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Full Length Research Paper

Phenotypic and genetic parameter estimates for grasscutter production traits. 2. Genetic and phenotypic correlations

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The objective of this work was to estimate genetic and phenotypic correlations among traits of the grasscutter. The study was conducted at the grasscutter section of the Department of Animal Science Education, University of Education, Winneba, Ghana, from 2005 to 2010. Data consisted of records of 502 kids born by 136 does and 40 sires over a period of 5 years. Data were analyzed by mixed model methodology using a full animal model and all known genetic relationships, in multiple trait analysis, using MTDFREML programme. Genetic correlations among size traits (body weight and growth rate) were medium to high (0.32 to 0.87), whilst their phenotypic correlations ranged from low to high (0.01 to 0.99). Antagonistic genetic relationship existed between size and reproductive traits. Phenotypic relationships between size and reproductive traits, survival, feed intake and feed efficiency were not important. Genetic correlations between size traits and survival ranged from no relationship (r = 0.00) to high (r = 0.80). Whilst genetic relationship between feed intake and size traits was positive, that between size traits and feed efficiency was negative. Litter size had little or no genetic relationship with pre-weaning survival but intermediate positive genetic relationship with post-weaning survival. Litter size had little phenotypic relationship with survival but pre-weaning survival had a high positive phenotypic relationship with litter size at weaning. In conclusion, findings in this study were in general agreement of what pertains to the grasscutter and other farm livestock species.

Keywords: *Thryonomys swinderianus,* cane rat, rodent, reproduction, growth, survival, feed intake, feed efficiency, domestication, phenotypic and genetic parameters

INTRODUCTION

Ghana is preparing to establish a genetic improvement programme to improve efficiency of grasscutter production (MoFA, 2004). To facilitate breeding of highly prolific, docile and fast growing animals, there is a need to know the phenotypic and genotypic characteristics of the current captive population. Estimates of heritability and phenotypic

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Table 1. Distribution of data used for estimating parameters

Trait	Acronym	Number of Records	Means	Range	Standard Deviation
Birth weight, g	BWT	502	123.6	63.0-216.0	24.6
Weaning weight, g	WWT	441	535.6	270.3-1271.7	162.4
4-month weight, g	BWT4	413	954.9	487.8-2540.8	303.2
6-month weight, g	BWT6	392	1374.4	731.0-2894.8	342.9
8-month weight, g	BWT8	339	1690.1	946.1-3417.0	352.7
Pre-weaning daily gain, g/day	PWADG	441	6.9	2.2-18.3	2.4
Daily gain from 2-4 months, g/day	ADG4	413	7.0	1.2-26.3	3.4
Daily gain from 4-6 months, g/day	ADG6	392	6.8	0.1-25.2	4.0
Daily gain from 6-8 months, g/day	ADG8	339	6.2	0.1-25.3	3.8
Litter size at birth, number	LS	502	4.3	1.0-7.0	1.6
Litter size at weaning, number	LSW	492	3.8	1.0-7.0	1.6
Days of joining to conception, days	DJC	502	20.8	1.0-58.0	14.2
Lactation weight loss, g	LWTL	473	-359.3	-1560.0-536.0	322.3
Pre-weaning survival, %	PRS	492	88.8	20.0-100.0	24.3
Post-weaning survival, %	POWS	380	87.7	25.0-100.0	12.8
Feed intake, gDM/day	FI	199	108.2	67.8-135.6	7.9
Feed conversion ratio	FCR	199	14.4	5.7-44.6	5.5

and genotypic correlations among traits are required inputs for designing breeding programmes and for many methods of genetic evaluation (Koots *et al.,* 1994). Genotypic and phenotypic parameter estimates for the grasscutter are scarce in the literature. There is only one paper that has reported on phenotypic and genotypic parameters of the grasscutter (Yewadan, 2000). The present paper complements a similar one on co (variance) components and heritability of traits of the grasscutter presented by Annor *et al*. (2012). The objective of this work was to estimate phenotypic and genotypic correlations among traits of the grasscutter.

