems to correspond well with the K5 position in Mukota pigs (Chen *et al*., 2002). The heritability for K5 was higher than K7.5, suggesting that more gain in leanness is achieved for selecting Mukota pigs using the former. Differences in heritability for growth rate at different stages of growth are consistent with literature (Crump *et al*., 1997; Hermesch *et al*., 2000b).

Simultaneous improvement of traits of economic importance requires the knowledge of genetic relationships to reduce antagonisms in selection. The observation that BWT was positively correlated with ADGWW indicates that heavy pigs at birth maintain their advantage in accessing feed and milk from the nursing sow. Kerr and Cameron (1995) and Kaufmann *et al*. (2000) also reported positive correlations between BWT and WWT. There is, therefore, scope in selecting for pigs that produce litters with heavy pigs at birth. In other words, selection for litter size should also be accompanied by selection for birth weight. This is especially so in the Mukota pigs where no negative genetic relationships have been reported between numbers of pigs born alive and the litter weight at birth.

The finding that both genetic and phenotypic correlation coefficients were of the same sign and magnitude suggest that the genetic and environmental (residual) correlations share the same pattern and developmental basis (Roff, 1996). The residual correlations observed in this study were low to moderate in comparison to the genetic correlations, which agrees with Cameron (1990) and de Vries *et al*. (1994). As such, the environmental correlations are not discussed explicitly in this study.

The high genetic correlations obtained between WWT and ADG1 suggests that, at 12 weeks, the pigs had not yet reached a plateau in growth rate, after which the growth rate is expected to decline (Kemm *et al*., 1995). The low genetic correlation between ADG1 and ADG2, therefore, suggests that the pigs could have been slaughtered when the ADG was at the plateau or even declining. The magnitude of the standard errors obtained for growth traits are similar to those reported in Hermesch *et al*. (2000c). The results obtained in this study suggest the need to determine the appropriate age and weight of slaughter for Mukota pigs. Feed intake was not monitored in this study, since all the growing pigs were fed in groups. It was, therefore, not possible to determine the genetic relationships of growth rate and feed conversion efficiency. The pigs in this study were fed on a fibrous diet containing 200 g maize cob meal/kg, and as such, feed conversion efficiency was not a critical factor. Feed efficiency tends to be critical when the cost of the feed is expensive, unlike when the feed resources are found in abundance and not much value is attached to them.

The genetic correlations among backfat measurements in this study were lower than those reported in Australian pigs (Hermesch *et al*., 2000b). The authors in that study obtained correlations that were not different from unity. When genetic correlations are not significantly different from unity, it suggests that the traits can be considered as one trait. In other words, a decrease or increase in one of the traits results in a similar change in the other. The high genetic correlation between K5 and K7.5, therefore, indicates the need to indicate that either position could be used in pig grading. The negative genetic correlation between CDM and K7.5 is difficult to explain. It is, however, generally accepted that high CDM are associated with high backfat thickness, as pigs tend to deposit more fat after reaching the plateau phase of growth (Whittemore, 1993). By that argument, the K7.5 position might not be an appropriate site to determine backfat thickness in Mukota pigs. The findings in this study, however, indicates the need to determine appropriate positions for taking backfat thickness that corresponds well with the meat or lean content in the carcasses.

Generally, reproductive traits are negatively correlated with production traits (Tholen *et al*., 1996; Perskovicova *et al*., 2002). The positive genetic correlation between BWT and production traits, therefore, suggests that BWT of individual pigs cannot best be described as a reproductive trait. These findings also suggest the lack of influence of litter size on growth performance from weaning up to peak growth rates. These findings agree with Hermesch *et al*. (2000a). As the pig grows beyond at reduced growth rates, the genetic relationships with weights recorded earlier in the life of the pig diminishes, as was confirmed by the lack of genetic relationships between ADGWW and ADG2.

