Bayesian Alternative Models In Genetic Analyses Of *In Vivo* Carcass Traits In Guzerá Cattle[6]

T.M. Gonçalves[1], J. Azevedo Jr.[3], J.C. de Sousa[2], V.D. Timpani[4], M.A.D. Dias[3], M.C.A.M. Bink[5]

Introduction

Animal breeding programs for the improvement of *Bos Indicus* carcass traits are imperative to increase meat quality and productivity. An effort to know the genetic architecture of these traits should be done before their inclusion in a breeding program. Generally, some quantitative traits, such ad, loin-eye area, rump fat thickness and back fat thickness are considered to be influenced by many genes with small effects. However, it was suggested that few genes could be responsible for a great part of the variation of quantitative traits (Lande, R. (1981)). These genes are known as major genes (MG). Carcass traits, generally, are modeled assuming an infinitesimal polygenic model (IPM), having a discreet distribution using a finite polygenic model (FPM) (Thompson, E.A. and Skolmick, M.H. (1977), Fernando, R.L., Stricker, C., Elston, R.L (1994), Lange, K. (1995)), or modeled with a combination of IPM and FPM (Bink, M.C.A.M., Uimari, P., Sillanpää, M.J. *et al*. (2002), Gonçalves, T.M., Oliveira, H.N., Bovenhuis, H. *et al.* (2005)), which considers polygenic and oligogenic effects.

The aim of this work was to adjust a combined model to describe the genetic architecture of three carcass traits evaluated by real-time ultrasonography in Guzerá cattle.

Material And Methods

Ultrasound data from 655 animals were used. Loin-eye area (LEA), rump fat thickness (RFT) and back fat thickness (BFT) images were obtained by positioning the transducer transversely between the 12ª and 13ª ribs, parallelly between 12ª and 13ª rib and at the junction between the *Biceps femoris* and *Gluteus medium* muscles, respectively. All ultrasound measurements were performed by a single experienced technician using an Aloka 500V unit with a 3.5 MHz/17.2cm linear transducer (Aloka Co. Ltd – Wallingford, EUA).

The combined model (IPM+FPM) adjusted for each trait analyzed was:

$$\underset{\sim}{y} = X\,\underset{\sim}{\beta} + W\,\underset{\sim}{u} + \sum_{K}^{N_{MG}} Z_{MG}\alpha_{MG,_K} + \underset{\sim}{e}$$

Where: $\boldsymbol{y}$ = is the vector of observations; $\boldsymbol{X}$ = incidence matrix of non-genetic factors, which connects the phenotypes of non-genetic effects; $\boldsymbol{\beta}$ = is a vector containing the mean (μ) and all non-genetic factors (NID) affecting the characteristics of interest: animal age and body weight at the time of measurement, contemporary group (sex, birth year, birth farm, feed management and date of measurement) and permanent environmental effect; $\boldsymbol{W}$ = incidence matrix of the genetic random direct effects, related to the observations to infinitesimal polygenic effects; $\boldsymbol{u}$ = is the vector of random effects of direct genetic values of animal, the effects of several genes with infinitesimal effect that are not explained by the major gene are computed here; $\boldsymbol{Z_{MG}}$ = incidence matrix that connects the phenotypic information to MG. It is typically unknown, since the genotypes of individuals are not known. However, this matrix can be inferred from the pedigree and phenotype (segregation indicators). It is assumed that the MG is biallelic allowing three different genotypes (AA, Aa and aa) and having genotypic values equal to + α, δ and -α, respectively. The variables α and δ represent the additive and dominance effects of a single gene. The matrix Z size depends on the number of MG in the model; $\boldsymbol{N_{MG}}$ = is the number of major genes. This number is considered a random variable and makes inferences about the distribution from the data analyzed; $\boldsymbol{\alpha_{MG}}$ = is a bidimensional vector for the k^{th} major gene (MG), i.e., additive (a) and dominance (d) effects were adjusted here. It was assumed that the loci for MG are biallelic; $\boldsymbol{e}$ = vector of the normally distributed residual associated to each observation. In this model the presence of a maximum of fifteen and at least one locus for major genes (MG), and one locus of infinitesimal polygenic effect were assumed to explain the genetic variation found.

