Are We Making Genetic Progress In The Southern African Simbra Composite Breed?

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[1]Introduction

Live weight traits throughout the animals' life have been shown to be an effective indicator of growth potential (Pico, 2004). Live weight traits include birth weight (BW), weaning weight (WW) and yearling weight (YW) measurements. Genetic parameter estimates enable beef breeders to genetically improve production by means of well-constructed breeding plans and precise selection. Even though studies estimating genetic parameters for the Simmental (Bennett *et al.,* 1996) and Brahman (Pico 2004; Martinez & Galindez, 2006), which form the genetic basis of the Simbra have been done, surprisingly none are available for the Southern African Simbra. Consequently the direction or magnitude of the genetic trends in this breed is not known. The objective of this study was to estimate (co) variance components for BW, WW (200-day) and YW (400-day) and assess the level of genetic trends for the Southern African Simbra cattle.

Materials and methods

Records. The Simmental and Simbra Breeders Society of South Africa availed a total of 148751 performance records for the Simbra breed. The available records ranged from the year 1987 to 2009. Animals were considered Simbra if they were of the following composition: 50% Simmental and 50% Brahman (SI50%BB50%), 25% Simmental and 75% Brahman (SI25%BB75%), 75% Simmental and 25% Brahman (SI75%BB25%). Only 12585 animals had all three records of interest ie BW, WW and YW. The details of the data set were described by Smith (2010).

Statistical analysis. The ASREML program (Gilmour *et al*., 2002) was then used for the estimation of (co) variance components for each trait separately (single-trait analyses) and all pairs of traits jointly (three-trait analysis). Six alternative models were implemented that included the direct genetic effect, maternal genetic and permanent environmental effects for the traits studied. Model six was the comprehensive model with another five reduced models, which ignored one or two of the maternal effects and/ or assumed no covariance between the direct and maternal genetic effects. The model with the higher Log-likelihood value will fit the data best.

Genetic trends were calculated by regressing trait predicted breeding value on time in years.

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Results and discussion

The direct additive heritability estimates, obtained during the single-trait analyses, for BW and WW were consistent with that of Gutierrez *et al.* (1997); Schoeman *et al.* (2000) and Wasike *et al.* (2006) respectively. Direct additive heritabilities (h^2) for BW (0.56 ± 0.08), WW measured at 200-days (0.67 ± 0.09) and YW measured at 400-days (0.70 ± 0.11) was relatively high compared to the bulk of estimates in literature for other beef breeds. Skrypzeck *et al.* (2000) found an even higher direct additive heritability for BW in a multibreed beef cattle population in South Africa with an estimate of 0.72. Skrypzeck *et al.* (2000) and Bennett & Gregory (1996) found that these high direct heritability estimates reported for composites are in fact fairly common compared to that of purebreds. Raphaka and Dzama (2010) have recently confirmed this trend. Direct additive heritability estimates (h^2) obtained during the three-trait analysis for BW (0.24 ± 0.07), WW (0.33 ± 0.06) and YW (0.38 ± 0.07) were consistent with the bulk of estimates reported in literature.

Rodriquez-Almeida *et al.* (1995) suggested that the variability in heritability estimates might be due to the inclusion of non-additive genetic variances. The dominance effect is one of the factors associated with the higher and possibly biased estimates in crossbred populations. Ferreira *et al.* (1999) suggested dominance effects as well as the epistatic variance to be partly responsible for inflated estimates associated with animal model estimates of composite breeds.

Maternal additive heritability was lower than direct heritability for BW, WW and YW. The latter implies that body weights were determined more by genetic characteristics of the calf than by those of the dam. This was consistent with most findings in literature and is a well-known feature. Maternal additive heritability estimates of 0.15 ± 0.05, 0.25 ± 0.07 and 0.18 ± 0.07 were obtained respectively for the weights measured. The current findings were more comparable to those of Wasike *et al.* (2006); Skrypzeck *et al.* (2000) and Schoeman *et al.* (2000) that obtained slightly higher maternal additive heritabilities.

The high additive maternal heritabilities for BW and WW indicate that, together with a high coefficient of genetic variation, considerable opportunity exists for the improvement of these traits. It must be kept in mind that the rather large direct and maternal genetic estimates are substantially inflated due to the exclusion of both heterosis and recombination effects. The inflation was of higher importance for maternal effects than the direct additive heritabilities (Demeke *et al*., 2003).

