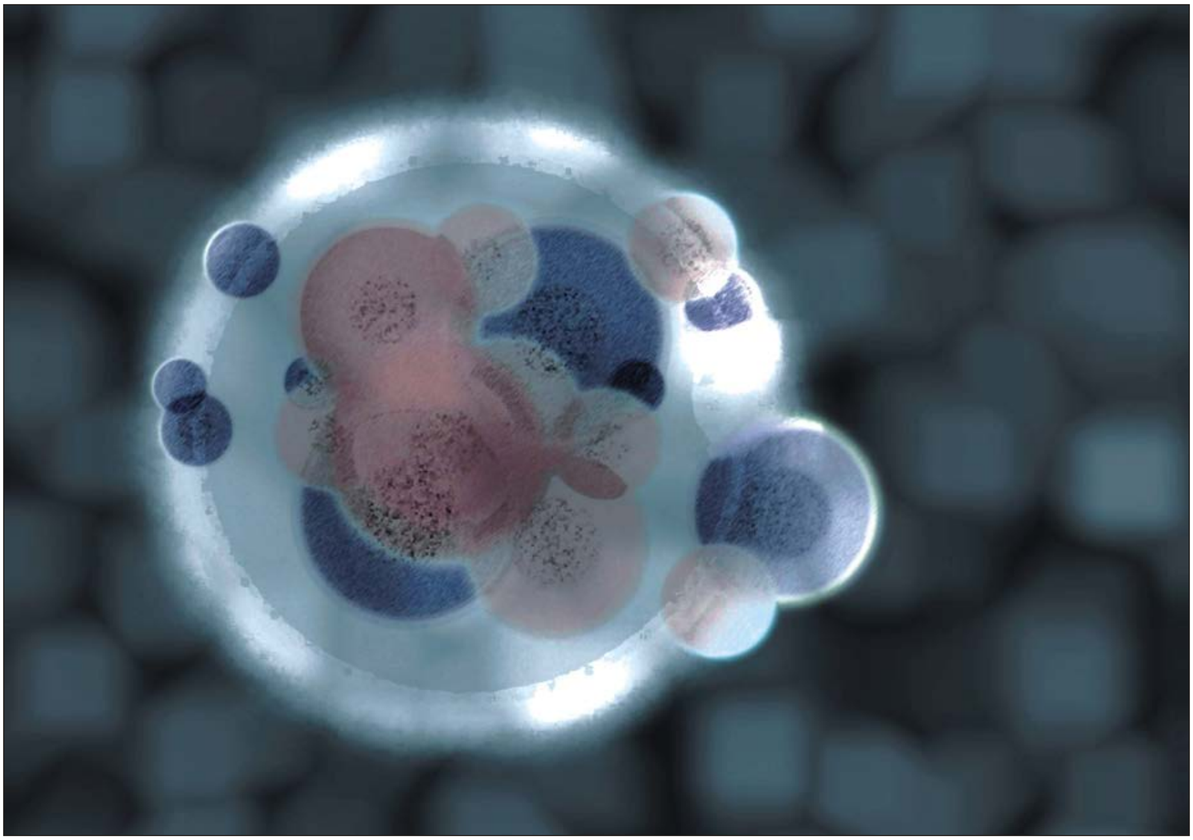

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Estimation of (Co) Variance Components for Type Traits in Charolais Cattle

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Abstract: Records of 3379 Charolais cattle were used to estimate (co) variance components for 20 type traits. The traits analysed in the study were back, back breadth, depth, frame, front leg, head, hind leg, hind length, hind round, hip width, hooves, pastern, pigment, rump flat, rump form, rump length, scrotum, sheath, tail placement and top line. Variance and covariance components were estimated using restricted maximum likelihood procedure with univariate and multivariate models. Heritability estimates ranged from 0.02 for hooves to 0.5 for pigment. Genetic correlations ranged from -0.78 (rump form and hooves) to 0.01 (hooves with frame and front leg). Phenotypic correlations ranging from -0.01 (sheath with back breadth and depth) to 0.84 were also observed.

Key words: Correlations, heritability and variance components

INTRODUCTION

Cattle breeders worldwide have long held the belief that type traits have important influence on cattle performance (Gutierrez and Goyache, 2002). Selection for type traits has been practised for many years and currently forms a major part of most livestock improvement programmes around the world. The importance of type traits stems from the realisation that they are related to traits of economic value in cattle such as herd life (Dekkers *et al*., 1994; Weigel, 2002).

