



Genomic growth curves of an outbred pig population

Fabyano Fonseca e Silva¹, Marcos Deon V. de Resende², Gilson Silvério Rocha¹,
Darlene Ana S. Duarte^{1,3}, Paulo Sávio Lopes³, Otávio J.B. Brustolini⁴, Sander Thus⁵,
José Marcelo S. Viana⁶ and Simone E.F. Guimarães³

¹*Departamento de Estatística, Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

²*Embrapa Florestas/Universidade Federal de Viçosa, Colombo, PR, Brazil.*

³*Departamento de Ciência Animal, Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

⁴*Instituto de Biotecnologia Aplicada à Agropecuária, Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

⁵*Department of Animal Sciences, Wageningen University, Wageningen, Netherlands.*

⁶*Departamento de Biologia Geral, Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

Abstract

In the current post-genomic era, the genetic basis of pig growth can be understood by assessing SNP marker effects and genomic breeding values (GEBV) based on estimates of these growth curve parameters as phenotypes. Although various statistical methods, such as random regression (RR-BLUP) and Bayesian LASSO (BL), have been applied to genomic selection (GS), none of these has yet been used in a growth curve approach. In this work, we compared the accuracies of RR-BLUP and BL using empirical weight-age data from an outbred F2 (Brazilian Piau X commercial) population. The phenotypes were determined by parameter estimates using a nonlinear logistic regression model and the halothane gene was considered as a marker for evaluating the assumptions of the GS methods in relation to the genetic variation explained by each locus. BL yielded more accurate values for all of the phenotypes evaluated and was used to estimate SNP effects and GEBV vectors. The latter allowed the construction of genomic growth curves, which showed substantial genetic discrimination among animals in the final growth phase. The SNP effect estimates allowed identification of the most relevant markers for each phenotype, the positions of which were coincident with reported QTL regions for growth traits.

Keywords: Bayesian LASSO, nonlinear regression, SNP effects.

Received: December 21, 2012; Accepted: July 7, 2013.

Introduction

The success of pig production systems, including the evaluation of alternative management and marketing strategies, requires knowledge of the body weight behavior over time, commonly referred to as the growth curve. This knowledge allows the assessment of growth characteristics in actual production situations and translates this information into economic decisions.

Differences among animal growth curves partly reflect genetic influences, with multiple genes contributing at different levels to the overall phenotype. Hence, selection strategies that attempt to modify the growth curve shape to meet demands of the pork market are very relevant. In the current post-genomic era, understanding the genomic basis of pig growth cannot be limited to simply estimating marker effects using body weight at a specific time as a

phenotype, but must also consider changes in body weight over time. According to Pong-Wong and Hadjipavlou (2010) and Ibáñez-Escriche and Blasco (2011) this can be done by estimating the marker effects for parameters of nonlinear regression models that are widely used to describe growth curves.

Regardless of the phenotype used, a major challenge in genome-wide selection (GS) is to identify the most powerful statistical methods for predicting phenotypic values based on estimates of marker effects. Since the seminal GS paper by Meuwissen *et al.* (2001), several studies have compared the efficiency of simple methods, such as the RR-BLUP (Random Regression Blup) (Meuwissen *et al.*, 2001), with more sophisticated methods, such as Bayesian LASSO (BL) (de los Campos *et al.*, 2009). The main difference between these two very popular GS methods is that the first one assumes, *a priori*, that all loci explain an equal amount of genetic variation, while the second one allows the assumption that each locus explains its own amount of this variation. Although these two methods have already been compared in other studies, so far there has been no

Send correspondence to Fabyano Fonseca e Silva. Departamento de Estatística, Universidade Federal de Viçosa, Avenida P.H. Hólfis, 36570-000, Viçosa, MG, Brazil. E-mail: fabyanofonseca@ufv.br.

comparison of these methods using a major gene, such as the halothane gene in pigs (Fujii *et al.*, 1991), as a marker. In addition, these methods have not yet been applied to the analysis of growth curves in conjunction with nonlinear regression models.

In this study, we compared the accuracies of RR-BLUP and BL for predicting genetic merit in an empirical application using weight-age data from an outbred F2 (Brazilian Piau X commercial) pig population (Silva *et al.*, 2011). In this approach, the phenotypes were defined by parameter estimates obtained with a nonlinear logistic regression model and the halothane gene was considered a single nucleotide polymorphism (SNP) marker in order to evaluate the assumptions of the GS methods in relation to the genetic variation explained by each locus. Genomic growth curves based on genomic estimated breeding values were constructed and the most relevant SNPs associated with growth parameters were identified.

