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Genetic parameters for growth and carcass traits of Duroc pigs

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ABSTRACT:

Objective: This study aimed to estimate genetic parameters for body weight and carcass traits in Duroc pigs to determine which traits could be more suitable to be included in breeding programs.

Methods: The following traits were analyzed: body weight at 70, 100, and 155 days of age (W70, W100, and W155), average daily gain (ADG1, ADG2, and ADG3), backfat thickness (BF), loin depth (LD), and intramuscular fat percentage (IMF).

Results: Direct heritability estimates for body weight ranged from 0.15±0.03 (W70) to 0.22±0.03 (W155), maternal heritabilities ranged from 0.02±0.01 (W155) to 0.04±0.02 (W70 and W100), and the proportion of common litter effect in the total variance ranged from 0.08±0.01 (W155) to 0.11±0.01 (W70). Heritability estimates for ADG ranged from 0.29±0.03 (ADG1) to 0.38±0.04 (ADG3). Higher heritability estimates were observed for BF, LD, and IMF (0.37±0.04 to 0.58±0.04). Genetic correlations between body weights, weight gains, and carcass traits ranged from 0.60 to 0.81, 0.22 to 0.80, and -0.03 to 0.56, respectively. Heritability estimates showed that selection for all traits is feasible.

Conclusion: The ADG2 trait may promote indirect and favorable gains in the other weight and weight gain traits studied, as well as in LD and IMF. Attention must be paid when selecting animals based on ADG2 because of the possibility of an increase in carcass fat. Direct selection for LD does not appear to affect BF or IMF.

Keywords: animal breeding; pig farming; selection criteria, *Sus scrofa domesticus*

INTRODUCTION

The Duroc breed has undergone intensive artificial selection to improve production efficiency and product quality [1], with reported superior performance in growth, conformation, and meat quality [2]. Industry-relevant traits, including average daily gain and carcass and meat attributes, are commonly targeted in breeding programs [3]. Growth traits show moderate heritability and can be efficiently selected [4], whereas carcass and meat quality traits are increasingly emphasized due to consumer demand [5].

Regarding body weight, breeding programs have used the number of days required to reach a specific weight as a selection criterion. In the European Union and the United States, market weight is approximately 130 kg, whereas in China it is around 105 kg [6]. In Duroc populations from the United States and Canada, Qiu et al. [7] reported mean values of 158.99 and 161.13 days, respectively, to reach 100 kg. Esfandyari et al. [8] estimated heritabilities of 0.20 and 0.26 for days to reach 80 and 120 kg, with mean ages of 119.08 and 167.48 days, respectively.

Another approach to evaluate growth is the assessment of body weight at different ages. In a study performing longitudinal monitoring of body weight in Duroc pigs, Herrera-Cáceres et al. [9] obtained mean weights of 66.03, 92.49 and 117.85 kg at 100 to 140, 141 to 170 and 171 to 200 days of age, respectively. The authors estimated heritability coefficients for weights at different ages (from 110 to 200 days of age, at 15-day intervals) that ranged from 0.18 to 0.32. The definition of body weight measures depends on the objectives of each breeding program and the requirements of the target market, highlighting the need for continuous investigation of these traits.

Average daily gain (ADG) is another trait of interest in pig breeding programs, as it reflects growth rate and the time required to reach market weight [10]. Ogawa et al. [11] estimated a heritability of 0.50 for ADG in 9,550 Duroc animals, with an observed ADG of 704.80 g/day. Homma et al. [12], in a study of 1,900 Duroc pigs, reported an ADG of 1,023.99 g/day, with a heritability estimate of 0.46.

In response to demand for meat with lower fat content, many countries have emphasized selection for lean meat yield, which has reduced both carcass fat and intramuscular fat thickness

[13], therefore these traits are relevant for meat quality [14]. Although the heritabilities for the carcass traits mentioned range from 0.25 to 0.58 [15–17], studies have reported the existence of negative genetic correlations between the percentage of lean meat and intramuscular fat, a fact that makes simultaneous selection for these traits a challenge [18].

The aim of the present study was to estimate heritability coefficients and genetic correlations for body weights measured at 70, 100 and 155 days of age, ADG between these ages, backfat thickness, loin depth, and intramuscular fat percentage to determine which trait(s) are more suitable to be included in a breeding program.

MATERIALS AND METHODS

Records from a Duroc herd selected for growth and meat quality, which belongs to a swine genetic improvement company called AcuFast™ (Saskatoon, SK, Canada), were used. Commercial diets specific to each life stage were provided to meet nutritional requirements. Water was available *ad libitum*. Stocking density, room temperature, and other rearing conditions (e.g., lighting and ventilation programs) were managed according to the Code of Practice of the Canadian Pork Council (https://www.cpc-ccp.com/uploads/userfiles/files/pig_code_of_practice.pdf).

