

# Sahiwal cattle in semi-arid Kenya: genetic aspects of growth and survival traits and their relationship to milk production and fertility

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**Abstract** The aim of this study was to estimate genetic and phenotypic parameters for growth and survival traits of Sahiwal cattle in Kenya and determine their relationship to milk production and fertility. Performance records of 5,681 animals were obtained from the National Sahiwal Stud and the traits considered were: birth weight (kilogrammes), weaning weight (kilogrammes), pre-weaning average daily gain (grammes per day), post-weaning average daily gain (grammes per day), yearling weight (kilogrammes), mature weight at 36 months (kilogrammes), pre-weaning survival rate (SR), post-weaning survival rate (PSR), lactation milk yield (kilogrammes), age at first calving (days), and calving interval (days). The data was analysed using univariate and bivariate animal model based on restricted maximum likelihood methods, incorporating all known pedigree relationship among animals. The additive direct effects

were more pronounced than maternal genetic effects in early and in post-yearling growth performance. The additive genetic variance and heritabilities were low for SR and PSR. The correlation between direct additive genetic and maternal genetic effect were negative for pre-yearling traits. Genetic and phenotypic correlations among growth traits and between growth and milk yield were positive, whilst those between growth and fertility were weak and negative. Correlations between survival and growth were generally low and positive. The estimates obtained in this study provide the necessary technical parameters for evaluating alternative breeding programmes and selection schemes for sustainable improvement of Sahiwal cattle.

**Keywords** Breeding programme · Correlations · Heritability · (Co)variances · Selection schemes

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## Introduction

The Sahiwal belongs to a class of large Zebu breeds that have primarily been used for dairy and beef production in tropical and sub-tropical regions. The breed has spread to several countries in Africa, Asia and Australia with purebred sub-populations in Pakistan, India, Kenya and Australia (FAO 2007). In Kenya, Sahiwal genetic resources are raised mostly by private and government ranches (which collectively form the nucleus herds), and the Maasai pastoralists, where they are kept as purebreds or crossbreds with local Small East African Zebu (Muhuyi 1997). Performance recording and selection for improved milk yield and growth performance is mainly practised in the nucleus herds, and the resultant genetic material transmitted to pastoral herds. The equally important fertility and

survival traits are mostly treated as secondary traits and therefore given less emphasis in the selection process. However a comprehensive selection programme involving all these traits requires knowledge on their performance levels and the extent of additive genetic variance in the population, as well as their degree of association amongst themselves.

Previous studies on performance evaluation of Sahiwal cattle in the tropics have mainly focused on milk production and fertility traits (e.g. Mwandotto 1994; Rege et al. 1992; Dahlin et al. 1998; Ilatsia et al. 2007). Appropriate models need to be used in order to obtain accurate and reliable estimates of (co)variances and genetic estimates. For example, in estimating growth performance traits, it is important to account for both direct additive and maternal effects and their interaction. Estimates of genetic parameters for growth performance of Sahiwal cattle have previously been presented (e.g. Rege et al. 1992; Mwandotto 1994). These studies assumed no relationship between the dams and that sires were mated randomly to the dams. However, with regard to the mating design in most nucleus herds, sires are usually assigned to particular dams. Furthermore, the analytical approach in those studies could not allow estimation of maternal effects, a fact that would lead to potential overestimation of (co)variance components and ultimately genetic parameters. Recently, Ilatsia et al. (2007) presented genetic parameters for milk and reproductive performance of the Sahiwal cattle. However, the selection process in most of the breeding herds has traditionally been based on both milk and growth performance. Therefore, estimate of (co)variance components and genetic parameters for growth traits and survival are equally important in order to design more comprehensive selection schemes that take account of the dual purpose role that the Sahiwal breed plays in low-input production systems. Such estimates are particularly scarce for Zebu cattle breeds in tropical and sub-tropical regions. This study is therefore a follow-up of earlier related studies by Ilatsia et al. (2007) that recommended further work to understand the genetic aspects of growth performance and survival rate of Sahiwal cattle and determines their relationship to milk production and fertility.

## Materials and methods

### Data source, herd management and selection

Data on growth performance were obtained from the National Sahiwal Stud (NSS) which is owned by the National Animal Husbandry Research Centre, one of the main centres of the Kenya Agricultural Research Institute.