Improvement of cow survival through indirect selection for these traits is appropriate as they are measured early in life, have close genetic relationship with herd life and exhibit considerable genetic variation (Short and Lawlor, 1992; Larroque and Ducrocq, 1999; Schneider *et al*., 1999; Cruickshank *et al*., 2002). Most of the work on type traits has been carried out in dairy because of their relatively higher influence on production and longevity traits (Gutierrez and Goyache, 2002). In beef cattle, type traits are also important and are expected to be useful for evaluating the animals as meat producers. Longevity has become an increasingly important trait in beef cattle since increased longevity decreases costs for the farmer and increases revenue (Forabosco *et al*., 2004) The type classification system is expected to describe the animal's conformation as far as its skeletal and muscular development so as to evaluate the animal's productive aptitude (Gutierrez and Goyache, 2002).

Genetic parameters are an important pre-requisite for a sound improvement programmes since they determine selection criteria and the potential for genetic improvement. Variance components are also required for estimation of breeding values. It is, therefore, essential to estimate (co) variance components for type traits in a given population as they may vary among populations.

The primary aim of this study was to determine variance and covariance components for conformation traits in the South African Charolais cattle population. Such estimates will be used to estimate breeding values for the individual type traits as well as to determine the usefulness of type traits in breeding programmes.

MATERIALS AND METHODS

The study was carried out at the Animal Improvement Institute (AII) in South Africa and records were collected between 1997 and from 2003. Data comprised of 3379 records on Charolais cattle from 63 herds. The data were obtained from the Charolais Cattle Breeders Society of South Africa and each record consisted of scores on 20 type traits. Each trait was scored on a nine-point biological scale.

A minimum of 5 animals per contemporary group was considered for the statistical analysis. A contemporary group was defined as animals from the same breeder that were classified on the same date, hence the concatenation of the breeder and the classification date (HCD) (Table 1).

To identify the effects of non-genetic sources to be included in the model, an analysis of variance was performed using the SAS (2001). Fixed effects included were a concatenation of breeder and classification date

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Table 1: Range of type scores, means and standard deviation of traits

Traits	Range of type scores	Mean±SE
Back	3-9	6.85±0.95
Back breadth	2-9	6.16±1.14
Depth	3-9	6.47±1.05
Frame	1-9	6.46±1.19
Front leg	2-9	6.65±1.06
Head	1-9	6.06±1.20
Hind leg	2-9	5.93±1.21
Hind length	1-9	6.08±1.08
Hind round	2-9	6.19±1.06
Hip width	2-9	6.89±1.02
Hooves	2-9	6.40±1.20
Pastern	1-9	6.43±1.22
Pigment	2-9	7.45±1.01
Rump flat	3-9	6.79±0.99
Rump form	1-9	6.56±1.08
Rump length	2-9	6.71±0.98
Scrotum	1-9	6.72±1.10
Sheath	2-9	7.49±1.46
Tail placement	2-9	6.42±1.21
Top line	2-9	6.67±1.19

Table 2: Fixed effects included in the analysis of different traits

Traits	HCD	AGEM	Age^2	Sex
Back	+	+	+	+
Back breadth	+	+	+	-
Depth	+	+	-	-
Frame	+	+	-	-
Front leg	+	-	-	-
Head	+	+	+	-
Hind leg	+	-	-	+
Hind length	+	+	+	+
Hind round	+	+	+	+
Hip width	+	+	+	+
Hooves	+	+	-	-
Pastern	+	+	-	-
Pigment	+	-	-	+
Rump flat	+	-	-	-
Rump form	+	+	+	-
Rump length	+	+	+	+
Scrotum	+	+	+	-
Sheath	+	-	-	+
Tail placement	+	-	-	+
Top line	+	-	-	+

+: Included in model; -: Excluded in model

(HCD), linear age effect (agem) in months and the quadratic effect of age (age^2) and the effect of sex. Only fixed effects identified as significant ($p<0.05$) were included in the model for (co) variance component estimation. A summary of the effects included in models is shown in Table 2.

The complete pedigree file was constructed by tracing animals/pedigree as many generations back as possible. The variance components were estimated using the Variance Components Estimate-Restricted Maximum Likelihood (VCE-REML) version 4.3 (Groeneveld, 1998) with the following univariate animal model:

$$Y_{ijklm} = \mu + HDC_i + agem_j + age^2_k + sex_l + a_m + e_{ijklm}$$

Where:

Y_{ijklm} = Linear type score

μ = Overall mean

HDC_I = The fixed effect of the ith herd classification date

$agem_j$ = The fixed effect of the kth quadratic age at classification (months)

sex_l = The fixed effect of the lth sex of the animal

a_m = Random additive genetic effect mth animal

e_{ijkl} = Random error

The following multivariate mixed model was fitted to the data to estimate the (co) variance components and genetic correlations.

$$Y = Xb + Zu + e$$

Where:

Y = The vector of phenotypic measurements for type traits

X = The incidence matrices relating observations to fixed effects

b = The vector of fixed effects

Z = The incidence matrices relating observations to random effects

u = The vector of additive genetic effects of the animal

e = The vector of random residual effects

Furthermore, genetic correlations among the traits were estimated using VCE-REML version 4.3 (Groeneveld, 1998).