Low genetic correlations between traits recorded early in life and production traits are one reason for evaluating production and reproduction traits separately. A causal relationship is, however, expected between reproductive and growth performance. It suggests that reproductive traits that are commonly measured do not take maximal advantage of this relationship. According to Perskovicova and co-workers (2002), the relationships are real and multitrait models, which include both reproduction and production traits should be used simultaneously to improve the accuracy of genetic evaluations. The observation that pre-weaning growth performance showed significant (though moderate) correlation coefficients with production traits further strengthens the justification for using multitrait models in pig genetic evaluation. No reports are available that reported genetic relationships between birth weight with carcass traits in pigs. Hermesch *et al*. (2000a), however, reported negative genetic relationships between litter birth weight and backfat measurements, which were of the same magnitude with those obtained in this study. These estimates are, however, of higher magnitude than the genetic correlation reported by Young and co-workers (1978) for backfat and litter birth weight.

The negative genetic correlation between ADG for weaning to 12 weeks of age and backfat measurements agrees with Hermesch *et al*. (2000b). In this study, the growing pigs were fed *ad libitum*. The genetic correlations obtained in this study agree with literature values that are based on *ad libitum* feeding systems (Lo *et al*., 1992; Ducos *et al*., 1993; Mrode and Kennedy, 1993; Cameron and Curran, 1994). The positive correlation between backfat thickness with ADG2 is also consistent with the observations made in Australian pigs (Hermesch *et al*., 2000c). These researchers observed a positive relationship between growth rate during the last four weeks to slaughter with backfat thickness. The genetic correlation between growth rate and leanness has been shown to be more favourable in young pigs, when feed intake capacity is limited (Campbell *et al*., 1986; McPhee *et al*., 1988; von Felde *et al*., 1996). Since younger pigs are limited in feed intake capacity, their lean growth potential exceeds their appetite, which might have lead to a favourable negative relationship between ADG1 and backfat. The unfavourable positive genetic correlation between ADG2 and backfat is, therefore, an indication that pigs at that age had a high feed intake which exceeded their maximum lean deposition. In such cases, the extra energy consumed is deposited as fat tissue. Von Felde *et al*. (1996) also reported that feed intake at the beginning of the growing period had a more favourable genetic correlation with leanness than feed intake over the entire growing period. The similarity of the genetic parameter estimates from rapidly growing pigs from Europe and the USA with Mukota pigs that were raised on a fibrous diets, tend to suggest the need to develop appropriate diets for the Mukota, as their slow growth rate is not ideal to feed them on the conventional feeds with high energy and protein concentrations. Such diets are likely to make them grow fat early and they become uneconomic to keep.

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Chapter 10: General Discussion

The Mukota pig is relatively small in size and is adapted to survive under low input production systems for the benefit of smallholder pig producers. Improvement of Mukota pigs requires knowledge of the genetic and non-genetic factors that influence their performance. Traits of economic importance in pigs include reproductive, growth, mortality, carcass and meat quality. Improving the environmental conditions enables animals to express their full genetic potential. It is, therefore, important to evaluate the non-genetic or environmental factors that influence Mukota pig growth. For the utilisation of the Mukota pig genetic resource to increase, there is need to evaluate the genetic determination of the traits of economic importance, besides the environmental factors. Generating genetic parameters, such as heritability and genetic correlations among traits, is essential to designing effective breeding programmes that incorporate the genes from the Mukota pigs. The objective of this study was to evaluate the production and genetic potential of Mukota pigs when raised on a high fibre diet based on maize cob meal. Pigs in smallholder areas are usually fed on fibrous diets. Conventional feeds that contain high levels of energy and protein have been demonstrated to be inappropriate for Mukota pigs, given their slow growth potential. Any improvement strategies should, thus be based on the conditions, under which the pigs are raised. The study endeavoured to mimic such conditions; such as the feeding regime and that farrowing crates were not provided. A diet containing 25 % cob meal was used for the growing pigs to mimic the fibrous poor quality diets that pigs are exposed to under the smallholder extensive production conditions.