The NSS is a research herd used for development of appropriate husbandry and breeding practices for cattle keepers mostly in the southern rangelands of Kenya. The stud constitutes purebred Sahiwal cattle and is the leading source of breeding stock for both pastoralists and other stud herds. Compared to other nucleus herds, the NSS keeps relatively good performance and pedigree records which are used to support selection and management decisions. The NSS was therefore chosen because of the reliability of such data which is crucial in estimation of (co)variance components within the animal model framework. The NSS is located approximately 100 km North West of Nairobi at an altitude of 1,829–2,330 m above sea-level in agro-ecological zone IV which is generally classified as semi-arid. The average rainfall is 680 mm per annum; the distribution is bimodal with peaks in April and November. The temperatures range from 8°C to 26°C, whilst the relative humidity varies from 60% to 75%. The vegetation consists mainly of Kikuyu grass (*Pennisetum clandestinum*), with scattered Acacia trees and shrubs.

All calves are weighed and identified at birth; they are allowed to suckle colostrum within 24 h of birth, after which they are transferred to separate calf pens where they are artificially fed on milk. Milk rations are given in reducing quantity depending on the age of the calves. Calves are weighed on weekly basis; however, this depends on the availability of sufficient labour to handle the animals, as well as the condition of the weighing equipment. Calves are weaned at approximately 6 months of age, and separated into different herds at approximately 1 year based on their sex. All animals are grazed on natural pastures without mineral or other feed supplements. Mandatory control of ectoparasites (mainly ticks) is done by routine weekly dipping. Control of endoparasites is usually not practised, but animals are occasionally treated depending on the number of animals showing symptoms of the parasites and availability of funds.

The primary breeding goal at the NSS is to increase milk and growth performance. Own and pedigree selection is practised, supported by a progeny testing programme for candidate bulls based on first lactation performance of their daughters and growth performance of their offspring. Improvement of fertility is achieved by culling cows based on their reproductive performance measures such as insemination counts and calving frequency. Adaptation is assumed to be improved as a correlated response by allowing animals to produce under the harsh semi-arid range conditions with minimal husbandry interventions.

### Description of traits and data characteristics

Growth performance and survival data of animals born from 1973 to 2004 were used in this study. However the

number of records and the years varied depending on the trait under consideration. Growth traits considered were: birth weight (BW, kilogrammes), weaning weight (WW, kilogrammes), pre-weaning average daily gain (DG, grammes per day), post-weaning average daily gain (PDG, grammes per day), yearling weight (YW, kilogrammes), mature weight (MWT, kilogrammes). Survival traits were pre-weaning survival rate (SR) and post-weaning survival rate (PSR). Milk production traits were lactation milk yield (MY, kilogrammes) in the first three parities considered as repeated measures whilst fertility traits were age at first calving (AFC, days), and calving interval (CI, days) considered also as a repeated measure in the first four parities. Data were edited for consistency of pedigree information and correct dates of birth, calving and weighing. Records with anomalies in pedigree information and dates were discarded. Mature weight (MWT) constitute both cow and bull weights at approximately 3 years, which is the expected service age for cows and sale weights for bulls. The final structure of the data and corresponding pedigree information is presented in Table 1.

Data analyses

Preliminary analyses to determine non-genetic factors that influence growth and survival rate were performed using PROC GLM and LIFETEST procedures, respectively (SAS 2004). Table 2 shows the relevant fixed effects fitted as well as the corresponding levels of significance for each of the traits. Analysis involving milk production and fertility traits, as well as definition of seasons of birth has already been presented in an earlier related study (see Ilatsia et al. 2007). (Co)variance components and genetic parameters were estimated by fitting linear mixed animal models using REML procedures (Meyer 1989). The full linear mixed model was:

$$y = Xb + Z_a a + Z_m m + Z_c c + e \tag{1}$$

where  $y$  is the observation whilst  $b, a, m, c$  and  $e$  are vectors for fixed effects, direct genetic effects, maternal genetic effects, maternal environmental effects and random residual effects, respectively. The incidence matrix for the fixed effects is represented by  $X$ , whilst the incidence matrices,  $Z_a, Z_m$  and  $Z_c$ , relate the respective random effects to the observation. The variance–covariance structure for the effects was;

$$v \begin{bmatrix} a \\ m \\ c \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I_c\sigma_c^2 & 0 \\ 0 & 0 & 0 & I_n\sigma_e^2 \end{bmatrix} \tag{2}$$

where:  $A$  is the numerator relationship matrix;  $I_c$  and  $I_n$  are the identity matrices for dams and animals, respectively; and  $\sigma_a^2, \sigma_m^2, \sigma_c^2$  and  $\sigma_e^2$  are variance components for the direct genetic, maternal genetic, permanent maternal environment, direct-maternal genetic covariance and residual effects, respectively. To assess the significance of maternal effects, preliminary analyses fitted a sequence of random models in univariate analyses for each of the growth traits. A maternal effect was only retained if there was a significant increase in the negative log-likelihood following the inclusion of that effect in the model. Table 2 shows the structure of the final models fitted for each of the traits.

