

ANIMAL GENETICS AND GENOMICS

Impact of including the cause of missing records on genetic evaluations for growth in commercial pigs

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Abstract

It is of interest to evaluate crossbred pigs for hot carcass weight (HCW) and birth weight (BW); however, obtaining a HCW record is dependent on livability (LIV) and retained tag (RT). The purpose of this study is to analyze how HCW evaluations are affected when herd removal and missing identification are included in the model and examine if accounting for the reasons for missing traits improves the accuracy of predicting breeding values. Pedigree information was available for 1,965,077 purebred and crossbred animals. Records for 503,716 commercial three-way crossbred terminal animals from 2014 to 2019 were provided by Smithfield Premium Genetics. Two pedigree-based models were compared; model 1 (M1) was a threshold-linear model with all four traits (BW, HCW, RT, and LIV), and model 2 (M2) was a linear model including only BW and HCW. The fixed effects used in the model were contemporary group, sex, age at harvest (for HCW only), and dam parity. The random effects included direct additive genetic and random litter effects. Accuracy, dispersion, bias, and Pearson correlations were estimated using the linear regression method. The heritabilities were 0.11, 0.07, 0.02, and 0.04 for BW, HCW, RT, and LIV, respectively, with standard errors less than 0.01. No difference was observed in heritabilities or accuracies for BW and HCW between M1 and M2. Accuracies were 0.33, 0.37, 0.19, and 0.23 for BW, HCW, RT, and LIV, respectively. The genetic correlation between BW and RT was 0.34 ± 0.03 , and between BW and LIV was 0.56 ± 0.03 . Similarly, the genetic correlation between HCW and RT was 0.26 ± 0.04 , and between HCW and LIV was 0.09 ± 0.05 , respectively. The positive and moderate genetic correlations between BW and other traits imply a heavier BW resulted in a higher probability of surviving to harvest. Genetic correlations between HCW and other traits were lower due to the large quantity of missing records. Despite the heritable and correlated aspects of RT and LIV, results imply no major differences between M1 and M2; hence, it is unnecessary to include these traits in classical models for BW and HCW.

Key words: animal identification, hot carcass weight, LR method, mortality, swine

Introduction

Profitability for commercial pig breeding is contingent on optimizing all traits contributing to the economic value of the terminal line. Mortality and culling of animals are the

most detrimental factors to financial gain. Many of the high economically valued traits, such as livability (LIV), have low heritabilities, resulting in a lengthy genetic progress (Dufresne et al., 2014). The occurrence of an animal not living to harvest

Abbreviations

BW	birth weight
EBV	estimated breeding values
HCW	hot carcass weight
LIV	livability
LR	linear regression, or Legarra-Reverter method
RT	retained tag

can be accounted for in the evaluations by including a censored trait if death records are available (Arango et al., 2005b). If an animal dies or is removed from the herd, then its survivability record becomes uncensored. Active animals in the herd have censored survivability records (Schaeffer, 2019). Harvested animals that obtain a hot carcass weight (HCW) measurement then have an uncensored record for survivability and HCW. To incorporate censored data in the analysis, the reason for death and the stage of life when the animal died must be recorded.

The growth and carcass traits are economically important, and breeders are continuously working to improve these rates of genetic gain. Because the rate of genetic process is slow at the commercial level in swine breeding, improving the model and individual identification methods will ultimately improve performance (Arango et al., 2005a). Selection for heavier birth weight (BW) is essential for commercial pig models as it leads to greater chances of LIV and faster growth rates (Grandinson et al., 2002; Arango et al., 2006). Previous studies have shown that it is possible to considerably improve several economically important traits by incorporating an associative social interaction effect in the breeding program (Muir and Schinckel, 2002; Bijma et al., 2007; Bergsma et al., 2008).

Individual identification is essential for traceability, phenotype tracking, and advancing breeding programs. The identification device must be retained and readable throughout the entire process to record measurements from birth to slaughter. A feasible identification method would accommodate the systematic processes at commercial harvest and provide a logical cost-benefit return. Efforts for social interaction models require a reliable animal identification method and group information, so group mates and their indirect genetic effects can be identified. However, group information is not usually attained in most commercial pig operations, and the percentage of animals that lose the identification tag can be as high as 30%. Accounting for the reason animals were unable to obtain a HCW measurement may help overcome this issue and provide better estimates of HCW, given that data were not available for some animals because of mortality and missing tags.