The dam permanent environment (c^2) estimates were only obtained for WW with a value of 0.04 ± 0.05. The c^2 was smaller than the maternal additive heritability. This was in concurrence with the results reported by Wasike *et al.* (2006) and Demeke *et al.* (2003).
The genetic correlation between direct and maternal effects (r_{am}) was highly negative for BW (r_{am} = -0.75 ± 0.07), WW (r_{am} = -0.93 ± 0.07) and YW (r_{am} = -0.85 ± 0.08). Negative estimates are however common in beef cattle for preweaning growth traits (Skrypzeck *et al.*, 2000). Although the estimates obtained by Sarmiento & Garcia (2007); De los Reyes *et al.* (2006); Burrow (2001); Schoeman *et al.* (2000); Skrypzeck *et al.* (2000); Haile-Mariam & Kassa-Mersha, (1995) and Koch (1972) showed a negative correlation between direct

additive and maternal additive effects, the values was still not as strongly negative than those obtained in the current study. The results were however in agreement with those reported by Melka (2001) for a muti-breed population in South Africa and Eler *et al.* (1995) for Nelore cattle in Brazil. Meyer (1992) also obtained relatively strong negative r_{am} values (-0.78) for WW and YW (-0.39) in Zebu cross cattle. It was indicated that these values are most possibly inflated by environmental co-variance. This environmental co-variance could have been the result of i.e. daughters of dams with superior maternal abilities that provide an inferior maternal environment for their offspring. The high negative values obtained in this study indicate an antagonistic effect between direct additive and maternal additive, suggesting a slow selection response for the three growth traits measured. Both effects should be taken into account in selection processes to achieve optimum genetic progress (Dezfuli & Mashayekhi, 2009). Thus selection of genetically superior animals for growth traits will result in genetically inferior animals for maternal genetic components for these traits.

The reason for this strong negative r_{am} estimates can be partially explained by the poor and small data/population structure and not the true antagonistic biological relationship between the direct and maternal genetic effects. Heydarpour *et al*. (2008) found that the data structure can affect both the magnitude as well as the standard error of the large negative values obtained for r_{am} estimates. The latter is primarily due to inconsistent recording and small herd sizes of the Simbra breed (Wasike *et al.*, 2006). Meyer (1997) attributed the negative r_{am} estimates to unaccounted sources of variation due to management practices. Meyer (1997) proposed that if models were to be fitted with regression of offspring performance on maternal phenotype and sire by herd-year interaction affects the magnitude of the direct-maternal correlation would decline. Wasike *et al.* (2006) reported the same results with Kenyan Boran cattle.

Genetic correlations between the traits studied were favorable but low indicating that selection for one trait will improve others in a desired direction. A value of 0.18 ± 0.16 was obtained for the genetic correlation between BW and WW indicating a small but positive relationship between the two traits. From the published literature available r_g estimates ranged from 0.23 to 0.79 (Eler *et al.*, 1995; Pico 2004). An r_g estimate of 0.27 ± 0.16 was obtained for BW and YW. Pico (2004) reported a value of 0.47 for the South African Brahman. Interesting enough Eler *et al.* (1995) reported an even lower genetic correlation estimate (0.16) between BW and YW. A value of 0.52 ± 0.10 was obtained for the genetic correlation between WW and YW indicating a strong positive correlation between the two traits.

The environmental correlations between BW and WW as well as BW and YW were relatively low (0.09 ± 0.06 and 0.07 ± 0.06) respectively. The r_e estimate (0.45 ± 0.05) between WW and YW was much higher and indicated a strong positive relationship between the two traits. These results were consistent with those reported by Pico (2004).

Genetic trends showed slight improvement for BW (0.01% per year) and small negative decline for both WW (-0.04% per year) and YW (-0.02% per year) leaving a lot of room for improvement in this breed.

Conclusion

Heritability estimates (both direct additive and additive maternal) were high compared to literature results from purebreds but not that of composites during single trait analyses for BW, WW and YW. The high to very high direct additive heritability estimates together with high coefficients of variation for the traits offers the opportunity of improvement for these traits through selection. Selection should be implemented in such a manner that growth rate is maximized while BW is kept at an optimal level to avoid dystocia. That genetic trends for growth traits were unfavourable for weaning and yearling weight is a cause for concern.

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