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Rethinking longevity: The boar perspective

A.O. Garcia[1*], C. Chen[2], J. Holl[2], I. Misztal[1], and D. Lourenco[1]

[1]University of Georgia, Athens, United States; [2]The Pig Improvement Company, Hendersonville, United States; [*]Corresponding author: arielly.garcia@uga.edu

Introduction

Longevity is generally defined as the length of time an animal remains alive or active within a production system. Research on longevity in swine has traditionally focused on females. Genetic analyses related to lifetime reproductive, longevity, and removal reasons have been conducted primarily in sows (Arango *et al.*, 2005; Plaengkaeo *et al.*, 2021). This emphasis reflects the greater output of data provided by sow farms than boar studs.

In contrast, studies on boar longevity are limited. In boars, longevity has been defined as either age at culling or productive days in the herd, from stud entry to culling (Koketsu and Sasaki, 2009; Wang *et al.*, 2017). Although these studies characterized longevity phenotypes and investigated which factors influence the reasons for removal, they did not investigate the genetic factors underlying boar removal. While short generation intervals are desirable and accelerate genetic progress, premature involuntary removal of boars represents both an operational challenge and an economic loss.

Evaluating longevity in boars is economically important, and the lack of information on its genetic basis represents a substantial knowledge gap. Managing boars in artificial insemination studs involves substantial costs, including replacement, rearing, feeding, and maintenance of males, semen collection labor, housing, biosecurity, quarantine, and mandatory health testing. Boar longevity, in this context, reflects the ability of a boar to remain in the stud until voluntary replacement, avoiding premature involuntary removal. Understanding the factors that influence boar longevity, particularly its genetic component, is essential for improving the efficiency and sustainability of artificial insemination stud operations. Therefore, this study aimed to estimate genetic parameters and evaluate genomic breeding values (GEBV) for boar longevity, considering three main involuntary removal reasons: Structure, Reproductive, and Other.

Materials & Methods

Animal care and use committee approvals were unnecessary as the data were obtained from preexisting databases.

Dataset. We analyzed data from 15,399 boars in a single purebred population that were removed from studs for eight different reasons. Removal reasons were grouped into three main involuntary removal categories: Structure, Reproductive, and Other. The Structure category included removals related to lameness (N= 4,724); the Reproductive category encompassed removals due to semen quality and libido (N= 4,027); and the Other category grouped health problems, euthanasia, death, miscellaneous, or unknown causes (N= 6,648). Boar longevity was defined as the number of days from arrival to removal from the stud.

Genetic parameters. Single and multi-trait animal models were used to estimate variance components, heritability estimates, and genetic correlations for the three removal reason groups:

$$\mathbf{y}=\mathbf{Xb}+\mathbf{Z}_1\mathbf{cg}+\mathbf{Z}_2\mathbf{u}+\mathbf{e} \quad (1)$$

where **y** is the vector of days in stud, **b** is the vector of fixed effects, **cg** and **u** are vectors for

the random effects of herd-year-season upon arrival at the stud and genetic effect of the phenotyped boar. The **X**, $\mathbf{Z}_1$, and $\mathbf{Z}_2$ are incidence matrices for the effects in **b**, **cg**, and **u**, and **e** is the vector of random residuals. Random effects were distributed as follows: $\mathbf{cg} \sim N(\mathbf{0}, \mathbf{I} \otimes \sum_{cg})$, $\mathbf{u} \sim N(\mathbf{0}, \mathbf{A} \otimes \sum_{u})$, and $\mathbf{e} \sim N(\mathbf{0}, \mathbf{I} \otimes \sum_{e})$. Variance components and genetic parameters were estimated without genomic information using the BLUPF90+ software (Misztal *et al.*, 2014; Lourenco *et al.*, 2022).

For estimating genomic breeding values (GEBV), we performed a multi-trait single-step GBLUP analysis (Eq. 1) with the algorithm for proven and young using 5,000 core genotyped animals selected at random, using the BLUP90IOD3 software (Misztal *et al.*, 2014; Lourenco *et al.*, 2022).

Validation. Prediction accuracy was assessed using the linear regression (LR) method, described by Legarra and Reverter (2018), which compared GEBV from partial and whole populations. In the partial datasets, phenotypes of 1,260, 1,044, and 1,428 boars born in 2023 and 2024 were omitted for Structure, Reproductive, and Other, respectively.

