INTERNATIONAL JOURNAL OF LATEST TECHNOLOGY IN ENGINEERING, MANAGEMENT & APPLIED SCIENCE (IJLTEMAS)

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XIV, Issue XI, November 2025

Initial Estimates of Variance Components and Genetic Parameters for Reproductive Traits in Large White Sows in Kenya.

Milka A. Kadenyi[1], Portas O. Olwande[1], Sophie Miyumo[2] and Chrilukovian B. Wasike[1,3*]

[1]Livestock Efficiency Enhancement Group (LEEG), Department of Animal and Fisheries Sciences, Maseno University, P.O. Box Private Bag 40105, Maseno, Kenya

[2]Department of Animal Breeding and Husbandry in the Tropics and Sub-tropics, University of Hohenheim, Garbenstr. 17, 70599 Stuttgart-Germany

[3]School of Agriculture, Food Security and Environmental Science, Maseno University, P.O. Box Private Bag 40105, Maseno, Kenya

DOI : https://doi.org/10.51583/IJLTEMAS.2025.1411000104

Received: 27 November 2025; Accepted: 05 December 2025; Published: 23 December 2025

ABSTRACT

This study aimed at estimating variance components and genetic parameters for reproductive traits of Large White sows in Kenya, in order to facilitate genetic improvement of reproductive efficiency in sows through selective breeding. 1145 records comprising 1129 records of litter size at birth (LSB), 1101 records of number of piglets born alive (NPBA), 1114 records of litter size at weaning (LSW) and 681 records of inter-farrowing interval (IFI) were obtained from 4 farms in western Kenya. After editing, a total of 1138 records of at least 2 traits were available for analysis. Genetic variance components were 0.10±0.03 for LSB, 1.33±1.80 for NPBA, 0.01±0.21for LSW and 23.28±22.71 for IFI. Phenotypic variance components were 7.63±0.33 for LSB, 6.67±0.29 for NPBA, 6.03±0.26 for LSW and 589.40±25.48 for IFI. Heritability estimates for reproductive traits were generally low. The estimates were 0.014±0.040 for LSB, 0.011±0.039 for NPBA, (0.001±0.035 for LSW and 0.039±0.038 for IFI. The standard errors for estimates were high. This is because, reproductive traits are strongly influenced by environmental factors. High environmental variability relative to genetic variability can make it difficult to accurately estimate heritability. The genetic correlation coefficients were 0.227.for LSB and NPBA, -0.555 for LSB and LSW, 0.865 for LSB and IFI, -0.924 for NPBA and LSW, -0.283 for NPBA and IFI as well as -0.079 for LSW and IFI. Phenotypic correlation coefficients were 0.810±0.011 for LSB and NPBA, 0.655±0.018 for LSB and LSW, 0.019±0.031 for LSB and IFI, 0.821±0.010 for NPBA and LSW, 0.004±0.031 for NPBA and IFI as well as 0.034±0.031 for LSW and IFI, The study concluded that, the low genetic variance compared to phenotypic variance across traits indicates a strong influence of environmental factors on reproductive traits, limiting the genetic contribution to variability. The very low heritability values with high standard errors highlight the limited potential for genetic improvement through selection and emphasize the use of other sources of information like progeny and ancestors. The genetic correlations with both positive and negative relationships, suggest the need for careful, balanced selection to avoid unfavorable genetic trade-offs between traits. Strong positive phenotypic correlations between traits like LSB and NPBA suggest shared environmental influences, underscoring the importance of improved management for overall reproductive performance.

Keywords: Pigs, fertility traits, heritability.

INTRODUCTION

Pork consumption in Kenya has seen steady growth over the past decade, largely attributed to urbanization, rising incomes, and shifting dietary preferences among the population (Bosire et al., 2017). Pork is increasingly recognized as an affordable and nutritious source of animal protein, making it an essential part of food security

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XIV, Issue XI, November 2025

strategies. However, the swine industry in Kenya faces significant challenges in meeting the growing demand for pork while maintaining sustainability and competitiveness (Murungi et al., 2021). Key barriers include low productivity, high disease prevalence, and inadequate infrastructure for pig farming. Western Kenya stands out as a region with great potential for pig farming, thanks to its conducive climate, abundant feed resources, and a growing population of farmers eager to adopt modern agricultural practices (Rudel et al., 2015). Despite these advantages, farmers in the region often struggle with limited access to quality breeding stock, poor disease control measures, and fragmented value chains, which hinder their ability to scale up operations. Addressing these issues is crucial for the growth of the swine industry and the country's efforts to meet the rising demand for animal protein.

