

*Short communication***Crossbreeding with a Bonsmara dam line****A. Theunissen^{1,2#}, M.M. Scholtz^{1,3}, F.W.C. Naser¹ & M.D. MacNeil^{1,3,4}**¹ Department of Animal, Wildlife and Grassland Sciences, UFS, P.O. Box 339, Bloemfontein, 9300, South Africa² Northern Cape Department of Agricultural, Land Reform and Rural Development, Private Bag X9, Jan Kempdorp 8550, South Africa³ ARC-Animal Production Institute, Private Bag X2, Irene, 0062, South Africa⁴ USDA Agricultural Research Service, Fort Keogh Livestock and Range Research Laboratory, Miles City, Montana 59301, USA

Abstract

Data from a crossbreeding trial in South Africa which involved the Bonsmara (Bo) as dam line and the Simmentaler (S), Brahman (Br), Charolais (C) and Herefords (H) as sire lines were used to estimate the additive and non-additive effects for weight traits in two-breed crosses. The average direct heterosis contributions, which were expressed as deviations from Bo were 1.4 kg and 13.6 kg for birth weight (BW) and weaning weight (WW) respectively in the four crossbred genotypes. The largest additive effect for BW was found in C x Bo while WW was the largest in S x Bo. The results indicate that C and S bulls could increase WW in the progeny of Bonsmara cows. C bulls should be used with caution due the additive effect on BW.

Keywords: Heterosis effects, Sanga cattle genotypes

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The world demand for meat is expected to rise by more than 200% from 229 million ton in 1999 to 465 million ton in 2050 (Steinfeld *et al.*, 2006), and global numbers of meat animals and their productivity will have to increase to meet such demand. The substantial increase in demand for livestock products in the developing countries (Delgado *et al.*, 1999), partly due to human population increase and improved financial incomes, could offer much larger market opportunities for the livestock producers in these countries. However, climate as such has also been changing and these changes are predicted to be highly dynamic (Jones and Thornton, 2009). An increase in the average global surface temperature of between 1.8 and 4.0°C to 2100 is predicted (IPCC, 2007), which will result in increasing frequencies of heat stress, drought and flooding events, and these will undoubtedly have adverse effects on crop and livestock productivity over and above the impacts due to changes in mean variable temperature alone (IPCC, 2007).

Therefore the type of production strategy to be followed in developing countries of the southern hemisphere will depend primarily on the environment and level of management. In harsh and undeveloped areas, pure breeding with Sanga, Zebu or locally developed breeds, may be the only production strategy that can be followed (Scholtz *et al.*, 2011). The availability of diverse cattle breed resources with large adaptive and productive differences allow breed types to be matched with the different environments, management capabilities and markets - thereby maximizing the opportunity for high productivity and profitability. It is therefore almost certain that the taurine content of cattle in the (sub) tropical environments will become larger in future (Frish and O'Neill, 1998, Prayaga, 2003a, 2003b; Burrow 2006) if productivity is to be increased.

Where managerial skills are better, but conditions are often harsh, with relatively poor pastures, crossbreeding with small framed indigenous or adapted cows may succeed in improving the output of beef cattle farming (Calegare *et al.*, 2007). A properly designed crossbreeding system takes advantage of appropriate combinations of superior traits of the different breeds, thereby resulting in heterosis. It is believed that crossbreeding will gain importance in many developing countries of the southern hemisphere, as climatic changes stand to affect the African and South American continents more substantially than the other continents (Anitei, 2006; Appel, 2006; Romanini *et al.*, 2008); and the demand for meat increases.

The aim of this paper is to estimate breed additive and heterosis effects in crosses between the Bonsmara (Bo) as dam line and the Brahman (Br), Charolais (C), Hereford (H) and Simmentaler (S) as sire lines, using the results from the Vaalharts Research Station in South Africa as reported by Els (1988). The Bonsmara is a composite breed developed by crossing the indigenous Afrikaner breed and the Hereford and Shorthorn breeds (Scholtz, 2010). Feedlots are an important segment of the beef production industry in South Africa supplying about 75% of beef to the consumer. In a survey conducted in 2004 (Scholtz, *et al.*, 2008) the Bonsmara breed and its crosses, had the highest percentage intake in feedlots of all breeds in South Africa.

The crossbreeding experiments were carried out at Vaalharts research station, situated near Jan Kempdorp. The research station is located in the centre of South Africa at 27°51' South and 24°50' East at an altitude of 1175 meters and is in an area with sandy red soil with lime rock underneath. These soils form part of the Hutton form and represents mainly the Manganese series (Laker, 2003). The veld type is mixed *Tarchonanthus* veld, Veld type No 16b, 4 (Acocks, 1988). The research station has a recommended carrying capacity of 10 ha/LSU.

The climate at the Vaalharts research station is classified as semi-arid. It is characterized by hot summers and cold winters with frost a common occurrence. The highest monthly average temperature is around 32°C and is experienced during December and January and the lowest monthly average temperature is around -0.5°C and is experienced during July. The average precipitation is around 450 millimeters per annum of which most is experienced during the summer months from October to April in the form of thunderstorms (Els, 1988).

Els (1988) evaluated four purebred sire lines Br, C, H) and S in crossings with the Bo dam line. The beef cattle herd was raised under extensive conditions. Management and selection procedure of the herd were described by Els (1988). Least square means for birth weight (BW) and weaning weight (WW) in different breed group combinations were published in the dissertation by Els (1988) and presented in Table 1. Genotype, contemporary group (year of birth, calving season, age of dam) and sex were significant ($P < 0.05$) sources of variation for all the traits.