Results & Discussion

The percentage of all removal reasons can be seen in Fig. 1. Lameness was the most frequent cause, accounting for 30.7% of all removals. Reproductive-related causes included removals due to semen quality (22.4%) and libido (3.7%). Several non-reproductive health-related causes contributed to removals as well: health problems (10.3%), death (11.2%), euthanasia (0.74%), and miscellaneous (1.56%). Additionally, unknown removals accounted for 19.35%. The eight reasons were grouped into three main removal categories: Structure (31%), Reproductive (26%), and Other (43%). Overall, structural issues and reproductive problems (mainly semen quality) were the predominant drivers of boar removal in AI studs.

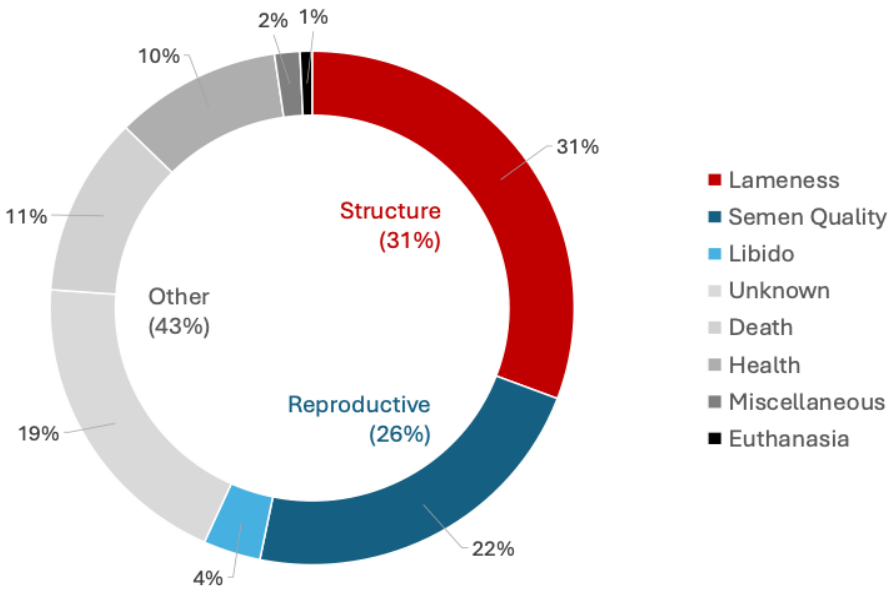

Figure 1. Percentage of involuntary removal reasons for 15,399 boars removed from studs. The eight original reasons were grouped into three main categories: Structure, Reproductive, and Other.

Heritability estimates and genetic correlations among the removal reasons are presented in Table 1. The heritability estimates were generally low to moderate across the three categories of removal reasons. Structure showed the highest heritability (0.12 ± 0.03), indicating a

relatively greater genetic contribution to removals associated with lameness compared with the other two categories. Reproductive and Other had lower heritability (0.05 ± 0.02 for both), suggesting that these removal reasons are strongly influenced by environmental or management factors, with limited genetic contribution.

Table 1. Heritability estimates (diagonal) and genetic correlations (off diagonal) with standard errors for boar longevity, defined as the number of days in the stud before removal for different reasons.

Reason[1]	**Structure**	**Reproductive**	**Other**
Structure	0.12 (0.03)	0.66 (0.31)	0.43 (0.19)
Reproductive		0.05 (0.02)	0.71 (0.40)
Other			0.05 (0.02)

[1] Structure category included removals related to lameness; Reproductive category encompassed removals due to semen quality, libido, or other reproductive issues; and Other category grouped health problems, miscellaneous, euthanasia, death, or unknown causes.

The genetic correlations showed moderate and positive associations, with high standard errors, among the removal categories. The genetic correlations between Structure and Reproductive (0.66 ± 0.31) and between Structure and Other (0.43 ± 0.19) imply that some genetic factors affecting removals due to lameness may also influence reproductive, health, or management-related removals. The highest correlation was observed between Reproductive and Other (0.71 ± 0.40), suggesting that individuals genetically predisposed to reproductive removal also tend to present issues that lead to removal for other reasons. However, the relatively large standard errors highlight the uncertainty of these estimates and emphasize the need for larger datasets to improve precision.