A simple bivariate animal model, with the direct additive effect as the only effect, was used to estimate genetic and phenotypic correlations between various traits. The traits considered in bivariate analysis were pairwise combinations of BW, WW, YW, DG, PDG, CWT, BWT, SR, PSR, MY, AFC and CI. Since genetic and phenotypic correlation between milk production and fertility traits have already been presented (Ilatsia et al. 2007), combinations amongst these traits were not considered here. The fixed effects were as those fitted in the univariate analysis; however, for milk production and fertility traits, the year×season of calving, and dam age at calving were fitted as fixed and covariable,

**Table 1** Data structure and summary statistics for growth performance traits and survival rates

	Trait							
	BW (kg)	WW (kg)	YW (kg)	DG (g/day)	PDG (g/day)	MWT (kg)	SR (%)	PSR (%)
Number of animals	5,681	4,525	3,309	4,525	3,803	3,803	4,525	3,803
Mean	21.86	48.59	133.98	162	322	337.62	81.33	93.33
SD	2.66	6.44	11.61	28.2	69.2	67.86	–	–
Number of sires	381	369	361	369	303	303	369	303
Number of dams	3,348	3,074	2,745	3,074	2,745	1,674	3,074	2,745
Progeny per sire	14.9	12.3	9.2	12.3	12.6	12.6	12.3	12.6
Progeny per dam	1.7	1.5	1.2	1.5	1.4	1.4	1.5	1.4

*BW* birth weight, *WW* weaning weight, *DG* pre-weaning average daily gain, *PDG* post-weaning average daily gain, *YW* yearling weight, *MWT* mature weight, *SR* pre-weaning survival rate, *PSR* post-weaning survival rate

**Table 2** Structure of the models used in the final analyses and levels of significance for growth and fertility traits

Effect	Type	Trait							
		BW (kg)	WW (kg)	YW (kg)	DG (g/day)	PDG (g/day)	MWT (kg)	SR (%)	PSR (%)
Sex	F	***	***	***	**	ns	ns	ns	ns
Year×season of birth	F	***	***	***	***	***	ns	***	ns
BW	C	–	***	ns	**	ns	ns	***	ns
WW	C	–	–	–	–	*	ns	–	*
Dam post partum weight	C	***	ns	ns	ns	ns	–	–	–
Age at weighing	C	–	***	***	–	–	ns	–	–
Maternal environmental	R	√	–	–	–	–	–	–	–
Direct genetic	A	√	√	√	√	√	√	√	√
Maternal genetic	A	√	√	√	√	–	–	–	–
Direct-maternal effects	A	√	√	√	–	–	–	–	–

F fixed factor, C linear covariate, A random factor with relationship matrix, R random factor with identity matrix, BW birth weight, WW weaning weight, DG pre-weaning average daily gain, PDG post-weaning average daily gain, YW yearling weight, MWT mature weight, SR pre-weaning survival rate, PSR post-weaning survival rate

ns=p>0.05; √, fitted

\*P<0.05; \*\*P<0.01, \*\*\*P<0.001

respectively. In this case, the animal model allowed for repeated records per cow by fitting an additional random effect that represented the permanent environment effect.

