Estimation of Genetic Parameters for Growth Traits in a Crossbred Population Derived from Piedmontese and Nanyang Cattle Using a Multi-Trait Animal Model

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Abstract: The objective of this study was to estimate the genetic parameters for growth traits in a cross between Piedmontese and Nanyang cattle. Data from the pure Italian Piedmontese and Chinese Nanyang breeds as well as from crosses between these two breeds were used to estimate genetic parameters and variance. Data were extracted from a base data set (49,646 growth records of 9,003 animals from 13 herds). The data were analyzed using the multiple-trait Restricted Maximum Likelihood (REML) Method to estimate the variance and the genetic parameters. The multiple-trait analysis included weights at birth, 6, 12, 18, 24 months and maturity. Weight heritability ranged from 0.34±0.01-0.54±0.03; the heritabilities at 24 months and at maturity were higher than at all other time points. Results indicated that growth traits were good traits for selection and cattle genetic evaluation. The estimates obtained in this study will be used in the breeding value estimation for national genetic evaluations of the Chinese crossbreed population between Piedmontese beef cattle and Nanyang Yellow cattle.

Key words: Animal model, growth traits, genetic parameters, crossing breeding, genetic evaluation, cattle

INTRODUCTION

A large number of cattle were imported to improve the local Chinese beef products. Crossbreeding between these imported cattle and the local Chinese breeds which has increased rapidly in the last decades of the 20th century. Crossbreeding was one of the primary ways that beef products were improved in China (Chen and Zhang, 2008). Piedmontese beef cattle from Italy were crossed with local Chinese breeds, particularly with the Chinese Nanyang Yellow cattle resulting in a significant improvement in the productivity of local cattle (Zhang et al., 2010).

Cattle weight affects many economic aspects of beef production including maintenance requirements (Costa et al., 2011; Williams and Jenkins, 2003; Nkrumah et al., 2007; Crowley et al., 2010), reproduction (Abeni et al., 2004; Albera et al., 2004; Carnier et al., 2000) and profitability. Therefore, growth traits have been considered in many beef cattle selection programs (Rumph et al., 2002; Mujibi and Crews, 2009). For selection programs to be effective, good estimates of the genetic parameters that are associated with weight should be available. Estimates of direct heritability as well as genetic and phenotypic correlations for growth traits have

been reported (MacNeil, 2005; Kaps et al., 1999). However, there is no information on genetic and phenotypic variation in composite populations derived from Piedmontese and Nanyang cattle.

The objective of the current study was to use a multi-trait animal model to estimate the variance components and genetic parameters for growth traits of a population generated by crossing Piedmontese beef cattle to Nanyang Yellow cattle.

MATERIALS AND METHODS

The data used in this study were recorded from 1988-2008 and were collected by the Chinese Academy of Agricultural Sciences. The recorded data were Weights at Birth (BW), 6 months (W_6), 12 months (W_12), 18 months (W_18), 24 months (W_24) and Maturity (MW). Data consisted of 49,646 growth records of 9003 cattle from 13 herds. The information studied in this research is related to 5 generations. The birth date of the oldest cattle was in 1988. First, Piedmontese beef cattle were used as sires to mate with the local Yellow cattle and then to mate with the crossbred offspring. After two generations of crossing, the most outstanding individuals were selected from the offspring of the second

crossing to mate with each other and their offspring were used to form the new nucleus breeding population after three generation.

Statistical analysis: A multi-trait animal model was used to estimate the genetic parameters of the crossbred population. The fixed effects included herd, generation and sex. The animal model included direct additive genetic effects and direct permanent environmental random effects. In matrix notation:

$$Y = X\beta + Z_a a + Z_p p + e \quad (1)$$

Where:
Y = An observation vector for a given trait
β = The vector of fixed effects (herd, generation and sex)
a = A vector of direct additive genetic effects of the animal
p = A vector of direct permanent environmental effects of the animal
e = A vector of random error
X = A known incidence matrix associating fixed effects with records in y
Z_a and Z_p = Known incidence matrices associating random effects with records in Y (with zero columns associated with animals that did not have records)