Material and Methods

The phenotypic data was obtained from the Pig Breeding Farm of the Department of Animal Science, Universidade Federal de Viçosa (UFV), MG, Brazil. A three-generation resource population was created and managed as described by Band *et al.* (2005). Briefly, two naturalized Piau breed grandsires were crossed with 18 granddams from a commercial line composed of Large White, Landrace and Pietrain breeds, to produce the F1 generation from which 11 F1 sires and 54 F1 dams were selected. These F1 individuals were crossed to produce the F2 population, of which 345 animals were weighed at birth and at 21, 42, 63, 77, 105 and 150 days of age. The use of these animals was reviewed and approved by the Bioethics committee of the Department of Veterinary Medicine (DVT-UFV) in agreement with the Guide to the Care and Use of Experimental Animals of the Canadian Council on Animal Care.

The SNPs used for fine mapping and estimation of marker effects were selected based on their spacing within chromosomes that contained quantitative trait loci (QTL) previously identified in this same population. These markers were distributed as follows: SSC1 (n = 56), SSC4 (n = 54), SSC7 (n = 59), SSC8 (n = 30), SSC17 (n = 25) and SSCX (n = 12), with the average distances (cM) being, respectively, 5.17, 2.37, 2.25, 3.93, 2.68 and 11.0. The animals were genotypes using Golden Gate/VeraCode technology, which provides a robust and flexible platform, in conjunction with a BeadXpress reader from Illumina. A total of 237 markers (236 SNPs plus the halothane gene) were used, with the halothane gene being considered a special marker for reasons explained later.

Five of the nonlinear regression models (Brody, Gompertz, logistic, von Bertalanffy and Richards) most widely used to describe animal growth curves were fitted to the weight-age data using the nls function of R (R Develop-

ment Core Team, 2011) software. The usefulness of the models was compared based on the goodness of fit, the adjusted coefficient of determination and the residual standard deviation, which showed a relative superiority of the logistic model. This model is given by (Ratkowsky, 1983):

$$w_{ij} = \frac{\alpha_{li}}{[1 + \exp(\alpha_{2i} - \alpha_{3i} t_{ij})]} + e_{ij}, \quad (1)$$

where w_{ij} is the animal weight i at age $(t)j$, α_{li} is the mature weight (kg), α_{2i} reflects the weight at time $t = 0$ (birth weight, kg), α_{3i} is a general growth rate (curve slope at the inflection point), and e_{ij} is a residual term, assumed to be independent and normally distributed.

Once the parameters estimates of the logistic model for each animal ($\hat{\alpha}_{li}$, $\hat{\alpha}_{2i}$ and $\hat{\alpha}_{3i}$) were obtained, these values were used as dependent variables in a linear model in order to perform a pre-correction for fixed effects (sex and lot). These pre-corrected observations (residual plus general mean) were used as phenotypes in the GS regression models in order to identify SNP marker effects. This is a well-known two-step procedure (Varona *et al.*, 1999; Pong-Wong and Hadjipavlou, 2010) in which, in the first step, a growth curve is fitted separately to the data of each animal and, in the second step, the growth curve parameter estimates from the previous step are taken as records. The main advantage of this method is its statistical simplicity since the growth model and GS model are fitted independently; however, more sophisticated methods, such as Bayesian joint analysis (Varona *et al.*, 1999) also have been used in GS (Ibáñez-Escriche and Blasco, 2011) and produced good results.

With respect to GS, the phenotypic outcomes (pre-corrected phenotypes for fixed effects), denoted from now on by y_i ($i = 1, 2, \dots, 345$), were regressed on marker covariates x_{ik} ($k = 1, 2, \dots, 237$) following the regression model proposed by Meuwissen *et al.* (2001):

$$y_i = \mu + \sum_{k=1}^{237} x_{ik} \beta_k + e_i, \quad (2)$$

where y_i is the phenotypic observation of animal I , μ is the general mean, β_k is the effect of marker k and e_i the residual term, $e_i \sim N(0, \sigma_e^2)$, in which are included the dominance and epistatic effects. In this model, x_{ik} take the values $2 - 2p_k$, $1 - 2p_k$ and $0 - 2p_k$ for the SNP genotypes AA, Aa and aa at each locus k , respectively, where p_k is the allele frequency at the locus k . Using matrix notation, this GS model can be rewritten as:

$$\mathbf{y} = \mathbf{1}'\mu + \mathbf{I} \sum_{k=1}^{237} \mathbf{X}_k \beta_k + \mathbf{e}, \quad (3)$$

where $\mathbf{1}'$ and \mathbf{I} are, respectively, a unit vector and an identity matrix with dimensions 345, where $\mathbf{y} = [y_1, y_2, \dots, y_{345}]'_{345 \times 1}$, $\mathbf{X}_k = [x_{1k}, x_{2k}, \dots, x_{345k}]'_{345 \times 1}$ and $\mathbf{e} = [e_1, e_2, \dots, e_{345}]'_{345 \times 1}$.