MATERIALS AND METHODS

The animals, location, experimental protocol and traits have been described in a companion paper (Annor *et al.,* 2012). Briefly, the experiment was done at the grasscutter section of the Department of Animal Science, University of Education, Winneba, Mampong-Ashanti Campus, Ghana. Data were obtained from a random mating population that was constituted in 2005 by randomly selecting and mating 48 does and 12 bucks from a base population of 100 breeding does and 25 bucks that were bought from 25 farmers in two grasscutter farming regions in Ghana. The breeding population was maintained at 48 does and 12 bucks. Replacement does and bucks were selected at random. Data were collected from this population for a period of 5 years (2006-2010). Five hundred and two (502) records were collected from kids during this period. The kids were born by 136 does and 40 sires. Dams from this group gave birth up to the third parity. Animals were fed on elephant grass and supplementary concentrate. They were reared and housed in concrete and wooden cages placed in a large animal house. Mating took place throughout the year. All animals were identified by using metal ear tags (HAUPTNER, GERMANY). Traits measured may be found in Table 1.

Data were analyzed by mixed model methodology using a full animal model and all known genetic relationships, in multiple trait analysis, using the MTDFREML programme (Boldman *et al.*, 1995). Parameters estimated were genetic and phenotypic correlations. The 2-trait animal model used for the estimates was:

$$\begin{matrix} y_I \\ y_J \end{matrix} = \begin{matrix} X_I & 0 \\ 0 & X_J \end{matrix} \begin{matrix} \beta_I \\ \beta_J \end{matrix} + \begin{matrix} Z_I & 0 \\ 0 & Z_J \end{matrix} \begin{matrix} a_I \\ a_J \end{matrix} + \begin{matrix} M_I & 0 \\ 0 & M_J \end{matrix} \begin{matrix} m_I \\ m_J \end{matrix} + \begin{matrix} W_I & 0 \\ 0 & W_J \end{matrix} \begin{matrix} p_I \\ p_J \end{matrix} + \begin{matrix} e_I \\ e_J \end{matrix}$$

Where, $\mathbf{y}_i$ and $\mathbf{y}_j$ are vectors of records of animals for trait i and trait j ; $\mathbf{ß}_i$ and $\mathbf{ß}_j$ are vectors of fixed effects for traits i and j; $\mathbf{a}_i$ and $\mathbf{a}_j$ are vectors of random additive genetic effects for animals for traits i and j; $\mathbf{m}_i$ and $\mathbf{m}_j$ are vectors of maternal genetic effects for traits i and j; $\mathbf{p}_i$ and $\mathbf{p}_j$ are vectors of random permanent environmental effects for dams for traits i and j; $\mathbf{e}_i$ and $\mathbf{e}_j$ are vectors of random residual effects for traits i and j; $\mathbf{X}_i$, $\mathbf{Z}_i$, and $\mathbf{W}_i$ are known design matrices for trait i; and $\mathbf{X}_j$, $\mathbf{Z}_j$, and $\mathbf{W}_j$ are known design matrices for trait j. Fixed effects included litter size at birth, sex, parity of dam, year of birth, season of mating and season of birth.

There were 572 animals in the pedigree file that included the base animals for the analysis of all traits. Local convergence was considered to be met if the variance of the -2 log likelihoods in the simplex was less than 1 x 10^{-6}. After first convergence, restarts were made to find global convergence, with convergence declared when values of -2 log likelihoods did not change to the second decimal. Correlations were classified as low (0.10 – < 0.30), medium (≥ 0.30 – < 0.50) and high (≥ 0.50 – 1.00), regardless of sign (Cohen, 1988).

RESULTS

The results of genetic and phenotypic correlations are presented in Table 2. Genetic correlation between BWT and BWT8 was moderate (0.49) but those between BWT and all other body weight traits were high (0.59 to 0.87) and those between BWT and all daily weight gains were also high (0.57 to 0.77). Phenotypic correlation between BWT and WWT was high (0.59) whereas those between BWT and BWT4, and BWT and PWADG were moderate (0.46 and 0.47, respectively). However, low phenotypic correlation existed between BWT and BWT6 (0.23), BWT and BWT8 (0.29), BWT and ADG4 (0.15), BWT and ADG6 (0.16), and BWT and ADG8 (0.15). There was high genetic correlation between WWT and BWT4 (0.51), WWT and ADG4 (0.55), and WWT and ADG6 (0.52), whereas moderate genetic correlation existed between WWT and BWT6 (0.34), WWT and BWT8 (0.32), WWT and PWADG (0.48), and WWT and ADG8 (0.50). There was high phenotypic correlation between WWT and BWT4 (0.81), WWT and BWT6 (0.54), WWT and BWT8 (0.60), and WWT and PWADG (0.99), but that between WWT and ADG4 was moderate (0.38) whereas those between WWT and ADG6, and WWT and ADG8 were low (0.01 and 0.27, respectively).