The objective of this study was to compare genetic parameters, correlations, and breeding values for BW and HCW in a two-trait model or a four-trait model that also accounted for retained tag (RT) and LIV records.

Materials and Methods

Animal Care and Use Committee approval was not needed because information was obtained from pre-existing databases.

Data

Data were recorded from two farms for animals born between 2014 and 2019 and were provided by Smithfield Premium Genetics (Rose Hill, NC). The pedigree included 1,965,077 animals; however, phenotypes were only available for

503,716 commercial three-breed cross terminal animals. The phenotyped animal's dams were crossbred Landrace and Large White, and sires were purebred Duroc. The traits included BW, HCW, and two binary traits, RT and LIV. All 503,716 animals used in the dataset had a BW record. There were 237,041 animals with a HCW measurement. Each farm brought their animals to a different harvest site, in which the instrumentation used to measure HCW may differ between sites. However, this potential difference is accounted for by including farms in the contemporary group.

RT and LIV traits consisted of reasons for the animals' inability to obtain a HCW record and were included in the model to analyze their effects on HCW evaluation. The RT categories were retained tag and non-retained tag and coded as 1 and 2, respectively. If an animal was missing its ear tag, the HCW trait was unobtainable, and death information was not recorded; thus, it is unknown if the animal was harvested. Once an animal loses its tag, phenotypes can no longer be recorded for the remainder of its life. There were no data available indicating at which life stage an animal lost its tag.

LIV evaluates if the animal lived to be a full-value pig and was harvested or if the animal failed to live until harvest. A missing ear tag is considered a missing record for LIV since it is unknown if the animal made it to harvest or was removed from the herd before harvest, and the animal could not obtain a HCW record. A total of 11,013 animals survived to harvest, retained their ear tag, but did not have a HCW measurement. This could be due to scale malfunction, errors in pig identification after initial processing, etc. Table 1 includes the number and proportion of animals that have each trait and level.

The dataset included 471,360 animals after editing. Summary statistics for all continuous traits and effects after editing are given in Table 2. Records were discarded for all animals born in 2014 due to the lack of LIV phenotypes. Animals in contemporary groups containing less than 10 animals were also excluded from the dataset. Contemporary groups were composed of farm, week, and year of birth. Group or pen information was not recorded and cannot be included in the contemporary groups. All animals were identified by a unique identification number on a plastic ear tag administered at birth.

Model and Analyses

Pedigree-based analyses were performed using a four-trait threshold-linear model (BW-HCW-RT-LIV) and a two-trait linear model (BW-HCW) defined as M1 and M2, respectively. M1 was considered to be the full model and compared with the reduced M2. The equation for both models can be expressed as:

Table 1. Number of animals with records for each trait and level

Trait	Code	Level	N	%
BW ¹			471,360	100.0
HCW ²			221,311	47.0
RT ³	1	Missing Tag	134,523	28.5
	2	Retained Tag	336,837	71.5
LIV ⁴	0	Missing Tag	134,523	28.5
	1	Died/Culled	104,513	22.2
	2	Harvested	232,324	49.3

¹Birth weight

²Hot carcass weight

³Retained tag

⁴Livability

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Wc} + \mathbf{e}, \quad (1)$$

where \mathbf{y} is the vector of phenotypes; \mathbf{b} is the fixed vector of systematic effects; \mathbf{u} is the vector of random additive genetic effects; \mathbf{c} is the vector of random litter effects; \mathbf{e} is the vector for random residual effects; \mathbf{X} , \mathbf{Z} , and \mathbf{W} are incidence matrices relating elements of \mathbf{y} to \mathbf{b} , \mathbf{u} , and \mathbf{c} , respectively. The systematic effects included in vector \mathbf{b} were contemporary group (farm, year, and week of birth), sex, age at harvest (only for HCW), and dam parity.