RESULTS AND DISCUSSION

The heritability of a trait is the fraction or portion of the transferable genetic value component, relative to the total measurement of the trait. Table 3 shows the additive genetic, error variance components, the estimated heritability and standard error values for studied traits.

Hooves had the lowest estimate (0.02), followed by the scrotum (0.09). The highest estimate was observed for the sheath (0.66) followed by pigment (0.57). This means that a good response to selection is expected from sheath and pigment as compared to the other traits. The body size traits (back, body depth, rump length, hip width) and hind traits (leg, length and round) had moderate estimates of heritability. The moderate estimates of heritability for body traits indicate that moderate selection response may be achieved in these traits if the selection goal is for large body size. Muscle development traits (rump flat, rump form) showed low heritabilities. However, other muscle development traits such as back breadth and hind round

Table 3: Genetic variance components (σ_a^2), error variance components (σ_e^2), heritability estimate (h^2) and standard errors for traits

Traits	σ_a^2	σ_e^2	h^2±SE
Back	0.33	0.67	0.33±0.01
Back breadth	0.23	0.75	0.23±0.01
Depth	0.23	0.56	0.29±0.02
Frame	0.16	0.89	0.15±0.03
Front leg	0.06	0.78	0.07±0.01
Head	0.17	0.93	0.15±0.03
Hind leg	0.32	1.20	0.21±0.01
Hind length	0.45	0.83	0.35±0.02
Hind round	0.33	0.87	0.27±0.02
Hip width	0.30	0.81	0.27±0.02
Hooves	0.02	0.83	0.02±0.02
Pastern	0.14	0.89	0.13±0.01
Pigment	0.57	0.57	0.50±0.02
Rump flat	0.04	0.78	0.05±0.02
Rump form	0.11	0.78	0.13±0.01
Rump length	0.29	0.75	0.28±0.02
Scrotum	0.09	0.82	0.10±0.02
Sheath	0.66	1.54	0.30±0.01
Tail placement	0.47	1.10	0.30±0.03
Top line	0.28	1.18	0.19±0.01

Table 4: Genetic correlations (above the diagonal) and phenotypic correlations (below the diagonal) among 20 linear-type traits of Charolais cattle