Four month weight (BWT4) was highly correlated genetically with BWT6 (0.80), BWT8 (0.69), ADG4 (0.84) and ADG8 (0.55) but BWT4 was moderately correlated genetically with PWADG (0.48) and ADG6 (0.42). Four month weight (BWT4) was highly correlated phenotypically with BWT6 (0.65), BWT8 (0.80), PWADG (0.81) and ADG4 (0.84) but BWT4 was lowly correlated phenotypically with ADG6 (0.01) and moderately correlated with ADG8 (0.44). High genetic correlation existed between BWT6 and BWT8 (0.72), BWT6 and PWADG (0.64), BWT6 and ADG4 (0.86), BWT6 and ADG6 (0.57), and ADG8 (0.65). Phenotypic correlation between 6MWT and ADG8 was low (0.04) but high phenotypic correlation was observed between BWT6 and BWT8 (0.75), BWT6 and PWADG (0.56), BWT6 and ADG4 (0.55), and BWT6 and ADG6 (0.72).

High genetic correlation was observed between BWT8 and PWADG (0.73), BWT8 and ADG4 (0.65), BWT8 and ADG6 (0.58), and BWT8 and ADG8 (0.54). High phenotypic correlation was observed between BWT8 and PWADG (0.61), BWT8 and ADG4 (0.69), and BWT8 and ADG8 (0.66) but the phenotypic correlation between BWT8 and ADG6 was moderate (0.33). Pre-weaning daily gain (PWADG) was highly correlated genetically with ADG4 (0.56), and ADG6 (0.52) but was moderately correlated genetically with ADG8 (0.44). In phenotypic terms, PWADG was moderately correlated with ADG4 (0.39) but lowly correlated with ADG6 (0.02) and ADG8 (0.27). Post-weaning daily gain from 2-4 months (ADG4) was highly correlated genetically with ADG6 (0.64) and ADG8 (0.59) but lowly correlated phenotypically with ADG6 (0.02) and moderately correlated phenotypically with ADG8 (0.41). Post-weaning daily gain from 4-6 months (ADG6) was highly correlated genetically with ADG8 (0.59) whereas their phenotypic correlation was low (0.26).

High negative genetic correlation was observed between LS and BWT (-0.51), and LS and WWT (-0.61) but low negative values were observed between LS and BWT4 (-0.28), LS and BWT6 (-0.03), and LS and BWT8 (-0.03), whereas moderate values were observed between LS and PWADG (-0.33), LS and ADG4 (-0.43), LS and ADG6 (-0.41), and LS and ADG8 (-0.44). High negative genetic correlation was observed between LSW and WWT (-0.59), whereas moderate values were observed between LSW and BWT (-0.47), LSW and ADG4 (-0.38), LSW and ADG6 (-0.41), and LSW and ADG8 (-0.43), whilst low negative values were observed between LSW and BWT4 (-0.29), LSW and BWT6 (-0.03), and LSW and BWT8 (-0.03). Moderate negative phenotypic correlations were observed between LS and BWT (-0.41), LS and WWT (-0.37), and LS and PWADG (-0.33) but low negative values were observed between LS and BWT4 (-0.29), LS and BWT6 (-0.17), LS and BWT8 (-0.23), LS and ADG4 (-0.11), LS and ADG6 (-0.02), and LS and ADG8 (-0.15). Except for WWT, which had moderate negative phenotypic correlation with LSW (-0.31), the phenotypic correlation between LSW and all other body weight traits were low negative (-0.21 to -0.25) and those between LWS and all growth rate traits were also low negative (-0.07 to -0.28).