The following traits were evaluated: weight at 70 days of age (W70), weight at 100 days of age (W100), weight at 155 days of age (W155), average daily gain between 70 and 100 days of age (ADG1), average daily gain between 70 and 155 days of age (ADG2), average daily gain between 100 and 155 days of age (ADG3), backfat thickness (BF), loin depth (LD), and intramuscular fat percentage (IMF).

W70, W100 and W155 correspond to the beginning, middle and end of the growth and finishing test, respectively. A variation of ± 15 days was allowed for each body weight to be evaluated. The ADG was obtained as the difference in weights between 100 and 70 days, between 155 and 70 days, and between 155 and 100 days of age, divided by the number of days between weight recordings. Carcass traits were measured with the BioQStation device (www.biotronics-inc.com) and obtained between the 3rd and 4th rib counted from the last rib.

Quality control of phenotypic data was performed using the *car* package [19], implemented in the R program [20]. The general linear model used to define the significance ($P < 0.05$) of fixed effects included the effects of year and month of birth and sex of the animal. Animals born between 2018 and 2023 were considered. To determine the normality of the distribution of residuals and to remove discrepant data, only standardized residuals ranging from -3.5 to +3.5 standard deviations were considered. After this step, the fixed effects were concatenated for the formation of contemporary groups. Contemporary groups containing fewer than five individuals, sires with fewer than five offspring, and contemporary groups composed of offspring from only one sire were removed.

Genetic parameters were estimated by the restricted maximum likelihood method under an animal model in single- and two-trait analyses using the WOMBAT program [21]. The complete statistical model (M4) is presented below:

$$y = X\beta + Za + Mm + Wc + e$$

where y is the vector of phenotypic data; β is the vector of fixed effects; a is the vector of random direct additive genetic effects; m is the vector of random maternal additive genetic effects; c is a vector of random common litter effects, and e is the vector of random environment effects. X, Z, M, and W are incidence matrices associated with the respective effects of the parameters on y.

For the other models tested, M1 included the random direct additive genetic and environmental effects; M2 included the random direct additive genetic, maternal additive genetic, and environmental effects; and M3 included the random direct additive genetic, common litter, and environmental effects. The complete relationship matrix included 195,694 animals. The convergence criterion adopted in all analyses was 10^{-6}. Single-trait analyses were performed to identify the most appropriate models. Model comparisons (Supplementary Table S1) were carried out using the likelihood ratio test at a significance level of 5% with *n* degrees of freedom [22].

After definition of the models, two-trait analyses were performed to estimate the genetic, environmental and phenotypic correlations between the traits studied. Significance ($P < 0.01$) of the genetic correlations was tested by the Student *t*-test using standardized Fisher transformation (Fisher, 1915).

RESULTS

The likelihood ratio test (Supplementary Table S1) indicated that all effects tested for W70, W100, and W155 were significant ($P < 0.05$); thus, direct additive genetic, maternal genetic, and the proportion of common litter to total variance effects were considered as adequate models. For the average daily gain traits, only the model including direct additive genetic effects was considered since the data structure was not sufficient for estimating the other parameters. For the carcass traits, there was no significant difference ($P > 0.05$) between the models tested; thus, the model that included direct additive genetic random effects and random effects of the environment was used. The genetic correlations between direct and maternal effects for W70, W100, and W155 were equal to -0.70, -0.61, and -0.50, respectively.

Table 1 shows the descriptive statistics of the data used for genetic parameter estimation. An important change was observed from W70 to W100, with a difference between means of 43.7 kg at an interval of 30 days between measurements. The difference between mean W100 and W155 was 42.82 kg, considering 55 days between measurements. The variations in the number of individuals for body weight and weight gain traits are due to the quality control applied to the phenotypes. Although carcass traits are evaluated at about 155 days of age, differences were observed in the number of individuals, which is also due to the quality control of phenotypes.

The estimates of direct and maternal heritability and the proportion of common litter effect in the total variance (obtained after the log likelihood test in single-trait analyses - Supplementary Table S1) and genetic correlations (obtained in two-trait analyses) are presented in Table 2. Heritability estimates for the body weight traits ranged from 0.21±0.04 (W70) to 0.27±0.04 (W155) and for the weight gain traits from 0.29±0.03 (ADG1) to 0.38±0.04 (ADG3). Maternal heritability estimates ranged from 0.05±0.02 (W155) to 0.12±0.03 (W70), and the proportion of common litter effect in the total variance ranged from 0.08±0.01 (W155) to 0.11±0.02 (W70). Higher heritability estimates were obtained for the carcass traits, with estimates ranging from 0.37±0.04 (IMF) to 0.58±0.04 (BF).

The genetic correlations (Table 2) ranged from 0.32±0.07 (ADG2 with IMF) to 0.87±0.03 (W100 with ADG1). High genetic correlations were observed between the body weight traits, with estimates ranging from 0.60±0.08 to 0.81±0.04. The genetic correlations between the weight gain traits ranged from 0.22±0.08 to 0.80±0.03. For the carcass traits, genetic correlations ranging from -0.03±0.07 to 0.56±0.05 were obtained. Table 3 shows the phenotypic and environmental correlations, which ranged from -0.03±0.03 to 0.89±0.01. There was concordance between most of the genetic and phenotypic correlations in terms of magnitude and sign. The environmental correlations were also similar to the genetic correlations for all traits studied.