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Back		0.72	0.60	0.79	0.69	0.73	0.62	0.70	0.75	0.77	0.39	0.60	0.32	0.84	0.76	0.95	0.77	0.24	0.50	0.64
Back breadth	0.47		0.76	0.81	0.70	0.80	0.72	0.91	0.95	0.93	0.00	0.00	0.09	0.00	0.00	0.69	0.00	-0.04	0.86	0.82
Depth	0.38	0.63		0.66	0.45	0.69	0.45	0.79	0.68	0.78	0.00	-0.01	0.04	0.44	0.56	0.66	-0.31	0.03	0.41	0.56
Frame	0.62	0.48	0.44		0.62	0.73	0.56	0.81	0.82	0.79	1.00	0.00	0.37	0.39	0.26	0.80	0.09	-0.12	0.42	0.31
Front leg	0.28	0.35	0.31	0.28		0.27	0.79	0.75	0.76	0.76	1.00	0.56	0.17	0.12	0.26	0.70	0.17	0.01	0.50	0.67
Head	0.44	0.49	0.48	0.44	0.30		0.55	0.92	0.93	0.81	0.28	0.10	0.28	0.17	0.29	0.75	0.12	0.17	0.60	0.62
Hind leg	0.30	0.45	0.36	0.28	0.35	0.84		0.71	0.82	0.72	0.68	0.82	0.37	0.31	0.73	0.68	0.65	-0.05	0.74	0.20
Hind length	0.43	0.67	0.67	0.48	0.33	0.45	0.45		0.91	0.91	0.52	0.52	0.08	0.73	0.91	0.70	0.57	-0.71	-0.75	-0.76
Hind round	0.41	0.73	0.62	0.44	0.35	0.46	0.51	0.76		0.95	0.50	0.65	0.20	0.54	0.92	0.48	0.52	-0.09	0.44	0.56
Hip width	0.45	0.79	0.61	0.46	0.31	0.47	0.42	0.65	0.71		0.45	0.53	0.20	0.77	0.91	0.78	0.67	0.32	0.15	-0.10
Hooves	0.21	0.27	0.24	0.24	0.36	0.26	0.33	0.28	0.25	0.21		0.77	0.19	-0.34	-0.78	0.36	-0.16	-0.05	0.31	0.29
Pastern	0.27	0.32	0.23	0.27	0.39	0.25	0.45	0.31	0.33	0.27	0.46		0.50	-0.17	0.64	0.56	0.57	0.31	0.69	0.64
Pigment	0.20	0.07	0.07	0.13	0.16	0.16	0.15	0.08	0.10	0.11	0.09	0.14		0.23	0.11	0.53	0.44	0.42	-0.19	-0.13
Rump flat	0.37	0.41	0.37	0.34	0.23	0.31	0.27	0.38	0.40	0.41	0.16	0.23	0.14		0.79	0.82	0.64	0.10	0.82	0.75
Rump form	0.39	0.59	0.51	0.40	0.30	0.42	0.39	0.57	0.58	0.61	0.27	0.31	0.07	0.57		0.67	0.62	0.13	0.87	0.86
Rump length	0.69	0.45	0.38	0.55	0.26	0.41	0.32	0.43	0.42	0.47	0.19	0.24	0.22	0.39	0.42		0.73	0.30	0.68	0.63
Scrotum	0.32	0.34	0.30	0.34	0.23	0.31	0.26	0.31	0.33	0.34	0.19	0.24	0.19	0.26	0.31	0.32		0.38	0.62	0.72
Sheath	0.06	-0.01	-0.01	0.05	0.09	0.08	0.12	0.01	0.02	0.03	0.12	0.11	0.24	0.01	0.01	0.07	0.18		0.10	0.14
Tail placement	0.29	0.43	0.34	0.28	0.25	0.28	0.31	0.40	0.40	0.41	0.25	0.30	0.09	0.42	0.52	0.30	0.21	-0.01		0.84
Top line	0.36	0.52	0.37	0.30	0.30	0.32	0.36	0.43	0.48	0.44	0.20	0.29	0.09	0.42	0.51	0.35	0.24	0.06	0.42	

1 = Back, 2 = Back breadth, 3 = Depth, 4 = Frame, 5 = Front leg, 6 = Head, 7 = Hind leg, 8 = Hind length, 9 = Hind round, 10 = Hip width, 11 = Hooves, 12 = Pastern, 13 = Pigment, 14 = Rump flat, 15 = Rump form, 16 = Rump length, 17 = Scrotum, 18 = Sheath, 19 = Tail placement, 20 = Top line

had moderate heritabilities which is in agreement with results reported by Veselá *et al.* (2005). On average, the heritability estimates were lower than expected, slightly, in agreement with study of Gutierrez and Goyache (2002). Heritability estimates for body traits were higher than those for leg traits and this was in agreement with findings from Gutierrez and Goyache (2002) and Brotherstone (1994).

The variation of type traits could be partly due to differential emphasis on selection for type traits by farmers in different herds. Variation in type traits could also be attributed to differences in feeding and management levels.

Table 4 shows the genetic and phenotypic correlations. Some traits were highly genetically correlated, indicating that they are controlled by the same genes e.g., hooves had a genetic correlation of 1.00 with frame and front leg. Sheath had a negative genetic correlation with most of the traits (i.e., back breadth, frame, hind leg, hind length, hind round and hooves) compared to others, followed by hooves. The phenotypic correlations ranged from -0.01 (between sheath and back breadth and between depth and tail placement) to 0.84 (between head and hind leg). In general, genetic correlations were higher than phenotypic correlations, as reported by Gutierrez and Goyache (2002).

Most body size traits were highly genetically correlated, ranging from 0.63 to 0.95. The same pattern was observed among muscle development traits. Most body traits were moderately correlated with muscle development traits. However, high genetic high genetic correlations were observed between rump traits associated with muscle development (flat and form) and rump length (body size trait). The high genetic correlation was also observed between back breadth and body size traits and between hind round and body size traits. As indicated earlier, most muscle development traits had low heritabilities while the body size traits had moderate heritabilities. The moderate to high genetic correlations between muscle development traits and body size traits indicate that there is potential to improve muscle development traits indirectly through selecting for increased body size.

CONCLUSION

Conformation traits in beef cattle breeding programmes are useful and essential during selection periods. Moderate genetic variation observed for some body traits may necessitate the incorporation of these traits in the Charolais beef selection efforts. However, due to the subjective nature of the scoring system, there may be a need to define and refine the system further before this could be embarked upon.

Type traits that are of economic importance but have low heritabilities could be improved indirectly through selection for those traits that show high genetic correlation with these traits.

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