Table 1 Least squares means for birth and weaning weight in the different genotypes

	Birth weight (kg)	Weaning weight (kg)
Bo (29)	38.8 ± 1.04	214.3 ± 4.3
Br x Bo (18)	39.4 ± 1.52	224.7 ± 6.2
C x Bo (19)	45.4 ± 1.45	245.8 ± 6.0
H x Bo (23)	39.6 ± 1.17	212.7 ± 4.8
S x Bo (20)	38.0 ± 1.37	217.4 ± 5.6
Average	40.2	223.0

(numbers of animals)

Dickerson (1973) modeled two-breed production systems as follows:

Two breed: $A \times B = \frac{1}{2}G^I_A + \frac{1}{2}G^I_B + h^I + G^M_B$ (0 recombination loss)

where G^I_A , and G^I_B represented direct additive effects of the specialized sire and dam breeds, respectively; h^I is the average heterosis (dominance: interactions within loci) effect, G^M is the maternal effect of the specialized dam breed.

In this study the least square means were equated to the breed additive and average heterosis (dominance) effects for all the sire lines. Predictions were based on multiple regressions. Constraints were imposed such that the sets of individual and maternal additive effects each summed to zero. The model then solved the following functions simultaneously to calculate the phenotypic values of the progeny:

a. Pure breeds

e.g. $C = G^I_C + G^M_C$

b. Two-breed crosses

$A \times B = \frac{1}{2}G^I_A + \frac{1}{2}G^I_B + H^I_{AB} + G^M_B$

where **A** and **B**, **G^I** and **G^M** are the individual additive and maternal parameters, respectively and **H^I** the individual heterosis parameters because of the assumed degrees of expected heterozygosities, respectively.

The single model is:

$$Y = Gm + \beta G^I + \beta G^M + \beta H^I + \varepsilon$$

where **Y** is the phenotypic value of the cross for the trait interest, **Gm** is the least square means of the Bo breed group for the trait of interest with no heterosis effect and **βG^I** and **βG^M** are the partial regression coefficients of individual and maternal breed composition representing additive effects expressed as deviation from the Bo breed mean and **βH^I** the regression coefficients of individual heterosis effects proportional to expected heterozygosities in the crossbred progeny. ε is random error (not estimated).

The GLM procedure of SAS (2010) was used for the analysis of the data set. The data set was formed by recording each least square mean along with breed composition and direct heterozygosity as covariates on a weighted (number of animals) LS regression. Each trait was analyzed separately. Breed solutions for each trait were expressed relative to the Bo breed similar to a method used, by amongst other, Williams *et al.* (2010).

For the estimation of genetic effects proportional contributions for the various dam breeds in their two- and three-breed and backcross combinations were derived (similar to Theunissen *et al.*, 2013). The genetic model was adapted because of the dependencies of the Br, C, H and S breeds on the A breed (Bonsmara) direct and maternal effects (which were set to zero and not included in the model) and the genetic components of the other breed were estimated as deviations from the A breed mean. Hence, composite estimates of all production trait means of all 24 crossbred genotypes could be derived using these contributions in models as follows:

Two-breed crosses

$$A \times B = I_B + (DG^I_B = 0) + \frac{1}{2}DG^I_A + H^I_{AB} + (DG^M_B = 0)$$

where **I_B** is the intercept or individual additive effect of the dam breed, **DG^I_A** is the individual additive deviation of sire breed from the dam breed, **H^I_{AB}** is the individual heterosis effects of genotypes AB.

The breed additive and heterosis effects for the weight traits in pure- and crossbred animals were estimated and are shown in Table 2.

Table 2 Additive and heterosis effects and standard errors* on weight traits

Effect	Breed	Birth weight (kg)	Weaning weight (kg)
Intercept	Bonsmara	38.8 ± 2.36	214.3 ± 11.5
<i>Additive</i>			
Individual	Brahman	-5.4 ± 3.3	-14.1 ± 16.0
	Charolais	8.3 ± 3.2	12.0 ± 15.5
	Hereford	-2.8 ± 3.2	-34.4 ± 15.3
	Simmentaler	2.9 ± 3.3	12.6 ± 16.1
<i>Heterosis</i>	Average for	1.4 ± 1.9	13.6 ± 9.2
Individual	all breeds		

*All standard errors are expressed in units and represent a lack of fit to the genetic model, rather than variation amongst animals in the same genotype

It needs to be mentioned that Els (1988) reported weaning rates (number of calves weaned as percentage of number of cows exposed to mating) of 98.8, 100.0, 96.6, 91.8, and 97.6 % for the Bo, Br x Bo, C x Bo, H x Bo and S x Bo dam groups respectively, which is extremely high under these extensive conditions. It should also be noted that the data did not take cognizance of the genetic trends in the growth

traits and the effects on heterosis parameters in any of the breeds since the conduction of the crossbreeding experiment some years ago.

The results indicate that C and S bulls could increase WW in the progeny of Bo cows. C bulls should be used with caution due the additive effect on BW. The use of Br and H sires on Bonsmara cows is not recommended due to the negative additive effect on WW. Because of the small number of animals in the study the results should be verified.

Acknowledgements

This work is based on research supported in part by Red Meat Research and Development South Africa and the National Research Foundation of South Africa, under grant UID 75122. The grant holder acknowledges that opinions, findings and conclusions or recommendations expressed in any publication generated by NRF-supported research are those of the authors and the NRF accepts no liability whatsoever in this regard.

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