**Results and discussion**

Estimates from univariate analyses

Estimates of (co)variance components and genetic parameters for growth traits and survival rate based on univariate analyses are presented in Table 3. The direct and maternal heritability estimate and permanent environmental variance as proportion of phenotypic variance for

BW were 0.23, 0.09 and 0.06, respectively. Maternal effects were also evident in WW and YW accounting for 0.27 and 0.14 of the total phenotypic variance (Table 3). Direct additive and maternal genetic effects were more pronounced at weaning resulting in high direct and maternal heritability estimates of 0.39 and 0.27 respectively. Direct additive and maternal genetic variances were low for DG accounting for 0.17 and 0.12 of the total variance, respectively. Maternal environmental variances were generally low in early stages of growth up to yearling and were 0.06, 0.07, 0.04 and 0.05 for BW, WW, YW and DG, respectively. Since inclusion of permanent maternal effects did not improve the negative log-likelihood for PDG and MWT, only direct additive genetic were considered for

**Table 3** Estimates of variance components and genetic parameters with their corresponding standard errors from various univariate analyses

Trait	Component									
	$\sigma^2_a$	$\sigma^2_m$	$\sigma^2_c$	$\sigma_{am}$	$\sigma^2_e$	$\sigma^2_p$	$h^2_a$	$h^2_m$	$c^2$	$r_{am}$
BW (kg)	1.55	0.62	0.41	-0.77	4.89	6.69	0.23±0.05	0.09±0.02	0.06±0.02	-0.65±0.08
WWT (kg)	7.22	5.14	1.40	-5.74	9.48	18.50	0.39±0.05	0.27±0.03	0.07±0.03	-0.66±0.08
YW (kg)	33.02	16.03	5.05	-20.46	84.00	117.63	0.28±0.06	0.14±0.06	0.04±0.03	-0.89±0.06
DG (g/day)	80.41	56.35	23.11	–	–	463.59	0.17±0.05	0.12±0.05	0.05±0.04	–
MWT (kg)	211.11	–	–	–	811.03	1,022.14	0.21±0.06	–	–	–
PDG (g/day)	135.12	–	–	–	532.90	668.02	0.20±0.05	–	–	–
SR (%)	3.03	–	–	–	98.09	101.12	0.03±0.02	–	–	–
PSR (%)	2.77	–	–	–	135.73	138.5	0.02±0.02	–	–	–

BW birth weight, WW weaning weight, DG pre-weaning average daily gain, PDG post-weaning average daily gain, YW yearling weight, MWT bull mature weight, SR pre-weaning survival rate, PSR post-weaning survival rate,  $\sigma^2_a$  direct genetic variance,  $\sigma^2_m$  maternal genetic variance,  $\sigma^2_c$  permanent maternal environment variance,  $\sigma^2_e$  residual error variance,  $h^2_a$  direct heritability,  $h^2_m$  maternal heritability,  $c^2$  maternal environmental variance as a proportion of phenotypic variance,  $r_{am}$  direct-maternal genetic correlation

these traits (see Table 2). They accounted for 0.20 and 0.21 for PDG and MWT, respectively.

In our study, early growth performance was under the influence of both an individual's genes as well as maternal genetic effects. However, the influence of the maternal environmental effects were minimal, a fact that resulted into very low estimate of  $c^2$  (Table 3). The low maternal environmental variance is a reflection of the artificial calf management system where the mother's environmental influence is reduced, with direct additive and maternal genetic effects playing a greater role in early growth performance. The observed low maternal environmental effects in the early stages of growth could be as a result of the residual prenatal maternal environment and cytoplasmic effects. Sahiwal cattle have traditionally been kept for milk production where they are routinely milked unlike other tropical beef cattle where dams are allowed to suckle their calves ad libitum. It is probably because of this that documentation of the extent of maternal environmental effects in Sahiwal dams based on cow-calf feeding system is scarce in literature. In a study on genetic and environmental causes of variation in body weight of Sahiwal cattle in Pakistan, Khan et al. (1999) reported  $c^2$  of 0.05 on calf weight under artificial milk feeding system. In a study on Boran cattle in Kenya, Wasike et al. (2009) reported low maternal environmental variance at birth ( $c^2=0.16$ ); however, unlike in our study and those mentioned, maternal environmental effects played a great role accounting for a significant variation in pre-weaning growth. The relatively large phenotypic variances for pre-weaning growth performance in tropical cattle breeds under the cow-calf feeding system is a reflection of differences in individual dam's milk production and mothering ability (Orenge et al. 2009; Wasike et al. 2009), compared to artificial feeding systems where calves are subjected to relatively uniform feeding regimes (e.g. Khan et al. 1999; Demeke et al. 2003). However, the dam environmental influence gradually diminishes with age as more of the growth and maturing characteristics get influenced by an individual's genes, an observation that has widely been acknowledged in various livestock species. This could be the reason why, in this study, inclusion of maternal environment effects had no significant influence on post-weaning growth performance (i.e. PDG, MWT). The direct additive genetic effects accounted for a very small proportion of the total variation in SR and PSR with correspondingly high residual error variances translating into low heritability estimates of 0.03 and 0.02 for the two traits respectively (Table 3). Survival traits have been reported to have low additive genetic variance with correspondingly low heritability probably due to high environmental influences (Burrow 2001; Kahi et al. 2003). Unlike fertility and growth traits, these traits are normally not directly included in the

selection programmes and therefore tend mostly to be changed as correlated traits.