Estimates of (co)variance components and breeding values for both models were obtained using THRGIBBS1F90 and were run as a single Gibbs chain of 50,000 rounds, with 1 in every 10 samples stored (Tsuruta and Misztal, 2006). The prior distributions were assumed to be uniform for fixed effects. The vectors \mathbf{u} , \mathbf{c} , and \mathbf{e} were assumed to be distributed as multivariate normal with mean zero and the following covariance structure:

$$\text{Var} \begin{bmatrix} \mathbf{u} \\ \mathbf{c} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{A} \otimes \mathbf{G}_0 & 0 & 0 \\ 0 & \mathbf{I} \otimes \mathbf{L}_0 & 0 \\ \text{symm} & 0 & \mathbf{I} \otimes \mathbf{R}_0 \end{bmatrix}, \quad (2)$$

in which \mathbf{A} is the numerator relationship matrix, \mathbf{I} is the identity matrix, \mathbf{G}_0 is the additive genetic (co)variance matrix, \mathbf{L}_0 is the litter (co)variance matrix, and \mathbf{R}_0 is the residual (co)variance matrix. After discarding the first 15,000 sampled as burn-in, 3,500 samples were kept to calculate the means and standard deviations of the posterior distributions of variance components used as estimations for the remainder of the analyses. Convergence and burn-in were assessed by visual inspection of the sample and distribution graphs. Additionally, the residual variances were set to 1.00 for the binary traits.

Validation metrics were estimated with the linear regression (LR) method to compare both models (Legarra and Reverter, 2018). The validation dataset consisted of 73,617 animals born in 2019. EBV were calculated for the animals in the validation set with all data available (\hat{u}_{whole}) and with phenotypes removed

for the validation animals (\hat{u}_{partial}). The validation measurements obtained were accuracy, dispersion, bias, and Pearson correlations. These measures were obtained to compare the estimability of HCW for both models. Accuracy was calculated for the focal animals using: $\hat{\rho}_{\text{cov}(\text{whole,partial})} = \sqrt{\frac{\text{cov}(\hat{u}_{\text{whole}}, \hat{u}_{\text{partial}})}{(1-F)\hat{\sigma}_u^2}}$ (Legarra and Reverter, 2018), where F is the average inbreeding coefficient for animals born in 2019, and $\hat{\sigma}_u^2$ is the estimated additive genetic variance of the whole dataset. INBUPGF90 was used to calculate inbreeding coefficients for each animal by a recursive method based on pedigree (Aguilar and Misztal, 2008). Dispersion (b_1) was measured as the regression coefficient of the regression of \hat{u}_{whole} on \hat{u}_{partial} : $b_1 = \frac{\text{cov}(\hat{u}_{\text{whole}}, \hat{u}_{\text{partial}})}{\text{var}(\hat{u}_{\text{partial}})}$. The bias is defined as the difference in the average EBV from partial and whole datasets. Lastly, Pearson correlations were calculated between \hat{u}_{whole} and \hat{u}_{partial} .

Results and Discussion

Variance components

Variances for the direct additive genetic, litter, and residual effects for both models are given in Table 3. The estimated BW variances were the same for both models (M1 and M2) and were 0.09, 0.24, and 0.48 for the direct additive genetic, litter, and residual effects, respectively. The estimated HCW variances for M1 (M2) were 26.4 ± 1.32 (25.9 ± 1.24), 45.1 ± 0.85 (43.6 ± 0.83), and 285.6 ± 2.25 (273.8 ± 1.13) for additive genetic, litter, and residual effects, respectively. There was no difference in variance estimates for BW and HCW between M1 and M2 in agreement with the lowly heritable aspects of RT and LIV. The variance estimates for RT (LIV) were 0.02 (0.05) and 0.10 (0.18) for the additive genetic and litter effects, respectively.

Table 4 shows the heritability and genetic correlations for both models and between all traits. Genetic correlations between traits were either weak or moderate. The genetic correlation between BW and RT was 0.34 ± 0.03 , and between BW and LIV

Table 2. Summary statistics for continuous traits and effects

Trait	Min	Max	Mean	Median	SD
BW ¹ , kg	0.24	2.70	1.42	1.40	0.41
HCW ² , kg	51.3	153.8	100.2	99.8	9.9
Age at Harvest, d	150.0	210.0	182.4	182.0	12.5

¹Birth weight

²Hot carcass weight

Table 3. Variances for direct additive genetic, litter, and residual effects for both models and all traits¹

	σ_u^2		σ_c^2		σ_e^2	
	M1	M2	M1	M2	M1	M2
BW ²	0.09	0.09	0.24	0.24	0.48	0.48
HCW ³	26.4 ± 1.32	25.9 ± 1.24	45.1 ± 0.85	43.6 ± 0.83	285.6 ± 2.25	273.8 ± 1.13
RT ⁴	0.02		0.10		1.00	
LIV ⁵	0.05		0.18		1.00	

¹Standard deviations are shown for HCW. All standard deviations for BW, RT, and LIV were less than 0.01.