The first method used to fit the GS model was RR-BLUP (Meuwissen *et al.*, 2001), in which β_k is considered a random marker effect, $\beta_k \sim N(0, \sigma_{\beta_k}^2)$ assuming that $\sigma_{\beta_1}^2 = \sigma_{\beta_2}^2 = \dots = \sigma_{\beta_{237}}^2 = \sigma_{\beta}^2$ (*i.e.*, all loci explain an equal amount of genetic variation). This method was implemented using an equivalent model (called G-BLUP) in the R software (R Development Core Team, 2011) by package *rrBLUP* (Endelman, 2011) and the function *mixed.solve*, which solves a mixed model equation of the form:

$$\begin{bmatrix} \mathbf{N} & \mathbf{1}' \\ \mathbf{1} & \mathbf{I} + \sigma_e^2 [\text{var}(\mathbf{u})]^{-1} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{u}} \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{1}' \mathbf{y} \\ \mathbf{y} \end{bmatrix},$$

where $\mathbf{u} = \sum_{k=1}^{237} \mathbf{X}_k \beta_k$ is the vector of genomic breeding values. Thus, admitting the additive genetic variance (σ_a^2) given by $\sigma_{\beta}^2 \sum_{k=1}^{237} 2p_k(1-p_k)$ (Habier *et al.*, 2007) it can be shown that:

$$\begin{aligned} \text{var}(\mathbf{u}) &= \text{var}\left(\sum_{k=1}^{237} \mathbf{X}_k \beta_k\right) = \sum_{k=1}^{237} \text{var}(\mathbf{X}_k \beta_k) = \\ &= \sigma_a^2 \left(\frac{\sum_{k=1}^{237} \mathbf{X}_k \mathbf{X}'_k}{\sum_{k=1}^{237} 2p_k(1-p_k)} \right) = \sigma_a^2 \mathbf{G}, \end{aligned}$$

with G being the so-called genomic relationship matrix. With this approach, it is possible to work through the well-known Henderson mixed model equation using the REML estimation method, which provides estimates of variance components for calculating the heritability by $\hat{h}^2 = \hat{\sigma}_a^2 / (\hat{\sigma}_a^2 + \hat{\sigma}_e^2)$. Since $\hat{\mathbf{u}} = \sum_{k=1}^{237} \mathbf{X}_k \hat{\beta}_k = \mathbf{X} \hat{\beta}$, with $\mathbf{X} = [\mathbf{X}_1 | \mathbf{X}_2 | \dots | \mathbf{X}_{237}]_{345 \times 237}$ and $\hat{\beta} = [\beta_1, \beta_2, \dots, \beta_{237}]_{237 \times 1}$, the estimated marker effects vector can be obtained by the simple normal equation system of $\hat{\beta} = (\mathbf{X}' \mathbf{X})^{-1} (\mathbf{X}' \hat{\mathbf{u}})$.

The second used method was BL (de los Campos *et al.*, 2009), which is a more general method because it assumes that each locus explains its own amount or contribution to the overall variation. This method has been used to solve multicollinearity problems and may also be employed in situations where there are more markers (covariates) than observations. The BL is a penalized Bayesian regression procedure, whose general estimator is given by

$$\hat{\beta} = \arg \min_{\beta} \left\{ (\hat{\mathbf{y}} - \mathbf{X}\beta)' (\hat{\mathbf{y}} - \mathbf{X}\beta) + \lambda \sum_{k=1}^{237} |\beta_k| \right\} \text{ where } \lambda \text{ is the}$$

regularization parameter. When $\lambda = 0$ there is no regularization and when $\lambda > 0$ there is a shrinkage of the marker effects toward zero, with the possibility of setting some identically equal to zero, resulting in a simultaneous estimation and variable selection procedure. This characteristic of the BL method is especially useful for F2 populations in which larger haplotype blocks with many redundant SNPs in each