---

[1]Animal Science Department's professor, Federal University of Lavras – Brazil.
[2]Animal Science Department's professor, Federal University of Lavras – Brazil.
[3]Animal Science Department's MSc student, Federal University of Lavras.
[4]Animal Science Department's DSc student, Federal University of Lavras.
[5] Biometris, PO Box 100, 6700AC Wageningen, The Netherlands.
[6] Support of FAPEMIG.

A Bayesian approach to the analyses was adopted. The Gibbs Sampling and a Markov Chain Monte Carlo methods were used to update the parameters considered in the model. A total of 1,500,000 cycles or iterations were generated initially. The sampling interval was 20 iterations, totalizing 75,000 samples. The Gibbs period (burn-in) adopted was 10%, or 6,750 samples, resulting in 67,500 samples of *posteriori* distributions of parameters considered in the models. The FLEXQTL^{TM} package was used (Bink, M.C.A.M., Version 0.98, Wageningen, (2009)).

Chain convergence was diagnosed when the effective chain size reached a number greater or equal to 100 (Sorensen, D.A., Andersen, S., Gianola, D. (1995)). The detection of a major gene affecting the expression traits was based on *posteriori* estimations for the number of MG (N_{MG}), on P*osteriori* probability for MG and on the Bayes factor (Kass, R.E.and Raftery, A.E. (1995)). Inferences about the *posteriori* distributions heritability were obtained based on Gibbs sampling of variance components.

Results And Discussion

Averages age and body weight on the day of measurement were 18 months and 391.45Kg, respectively. Phenotypic means from LEA, RFT and BFT were 58.17cm^2, 2.36mm and 3.36mm, respectively.

LEA, RFT and BFT variance components and their effectives chains sizes (ECS) adjusted by the combined model (MPF + IPM), are presented on Table 1. Except for RFT, the ECS of the variance components was over 100. This result means that, the chains converged, providing reliable inferences of variance components when adjusted these model for these characteristics (Sorensen, D.A., Andersen, S., Gianola, D. (1995)). The RFT trait has yet to be analyzed genetically through the infinitesimal polygenic model, because the combined model adjusted did not reach chain convergence for all model parameters. This result did not allow inferences on RTF parameters.

The *posteriori* estimative of number of major genes (N_{MG}) affecting the expression of LEA and BFT traits are shown on Table 1. The same number of MG for LEA (three major genes) and BFT (two major genes) are obtained in the *posteriori* probabilities (Table 2), where one of the major probabilities was located in three MG for LEA and a large probability of two major genes for BFT. When Bayes factors are considered (Table 3), there is positive evidence that three MGs control LEA and a decisive evidence for two MG for BFT. So, it is possible to confirm the evidence of major genes being segregated in this population concerning LEA and BFT. Furthermore, these findings imply that these traits must be evaluated genetically considering the presence of polygenes and oligogenes controlling their expression.

A partial dominance action over LEA and an over dominance action over BFT were observed (Table 4). Negative dominance values were observed in both traits analyzed, indicating that the heterozygote genotype can decrease the phenotypic value of these traits.

LEA heritability estimations were 0.15 for the polygenic and 0.10 for the oligogenic fractions (Table 4). These were lower than those observed for BFT, of 0.19 and 0.13 for the polygenic and to oligogenic fractions, respectively. The low heritability found for the LEA and BFT traits can be explained by the fact that these traits are dependent on the gene expression of a few MG and, thus, may have already been fixed in that population.

Table 1 - Variance components to polygenic variance (σ^2_{IPM}), oligogenic variance (σ^2_{FPM}), residual variance (σ^2_r), *posteriori* estimative to major gene number (N_{MG}) and their respective effective chains sizes (ECS), in parentheses, when adjusting the combined model to the Loin Eye Area (LEA), Rump Fat Thickness (RFT) and Back Fat Thickness (BFT) traits.