The first three chapters (3, 4 and 5) describe the phenotypic characterisation of the pigs, in comparison with Large White × Mukota pigs that were raised under the same environmental conditions. The Large White × Mukota pigs are common in rural areas, largely as a result of the introduction of Large White pigs by the Pig Industry Board of Zimbabwe. The major non-genetic or environmental factors that influence pig performance were evaluated. The influences of these non-genetic factors on the reproductive, growth and carcass traits were determined. The genetic determination of the traits of economic importance is described in Chapters 6 through 9. Genetic determination of traits recorded at birth was first discussed (Chapter 6), followed by traits up to weaning (Chapter 7). In each case, the relationship of the individual weight traits and litter performance traits were compared, using models that included or excluded maternal genetic effects of the sow. Growth and carcass traits were then discussed (Chapter 8). The genetic and phenotypic correlations of the traits from birth to carcass performance are the subject of Chapter 9.

Chapter 3 discussed the influence of non-genetic factors on the reproductive performance of Mukota sows. The primary determinant of the profitability of any pig enterprise is not only the size of the litter, but also the weight of the pigs born, with the latter being, arguably, more important than the former under smallholder extensive pig production systems. The general absence of repeat breeding, which is, usually, a sign of presence of stress factors, suggests that these sows are tolerant to high stress and low nutrition levels. This was shown by the low number of matings per conception observed in this study. The sows were not subjected to any selection based on repeat breeding. The influence of heat stress on the exhibition of oestrus in Mukota sows is considerably low. Low number of repeat breeders indicates that, where possible, there is scope of using modern reproductive technologies, such as artificial insemination to improve reproductive efficiency of Mukota pigs. The fact that the sows were not sprinkled with water, as is widely recommended (Whittemore, 1993), suggests the need to use Mukota pigs where production environments are relatively harsh.

The large weights at birth of the crossbred piglets could suggest that there is possible hybrid vigour on birth weight. Sows mated to large White boars also exhibited large litters. Crossbreeding is, therefore, an option that can be used to boost productivity. It needs to be highlighted that crossbreds have faster growth rates and so require more inputs and good management than Mukota pigs. Such animals could be more suitable for the small-scale commercial farmers, while the Mukota are appropriate for the rural poor. Crossbreeding calls for accurate recording of the dams and sires and also requires good management practices, since the crossbred pigs also had higher growth rates than for the Mukota. Such findings could support the argument that crossbred pigs can be utilised under smallholder farming systems. Mashatise (2002) reported that farmers in rural areas cull their sows early (at around parity 2). These findings highlight the different objectives of keeping pigs between rural and commercial farmers. Early culling is practised to take advantage of the good meat quality in gilts than in mature sows, and partly explains the low litter sizes recorded in rural areas. Mukota sows, however, need not be culled at parity 6, as is recommended for exotic breeds. More work, therefore, needs to be done to evaluate the appropriate culling age.

Sow performance at birth does not give an adequate picture of the productivity of a pig enterprise. Evaluating the performance to weaning is crucial. The performance is presented in Chapter 4. Performance of pigs before weaning measures the level of management on the farm. In addition, survival and growth rates up to weaning, describes, to a great extent, the mothering ability of the sow. Although mothering ability is defined in numerous ways, it is a crucial trait to monitor under smallholder pig production conditions, where the level of management is low. Pigs under extensive production conditions scavenge for food and are subjected to draughts and excesses of weather and predation.

Total weaning weight was higher in the crossbred than Mukota pigs, suggesting that crossbreeding of Large White boars and Mukota sows can be a viable option to increase pig productivity, especially to small-scale commercial pig producers. The higher weights at weaning could be explained by the superior genes for growth in Large White pigs. Both the total and average weights at weaning were similar across seasons, suggesting that there is little or minimal manipulation of the production environments when either or both these genotypes are used in smallholder pig production systems. The growth rates of Mukota pigs before weaning were comparable to the crossbred pigs and even with literature (Mungate *et al*., 1999). Efficient utilisation of Mukota pigs, therefore, lies in determining the appropriate age and body weight for slaughter.

Chapter 5 was designed to evaluate the performance and carcass traits of growing Mukota and Large White × Mukota pigs fed on diets based on maize cob meal up to slaughter. Crossbred pigs had low growth rates during the cool season, suggesting that Mukota pigs have lower maintenance requirements than their crossbred counterparts. The observation that Mukota pigs matured earlier than the crossbred pigs agree with Kanengoni *et al*. (2004), and indicate that age at slaughter should be breed-specific. Keeping Mukota pigs for longer periods than is optimum reduces efficiency of feed conversion into muscle since most of the dietary nutrients are converted into fat. Crossbred pigs are, therefore, appropriate to produce in commercialised smallholder pig production system. One major distinction between the Mukota and the crossbred pigs was in the growth rates post-weaning. Mukota pigs showed a marked drop in growth rate after around 12 weeks of age, suggesting that these phases should be treated as different traits in genetic evaluation.