DISCUSSION

Considering the estimates obtained for body weight (Table 2), selection for W155 would be more efficient because of the higher heritability compared to the other traits, increasing genetic progress in this population of Duroc pigs. However, the selection process could be anticipated using W70 or W100, but genetic gains are expected to be slightly lower when compared to selection for W155. According to Ruan et al. [24], growth traits in Duroc pigs have moderate heritabilities and can be genetically improved by direct selection.

All body weight traits were influenced by maternal genetic effects, whose influence decreased at later ages, as also reported by Lee et al. [25]. Therefore, maternal genetic effects must be considered in the estimation of genetic parameters for body weight in pigs to reduce bias in the estimation of direct breeding values and, consequently, in animal ranking. The estimates of both maternal genetic effects and the proportion of common litter effect in the total variance on body weight traits tended to decrease as the animals got older across the ages studied. Despite low magnitudes, the maternal effect can influence offspring performance at 70, 100 and 155 days of age in Duroc pigs.

We found no studies using body weight at 70, 100 and 155 days of age, or weight gains between these ages. We therefore compared the findings with studies in the literature that evaluated ages close to those used here. For example, Hong et al. [26] reported a heritability of 0.31 for the age to reach 90 kg, with a mean age of 160 days in Duroc animals. Esfandyari et al.

196 [8] obtained heritabilities of 0.20 and 0.26 for the age to reach 80 and 120 kg, respectively, in
197 Duroc animals. The mean ages to reach the weights studied were 119.08 and 167.48 days. In
198 crossbred pigs, Bonfatti et al. [27] estimated a heritability of 0.45 for body weight at 270 days of
199 age. Studying Duroc pigs from three breeding nucleus farms, Wei et al. [28] reported heritability
200 estimates of 0.07 to 0.29 for the age to reach a body weight of 100 kg, with the mean ages ranging
201 from 148.69 to 156.90 days.

202 The variations in the estimates can be explained by the different data structures and
203 methods used in the cited studies that investigated body weight or age to reach a certain weight.
204 However, comparison of the ages analyzed in this study (70, 100 and 155 days) with the mean
205 ages at which animals reached a certain weight, as well as the heritability estimates, showed
206 consistency among the results. It is worth noting that the weight of 116.41 kg at 155 days of age
207 was higher than those reported in the other studies, indicating that selection for body weight has
208 been efficient in the Duroc population studied.

209 The heritability estimates for ADG1, ADG2 and ADG3 were higher than the heritabilities
210 obtained for body weights and lower than those obtained for carcass traits. Since ADG3 showed
211 the highest heritability, it can be indicated as a selection criterion and genetic gains in this trait
212 are expected. The heritability estimates for ADG were higher than those reported by Herrera-
213 Cáceres et al. [29] for the Duroc breed. In that study, the animals started and finished the
214 evaluation at 10 and 26 weeks of age, respectively, and the heritability for ADG over this period
215 was 0.19. Studying Duroc animals, Seong et al. [30] obtained a heritability estimate of 0.16 for
216 weight gain of animals with an initial and final weight of 30 and 100 kg, respectively. In a study
217 comprising the period from 149.32 to 159.88 days of age of Duroc and Yorkshire pigs, Li et al.
218 [31] reported heritability estimates ranging from 0.13 to 0.16. For ADG of Duroc animals from
219 159 to 219 days of age, Green et al. (2024) estimated a heritability of 0.23.

220 The heritability estimates for the carcass traits were 0.58 (BF), 0.44 (LD), and 0.37 (IMF),
221 indicating that the traits can be used as efficient selection criteria. Swine genetic evaluation
222 programs therefore face the challenge to increase the proportion or percentage of lean meat and
223 to reduce fat in the carcass while maintaining certain levels of intramuscular fat to ensure

palatability of the products. The heritability estimated for BF in this study corroborates the findings of Bergamaschi et al. [32], Willson et al. [33], Hong et al. [26], Green et al. [5], and Jové-Juncà et al. [34], who reported values ranging from 0.30 to 0.61 in Duroc pigs. These results indicate that targeted selection can be applied to reduce or maintain BF, thereby adjusting carcass fat composition and ensuring a balance in subcutaneous fat deposition.

Similarly, the heritability estimated for LD is consistent with the values reported by Zhuang et al. [35], Esfandyari et al. [8], and Lozada-Soto et al. [36] which ranged from 0.18 to 0.48 in Duroc pigs. Our results suggest that it would be feasible to select boars and sows with high genetic potential for LD, potentially leading to a greater proportion of muscle in the carcass and, consequently, improved lean meat yield. The heritability estimate obtained for IMF indicated that it can be effectively improved through selection. Our result was higher compared to that obtained by Lozada-Soto et al. [36] and Esfandyari et al. [8] for Duroc pigs (0.11 and 0.24, respectively). Green et al. [5] and Willson et al. [33] reported heritability estimates of 0.34 and 0.42, respectively.