	Traits	LEA	RFT	BFT
Variance Components	σ^2_{IPM}	23.14	0.02	0.42
	(ECS)	*(204)*	*(185)*	*(142)*
	σ^2_{FPM}	29.57	0.30	0.72
	(ECS)	*(564)*	*(538)*	*(323)*
	σ^2_r	10.56	0.08	0.13
	(ECS)	*(549)*	*(96)*	*(145)*
	N_{MG}	3	2	2
	(ECS)	*(164)*	*(40)*	*(205)*

Table 2 - *Posteriori* probabilities for the major gene (MG) number affecting Loin Eye Area (LEA) and Back Fat Thickness (BFT) traits, after adjusting for the combined model (FPM+IPM)

MG	0	1	2	3	4	5	6	7	8	9 … 15
Priori	***0.37***	***0.37***	***0.18***	***0.06***	***0.01***	***0***	***0***	***0***	***0***	***0***
	Traits					***Posteriori* Probabilities**				
LEA	0.001	0.092	**0.332**	**0.304**	0.163	0.065	0.026	0.005	0.002	0
BFT	0	0.002	**0.889**	0.091	0.013	0.001	0	0	0	0

Table 3 - Bayes Factor[1] for the major gene (MG) number affecting Loin Eye Area (LEA) and Back Fat Thickness (BFT) after adjusting for the combined model (FPM+IPM)

Traits	1/0[2]	2/1	3/2	4/3	5/4	6/5	7/6	8/7 - 15/14
LEA	19.3	6.9	**3.3**	1.5	0.9	0.7	1.0	NA
BFT	NA	**14.0**	-2.4	-1.1	-2.9	NA	NA	NA

[1]Twice the natural logarithm (2ln) of the Bayes factor is similar to the statistical test because of the likelihood.
[2]Evidence of the 1 MG in the model versus 0 MG in the model: 0 to 2 = low, 2 to 5 = positive, 5 to 10 = strong, > 10 = decisive; NA = not available due to lack of MCMC samples. Negative values indicate evidence of the MG number, indicated by the denominator of the ratio.

Table 4 – *Posteriori* means to additive effect (*a*), dominance effect (*d*), additive variance (σ^2_a), dominance variance (σ^2_d), major gene variance (σ^2_{MG}), polygenic variance (σ^2_{IPM}), phenotypic variance (σ^2_P), polygenic heritability (h^2_{IPM}) and oligogenic heritability (h^2_{FPM}) adjusting the combined model to the Loin Eye Area (LEA) and Back Fat Thickness (BFT)

		Parameters								
		a	d	σ^2_a	σ^2_d	σ^2_{MG}	σ^2_{IPM}	σ^2_P	h^2_{IPM}	h^2_{FPM}
Traits	**LEA**	9.93	-7.45	15.78	12.03	29.57	23.14	156.71	0.15	0.10
	BFT	1.97	-2.19	0.30	0.43	0.72	0.42	2.23	0.19	0.13

Conclusion

There are major genes segregating in the population studied for LEA and BFT. The genetic analysis of LEA and BFT should be performed combining oligogenic and polygenic effects (FPM + IPM). RFT should be analyzed using the infinitesimal polygenic model (IPM).

References

Lande, R. (1981). *Genetics. Sel Evol*. 99:541-553.

Thompson, E.A. and Skolmick, M.H. (1977). In *Proc. Of the International Conference on Quantitative Genetics,* p. 815-818 Ames, Yowa State University Press.

Fernando, R.L., Stricker, C., Elston, R.L. (1994). *Theoretical and Applied Genetics Sel. Evol*. 88:573-580.

Lange, K. (1997). *Genetics. Sel Evol*. 147:1423-1430.

Bink, M.C.A.M., Uimari, P., Sillanpää, M.J. *et al*. (2002). *Theoretical and Applied Genetics Sel Evol.* 104: 751-762.

Gonçalves, T.M., Oliveira, H.N., Bovenhuis, H. *et al.* (2005). *R. Bras. Zootec*. 34(5):1531-1539.

Sorensen, D.A., Andersen, S., Gianola, D. (1995). *Genet Sel Evol*. 27:229-249.

Kass, R.E.and Raftery, A.E. (1995). *J. Amer. Statist. Assoc*. 90:773–795.