Chapters 6 to 9 evaluated the genetic contribution of the traits of economic importance in Mukota pigs. The crossbreds were not considered because of the lack of adequate records on the Large White pigs, which made it impossible to estimate heterosis effects. A reasonable genetic variation was obtained in the birth weight of Mukota pigs, indicating the scope to achieve genetic improvement through selection. Common environmental litter effects were low for the Mukota pigs. The finding that adjustments of individual birth weight for NBT had marginal or insignificant influences on the variance components suggest that number of pigs in the litter had no substantial influence on the ability of the embryos or foetuses to grow. Individual birth weight should also be incorporated in the genetic evaluation of sows, rather than using derivatives such as average birth weight or total litter weight.

Chapter 7 showed that using a simplified model tends to overestimate the heritability of a trait, as some non-additive and common environmental litter effects inflate the additive genetic variance. Maternal and litter influences should, therefore, be accounted for in estimating heritabilities in pigs. More importantly, the maternal genetic influence in this study was higher for traits at weaning than at birth. The maternal genetic effect for WWT was higher than the additive direct animal effect. These findings suggest that Mukota pigs possess superior genetically controlled effects of milk production and caring for their piglets. The maternal influence is genetically controlled, which makes them suitable for smallholder production, where the maternal influence would have a bigger role than in commercial set ups. Individual animal records and cumulative traits, however, produced different genetic parameter estimates. Although individual pig weights are expensive and labour intensive to obtain, they tend to give more accurate estimates of genetic parameters, as also pointed out with other breeds (Roehe, 1999; Kaufmann *et al*., 2000).

In smallholder production systems, mothering ability relates to the number of pigs that survive to weaning. The survival is a result of the pig's ability to grow and the care provided for by the nurse sow. The heritability for mothering ability was higher than values reported in European pigs, for example, the Dutch Landrace (Hahenberg *et al*., 2001), indicating that it should be incorporated in pig improvement programmes for Mukota pigs.

One sustainable way to conserve a breed at risk is to develop niche markets for its products. Post-weaning growth performance and carcass traits are, thus crucial traits to evaluate to promote the *in-situ* conservation of Mukota pigs. For example, the grading of carcasses at the formal pig markets should not disadvantage the Mukota pigs, as is currently the case in Zimbabwe. In Chapter 8, different linear models were compared to estimate the heritability of growth performance and carcass traits for Mukota pigs. Appropriate models should incorporate both common environmental and maternal genetic effects. Growth performance was split into two phases, before and after 12 weeks of age and the heritability estimates were 0.27 and 0.12, respectively. The heritability for carcass traits was moderate to high, indicating that selection is a potent tool for the genetic improvement of Mukota pigs for these traits.

Selecting for one trait can reduce the performance of another trait, if negative genetic relationships exist between such traits. Such antagonisms are reduced through simultaneous selection of traits. The relationships among traits, generated using a multi-trait model, are the subject of Chapter 9. High genetic correlations existed between weight at weaning and post-weaning growth performance up to 12 weeks. Keeping Mukota pigs well beyond this age could be uneconomic. The pigs in this study were fed on a fibrous diet, and it is likely that changing the diet will also influence the environmental correlations of the traits, and hence the genetic correlation estimates. The observation that pre-weaning growth performance showed a positive correlation with post-weaning growth rate further strengthens the justification for using multi-trait models in pig genetic evaluation (Perskovicova *et al*., 2002).