block are expected; the latter implies multicollinearity that impairs fitting of the model (Eq. (2)). Thus, the regularization imposed by BL reduces some redundant SNPs to zero, thereby bypassing the problem of multicollinear SNPs in haplotype blocks. The package *BLR* (de los Campos *et al.*, 2009; Pérez *et al.*, 2010) of R software was used for this analysis. This package assumes that the joint prior distribution of marker effects ($\beta_1, \beta_2, \dots, \beta_{237}$) is $\prod_{k=1}^{237} N(0, \sigma_{\beta_k}^2)$,

where $\sigma_{\beta_k}^2 = \sigma_e^2 \tau_k^2$, σ_e^2 is the residual variance, with a scaled inverse χ^2 prior distribution, and τ_k^2 is the scale parameter related to each marker. The BLR method also assumes that the joint prior distribution for the scale parameters ($\tau_1^2, \tau_2^2, \dots, \tau_{237}^2$) is the product of exponential distributions, $\prod_{k=1}^{237} \exp(\lambda)$, and that the λ prior distribution is Gamma(v_1, v_2). The BL method was implemented using 10,000 MCMC (Markov chain - Monte Carlo) iterations, with a burn-in and thin of 5,000 and 2 iterations, respectively. The plausibility of these values was assessed for each MCMC chain separately using Raftery-Lewis and Geweke convergence diagnostics in *boa* (Smith, 2007) R package. Since the BLR method provides the posterior mean ($\hat{\beta}_k$) as a marker effect estimate, the vector of the genomic estimated breeding values (GEBV) was obtained as $\hat{\mathbf{u}} = \sum_{k=1}^{237} \mathbf{X}_k \hat{\beta}_k = \mathbf{X} \hat{\beta}$. Using this approach, the additive genetic variance needed to calculate h^2 was $\sigma_a^2 = 2 \sum_{k=1}^{237} \sigma_{\beta_k}^2 p_k(1-p_k)$ because each locus presents a particular variance ($\sigma_{\beta_k}^2$).

As stated earlier, the main difference between RR-BLUP and BL is the assumption related to the equality of marker effects variance, and some studies has used simulated (Meuwissen *et al.*, 2001) and real (Moser *et al.*, 2009) data to verify this assumption. However, to date no studies have applied this assumption to real scenarios in which known major genes are postulated as markers. For this reason, the well-known halothane gene that affects growth traits (Miller *et al.*, 2000) was included in the analysis as a simple marker to provide a real situation of unequal marker effects variances. Of the 345 animals, 291 (84.3%) and 54 (15.7%) had the normal (HAL^{NN}) and heterozygous (HAL^{Nn}) halothane genotype, respectively; none of the animals had a double recessive genotype (HAL^{nn}). The allelic frequencies of N and n were 7 and 93%, respectively.

The leave-one-out cross-validation was used to compare RR-BLUP and BL. For this, the original data set with 345 animals was divided into 345 training data sets (\mathbf{D}_{-i}) of 344 individuals, $\mathbf{D}_{-1}, \mathbf{D}_{-2}, \dots, \mathbf{D}_{-345}$, with each containing marker and phenotypic information of all the animals, except for animal -i. With this approach, there was no loss of generality for each method and each phenotype. In these

analyses, the predicted genomic breeding value of animal **i** for each trait (parameter estimates $\hat{\alpha}_1$, $\hat{\alpha}_2$ and $\hat{\alpha}_3$ of the logistic model) was calculated as $\hat{u}_i = \mathbf{X}_i \hat{\beta}_{\cdot i}$, where \mathbf{X}_i denotes the SNP genotype vector of animal **i** and $\hat{\beta}_{\cdot i}$ denotes the estimated marker effects vector from the analysis that considered all animals, except animal **i**. All codes related to the leave-one-out cross-validation implemented for the RR-BLUP and BL method are provided in the Supplementary Material.

The vector containing all predicted values was $\hat{\mathbf{u}} = [\hat{u}_1, \dots, \hat{u}_{345}]$ and the accuracy (r) used to measure the efficiency of RR-BLUP and BL was given by $r = r_{y\hat{u}} / \sqrt{h^2}$, where $r_{y\hat{u}}$ is the correlation between observed phenotype (**y**) and $\hat{\mathbf{u}}$, and h^2 is the estimated heritability. A linear regression with **y** as the dependent variable and $\hat{\mathbf{u}}$ as the independent variable was used to screen for bias produced by each method; in this case, a regression coefficient of one indicated an unbiased method.