Kenya's pig breeding programs are in their infancy, with limited coordination and inconsistent implementation across farming regions. While some medium and large-scale farms have adopted structured breeding programs, smallholder farmers—who form the majority—lack access to the resources and knowledge needed to improve their herds. The absence of systematic genetic improvement strategies has resulted in low reproductive performance and overall productivity. For instance, farmers often rely on unverified breeding stock with unknown genetic potential, leading to suboptimal litter sizes, growth rates, and fertility (Levit & Verchick, 2016). Furthermore, technical support services such as veterinary care, extension services, and genetic evaluation programs remain underdeveloped, leaving farmers to rely on traditional practices that do not maximize genetic potential. The collection and analysis of reproductive performance data, such as litter size, inter-farrowing intervals, and the number of piglets born alive, are critical steps toward addressing these gaps. Enhanced breeding programs should focus on integrating local and imported genetics, supported by robust technical support systems, to improve production efficiency and profitability. Genetic improvement is essential to boosting productivity in Kenya's pig industry, particularly in smallholder and tropical farming systems. Estimating variance components and genetic parameters provides critical insights into the heritability of traits such as litter size, growth rate, and disease resistance, enabling breeders to make informed decisions (Dumont et al., 2014). By identifying traits with high heritability, breeders can focus on those with the greatest potential for genetic gain, optimizing the use of limited resources. Genetic variation plays a pivotal role in enhancing adaptability, resilience, and disease resistance in pigs—qualities that are indispensable in tropical environments where heat stress and endemic diseases pose significant challenges (Phocas et al., 2016). Moreover, understanding genotype-environment interactions helps breeders tailor selection strategies to specific ecological conditions, ensuring the sustainability of genetic progress (Rose et al., 2016).

Accurate estimates of genetic parameters also mitigate the risks of inbreeding, preserving genetic diversity and ensuring long-term population viability. For smallholder farmers, the benefits are particularly pronounced. Genetic improvement enhances productivity, reduces production costs, and ultimately increases profitability. Beyond economic benefits, genetic improvement contributes to food security by ensuring a consistent supply of high-quality pork. However, achieving these outcomes requires investments in data collection, research, and the establishment of breeding programs that prioritize the unique needs of smallholder systems. Through a combination of science-based breeding and capacity building, Kenya's swine industry can realize its full potential while improving livelihoods and advancing national food security goals.

MATERIALS AND METHODS

Data source

Data for this study was collected from medium-scale pig farms located in Kisumu and Trans-Nzoia counties in the Western region of Kenya. Farm 1 in Kisumu County was located within longitudes 33^0 20'E and $35^0$20'E and latitudes $0^0$20'S and $0^0$50'S, at an altitude of 1131 m above Sea level, 72 km west of Kisumu city along Kisumu-Bondo road. Temperatures on this farm were high and ranged between 16 ^{0}C to 31 ^{0}C with an annual rainfall of 1311 mm. Farms 2, 3, and 4 were located in Trans-Nzoia county within longitudes $34.97^0$58'E and $34^0$58' E and latitude $1^0$45'N and $1^0$2'N, at an altitude of 1864.59 m above sea level, East of Kitale airstrip. The farms received an annual rainfall that ranged from 1100 mm to 2700 mm per year with an annual average rainfall of 1172 mm (Blanford et al., 2013; Okayo et al., 2015). Temperatures on these farms were mild and generally warm throughout the year and ranged between 10^0C- 28^0C (Blanford et al., 2013). The study site experienced a

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XIV, Issue XI, November 2025

bimodal rainfall pattern with four seasons; long rains from March to May, short rains from September to November, long dry season from December to February, and short dry season from June to August (Mugalavai et al., 2008).

The farms under study were medium-scale pig farms, keeping large white breeds for commercial pork production with an average herd size of 100 sows. In farm 1, sows were housed in specialized housing in group pens on the basis of their age, physiological status, and climatic conditions. The houses were made of concrete floors and walls and had large open windows for ventilation and free air circulation. Pigs were fed on concentrate diets formulated on the farm. Feeding was done twice daily and the ration composition and quantity varied based on the age and physiological status of sows. The farm kept both reproduction and production records. Like farm 1, housing in farm 2 had concrete floors with open windows. Commercial concentrates were used in feeding pigs. Feeding was done twice a day, with the sows being fed together with their young ones, weaners in a group, and boars fed individually. This farm practiced hand-mating, with the sow being mated two to three times during estrus. Primarily, disease management was by curative treatment with low-level prophylaxis. Housing in Farm 3 was similar to Farm 2. Pigs were fed once a day (at midday), but the young ones were fed twice daily on commercial concentrates. Water was given adlib to cater for the rest of the hours without feed. Pregnant and nursing sows were fed on sow and weaner meals. The farm leased boars from the neighborhood for mating sows on the farm whenever one manifested signs of estrus. Like farms 1 and 2, disease management on the farm was predominantly curative. Like the other farms, pigs were housed in group pens except for nursing and pregnant sows. Farm 4 had a relatively high stocking rate compared to other farms. Feeding was done twice a day using commercial concentrate feeds. Pregnant sows were given an additional snack of sow and weaner meal in the afternoon. Disease management on the farm was largely curative with treatment given whenever a disease was reported. There were no biosecurity measures, just like on the other farms. Other routine management procedures on the farm including teeth clipping, notching for identification, administration of iron dextran, and tail docking were done based on standard schedule.