Genetic correlations between direct and maternal effects for W70, W100, and W155 presented negative signs and decreased as animals grew older (Supplementary Table S1). According to Eler et al. [37], accounting for the genetic correlations between direct and maternal effects when estimating genetic parameters can help avoid biased estimates and lead to greater long-term economic benefits compared with selection based solely on direct genetic effects.

Comparison of the genetic (Table 2) and phenotypic (Table 3) correlations showed similarity in magnitude and sign (positive and negative), indicating that, depending on the trait and whether there is a correlation of moderate to high magnitude, concordance exists between the genetic potential and phenotypic performance of the animals. This fact was mainly observed between the body weight and weight gain traits. Environmental correlations, if high, indicate that the traits are affected by similar environmental components. Low environmental correlations or correlations close to zero indicate that different environmental effects influence the traits.

In the present study, the genetic correlations were significant ($P < 0.01$); the minimum value observed was 0.32. Non-significant genetic correlations indicate that it was not possible to

genetically associate the traits studied. The genetic correlations between the body weight traits were high and positive (0.60±0.08 to 0.81±0.04), indicating that these traits are influenced by similar set of genes of additive action. In this case, selection at early ages will favor subsequent traits and allow the early identification of genetically superior animals, thereby accelerating genetic progress and reducing maintenance costs on the farm. The high genetic correlations between ADG1 and ADG2 and between ADG2 and ADG3 indicate the existence of a set of genes that influence weight gain at different ages. Selection in Duroc pigs has primarily focused on growth [31], and evidence suggests that selection during a specific growth phase can have positive effects on later stages. Consequently, ADG2 can be prioritized as a selection criterion for improving growth efficiency.

The genetic correlations between body weights and weight gains were high and favorable, except for W70 and W100 with ADG2 (-0.10±0.10 and 0.11±0.10, respectively). Thus, selection aimed at increasing body weight may alter ADG. Willson et al. [33] reported high and favorable correlation for ADG and live weight (0.97), indicating that one trait could be used as a predictor of the other. In a study of Korean Duroc pigs, Alam et al. [16] estimated the genetic correlation between days to reach 105 kg and ADG from weaning (mean weight of 30 kg) to the age at which they reached approximately 105 kg, which was -0.97, indicating that animals with greater weight gains reached 105 kg at a younger age. Although very high, this result agrees with the present study in which the estimated genetic correlation between W70 and ADG1 was 0.68.

The body weight and weight gain traits showed moderate to high genetic correlations with LD and BF (0.35 to 0.58), except for the correlation between ADG3 and LD (0.09), suggesting that selection based on growth and weight gain traits will result in favorable responses in LD and unfavorable responses in carcass fat deposition. In the latter case, if it is necessary to reduce the fat percentage in the carcass, individuals with breeding values close to zero or negative values should be selected and their performance regarding the other growth and carcass traits should be evaluated.

Zhou et al. [38] observed moderate and favorable genetic correlations between ADG and lean meat percentage in Canadian and American Duroc pigs. Lopez et al. [39] reported genetic

correlations between days to reach 90 kg (mean of 141.70 days) and fat thickness and loin muscle area of 0.04 and 0.02, respectively, indicating the absence of a linear genetic association. Regarding fat percentage, the authors obtained an estimate of 0.31. In addition, the genetic correlations between ADG and the carcass traits described above were -0.05, -0.37 and -0.03, respectively.

The IMF showed a genetic correlation with ADG1 and ADG2 of 0.32. Therefore, selection for weight gain may have benefits for IMF. This suggests that animals exhibiting higher growth performance may also show improved meat marbling, a sensory trait with economic significance in the market. The genetic correlation between BF and IMF was high (0.56), suggesting that selection for one trait will cause changes in the same direction in the other. However, an increase in BF in the carcass is not desired since consumers want carcasses with intramuscular fat, which ensures flavor and tenderness of the meat but without excess fat coverage.

Suzuki et al. [40] observed a genetic correlation between BF and IMF of 0.28 in Duroc pigs, suggesting that the genetic variation in muscle lipid content is independent of total carcass fat. In crossbred Jinhua-Duroc animals, Terada et al. [41] estimated a negative and non-significant genetic correlation (-0.11) between BF and IMF and suggested that it would possibly not be difficult to improve intramuscular fat and to maintain fat thickness at certain levels.

In the present study, the genetic correlation between BF and LD was low and negative, suggesting that selection for one trait will not necessarily affect the other. In crossbred pigs, Miar et al. [42] obtained high and negative correlations between these traits (-0.34). The study conducted by Lozada-Soto et al. [36] found a high and positive genetic correlation between loin depth and fat thickness (0.49) in a population of Duroc animals.