Once the most appropriate method (RR-BLUP or BL) had been chosen, the vectors of the estimated genomic breeding values for each parameter of the logistic growth curve were obtained, assuming that $\hat{\mathbf{u}}_{\hat{\alpha}_1} = [\hat{u}_{\hat{\alpha}_1}, \dots, \hat{u}_{\hat{\alpha}_1 345}]$, $\hat{\mathbf{u}}_{\hat{\alpha}_2} = [\hat{u}_{\hat{\alpha}_2}, \dots, \hat{u}_{\hat{\alpha}_2 345}]$ and $\hat{\mathbf{u}}_{\hat{\alpha}_3} = [\hat{u}_{\hat{\alpha}_3}, \dots, \hat{u}_{\hat{\alpha}_3 345}]$. Subsequently, the “genomic growth curve” for each animal could be estimated using the relationship:

$$\hat{y}_{ij} = \frac{(\mu_{\hat{\alpha}_1} + \hat{u}_{\hat{\alpha}_1 i})}{\{[1 + \exp((\mu_{\hat{\alpha}_2} + \hat{u}_{\hat{\alpha}_2 i}) - (\mu_{\hat{\alpha}_3} + \hat{u}_{\hat{\alpha}_3 i})t_{ij})]\}}, \quad (4)$$

where \hat{y}_{ij} is the genomic breeding value of each animal **i** for weight at each age (t_{ij}) of interest *j* (even for no observed ages), $\mu_{\hat{\alpha}_1}$, $\mu_{\hat{\alpha}_2}$ and $\mu_{\hat{\alpha}_3}$ are the average of each phenotype (parameter estimates for the logistic model) and $\hat{u}_{\hat{\alpha}_1 i}$, $\hat{u}_{\hat{\alpha}_2 i}$ and $\hat{u}_{\hat{\alpha}_3 i}$ are the GEBVs for these phenotypes.

Results and Discussion

Table 1 shows the performance of BL and RR-BLUP. Overall, the two methods provided highly accurate values (mean overall accuracy: 0.69 ± 0.09), as shown by the strong association between the phenotypic assessment and the true breeding values. To date, there has been no evaluation of the accuracy of genomic selection for growth traits in pigs using real data, although Akanno (2012) reported a simulation study in which a performance trait (average daily gain) was simulated for different populations. In this simulation, the so-called synthetic population, which was similar to the F2 population of the present study, showed an accuracy of 0.61.

Comparison of the two methods showed that the BL method yielded more accurate values than RR-BLUP for all of the phenotypes. The mean accuracy of BL (0.70 ± 0.09) was greater than for RR-BLUP (0.62 ± 0.06), indicating that in a real data set in which one locus is known

Table 1 - Accuracy and bias estimates for the Bayesian LASSO (BL) and RR-BLUP genomic selection methods used to determine the logistic growth curve parameters of an F2 Piau X commercial pig population evaluated from birth to 150 days of age.

Phenotypes	Method	Accuracy	Regression coefficient
Mature weight (α_1)	RR-BLUP	0.72	1.56
	BL	0.86	1.39
Birth weight (α_2)	RR-BLUP	0.61	1.31
	BL	0.68	1.26
Growth rate (α_3)	RR-BLUP	0.62	1.39
	BL	0.70	1.29

to have a larger effect (in this case, the halothane gene) the BL property of assuming different variances for markers ensures greater efficiency in genomic selection. Although both methods underestimated the breeding values, *i.e.*, the regression coefficient estimates between the observed and predicted phenotypes were slightly greater than 1.0, for the BL method these coefficients were closer to unity for all phenotypes (indicating low bias) when compared to the corresponding values for RR-BLUP. These findings agreed with those of Ogutu *et al.* (2012), who used a simulated data set to show that LASSO type regressions were more efficient than RR-BLUP for genomic selection because they provided more accurate and less biased predictions.

Table 1 also shows that the accuracy of the differences between the two methods was more pronounced for the trait mature weight (α_1) than for the traits birth weight (α_2) and growth rate (α_3). This finding provides an indirect indication that the genetic architecture of α_1 is possibly more influenced by loci that exert larger effects, such as the halothane gene, than the other two traits. This conclusion reflects the fact that BL works better than RR-BLUP when the assumption of an equal contribution of genetic variance in the latter model is violated, as was the case here with the large-effect halothane gene that was used as a marker.

The effect of the halothane gene on estimates of growth curve parameters has not been examined before and this precludes a direct assessment of the effects of this major gene on mature weight. However, Band *et al.* (2005) observed a significant effect of the halothane gene on weight at 105 days of age (W105) in animals from this same population (F2 Piau X commercial). These authors also evaluated the weight at birth in relation to parameter α_1 and the average daily gain in relation to parameter α_3 . The halothane gene had a significant effect only on W105, indicating that this gene has a greater influence on final weight than on other performance traits.