²Birth weight

³Hot carcass weight

⁴Retained tag

⁵Livability

Table 4. Estimates of heritability (diagonal) and genetic correlations (off-diagonal) for both models

	BW ¹	HCW ²	RT ³	LIV ⁴
Model 1				
BW ¹	0.11 ± 0.00	0.31 ± 0.03	0.34 ± 0.03	0.56 ± 0.03
HCW ²		0.07 ± 0.00	0.26 ± 0.04	0.09 ± 0.05
RT ³			0.02 ± 0.00	0.00 ± 0.06
LIV ⁴				0.04 ± 0.00
Model 2				
BW ¹	0.11 ± 0.00	0.32 ± 0.03		
HCW ²		0.07 ± 0.00		

¹Birth weight²Hot carcass weight³Retained tag⁴Livability

was 0.56 ± 0.03. These positive, moderate genetic correlations are logical with the code used for RT and LIV (Table 1). Previous studies have shown that piglets with a heavier BW have greater survival chances (Arango et al., 2006). As BW increases, the probability of an animal to live to harvest increases. Similarly, piglets with a lighter BW have a higher probability of early death, culling, or not retaining their ear tag. Both HCW and BW had positive genetic correlations between the two binary traits; however, the lower correlations between HCW can be explained by the inability of 53% of this population to obtain HCW records. The heritability of HCW was less than BW, which explains the more significant impact of HCW between RT and LIV.

It should be noted that no information was given on the number of animals in each pen or if animals were removed from the pen at different times. If the larger animals were removed from the pen first, and the smaller animals had more time and pen space available to grow, this could impact the predictions for HCW. The genetic correlations between BW and HCW also showed no significant difference between models and were 0.31 ± 0.03 and 0.32 ± 0.03 for M1 and M2. Comparably, Dufasne et al. (2014) reported a genetic correlation of 0.55 between BW and HCW for a commercial pig population.

The heritabilities for BW (0.11) and HCW (0.07) showed no difference between models. Heritability estimates for RT and LIV were 0.02 and 0.04. Heritability estimate ranges in previous literature seem to be lower for BW (0.03–0.06) and higher for HCW (0.12–0.28) than the estimates found in this study (Knol et al., 2002; Arango et al., 2006; Zumbach et al., 2007; Dufasne et al., 2013; Miar et al., 2014). Analogously to LIV, (Dufasne et al., 2014) analyzed a binary culling trait including death for all stages of life and found the heritability estimate to be 0.06. Currently, there is no published research in estimating the heritability of RT for any species. As the genetic correlations are moderate between RT and LIV and the weight traits, as well as the higher h^2 for weight traits, the indirect selection for weight may move the population means for RT and LIV to more desirable values. Accounting for RT and LIV gives no additional benefits for variance component estimations of HCW and BW evaluations.

Validation

The validation measures give a further justification of the insignificant differences between the models (Table 5). Bermann et al. (2021) showed that the LR method is suitable for binary traits and yields consistent accuracy measures (Legarra and Reverter, 2018). The accuracy, dispersion, and correlations for HCW were higher than BW (Table 5). The EBV for HCW and BW

Table 5. Validation statistics for both models

Trait	Model	acc _{LR} ¹	b_1 ²	Bias ³	cor(\hat{u}_{whole} , $\hat{u}_{partial}$) ⁴
BW ⁵	M1	0.33	0.74	0.00	0.59
	M2	0.33	0.75	0.01	0.59
HCW ⁶	M1	0.37	0.93	-0.01	0.74
	M2	0.37	0.91	0.06	0.74
RT ⁷	M1	0.19	0.65	0.00	0.56
LIV ⁸	M1	0.23	0.78	0.00	0.56

¹Accuracy as defined in the LR method²Dispersion: the coefficient of the regression of $\hat{u}_{partial}$ on \hat{u}_{whole} ³The difference in the average of \hat{u}_{whole} and $\hat{u}_{partial}$ in terms of genetic standard deviation⁴Pearson correlation between \hat{u}_{whole} and $\hat{u}_{partial}$ ⁵Birth weight⁶Hot carcass weight⁷Retained tag⁸Livability

were more biased in M2 than M1. Bias was less than 0.01 for BW and -0.01 for HCW in M1. In M2, bias was 0.01 for BW and 0.06 for HCW. Biases were less than 0.01 for RT and LIV. The dispersion for HCW was less than for LIV and BW. The greatest dispersion was for RT ($b_1 = 0.65$). The binary traits had lower accuracy and correlations than both linear traits, indicating the difficulty of modeling binary traits of low heritability.