The genetic correlation between LD and IMF was close to zero, indicating the absence of genetic association between the two traits. This result indicates that breeding programs can direct selection toward increasing LD (with expected improvements in carcass musculature) and increasing IMF to optimize meat quality. Based on our findings, there would be no adverse genetic effects acting on the selection for these traits, which could be improved independently. In

crossbred pigs, Miar et al. [42] found a genetic correlation of -0.47 between LD and IMF and suggested that selection aimed at increasing marbling may imply a decrease in LD. However, Lozada-Soto et al. [36] estimated a favorable genetic correlation (0.38) between these traits in Duroc animals, which suggests the positive interactions between these traits might exist.

CONCLUSION

In general, the heritability estimates obtained for the traits studied in Duroc pigs showed that selection for weight, weight gain and carcass traits is feasible. The use of ADG2 may promote direct gains in the trait itself, as well as in the other weight and weight gain traits studied. Regarding carcass traits, selection for ADG2 will promote indirect and favorable gains in LD and IMF but must be carried out carefully because of the possibility of increasing carcass fat. Direct selection for LD does not appear to affect BF or IMF, a desirable situation if the objective is to increase the amount of meat produced without a concomitant increase in fat percentage.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

AUTHORS' CONTRIBUTION

Conceptualization: Câmara GMS, Araujo AC, Grossi DA, Buzanskas ME.

Data curation: Araujo AC, Grossi DA

Formal analysis: Câmara GMS, Buzanskas ME.

Methodology: Câmara GMS, Buzanskas ME.

Software: Buzanskas ME.

Validation: Câmara GMS, Silva JAIIV, Araujo AC, Grossi DA, Buzanskas ME.

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Writing - original draft: Câmara GMS, Araujo AC, Grossi DA, Buzanskas ME.

Writing - review & editing: Câmara GMS, Zucatelle C, Futema FK, Teixeira R, Silva JAIIV, Chardulo LAL, Curi RA, Baldassini WA, Pereira GL, Araujo AC, Grossi DA, Buzanskas ME.

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SUPPLEMENTARY MATERIAL

Supplementary Table S1. Genetic parameters and likelihood ratio test (LRT) at a 5% significance level considering degrees of freedom (d.f.) of one (X^2=3.84) and two (X^2=5.99)

DATA AVAILABILITY

Upon reasonable request, the datasets of this study can be available from the corresponding author.

ETHICS APPROVAL

Not applicable, as historical databases from the breeding program were used.

DECLARATION OF GENERATIVE AI

No AI tools were used in this article

REFERENCES

1. Diao SQ, Luo YY, Ma YL, et al. Genome-wide detection of selective signatures in a Duroc pig population. Journal of Integrative Agriculture 2018;17: 2528–2535. https://doi.org/10.1016/S2095-3119(18)61984-7

2. Wang S, Yang J, Li G, et al. Identification of Homozygous Regions With Adverse Effects on the Five Economic Traits of Duroc Pigs. Frontiers in Veterinary Science 2022;9. https://doi.org/10.3389/fvets.2022.855933

3. Tecku PKM, Chen D, Wang K, Yu S, Chen J, Tang G. Comprehensive co-expression analysis reveals candidate regulatory genes associated with carcass and meat quality traits in Neijiang and Large White pigs. Animal Bioscience 2025;38: 2568–2583. https://doi.org/10.5713/ab.25.0259

4. Hoque MA, Suzuki K, Kadowaki H, Shibata T, Oikawa T. Genetic parameters for feed efficiency traits and their relationships with growth and carcass traits in Duroc pigs. Journal of Animal Breeding and Genetics 2007;124: 108–116. https://doi.org/10.1111/j.1439-0388.2007.00650.x

5. Green HE, Oliveira HR de, Alvarenga AB, et al. Genomic background of biotypes related to growth, carcass and meat quality traits in Duroc pigs based on principal component analysis. Journal of Animal Breeding and Genetics 2024;141: 163–178. https://doi.org/10.1111/jbg.12831

6. Kim SW, Gormley A, Jang KB, Duarte ME. Current status of global pig production: an overview and research trends. Animal Bioscience 2024;37: 719–729. https://doi.org/10.5713/ab.23.0367

7. Qiu Y, Ding R, Zhuang Z, et al. Genome-wide detection of CNV regions and their potential association with growth and fatness traits in Duroc pigs. BMC Genomics 2021;22: 332. https://doi.org/10.1186/s12864-021-07654-7

8. Esfandyari H, Thekkoot D, Kemp R, Plastow G, Dekkers J. Genetic parameters and purebred–crossbred genetic correlations for growth, meat quality, and carcass traits in pigs. Journal of Animal Science 2020;98. https://doi.org/10.1093/jas/skaa379