In summary, the results in Table 1 indicate a superiority of BL in providing accurate estimates and suggest that this method can be recommended for estimating SNP effects and GEBV vectors. However, before using these vec-

tors to select markers and animals it is important to estimate heritabilities and genetic correlations (Table 2) in order to assess whether the three traits (α_1 , α_2 and α_3) are really relevant in a breeding program.

The high values of h^2 (estimated with the BL method) in Table 2 indicate that these traits can be a viable alternative for pig breeding in which the aim is to produce efficient high growth animals. However, direct selection for high α_1 implies a selection for low α_3 (as indicated by the high negative genetic correlation, -0.69, between these two parameters), *i.e.*, in general terms such selection will result in less precocious animals (low growth rate) with a larger body size at maturity. On the other hand, direct selection for high α_3 can result in more precocious animals with high α_2 (birth weight) but low maturity weight (α_1). This negative correlation is expected and has been reported in most studies of growth curves and animal breeding, *e.g.*, Koivula *et al.* (2008) in pigs, Mignon-Grasteau *et al.* (1999) in chickens and Forni *et al.* (2007) in beef cattle.

In practical terms, in pig breeding it is better to select for high growth rate (α_3) since slaughter occurs at a standard slaughter weight (~65 kg for this F2 Piau X commercial population). As a result, the time to slaughter will be significantly lower with a high growth rate, resulting in lower production costs because the slaughter weight is practically the same for all animals (65 kg), with the difference between them reflecting the time required to reach this standard weight. Thus, animals slaughtered at an early age will generate substantially lower feeding costs. The high positive correlation between α_3 and α_2 means that young pigs do not show a loss in early growth and consequently guarantees good nutrition and health for subsequent growth phases.

As mentioned earlier, the main focus of this paper was to construct genomic growth curves using the genomic estimated breeding values (GEBVs) for each parameter of a logistic growth curve (Eq. (4)). Figure 1 shows the genomic growth curve for each animal of the F2 population.

The sigmoidal behavior of the curves in Figure 1 was ensured by the average estimates of the growth curve parameters ($\mu_{\hat{\alpha}_1}$, $\mu_{\hat{\alpha}_2}$ and $\mu_{\hat{\alpha}_3}$) and the GEBVs ($\hat{u}_{\hat{\alpha}_{1i}}$, $\hat{u}_{\hat{\alpha}_{2i}}$ and

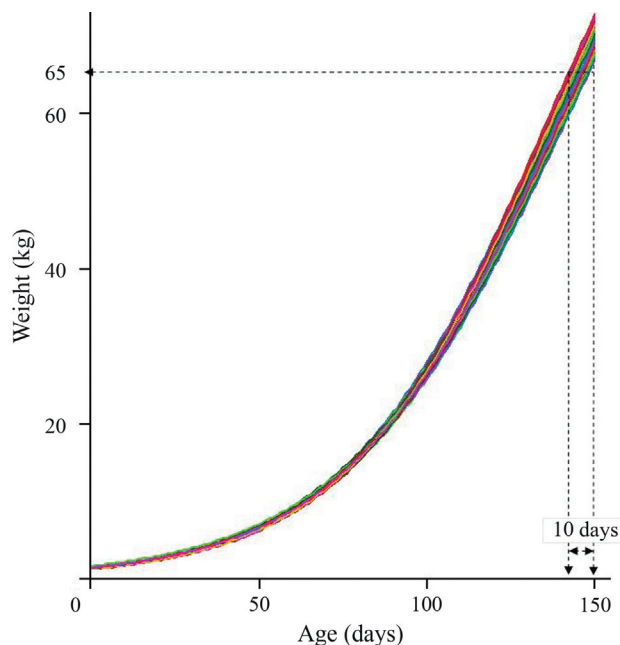


Figure 1 - Genomic growth curves for 345 pigs of an F2 Piau X commercial outbred population from birth to 150 days of age.

$\hat{u}_{\hat{\alpha}_{3i}}$); the latter parameters do not predict this behavior as they may have positive or negative values and are thus outside the limits of the logistic model. The estimates for $\mu_{\hat{\alpha}_1}$, $\mu_{\hat{\alpha}_2}$ and $\mu_{\hat{\alpha}_3}$ were, respectively, 118 kg, 1.4 kg and 0.03 kg/day. There are no data in the literature regarding maturity weight ($\mu_{\hat{\alpha}_1}$) of the present F2 population because the animals are slaughtered at a live weight of 60-65 kg.