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Chapter 11: Conclusions, Recommendations and Further Studies

11.1 Conclusions

Reproductive performance of Mukota sows, as measured by number of matings per conception, farrowing intervals, farrowing indices, is comparable to improved exotic pigs. Crossbreeding of Mukota sows and Large White boars increased reproductive performance of the sows, possibly due to hybrid vigour. Total weaning weight was higher in the crossbred than Mukota pigs, further indicating that crossbreeding is a viable option to increase smallholder pig productivity. Growth rates of Mukota pigs before weaning were comparable to that of crossbred pigs and even with that of exotic pigs in Zimbabwe. The crossbred pigs had a higher growth rate post-weaning than Mukota pigs. Mukota pigs matured earlier than the crossbred pigs. The ADG of Mukota tends to peak at around 10 to 12 weeks of age.

In improving the reproductive performance of Mukota sows, individual birth weight should also be incorporated. The number of piglets in the uterus did not affect the ability of the embryos or foetuses to grow, suggesting that there is scope to select for large litter sizes in Mukota pigs. The maternal genetic influence was higher for traits at weaning than at birth. Mukota pigs tend to possess superior genetically controlled effects of milk production and caring for their piglets. Maternal and litter influences should be accounted for in estimating heritabilities for growth and carcass performance in Mukota pigs. The heritability for mothering ability was high.

Growth rate before and after 12 weeks had different heritability estimates. The heritability for carcass traits was moderate to high. There was a high genetic correlation between weight at weaning and post-weaning growth performance up to 12 weeks. Multi-trait models should be used in pig genetic evaluation. Mukota pigs could, therefore, be reared commercially on fibrous diets.

11.2 Recommendations

Selection can be used to improve smallholder pig production. The additive genetic variances for most of the traits are huge, giving room for selection. There is need to design methods of keeping accurate records for effective genetic evaluation. Traits to be included in the selection index should be biased towards adaptation to take advantage of the strengths of the Mukota pigs. Open nucleus schemes could be a viable option to achieve genetic improvement in Mukota pigs, provided measures are put in place to control the spread of diseases.

Crossbreeding has the potential to increase smallholder pig productivity. One sustainable way is to use the Mukota pigs as the dam line, since they are adapted to the local conditions and replacement stock is readily available. The imported pigs should be used as the sires. This will take advantage of the complementarity between the different breeds. Crossbreeding should be planned and based on records to ensure the appropriate contribution of each line and to maintain the genes of the Mukota pigs. Indiscriminate crossbreeding, as is currently practised, threatens the Mukota genotype.

Keeping either the Mukota or the Large White × Mukota genotypes should be based on diets with higher fibre content than are found in the conventional pig diets. The high energy density diets are more suitable for rapidly growing genotypes, which require high levels of inputs and management. Such diets tend to make Mukota pigs deposit fat early.

Smallholder pig producers should be recommended to keep records on reproduction and growth performance of their pigs. To start with, the recording scheme can be initiated, managed and monitored centrally, ideally by the Pig Industry Board, which has the mandate to develop pigs in Zimbabwe. The data gathered will then be crucial in estimating genetic parameters for pigs under the smallholder conditions. In addition, record keeping, has been shown to lead to improvements in management of livestock.

It is also recommended that a nucleus herd of Mukota pigs be set up for effective research and selection. The indigenous pigs should be obtained from diverse agro-ecological regions to increase diversity and also to determine whether the Mukota pig populations are uniform or have the same gene frequencies. Detailed characterisation of the Mukota genotypes is likely to promote their widespread use.

11.3 Further studies

Future research should focus on ways of commercialising smallholder pig production based on indigenous Mukota pigs. This requires understanding their genetic and physiological make up. Possible study areas include:

1. Reproductive performance of gilts, e.g. cyclicity and attainment of puberty;

2. Phenotypic and molecular characterisation of the local pigs in the different agro-ecological zones of Zimbabwe;
3. Determining the genetic distances of the local genotypes and using molecular techniques to evaluate the genetic basis of adaptive traits;
4. Conducting extensive crossbreeding experiments to identify the most appropriate genotype to recommend for small-scale and large-scale pig producers;
5. Mothering ability in Mukota sows, such milk yield and quality characteristics;
6. Evaluating meat quality characteristics and conducting extensive organoleptic tests to determine the quality of Mukota pig meat; and
7. Developing pig genetic improvement strategies in rural areas to promote in-situ conservation of the indigenous pig genotypes.