9. Herrera-Cáceres W, Ramayo-Caldas Y, Sánchez JP. Longitudinal modelling of performance and feed efficiency traits in growing Duroc pigs. Livestock Science 2022;256: 104824. https://doi.org/10.1016/j.livsci.2022.104824

10. Quan J, Ding R, Wang X, et al. Genome-wide association study reveals genetic loci and

391 candidate genes for average daily gain in Duroc pigs. Asian-Australasian Journal of
392 Animal Sciences 2018;31: 480–488. https://doi.org/10.5713/ajas.17.0356
393 11. Ogawa S, Kimata M, Tomiyama M, Satoh M. Heritability and genetic correlation
394 estimates of semen production traits with litter traits and pork production traits in
395 purebred Duroc pigs. Journal of Animal Science 2022;100: 1–10.
396 https://doi.org/10.1093/jas/skac055
397 12. Homma C, Hirose K, Ito T, et al. Estimation of genetic parameter for feed efficiency and
398 resilience traits in three pig breeds. Animal 2021;15: 100384.
399 https://doi.org/10.1016/j.animal.2021.100384
400 13. Solanes FX, Reixach J, Tor M, Tibau J, Estany J. Genetic correlations and expected
401 response for intramuscular fat content in a Duroc pig line. Livestock Science 2009;123:
402 63–69. https://doi.org/10.1016/j.livsci.2008.10.006
403 14. Font-i-Furnols M, Tous N, Esteve-Garcia E, Gispert M. Do all the consumers accept
404 marbling in the same way? The relationship between eating and visual acceptability of
405 pork with different intramuscular fat content. Meat Science 2012;91: 448–453.
406 https://doi.org/10.1016/j.meatsci.2012.02.030
407 15. Déru V, Bouquet A, Hassenfratz C, Blanchet B, Carillier-Jacquin C, Gilbert H. Impact of
408 a high-fibre diet on genetic parameters of production traits in growing pigs. Animal
409 2020;14: 2236–2245. https://doi.org/10.1017/S1751731120001275
410 16. Alam M, Chang HK, Lee SS, Choi TJ. Genetic Analysis of Major Production and
411 Reproduction Traits of Korean Duroc, Landrace and Yorkshire Pigs. Animals 2021;11:
412 1321. https://doi.org/10.3390/ani11051321
413 17. Ding R, Zhuang Z, Qiu Y, et al. Identify known and novel candidate genes associated
414 with backfat thickness in Duroc pigs by large-scale genome-wide association analysis.
415 Journal of Animal Science 2022;100. https://doi.org/10.1093/jas/skac012
416 18. Knapp P, Willam A, Sölkner J. Genetic parameters for lean meat content and meat
417 quality traits in different pig breeds. Livestock Production Science 1997;52: 69–73.
418 https://doi.org/10.1016/S0301-6226(97)00120-6

19. Fox J, Weisberg S. An R Companion to Applied Regression. Third edit. Thousand Oaks: Sage; 2019.

20. R Core Team. R: A language and environment for statistical computing. R Foundation for Statistical Computing. Vienna, Austria; 2025. Available: http://www.r-project.org/

21. Meyer K. WOMBAT: a tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). Journal of Zhejiang University Science B 2007;8: 815–21. https://doi.org/10.1631/jzus.2007.B0815

22. Dobson AJ, Barnett AG. An introduction to generalized linear models. 4th ed. Boca Raton: CRC Press; 2018.

23. Fisher RA. Frequency Distribution of the Values of the Correlation Coefficient in Samples from an Indefinitely Large Population. Biometrika 1915;10: 507–521. https://doi.org/10.2307/2331838

24. Ruan D, Zhuang Z, Ding R, et al. Weighted Single-Step GWAS Identified Candidate Genes Associated with Growth Traits in a Duroc Pig Population. Genes 2021;12: 117. https://doi.org/10.3390/genes12010117

25. Lee HL, Lin MY, Wang HS, et al. Direct–Maternal Genetic Parameters for Litter Size and Body Weight of Piglets of a New Black Breed for the Taiwan Black Hog Market. Animals 2022;12: 3295. https://doi.org/10.3390/ani12233295

26. Hong JK, Cho KH, Kim YS, et al. Genetic relationship between purebred and synthetic pigs for growth performance using single step method. Animal Bioscience 2021;34: 967–974. https://doi.org/10.5713/ajas.20.0261

27. Bonfatti V, Rostellato R, Carnier P. Estimation of Additive and Dominance Genetic Effects on Body Weight, Carcass and Ham Quality Traits in Heavy Pigs. Animals 2021;11: 481. https://doi.org/10.3390/ani11020481

28. Wei C, Zeng H, Zhong Z, et al. Integration of non-additive genome-wide association study with a multi-tissue transcriptome analysis of growth and carcass traits in Duroc pigs. animal 2023;17: 100817. https://doi.org/10.1016/j.animal.2023.100817