The linear regression validation results (Table 2) indicate moderate predictive ability and minimal bias across all three categories of removal reasons. Slopes lower than 1 suggest that GEBV tend to be over-dispersed, meaning that extreme predicted values are overestimated. The slope values were below 1 for all traits (0.78 for Structure and Reproductive, and 0.87 for Other), indicating a general inflation of GEBV in the partial dataset relative to the whole dataset. Among the three traits, Other removal category showed the slope closest to 1, suggesting slightly better estimation compared to Structure and Reproductive. It may have happened because Other was the removal category with the largest dataset.

Table 2. Linear regression (LR) validation metrics for boar longevity, defined as the number of days in the stud before removal for different reasons.

Reason[1]	**Slope**	**Bias**[2]	**Accuracy**[2]
Structure	0.78	-0.01	0.34
Reproductive	0.78	-0.02	0.32
Other	0.87	0.00	0.30

[1] Structure category included removals related to lameness; Reproductive category encompassed removals due to semen quality, libido, or other reproductive issues; and Other category grouped health problems, euthanasia, death, or unknown causes.

[2] Where: Bias=(GEBVw - GEBVp)/Var(u); and Accuracy=sqrt[Cov(GEBVw, GEBVp)/(1-F)Var(u)]

Bias values were near zero for all traits (–0.02 to 0.00), indicating that, on average, the predictions did not systematically overestimate or underestimate genetic merit. This minimal mean bias is desirable and suggests that the model is providing unbiased expectations of genetic values at the population level.

Accuracy estimates ranged from 0.30 to 0.34, consistent with the low heritability found in this study. Structure showed the highest accuracy (0.34), aligning with its relatively higher

heritability, whereas Reproductive and Other presented slightly lower accuracies (0.32 and 0.30, respectively). These levels of accuracy reflect the inherent challenge of predicting genetic merit for traits with low heritability and complex phenotypic definitions.
Overall, the LR validation showed that the GEBV are essentially unbiased, moderately stable, and have reasonable predictive ability, consistent with expectations for low-heritability, complex traits such as boar removal reasons.

Conclusions

This study provides one of the first genomic predictions of boar longevity through the analysis of involuntary removal reasons and their underlying genetic parameters. The findings suggest that boar longevity is heritable and moderately correlated across removal causes. Accounting for specific removal reasons provides a more comprehensive understanding of the genetic determinants of longevity in breeding males. Validation results indicated minimal bias in GEBV with predictive performance consistent with expectations for low-heritability, complex traits. Although the accuracies were moderate, the results showed only mild inflation. Overall, accounting for the genetic contribution of removal reasons in selection decisions could offer a path toward reducing premature boar losses, lowering replacement and health testing costs, and ultimately increasing the efficiency of AI stud operations. Future studies with larger datasets will be important to confirm these findings and further refine strategies for selecting boars with improved longevity.

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References

Arango J., Misztal I., Tsuruta S., *et al*. (2005) J. Anim. Sci. 83:2052–2057. https://doi.org/10.2527/2005.8392052x

Koketsu Y., and Sasaki Y. (2009) Theriogenology 71:1186–1191. https://doi.org/10.1016/j.theriogenology.2008.12.018

Legarra A., and Reverter A. (2018) Genet. Sel. Evol. 50:53. https://doi.org/10.1186/s12711-018-0426-6

Lourenco D., Tsuruta S., Masuda Y., *et al*. (2022) Proc. 10th WCGALP, Rotterdam, Netherlands.

Misztal I., Tsuruta S., Lourenco D., *et al*. (2014) Manual for BLUPF90 family of programs. Available at: nce.ads.uga.edu/wiki/doku.php?id=documentation, visited on: 23-04-2025.

Plaengkaeo S., Duangjinda M., and Stalder K.J. (2021) Trop. Anim. Health Prod. 53:319. https://doi.org/10.1007/s11250-021-02579-5

Wang C., Li J.-L., Wei H.-K., *et al*. (2017) Theriogenology 93:105–110. https://doi.org/10.1016/j.theriogenology.2017.01.038