Except for BWT, which had moderate negative genetic correlation with DJC (-0.31), the genetic correlation between DJC and all other body weight traits were low negative (-0.03 to -0.27) and those between DJC and all growth rate traits were also low negative (-0.23 to -0.26) whilst phenotypic correlations between DJC and both body weight and growth rate traits were low negative (-0.01 to -0.18). Low negative genetic correlations were observed between BWT and LWTL (-0.01), WWT and LWTL (-0.01), and PWADG and LWTL (-0.04). The phenotypic correlations between the same traits were also low negative (-0.14 to -0.18). Except for BWT, which had moderate genetic correlation with PRS (0.42), the genetic correlation between PRS and all other body weight traits were zero to low (0.00 to 0.10) and those between PRS and all growth rate traits were also low (0.01 to 0.25) whilst

Table 2. Genetic (above diagonal) and phenotypic (below diagonal) correlations among 17 traits

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
BWT (1)		0.87	0.59	0.66	0.49	0.77	0.76	0.60	0.57	-0.51	-0.47	-0.31	-0.01	0.42	0.67	-	-
SE		*0.024*	*0.040*	*0.038*	*0.047*	*0.031*	*0.032*	*0.041*	*0.045*	*0.038*	*0.040*	*0.043*	*0.046*	*0.041*	*0.038*		
WWT (2)	0.59		0.51	0.34	0.32	0.48	0.55	0.52	0.50	-0.61	-0.59	-0.27	-0.01	0.07	0.76	-	-
SE	*0.039*		*0.042*	*0.048*	*0.052*	*0.042*	*0.041*	*0.043*	*0.047*	*0.038*	*0.041*	*0.046*	*0.048*	*0.048*	*0.033*		
BWT4 (3)	0.46	0.81		0.80	0.69	0.48	0.84	0.42	0.55	-0.28	-0.29	-0.10	-	0.04	0.56	0.33	-0.82
SE	*0.044*	*0.029*		*0.030*	*0.039*	*0.043*	*0.028*	*0.046*	*0.045*	*0.047*	*0.047*	*0.049*		*0.049*	*0.043*	*0.067*	*0.041*
BWT6 (4)	0.23	0.54	0.65		0.72	0.64	0.86	0.57	0.65	-0.03	-0.03	-0.03	-	0.10	0.66	0.70	-0.77
SE	*0.049*	*0.043*	*0.038*		*0.038*	*0.039*	*0.026*	*0.042*	*0.041*	*0.051*	*0.051*	*0.051*		*0.050*	*0.039*	*0.051*	*0.045*
BWT8 (5)	0.29	0.60	0.80	0.75		0.73	0.65	0.58	0.54	-0.03	-0.03	-0.04	-	0.00	0.80	-	-
SE	*0.052*	*0.044*	*0.033*	*0.036*		*0.037*	*0.041*	*0.044*	*0.046*	*0.054*	*0.054*	*0.054*		*0.055*	*0.031*		
PWADG (6)	0.47	0.99	0.81	0.56	0.61		0.56	0.52	0.44	-0.33	-0.17	-0.25	-0.04	0.25	0.65	-	-
SE	*0.042*	*0.006*	*0.030*	*0.040*	*0.043*		*0.041*	*0.043*	*0.049*	*0.045*	*0.047*	*0.046*	*0.048*	*0.046*	*0.039*		
ADG4 (7)	0.15	0.38	0.84	0.55	0.69	0.39		0.64	0.59	-0.43	-0.38	-0.23	-	0.13	0.62	-	-
SE	*0.049*	*0.046*	*0.027*	*0.041*	*0.039*	*0.045*		*0.039*	*0.044*	*0.045*	*0.046*	*0.048*		*0.049*	*0.040*		
ADG6 (8)	0.16	0.01	0.01	0.72	0.33	0.02	0.02		0.59	-0.41	-0.41	-0.26	-	0.01	0.79	0.50	-0.46
SE	*0.050*	*0.051*	*0.051*	*0.035*	*0.051*	*0.051*	*0.051*		*0.044*	*0.046*	*0.046*	*0.049*		*0.051*	*0.032*	*0.062*	*0.063*
ADG8 (9)	0.15	0.27	0.44	0.04	0.66	0.27	0.41	0.26		-0.44	-0.43	-0.26	-	0.09	0.66	-	-
SE	*0.054*	*0.052*	*0.049*	*0.054*	*0.041*	*0.052*	*0.050*	*0.053*		*0.049*	*0.049*	*0.053*		*0.054*	*0.039*		
LS (10)	-0.41	-0.37	-0.29	-0.17	-0.23	-0.33	-0.11	-0.02	-0.15		0.96	-	-0.04	0.13	0.31	-	-
SE	*0.041*	*0.042*	*0.043*	*0.044*	*0.053*	*0.045*	*0.049*	*0.051*	*0.054*		*0.013*		*0.046*	*0.045*	*0.049*		
LSW (11)	-0.24	-0.31	-0.25	-0.21	-0.23	-0.28	-0.12	-0.07	-0.15	0.69		-	-0.03	0.13	0.35	-	-
SE	*0.044*	*0.043*	*0.044*	*0.044*	*0.043*	*0.046*	*0.049*	*0.051*	*0.054*	*0.033*			*0.046*	*0.045*	*0.048*		
DJC (12)	-0.01	-0.05	-0.12	-0.18	-0.01	-0.04	-0.12	-0.14	-0.08	-	-		-0.02	-	-	-	-
SE	*0.045*	*0.045*	*0.044*	*0.044*	*0.054*	*0.048*	*0.048*	*0.050*	*0.054*				*0.046*				
LWTL (13)	-0.18	-0.16	-	-	-	-0.14	-	-	-	-0.38	-0.34	0.00		0.07	-	-	-
SE	*0.045*	*0.045*				*0.047*				*0.043*	*0.043*	*0.046*		*0.046*			
PRS (14)	0.08	0.02	0.01	0.09	0.00	0.02	0.04	0.13	0.04	-0.01	0.68	-	-0.10		0.94	-	-
SE	*0.045*	*0.045*	*0.045*	*0.045*	*0.055*	*0.048*	*0.049*	*0.050*	*0.054*	*0.045*	*0.033*		*0.046*		*0.018*		
POWS (15)	0.09	0.11	0.11	0.16	0.09	0.14	0.08	0.25	0.06	-0.02	0.11	-	-	0.64		-	-
SE	*0.051*	*0.051*	*0.051*	*0.050*	*0.054*	*0.051*	*0.051*	*0.050*	*0.051*	*0.051*	*0.051*			*0.040*			