One of the advantages of nonlinear growth curve models (such as the logistic curve) is the ability to predict maturity weight using partial weight-age data, *i.e.*, it is possible to estimate the maturity weight before this weight is reached. The value observed here (118 kg) was lower than in other populations such as Yorkshire pigs (201 kg; Koivula *et al.*, 2008) and 4-way-cross pigs (160 kg; Kusec *et al.*, 2007). This lower weight reflects the characteristically small body size of the Piau breed compared to commercial breeds. The estimated growth rate ($\mu_{\hat{\alpha}_3}$) (0.03 kg/day) was higher than that reported by Koivula *et al.* (2008) (0.016 kg/day) and lower than that reported by Kusec *et al.* (2007) (0.05 kg/day) for Yorkshire pigs and commercial crosses, respectively. Kusec *et al.* (2007) also reported estimates for the time until maximum gain (time to inflection point), which were ~120 and 105 days, respectively, for intensive and restrictive feeding systems. In summary, even though the values cited above were obtained in different populations, the comparisons nevertheless provide a useful means of obtaining a general characterization of the growth patterns in the F2 population. Furthermore, as mentioned earlier, there are no data on the growth behavior of this experimental population, which was initially developed to combine the precocity of com-

Table 2 - Heritabilities (diagonal) and genetic correlations (above the diagonal) for the parameters α_1 , α_2 and α_3 estimated by the Bayesian LASSO genomic selection method from the logistic growth curve of an F2 Piau X commercial pig population evaluated from birth to 150 days of age.

	Phenotypes		
	α_1	α_2	α_3
α_1^*	0.42	-0.45	-0.69
Phenotypes α_2	-	0.34	0.92
α_3	-	-	0.36

*Mature weight (α_1), birth weight (α_2) and growth rate (α_3).

mercial lines with the resistance and fat attributes of Piau, a native Brazilian breed.

From a genetic point of view, Figure 1 shows that the weight differences among GEBVs were accentuated over time such that the genetic variance for weight increased with age. This finding may be related to the greater heritability of mature weight (α_1) compared to birth weight (α_2) (Table 2) since this value is directly proportional to genetic variance for a given value of residual variance. Similar curves can be obtained using other approaches, *e.g.*, random regression (Meyer, 1998), but in the present study a different approach was used in which (1) the plotted values were GEBVs that had been estimated by a sophisticated method (Bayesian LASSO) that simultaneously considered regularization and variable selection (SNP markers) and (2) the use of a nonlinear (logistic) growth model allowed estimation of the genetic parameters for traits with direct biological interpretation, *e.g.*, maturity weight and growth rate, that could not be estimated by random regression. In practical terms, Figure 1 shows that the greatest genetic difference (based on GEBV) among animals at slaughter was 10 days since the animals were killed at a live weight of ~65 kg.

Since there have been no reports on QTL detection for the three phenotypes considered in this study and since genomic selection is based on SNP marker estimates, the 5% most relevant SNPs (12 SNPs out of 237 SNPs) for each phenotype (α_1 , α_2 and α_3) were used to assess whether their chromosomal positions coincided with others already reported in the literature as being QTLs related to general growth traits. Table 3 shows these selected SNP markers and the absolute values of their estimated effects and chromosomal positions in cM.

The SNPs with the greatest effects on α_1 were located mainly on chromosomes SSC6, SSC7, SSC17 and SSCX, with particular emphasis on the magnitude of the effect of the halothane gene (0.9114) on this phenotype, as already mentioned for Table 1. The position of marker ALGA0042216 at SSC7 (60.4 cM) agreed with Yue *et al.* (2003), who found a significant QTL for weight at slaughter at position 65.2 cM in crosses between Meishan (M), Pietrain (P) and European Wild Boar (W). Pierzchala *et al.* (2003), using a population similar to those studied by Yue *et al.* (2003), found a significant QTL for weight at slaughter at position 51.1 cM of SSC17, *i.e.*, close to position 45.2 cM for marker ALGA0095662. In general, in the absence of QTL detection for mature weight (α_1), these references to weight at slaughter may be useful for validating the relevance of the identified SNPs for this phenotype.