We hypothesized that by including the reasons for missing records, RT, and LIV information, HCW evaluations would have better predictions. However, no performance distinctions were observed when this information was accounted for in the model. Bias was marginally less in M1 compared to M2 for both BW and HCW. The dispersion was 0.02 greater for HCW and 0.01 less for BW when missing record information was included in the analyses. The Pearson correlation of \hat{u}_{whole} and $\hat{u}_{partial}$ is a direct estimator of the magnitude of change between evaluations when phenotypes are added; therefore, a higher Pearson correlation indicates a more stable model (Legarra and Reverter, 2018). There was no difference in correlations between M1 and M2 for both BW and HCW, which further indicates the lack of dissimilarity between the models. It is logical that including the missing trait information does not benefit models for BW evaluations since RT and LIV are traits measured after BW is recorded and can cause extra noise in the model. Despite subtle differences between the models, the inconsistencies are negligible, and the prediction performance is the same for both models. As in Arango et al. (2005b), censoring models could not be implemented with this dataset since there were no records of in which life stage each animal lost its ear tag. An alternative would be to link animals with missing tags back to the data by using parentage tests based on SNP (Maiorano et al., 2019); however, this would require much cheaper genotyping platforms because the crossbreds are terminal animals.

Conclusions

HCW and BW accuracies were unchanged when the causes of missing records were included in the model. Positive genetic correlations were observed between BW and HCW and the binary traits indicating relationships exist between these traits. Low genetic correlations between HCW can be attributed to this trait's high percentage of missing records. Results imply a higher survival probability with heavier BW, shown in the

moderate and positive genetic correlations between BW and RT and LIV. The low heritabilities of RT and LIV potentially explain the small impact of including animal removal reasons on HCW evaluations. An alternative option would be to implement a social interaction model; however, group information and a more reliable identification method are needed. A low-density, inexpensive parentage SNP panel could possibly help with the latter. This study shows no major differences in results when accounting for causes of missing records, and RT and LIV traits are not necessary to include in HCW evaluations.

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Conflict of interest statement

The authors declare no real or perceived conflicts of interest.