Table 2. Continue

FI	(16)	-	-	0.19	0.17	-	-	-	0.03	-	-	-	-	-	-	-		0.68
SE				*0.070*	*0.070*				*0.071*									*0.052*
FCR	(17)	-	-	-0.19	-0.23	-	-	-	-0.11	-	-	-	-	-	-	-	0.15	
SE				*0.069*	*0.069*				*0.071*								*0.070*	

Birth weight (BWT); weaning weight (WWT); 4-month weight (BWT4); 6-month weight (BWT6); 8-month weight (BWT8); pre-weaning daily gain (PWADG);

Post-weaning daily gain from 2-4 months (ADG4); Post-weaning daily gain from 4-6 months (ADG6); post-weaning daily gain from 6-8 months (ADG8); litter size at birth (LS); litter size at weaning (LSW); day from joining to conception (DJC); lactation weight loss of dam (LWTL); pre-weaning survival (PRS); post-weaning survival (POWS); feed intake (FI); feed conversion ratio (FCR); standard error (SE) below trait values in italics.

phenotypic correlations between PRS and both body weight and growth rate traits were zero to low (0.00 to 0.13).Whilst genetic correlations between POWS and all body weight traits, and POWS and all growth rate traits were all high (0.56 to 0.80) and (0.62 to 0.79), respectively, the phenotypic correlations between POWS and both body weight and growth rate traits were all low positive (0.06 to 0.25).