In relation to trait α_2 , other studies have identified QTLs associated with birth weight at positions close to those of SNPs indicated in Table 3. Su *et al.* (2002) analyzed data from a Large White (LW) x M intercross population and found a significant QTL at position 153 cM of

Table 3 - Absolute values of the estimated effects of the 5% most relevant SNPs on parameters (α_1 , α_2 and α_3) determined from the logistic growth curve of an F2 Piau X commercial pig population evaluated from birth to 150 days of age. SNPs shaded in gray correspond to putative QTLs based on previous literature reports (see text for details).

Phenotype	SNP marker	Estimated effect (abs)	Chromosome	Position (cM)
Mature weight (α_1)	HALOTANO	0.9114	SSC6	112.0
	ALGA0042216	0.0148	SSC7	60.4
	ALGA0099785	0.0092	SSCX	35.1
	ALGA0095662	0.0092	SSC17	45.2
	ALGA0024031	0.0084	SSC4	20.2
	ALGA0039607	0.0080	SSC7	26.4
	ALGA0098944	0.0080	SSCX	0.06
	ALGA0042327	0.0078	SSC7	65.5
	ALGA0111404	0.0076	SSCX	100.7
	ALGA0026446	0.0067	SSC4	85.0
	ALGA0044519	0.0066	SSC7	115.2
	ALGA0000022	0.0065	SSC1	0.3
Birth weight (α_2)	ALGA0010089	0.0169	SSC1	153.3
	ALGA0049219	0.0152	SSC8	55.0
	ALGA0021973	0.0132	SSC4	0.3
	MARC0051258	0.0110	SSCX	112.2
	ALGA0044984	0.0098	SSC7	120.6
	ALGA0049546	0.0097	SSC8	60.0
	ALGA0029483	0.0092	SSC4	123.2
	ALGA0025813	0.0087	SSC4	70.3
	ALGA0021974	0.0084	SSC4	0.3
	ALGA0006708	0.0084	SSC1	141.3
	ALGA0047440	0.0081	SSC8	15.0
	ALGA0027861	0.0079	SSC4	105.0
Growth rate (α_3)	ALGA0047440	0.000180	SSC8	15.0
	ALGA0010089	0.000134	SSC1	153.3
	MARC0051258	0.000118	SSCX	112.2
	ALGA0029483	0.000076	SSC4	123.3
	ALGA0006708	0.000064	SSC1	141.4
	ALGA0093254	0.000059	SSC17	10.3
	ALGA0037853	0.000056	SSC7	0.4
	ALGA0006721	0.000051	SSC1	142.0
	ALGA0047444	0.000049	SSC8	15.2
	ALGA0029781	0.000049	SSC4	127.9
	ALGA0026787	0.000049	SSC4	90.3
	ALGA0050287	0.000048	SSC8	66.5

SSC1, which coincided with the position of marker ALGA0010089. Cepica *et al.* (2003) used F2 families based on crosses of M, W and P breeds and identified a significant QTL at position 117 cM of SSCX, close to the position of marker MARC0051258 (112.2 cM).

With respect to phenotype α_3 , the SNPs positions in Table 3 were compared with significant QTL positions for the trait average daily gain (ADG), which is frequently mentioned in the literature and is highly related to the estimated growth (α_3) rate in the present study. The position of marker ALGA0047440 on SSC8 (15 cM) was close to position 10 cM reported by de Koning *et al.* (2001) who used data from an experimental cross between M and Dutch commercial lines. Sanchez *et al.* (2006) used data from a backcross M x LW and found a significant QTL at position 143 cM of SSC1, close to marker ALGA0010089 (1553.3 cM).

Five SNPs (ALGA0006708, ALGA0010089, ALGA0029483, ALGA0047440 and MARC0051258) in Table 3 were simultaneously among the most important for α_2 and α_3 , which could perhaps explain the greater genetic correlation between birth weight and growth rate in Table 2. In summary, the relevant SNPs listed in Table 3 were associated with QTL regions for growth traits previously reported in the literature. This finding indicates that these regions can be exploited molecularly to enhance pig breeding.

As a general conclusion, Bayesian LASSO provided more accurate values than RR-BLUP for all of the phenotypes evaluated and worked best when the assumption of an equal contribution to genetic variance was violated, *e.g.*, when the halothane major gene was used as a marker in this study. The GEBV vectors allowed the construction of genomic growth curves that revealed substantial genetic discrimination among animals in the final phase of growth. Estimates of the effects of SNPs allowed identification of the most relevant markers for each phenotype, the positions of which coincided with already well-known QTL regions for growth traits.

Acknowledgments

This work was supported by CNPq (grant no. 473601/2010-9) and FAPEMIG (grant no. PPM-00483-11).

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Associate Editor: Louis Bernard Klaczko

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