29. Herrera-Cáceres W, Ragab M, Sánchez JP. Indirect genetic effects on the relationships

between production and feeding behaviour traits in growing Duroc pigs. Animal 2020;14: 233–242. https://doi.org/10.1017/S1751731119002179

30. Seong HS, Kim YS, Sa SJ, Jeong Y, Hong JK, Cho ES. Genetic Parameter Estimation and Genome-Wide Association Analysis of Social Genetic Effects on Average Daily Gain in Purebreds and Crossbreds. Animals 2022;12: 2300. https://doi.org/10.3390/ani12172300

31. Li W, Wang Z, Luo S, Wu J, Zhou L, Liu J. Genome-Wide Association Analysis and Genetic Parameters for Feed Efficiency and Related Traits in Yorkshire and Duroc Pigs. Animals 2022;12: 1902. https://doi.org/10.3390/ani12151902

32. Bergamaschi M, Maltecca C, Fix J, Schwab C, Tiezzi F. Genome-wide association study for carcass quality traits and growth in purebred and crossbred pigs1. Journal of Animal Science 2020;98. https://doi.org/10.1093/jas/skz360

33. Willson HE, Rojas de Oliveira H, Schinckel AP, Grossi D, Brito LF. Estimation of Genetic Parameters for Pork Quality, Novel Carcass, Primal-Cut and Growth Traits in Duroc Pigs. Animals 2020;10: 779. https://doi.org/10.3390/ani10050779

34. Jové-Juncà T, Crespo-Piazuelo D, González-Rodríguez O, et al. Genomic architecture of carcass and pork traits and their association with immune capacity. animal 2024;18: 101043. https://doi.org/10.1016/j.animal.2023.101043

35. Zhuang Z, Li S, Ding R, et al. Meta-analysis of genome-wide association studies for loin muscle area and loin muscle depth in two Duroc pig populations. Davoli R, editor. PLOS ONE 2019;14: e0218263. https://doi.org/10.1371/journal.pone.0218263

36. Lozada-Soto EA, Lourenco D, Maltecca C, et al. Genotyping and phenotyping strategies for genetic improvement of meat quality and carcass composition in swine. Genetics Selection Evolution 2022;54: 42. https://doi.org/10.1186/s12711-022-00736-4

37. Eler JP, Van Vleck LD, Ferraz JBS, Lôbo RB. Estimation of variances due to direct and maternal effects for growth traits of Nelore cattle. Journal of Animal Science 1995;73: 3253–3258.

38. Zhou S, Ding R, Meng F, et al. A meta-analysis of genome-wide association studies for

475 average daily gain and lean meat percentage in two Duroc pig populations. BMC
476 Genomics 2021;22: 12. https://doi.org/10.1186/s12864-020-07288-1
477 39. Lopez BI, Viterbo V, Song CW, Seo KS. Estimation of genetic parameters and accuracy
478 of genomic prediction for production traits in Duroc pigs. Czech Journal of Animal
479 Science 2019;64: 160–165. https://doi.org/10.17221/150/2018-CJAS
480 40. Suzuki K, Irie M, Kadowaki H, Shibata T, Kumagai M, Nishida A. Genetic parameter
481 estimates of meat quality traits in Duroc pigs selected for average daily gain, longissimus
482 muscle area, backfat thickness, and intramuscular fat content. Journal of Animal Science
483 2005;83: 2058–2065. https://doi.org/10.2527/2005.8392058x
484 41. Terada K, Ohtani T, Ogawa S, Hirooka H. Genetic parameters for carcass and meat
485 quality traits in Jinhua, Duroc, and their crossbred pigs. Journal of Animal Breeding and
486 Genetics 2024;141: 33–41. https://doi.org/10.1111/jbg.12823
487 42. Miar Y, Plastow G, Bruce H, et al. Genetic and Phenotypic Correlations between
488 Performance Traits with Meat Quality and Carcass Characteristics in Commercial
489 Crossbred Pigs. Zhao S, editor. PLoS ONE 2014;9: e110105.
490 https://doi.org/10.1371/journal.pone.0110105
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493 **Table 1.** Traits, number of animals, boars, sows, phenotypic mean, standard deviation (SD),
494 minimum and maximum values, and number of contemporary groups (CG)

Traits	Animals	Boars	Sows	Mean	SD	Minimum	Maximum	CG
W70 (kg)	7,942	265	2,226	29.89	4.24	20.20	42.80	102
W100 (kg)	6,834	246	2,038	73.59	10.22	50.20	101.40	94
W155 (kg)	7,934	289	2,366	116.41	12.44	61.60	152.00	110
ADG1 (kg/day)	6,853	245	2,030	0.906	0.12	0.460	1.300	94
ADG2 (kg/day)	6,915	253	2,135	0.957	0.94	0.640	1.290	100
ADG3 (kg/day)	5,979	233	1,923	1.020	0.14	0.520	1.510	91
BF (mm)	5,319	224	1,826	11.48	2.64	5.20	20.70	85
LD (mm)	5,063	198	1,741	72.91	5.83	52.20	91.90	51
IMF (%)	5,326	224	1,821	2.39	0.63	0.90	4.32	84

495 W70, W100 and W155 = body weights adjusted to 70,100 and 155 days of age; ADG1 = average
496 daily gain from 70 to 100 days of age; ADG2 = average daily gain from 70 to 155 days of age;
497 ADG3 = average daily gain from 100 to 155 days of age; BF = backfat thickness; LD = loin depth;
498 IMF = intramuscular fat percentage.