Expectations for random effects were:

$$E \begin{bmatrix} y \\ a \\ p \\ e \end{bmatrix} = \begin{bmatrix} X\beta \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad (2)$$

and the (co) variance structure for random effects for growth traits was:

$$Var \begin{bmatrix} a_i \\ p_i \\ e_i \\ \vdots \\ a_j \\ p_j \\ e_j \end{bmatrix} = \begin{bmatrix} A\sigma^2_{a_i} & 0 & 0 & & A\sigma_{a_i a_j} & 0 & 0 \\ 0 & I\sigma^2_{p_i} & 0 & \cdots & 0 & IA\sigma_{p_i p_j} & 0 \\ 0 & 0 & I\sigma^2_{e_i} & & 0 & 0 & I\sigma_{e_i e_j} \\ & \vdots & & \ddots & & \vdots & \\ A\sigma_{a_i a_j} & & & & A\sigma^2_{a_j} & 0 & 0 \\ & IA\sigma_{p_i p_j} & & \cdots & 0 & I\sigma^2_{p_j} & 0 \\ & & I\sigma_{e_i e_j} & & 0 & 0 & I\sigma^2_{e_j} \end{bmatrix}$$

$$(3)$$

Where:
Matrix A = The numerator relationship matrix of all animals in the pedigree including those without records

Matrix I = An identity matrix of the appropriate order
σ^2_a = The variance due to the direct additive genetic effects
σ^2_p = The variance due to the direct permanent environmental random effects
$\sigma_{a_i a_j}$ = The additive genetic covariance between different weight traits
σ^2_e = The variance due to random error

Co variance components were estimated using the multiple-trait REML program (Software named VCE 6.0) of Groeneveld *et al.* (2008). The optimization in VCE was done with a Quasi-Newton procedure included setting up the mixed model equations, solving the sparse inverse, numerical factorization and assembling the gradients. The convergence criterion of the maximum difference between two successive solutions was set to 0.0001. The dispersion parameters were obtained by the Restricted Maximum Likelihood (REML) method using an analytical gradients algorithm. Analyses were repeated for confirmation of convergence. The resulting variance and covariance components were used to estimate heritabilities and genetic correlations.

RESULTS AND DISCUSSION

Phenotypic performance: The phenotypic means and standard deviations of six growth traits are shown in Table 1. The phenotypic estimates (and standard deviations) for the basic statistics analyses were 36.39±4.92, 194.49±18.42, 293.38±36.79, 358.48±40.82, 419.35±44.05 and 487.93±55.94 for weights at birth, 6, 12, 18, 24 months and maturity.

Variance components and heritabilities: Multivariate analyses were conducted with data from all of the traits studied. The variance components and heritabilities of weight traits that were analyzed with a multi-trait animal model are shown in Table 2.

The additive genetic variance, direct permanent environmental variance and residual variance increased as

Table 1: A summary of basic statistics (Mean±SD) for growth records of the crossbred Piedmontese and Nanyang population

Trait[a] (kg)	Records	Mean±SD	Min.	Max.
BW	9003	36.39±4.920	21	50
W_6	8945	194.49±18.42	145	255
W_12	8867	293.38±36.79	235	470
W_18	7948	358.48±40.82	280	600
W_24	7797	419.35±44.05	330	780
MW	7086	487.93±55.94	385	900

[a]BW = Birth Weight; W_6 = 6 months Weight; W_12 = 12 months Weight; W_18 = 18 months Weight; W_24 = 24 months Weight; MW = Mature Weight

Table 2: Estimates of parameters (Mean±SD, additive variance σ_a^2, permanent environmental variance σ_p^2, phenotypic variance σ_{phe}^2, residual variance σ_e^2, heritability h^2) for growth traits of the population using a multi-trait animal model

Traits[a] (kg)	σ_a^2	σ_p^2	σ_e^2	σ_{phe}^2	h^2
BW	7.93	0.48	12.39	20.80	0.38±0.01
W_6	106.26	37.31	166.69	310.27	0.34±0.01
W_12	169.57	132.53	118.91	421.01	0.40±0.02
W_18	262.96	132.37	269.56	664.89	0.39±0.02
W_24	531.38	217.79	453.25	1202.42	0.44±0.02
MW	1059.89	279.07	596.89	1935.85	0.54±0.03