The genetic correlations between additive direct and maternal genetic effects were antagonistic and were  $-0.66$ ,  $-0.65$  and  $-0.89$  for BW, WW and YW, respectively (Table 3). The reported estimates for additive-maternal genetic correlations in cattle breeds reared in the tropics vary in magnitude but are generally negative for most traits presented (e.g. Khan et al. 1999; Maiwashe et al. 2002; Wasike et al. 2009). However, positive correlations of 0.47 and 1.00 for BW were reported for Zebu crossbreds in Ethiopia (Demeke et al. 2003) and Hereford calves in Kenya (Orenge et al. 2009), respectively. The correlation estimated for WW ( $-0.65$ ) in this study is lower than the estimate of  $-0.25$  reported by Wasike et al. (2009) for Boran calves under cow-calf management. Orenge et al. (2009) reported moderate to high negative correlations for BW, ADG and WW of  $-46$ ,  $-0.51$  and  $-0.47$  for Charolais, and 1.00,  $-1.00$  and  $-0.39$  for Hereford beef cattle breeds, respectively, in the tropical highlands of Kenya. On the other hand, Maiwashe et al. (2002) reported an estimate of  $-0.54$  for WW in Bonsmara cattle in South Africa. Such differences in the reported estimate would be expected bearing in mind that large variations exist in gene pools among populations, breed differences, previous selection strategies, environmental influences as well as the amount of performance data used and model used in analysis. Nonetheless, the moderate to high negative estimate of direct-maternal genetic correlation reported for the Sahiwal breed in this study and other tropical cattle breeds indicates an antagonistic relationship between these components. Therefore, future performance evaluation of growth performance should take into account the potential influence of this covariance component; otherwise, its omission would result in an upward bias in estimates of direct and maternal heritability.

#### Genetic and phenotypic correlations

Table 4 shows estimates of genetic and phenotypic correlations among the various traits from bivariate analyses. Genetic correlations among pre-yearling growth (i.e. BW, WW and YW) were moderately high and were 0.63, 0.65 and 0.59 for BW vs WW, BW vs YW and WW vs YW, respectively. Genetic correlations between these pre-yearling growth weights (i.e. BW, WW and YW) and mature weights (MWT) were comparably low and were 0.22, 0.20 to 0.49, respectively. The high genetic correlations among pre-yearling growth weights indicate the high degree of similarity in additive gene effects at different ages. Given the favourable high genetic correlation among pre-yearling growth weights and their corresponding positive, though low, genetic association with mature



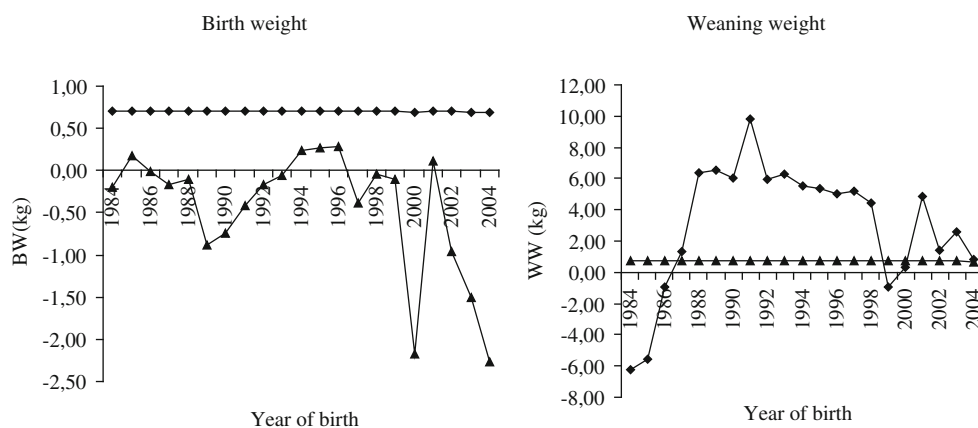
cows with relatively higher milk yield in the future under good feeding management. Khan et al. (1999) reported favourable genetic relationship (0.57) between cow mature weight and milk yield in Sahiwal cattle in Pakistan. They (Khan et al. 1999) also reported moderate to high (range of 0.38 to 0.79) genetic correlations between weight up to two years and cow mature weight. Genetic and phenotypic correlations between growth and fertility were low and negative. There were no correlation between growth and CI except YW vs CI and MWT vs CI where low correlations of  $-0.03$  and  $-0.17$ , respectively were estimated. The relatively large standard errors (Table 4) associated with the genetic correlation estimates in this study could be due to the large sampling variation resulting from the limited number of sires and progeny per sire (see Table 2).