Moderate genetic correlations were observed between BWT4 and FI (0.33), and ADG4 and FI (0.50) whilst high genetic correlation was observed between BWT6 and FI (0.70), whereas phenotypic correlations between the same traits were low (0.19, 0.03 and 0.17, respectively). Genetic correlations between FCR and body weight, and FCR and growth rate traits were negative values. They ranged from moderate (-0.46 for FCR and ADG6) to high (-0.77 and -0.82 for FCR and BWT6, and FCR and BWT4, respectively). Low negative phenotypic correlations were observed between FCR and BWT4 (-0.19), FCR and BWT6 (-0.23), and FCR and ADG6 (-0.11).

Genetic and phenotypic correlations between LS and LSW were both high positive (0.96 and 0.69, respectively). Weak negative genetic relationship existed between LS and LWTL (-0.04), and between LSW and LWTL (-0.03), whilst phenotypic correlations between the same traits were both moderate negative (-0.38 and -0.34, respectively). Weak positive genetic relationship existed between LS and PRS (0.13), and LSW and PRS (0.13), but the genetic relationship between LS and POWS, and LSW and POWS was moderate positive (0.31 and 0.35, respectively). The phenotypic correlations between LS and PRS, and LS and POWS were low negative (-0.01 and -0.02, respectively). That between LSW and PRS, and LSW and POWS was high (0.68) and low (0.11), respectively.

There were virtually no genetic and phenotypic relationships between DJC and LWTL, since their correlations were almost zero (-0.02) and zero (0.00), respectively. There were low genetic and phenotypic relationships between LWTL and PRS (0.07 and -0.10, respectively). There was a strong positive genetic relationship between PRS and POWS (0.94), and a high positive phenotypic relationship (0.64) between the same traits. There was a positive genetic correlation between FI and FCR (0.68) and a low positive phenotypic correlation (0.15) between the same traits.

DISCUSSION

The moderate to high positive genetic correlations obtained between body weight and growth rate, between different body weight traits, and between different growth rate traits indicate that selection for any one of them will improve the other (Hohenboken, 1985; Nicholas, 1987; Van Vleck *et al.,* 1987). Moderate to high positive phenotypic correlations were also observed between most of these traits. Similar results to this work on genetic and phenotypic correlations have been reported in the grasscutter and other livestock species. Yewadan (2000) reported high positive genetic and phenotypic correlations between 4-month weight and 8-month weight in the grasscutter. Koots *et al.* (1994) also reported medium to high positive phenotypic and genetic correlations among body weight and growth traits in beef cattle. These results were expected because many of the body and growth traits were simply measures of growth at different ages (Koots *et al.,* 1994). From the results of the phenotypic correlation studies, it appears as if BWT and WWT are not useful indicators of growth rate from 4-6 and 6-8 months in the grasscutter, since BWT and WWT come first in the life cycle..

Genetic correlations between size traits (body weight and growth rate) and LS and LSW were all negative, indicating that bigger animals tended to come from small litters. Contrary to the results of this study, Yewadan (2000) reported low to medium positive genetic correlation between litter size and body weight. However, unfavourable genetic correlation between growth traits and litter size has been observed in other litter bearing farm species (e.g. Hermesch *et al.,* 2000; Holm *et al.,* 2004). The phenotypic relationship between size traits and all reproductive traits were low negative, indicating weak or no relationship. Yewadan (2000) obtained similar results in the grasscutter. He observed weak phenotypic relationship between BWT4 and LS and BWT8 and LS. Genetic correlations between size traits and DJC and LWTL were generally low negative, indicating little or no relationship between these traits.

There was little or no genetic relationship between all size traits and PRS except with BWT. The positive medium genetic correlation between PRS and BWT indicates that direct selection for birth weight will bring about increase survival of kids (Burfening & Carpio, 1993). The high positive genetic relationship between all size traits and POWS also indicates that genetic improvement of body weight and growth traits will bring about improvement in post-weaning survival (Koots *et al.,* 1994). The study also observed little or no phenotypic relationship between size traits and pre- and post-weaning survival, indicating that body weight or growth traits cannot be used as measures for survival. Estimates of genetic correlations between size traits and feed intake support the theory that as body weight or growth rate increases feed intake also increases (Koots *et al.,* 1994; Arthur *et al.,* 2001). This resulted from the medium to high positive genetic correlation between size traits and FI. Medium to high negative genetic correlations between FCR and size traits have been observed in other studies in farm animals (e.g. Koots *et al.,* 1994; Arthur *et al.,* 2001). A correlation between a ratio such as FCR and its denominator is negative whilst that between a ratio and its numerator is positive (Koots *et al.,* 1994). It was concluded that selection for body weight and growth rate will produce efficient animals that will convert feed into gain at a faster rate.