[a]Values are expressed as the mean±SD; BW = Birth Weight; W_6 = 6 months Weight; W_12 = 12 months Weight; W_18 = 12 months Weight; W_24 = 24 months Weight; MW = Mature Weight

Table 3: Genetic correlations (Mean±SD, above diagonal) and phenotypic correlations (below diagonal) for growth traits of the population

Trait[a] (kg)	Body weight (kg)					
	BW	W_6	W_12	W_18	W_24	MW
BW	1	0.60±0.03	0.53±0.04	0.68±0.03	0.68±0.03	0.53±0.04
W_6	0.52	1	0.86±0.02	0.90±0.02	0.77±0.02	0.71±0.04
W_12	0.51	0.79	1	0.96±0.02	0.87±0.02	0.77±0.01
W_18	0.53	0.72	0.87	1	0.96±0.02	0.85±0.05
W_24	0.50	0.62	0.80	0.90	1	0.88±0.05
MW	0.50	0.65	0.78	0.84	0.87	1

[a]BW = Birth Weight; W_6 = 6 months Weight; W_12 = 12 months Weight; W_18 = 18 months Weight; W_24 = 24 months Weight; MW = Mature Weight

the animals aged (Table 2). The highest additive variance was observed for the mature weight. The heritability estimates for all six traits were similar. The direct heritability estimates (and standard deviations) for the multivariate analyses were 0.38±0.01, 0.34±0.01, 0.40±0.02, 0.39±0.02, 0.44±0.02 and 0.54±0.03 for weights at birth, 6, 12, 18, 24 months and maturity, respectively. These estimates are greater than those of Brandt *et al.* (2010) and smaller than those of Rumph *et al.* (2002). However, these estimates are similar to those reported by various groups including Kaps *et al.* (1999) and MacNeil (2005).

Genetic correlations: Estimates of the genetic and phenotypic correlations among body weight traits are shown in Table 3. There were strong genetic and phenotypic correlations among weights at birth, 6, 12, 18, 24 months and maturity.

As expected, estimates of the genetic correlation between any two weights were large. Estimates of the direct genetic correlation between pairs of weights ranged from 0.53±0.04-0.96±0.02. Estimates of phenotypic correlations were also large with estimates that ranged from 0.50-0.90. Although, the genetic correlations for weights at birth and other time points and the phenotypic correlations between body weights were lower those for other growth traits, all traits had high phenotypic correlations (r>0.5) and genetic correlations (>0.53). The genetic correlations were similar to estimates reported by others (Costa *et al.*, 2011; Boligon *et al.*, 2010) using animal model for single and multiple trait analysis, reported a genetic correlation of 0.80 between weaning weights and yearling weight for Nellore cattle. Using different models, Arango *et al.* (2002) found an even higher genetic correlation of 0.92 for crosses of breeds

with Angus and Hereford cattle whereas (Kaps *et al.*, 1999) reported a value of 0.63 for Angus cattle. The strong correlations between any two weights suggest that any of the weight traits could be used to estimate breeding values for growth traits.

CONCLUSION

Above all, estimation of genetic parameters for growth traits of the crossbred population between Piedmontese and Nanyang cattle in China produced moderate to high heritability estimates, indicating that genetic variability of these traits exists in this population and that improvement can be made by the proper selection scheme. The differences observed among the estimated phenotypic and genetic parameters with others reported elsewhere in the world could be attributed to differences in sample size, management, feeding practices, models and procedures employed to estimate parameters and so on. However, since these estimates were found using data on animals maintained under the standard conditions of feeding, management and environmental conditions of China, these values of genetic evaluation may well be used for genetic evaluation of animals at national beef cattle herd. Meanwhile, a selection program that includes body weight can benefit producers who want to change or maintain a specific cattle weight. High estimates of genetic correlations between body weights indicate that selection for one trait in a particular direction would also yield nearly the same change in the same direction in other traits. The mature weight can be used as a selection criterion to change or maintain a desired body weight; other growth traits of interest such as weights at

birth and later stages can also be used as selection criteria if a selection decision must be made earlier. Moreover, scientific animal breeding practices need to be better supported by the national cattle breeding program including individual animal recording, genetic parameter estimation using REML Method and animal selection based on breeding values in order to maximize genetic improvement in the national cattle herds.

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