Genetic and phenotypic correlations between growth and survival traits were generally low (ranges of 0 to 0.11). This could also be a reflection of the selection process that is skewed towards production. To examine the effect of this selection procedure, our study evaluated genetic and environment trends over a period of 20 years for pre-weaning growth performance. Figure 1 shows genetic and environment trends for BW and WW over this period. Direct selection for pre-weaning growth performance notwithstanding, estimate of genetic trends for pre-weaning growth weights (Fig. 1) reveals that there has been very little genetic progress made over the years. Even in cases where environmental conditions seemed to have been favourable (e.g. between the years 1987 and 1995 for WW, Fig. 1), there was still not much improvement in WW. This could possibly be due to adverse environmental conditions that obstruct full genetic expression at birth (Fig. 1) that was carried over to weaning. It is likely that various environmental factors interact to suppress and restrict the realisation of full genetic potential for pre-weaning growth performance. This could, probably over time, confer the Sahiwal calves

with coping mechanism that enhances their ability to withstand the challenging production conditions whilst maintaining steady level of genetic performance, bearing in mind that the all important pre-weaning maternal environment influence is deliberately denied.

Given the low additive genetic variance and the environmental influence on survival, two options for improving both the production and adaptation could be explored. The first one is to maintain the status quo, i.e. pursue selection for improved production and allow adaptation to be improved as a correlated response in the strenuous production environment. The second alternative is to exploit the biology of direct measures of adaptation and determine their association with production, then develop criteria that support improvement of both adaptation and production. In this study, pre- and post-weaning survival rates, normally considered as herd traits, were used as indicators of tolerance or resistance to pathogenic parasites and other production challenges. In most livestock breeding programmes in the tropics, survival traits are selected for indirectly during direct selection for production traits under restrictive production environments (Burrow 2001). Whilst production can be measured in terms of quantity and quality of products, the greatest challenge is identifying selection criteria of adaptation and incorporating them into technically and economically feasible recording schemes. For example, resistance/tolerance to diseases can be measured in terms of the actual parasite levels such as tick counts or parasite count per volume of blood, or its direct effects such packed cell volume or the faecal egg count. However, with the already over constrained livestock recording schemes in developing countries, the practicality of recording such traits becomes very remote given the highly specialised human and enormous financial resources that would be required to realise this.

**Fig. 1** Genetic (*diamond*) and environmental (*triangle*) trends in birth weight and weaning weight. Genetic trends are expressed as deviations of breeding value from the population mean



## Implications to a breeding programme

There exists considerable additive and maternal genetic variance in growth performance to enhance growth performance of Sahiwal cattle under semi-arid conditions through appropriate selection procedures. Previous studies have demonstrated the negative shift in performance of Sahiwal cattle especially when climatic conditions get extremely hostile under limited husbandry mitigation measures (Ilatsia et al. 2007). This situation will continue to be a challenge to the realisation of the full genetic potential of the Sahiwal breed in the tropics, as demonstrated in Fig. 1. In most cases, the management has assumed that the population poses the requisite capabilities to cope with such extremes. However, such an assumption could frustrate any breeding efforts because the potential of promising genotypes are either disrupted or lost and thus complicating selection or mating plans to alter performance. Realisation of the full benefits of the breeding programme could therefore be achieved by improving the herd welfare especially when climatic conditions become extremely challenging. The results reported in this study compliment those reported earlier by Ilatsia et al. (2007) in providing a comprehensive array of the requisite biological parameters that would be necessary in evaluating the efficiency of alternative breeding programmes for genetic improvement and conservation of Sahiwal genetic resources in Kenya.

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