499 **Table 2.** Estimates of direct heritability[A], maternal heritability[B], and proportion of common litter effect in the total variance[C] (diagonal, in bold) and genetic
500 correlations (above the diagonal) and their respective standard errors

Traits	W70	W100	W155	ADG1	ADG2	ADG3	BF	LD	IMF
W70	**0.21±0.04[A]** **0.12±0.03[B]** **0.11±0.02[C]**	0.81±0.04*	0.60±0.08*	0.68±0.06*	0.48±0.08*	-0.10±0.10	0.36±0.09*	0.51±0.08*	0.09±0.11
W100	-	**0.26±0.04[A]** **0.11±0.03[B]** **0.09±0.02[C]**	0.78±0.05*	0.87±0.03*	0.73±0.05*	0.11± 0.10	0.48±0.08*	0.58±0.07*	0.29±0.09
W155	-	-	**0.27±0.04[A]** **0.05±0.02[B]** **0.08±0.01[C]**	0.83±0.03*	0.85±0.03*	0.68±0.05*	0.51±0.06*	0.45±0.07*	0.28±0.08
ADG1	-	-		**0.29±0.03[A]**	0.74±0.04*	0.22±0.08	0.44±0.07*	0.49±0.07*	0.32±0.08*
ADG2	-	-	-	-	**0.36±0.03[A]**	0.80±0.03*	0.44±0.06*	0.38±0.07*	0.32±0.07*
ADG3	-	-	-	-	-	**0.38±0.04[A]**	0.35±0.07*	0.09±0.08	0.11±0.09
BF	-	-	-	-	-	-	**0.58±0.04[A]**	-0.03±0.07	0.56±0.05*
LD	-	-	-	-	-	-	-	**0.44±0.04[A]**	0.04±0.08
IMF	-	-	-	-	-	-	-	-	**0.37±0.04[A]**

501 * Significant genetic correlations (P < 0.01). W70, W100, and W155 = body weights adjusted to 70,100, and 155 days of age; ADG1 = average daily gain from
502 70 to 100 days of age; ADG2 = average daily gain from 70 to 155 days of age; ADG3 = average daily gain from 100 to 155 days of age; BF = backfat thickness;
503 LD = loin depth; IMF = intramuscular fat percentage.

504 **Table 3.** Estimates of phenotypic (above the diagonal) and environmental (below the diagonal) correlations and their respective standard errors obtained in two-
505 trait analyses

Traits	W70	W100	W155	ADG1	ADG2	ADG3	BF	LD	IMF
W70	-	0.76±0.00	0.62±0.00	0.35±0.01	0.27±0.01	0.04±0.02	0.19±0.02	0.32±0.02	0.03±0.02
W100	0.71±0.01	-	0.80±0.00	0.84±0.00	0.60±0.01	0.06±0.02	0.30±0.02	0.41±0.02	0.12±0.02
W155	0.60±0.02	0.79±0.01	-	0.69±0.00	0.86±0.00	0.62±0.01	0.42±0.02	0.45±0.01	0.18±0.02
ADG1	0.26±0.02	0.85±0.01	0.66±0.01	-	0.68±0.00	0.05±0.02	0.30±0.02	0.36±0.02	0.16±0.02
ADG2	0.23±0.03	0.59±0.02	0.89±0.01	0.65±0.02	-	0.74±0.00	0.42± 0.02	0.39±0.01	0.21±0.02
ADG3	0.09±0.03	0.04±0.03	0.61±0.02	-0.03±0.03	0.71±0.01	-	0.29±0.02	0.17±0.02	0.12±0.02
BF	0.13±0.04	0.24±0.04	0.41±0.03	0.24±0.04	0.43±0.04	0.26±0.04	-	0.09±0.02	0.45±0.02
LD	0.29±0.03	0.36±0.03	0.47±0.03	0.29±0.03	0.39±0.03	0.22±0.04	0.23±0.05	-	0.09±0.02
IMF	0.01±0.03	0.05±0.03	0.15±0.03	0.07±0.03	0.14±0.03	0.13±0.04	0.36±0.04	0.13±0.04	-

506 W70, W100, and W155 = body weights adjusted to 70,100, and 155 days of age; ADG1 = average daily gain from 70 to 100 days of age; ADG2 = average daily
507 gain from 70 to 155 days of age; ADG3 = average daily gain from 100 to 155 days of age; BF = backfat thickness; LD = loin depth; IMF = intramuscular fat
508 percentage.

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