Literature Cited

- Aguilar, I., and I. Misztal. 2008. Technical note: recursive algorithm for inbreeding coefficients assuming nonzero inbreeding of unknown parents. *J. Dairy Sci.* **91**:1669–1672. doi:[10.3168/jds.2007-0575](https://doi.org/10.3168/jds.2007-0575).
- Arango, J., I. Misztal, S. Tsuruta, M. Culbertson, and W. Herring. 2005a. Estimation of variance components including competitive effects of Large White growing gilts. *J. Anim. Sci.* **83**(6):1241–1246. doi:[10.2527/2005.8361241x](https://doi.org/10.2527/2005.8361241x)
- Arango, J., I. Misztal, S. Tsuruta, M. Culbertson, and W. Herring. 2005b. Study of codes of disposal at different parities of Large White sows using a linear censored model. *J. Anim. Sci.* **83**(9):2052–2057. doi:[10.2527/2005.8392052x](https://doi.org/10.2527/2005.8392052x)
- Arango, J., I. Misztal, S. Tsuruta, M. Culbertson, J. W. Holl, and W. Herring. 2006. Genetic study of individual preweaning mortality and birth weight in Large White piglets using threshold-linear models. *Livest. Sci.* **101**(1–3):208–218. doi:[10.1016/j.livprodsci.2005.11.011](https://doi.org/10.1016/j.livprodsci.2005.11.011)
- Bergsma, R., E. Kanis, E. F. Knol, and P. Bijma. 2008. The contribution of social effects to heritable variation in finishing traits of domestic pigs (*Sus scrofa*). *Genetics* **178**:1559–1570. doi:[10.1534/genetics.107.084236](https://doi.org/10.1534/genetics.107.084236).
- Bermann, M., A. Legarra, M. K. Hollifield, Y. Masuda, D. Lourenco, and I. Misztal. 2021. Validation of single-step GBLUP genomic predictions from threshold models using the linear regression method: an application in chicken mortality. *J. Anim. Breed. Genet.* **138**:4–13. doi:[10.1111/jbg.12507](https://doi.org/10.1111/jbg.12507).
- Bijma, P., W. M. Muir, E. D. Ellen, J. B. Wolf, and J. A. Van Arendonk. 2007. Multilevel selection 2: estimating the genetic parameters determining inheritance and response to selection. *Genetics* **175**:289–299. doi:[10.1534/genetics.106.062729](https://doi.org/10.1534/genetics.106.062729).
- DufRASNE, M., I. Misztal, S. Tsuruta, J. Holl, K. A. Gray, and N. Gengler. 2013. Estimation of genetic parameters for birth weight, preweaning mortality, and hot carcass weight of crossbred pigs. *J. Anim. Sci.* **91**:5565–5571. doi:[10.2527/jas.2013-6684](https://doi.org/10.2527/jas.2013-6684)
- DufRASNE, M., I. Misztal, S. Tsuruta, N. Gengler, and K. A. Gray. 2014. Genetic analysis of pig survival up to commercial weight in a crossbred population. *Livest. Sci.* **167**:19–24. doi:[10.1016/j.livsci.2014.05.001](https://doi.org/10.1016/j.livsci.2014.05.001)
- Grandinson, K., M. S. Lund, L. Rydhmer, and E. Strandberg. 2002. Genetic parameters for the piglet mortality traits crushing, stillbirth and total mortality, and their relation to birth weight. *Acta Agric. Scand. Section A — Anim. Sci.* **52**(4):167–173. doi:[10.1080/090647002762381041](https://doi.org/10.1080/090647002762381041)
- Knol, E. F., B. J. Ducro, J. A. M. van Arendonk, and T. van der Lende. 2002. Direct, maternal and nurse sow genetic effects on farrowing-, pre-weaning- and total piglet survival. *Livest. Prod. Sci.* **73**(2):153–164. doi:[10.1016/S0301-6226\(01\)00248-2](https://doi.org/10.1016/S0301-6226(01)00248-2)
- Legarra, A., and A. Reverter. 2018. Semi-parametric estimates of population accuracy and bias of predictions of breeding values and future phenotypes using the LR method. *Genet. Sel. Evol.* **50**(1):53. doi:[10.1186/s12711-018-0426-6](https://doi.org/10.1186/s12711-018-0426-6)
- Maiorano, A. M., A. Assen, P. Bijma, C.-Y. Chen, J. A. I. V. Silva, W. O. Herring, S. Tsuruta, I. Misztal, and D. A. L. Lourenco. 2019. Improving accuracy of direct and maternal genetic effects in genomic evaluations using pooled boar semen: a simulation study1. *J. Anim. Sci.* **97**(8):3237–3245. doi:[10.1093/jas/skz207](https://doi.org/10.1093/jas/skz207)
- MiAR, Y., G. S. Plastow, S. S. Moore, G. Manafazar, P. Charagu, R. A. Kemp, B. Van Haandel, A. E. Huisman, C. Y. Zhang, R. M. McKay, et al. 2014. Genetic and phenotypic parameters for carcass and meat quality traits in commercial crossbred pigs1. *J. Anim. Sci.* **92**(7):2869–2884. doi:[10.2527/jas.2014-7685](https://doi.org/10.2527/jas.2014-7685)
- Muir, W., and A. Schinckel. 2002. *Incorporation of competitive effects in breeding programs to improve productivity and animal well being*. Proceedings of the 7th World Congress on Genetics Applied to Livestock Production.
- Schaeffer, L. R. 2019. *Animal models*. Volumes Direct.
- Tsuruta, S., and I. Misztal. 2006. *THRGI BBS1F90 for estimation of variance components with threshold-linear models*. Proceedings of the 8th World Congress on Genetics Applied to Livestock Production **89**:27–31.
- Zumbach, B., I. Misztal, S. Tsuruta, J. Holl, W. Herring, and T. Long. 2007. Genetic correlations between two strains of Durocs and crossbreds from differing production environments for slaughter traits. *J. Anim. Sci.* **85**:901–908. doi:[10.2527/jas.2006-499](https://doi.org/10.2527/jas.2006-499)