Low positive phenotypic correlations were observed between size traits (body weight and growth rate) and FI, and size traits and FCR. These results differ from many studies that reported medium to high positive or negative phenotypic correlations between these traits. For example, weighted mean values for phenotypic correlation coefficients reported in the review by Koots *et al.* (1994) were −0.64 and −0.46 for post-weaning FCR with average daily gain and FCR with yearling live weight, respectively. Corresponding phenotypic correlations between FI and the same traits were 0.51 and 0.64, respectively (Koots *et al.,* 1994).

The high genetic and phenotypic correlation observed between LS and LSW indicates that either of them can be used as a measure for the other, and improving one of them will bring about improvement in the other (Garcia & Baselga, 2002; Su *et al.,* 2007). The genetic relationships between LS and LWTL, and LSW and LWTL were almost zero. This means that improvement in LS and LSW will have little or no effect on LWTL. The current moderate negative phenotypic correlation between litter size and LWTL indicates that high litter size is associated with deterioration in dam weight during lactation. This observation was also made by Ferguson *et al.* (1985) in pigs. They reported high negative phenotypic and genetic correlations between dam weight loss and litter size. They suggested that increases in weight loss accompanied by high litter size may be due to high milk production by sows that lose more weight from parturition to weaning their litter.

The moderate positive genetic correlations between LS and POWS, and LSW and POWS observed in this study were also reported in pigs (Su *et al.,* 2007) and in mink (Hansen *et al.,* 2010). They all concluded that selection for high litter size could improve survival, and vice versa. For example Su *et al.* (2007) observed that selection for high litter size at day 5 of birth could improve piglet survival. Most of the phenotypic correlations between litter size and survival were low, indicating little or no phenotypic relationship. There was little genetic and no phenotypic relationship between DJC and LWTL. This means that DJC cannot be used as measures for LWTL, and selection of DJC cannot bring about correlated response in the latter. Low genetic and phenotypic relationships between days to calving and dam weaning weight were reported in Angus cattle by Johnston & Bunter (1996). The low genetic and phenotypic correlation between LWTL and PRS indicates no relationship between the two traits. Contrary to the results of this study, Ferguson *et al.* (1985) observed high negative phenotypic and genetic correlations between the two traits in pigs, and suggested that as weight of sow at weaning decreases, a tendency exists for pre-weaning survival to increase.

The high positive genetic and phenotypic correlations observed between PRS and POWS indicates that either of them can be used as a measure for the other, and improving one of them will bring about correlated response in the other. Moderate to high genetic correlation between PRS and POWS have been reported in goats (Bett *et al.,* 2007) and dairy cattle (Visscher & Goddard, 1995).

The genetic correlation estimate between FCR and FI is in general agreement with the findings in the literature. Koots *et al.* (1994) summarized available estimates between FI and FCR as 0.71 and Arthur *et al.* (2001) obtained an estimate of 0.64 for the same traits. The genetic correlations indicate that selection against FI will improve feed efficiency but will have an undesirable consequence of reducing growth potential. One of the best ways of improving FCR is to select for increased body weight or growth rate, since these traits are highly correlated with FCR (Mrode *et al.,* 1990; Arthur *et al.,* 2001). The phenotypic correlation between FI and FCR reported in this study is lower than literature estimates. Koots *et al* (1994) reported a phenotypic correlation of 0.75 between the two traits, and Arthur *et al* (2001) also obtained a value of 0.48. The results obtained in this work could probably be due to the low genetic variance obtained for feed intake in the grasscutter (Annor *et al.,* 2011).

CONCLUSION

The findings in this study are in general agreement of what pertains to the grasscutter and other farm livestock species. The results could therefore be used to initiate grasscutter selection breeding programmes through estimating breeding values, defining breeding objectives and calculating annual rate of genetic gain.

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