Data collection

Records on reproductive performance of sows were extracted from farm record books targeting sows born between the years 2010 to 2020 in the four farms. The information collected included sow identification, sire, dam, dates of birth, farrowing dates, parity, litter size at birth, number of stillbirths, and number of litters weaned. Information on litter size at birth and weaning formed two traits of interest namely; litter size at birth (LSB) and litter size at weaning (LSW). Inter-farrowing interval (IFI) was determined as the difference between the date of a farrowing and the subsequent one, while number of piglets born alive (NPBA) was the difference between litter size at birth and number of stillbirth. Some individuals had only two parities while others had up to five and therefore, parities were truncated to three resulting in a dataset that had two inter-farrowing intervals. Months were clustered into four seasons namely: long rains from March to May, short rains from September to November, long dry season from December to February, and short dry season from June to August. The data were edited to remove individuals that had only one record, records of farrowing following abortions and farrowings whose activity dates were missing. Further edits involved the removal of records with inconsistent dates of birth and farrowing. 1138 records of at least 2 traits per animal were available for analysis.

Data analysis

Data on reproductive traits (LSB, NPBA, LSW, IFI, and AFF) was subjected to preliminary fixed model analysis to determine fixed effects of significant influence on reproductive traits using GLM package of R software (R Core Team 2023). The effects fitted included Herd, Yob, Sob, Sof, Yof. The effects that were significant were used in animal model evaluation as fixed effects. A multivariate animal model fitting 4 traits at a time was used for genetic analyses that were performed using restricted maximum likelihood methodology based on average information algorithm (AI-REML) in WOMBAT (Meyer, 2007). Mixed model equations in the analyses were solved iteratively and estimates at convergence of previous runs were used as starting values for the subsequent runs until no differences were observed in variance components in at least two consecutive runs, a global convergence was then assumed. The multivariate animal model in matrix notation is presented in equation 1:

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XIV, Issue XI, November 2025

$$\begin{bmatrix} y_1 \\ \vdots \\ y_n \end{bmatrix} = \begin{bmatrix} x_1 & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & x_n \end{bmatrix} \begin{bmatrix} b_1 \\ \vdots \\ b_n \end{bmatrix} + \begin{bmatrix} z_1 & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & z_n \end{bmatrix} \begin{bmatrix} a_1 \\ \vdots \\ a_n \end{bmatrix} + \begin{bmatrix} e_1 \\ \vdots \\ e_n \end{bmatrix} \text{……………………………………equation 1}$$

where: $y_1 \ldots y_n$ is the vector of observations on sow reproductive performance traits, $b_1 \ldots \mathrm{b_n}$ is the vector of fixed effects (only effects that were significant in the preliminary analysis); $a1 \ldots \mathrm{a_n}$ is the vector of random animal additive genetic effects assumed to be a ~ N ($\mathrm{A}\sigma_\mathrm{a}^2$) in which the random vector a, follows a multivariate normal distribution. **A** is the numerator relationship matrix, which describes the genetic relationships among individuals based on their pedigree and σ_a^2 is the additive genetic variance, representing the variability in the trait due to genetic factors. $e1 - \mathrm{e_n}$ is the vector of random residual effect assumed to be e ~N (0, $\mathbf{I}\sigma_\mathrm{e}^2$) in which the random vector e follows a multivariate normal distribution. **I** is an identity matrix, ascertaining that residual effects are independent across individuals and σ_e^2 is the residual variance, representing the variability in the trait due to non-genetic, random factors; $x1 \ldots \mathrm{x_n}$ and z1- $\mathrm{z_n}$ are incidence matrices relating records to fixed and random animal effects, respectively.

The random effects were assumed to follow a normal distribution with mean zero and covariance structure as presented in equation 2:

$$\mathrm{var}\begin{bmatrix} \mathrm{a} \\ \vdots \\ \mathrm{e} \end{bmatrix} = \begin{bmatrix} \mathrm{A}_{\boldsymbol{\sigma a2}} & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & \mathrm{I}_{\boldsymbol{\sigma e2}} \end{bmatrix} \text{……………………………………………………………equation 2}$$

in which,a is a vector of additive genetic effects; e is a vector of random residual effects; A is the numerator relationship matrix; I is the identity matrix; σa^2 is the direct additive genetic variance; σe^2_s is the residual variance.

The (co)variance components and variance ratios from the several analyses were pooled, weighting each estimate by the inverse of its sampling variance (S.E^2). This means that variances, heritability estimates and correlations estimates or any other mean was pooled using this equation as below.

$$\bar{\mathrm{E}} = \frac{\sum(\mathrm{w\ x\ E})}{\sum \mathrm{w}} \text{ ……………………………………… …………………………..equation 3}$$

$\bar{\mathrm{E}}$ is the weighted mean, W is the reciprocal of the sampling variance (weight), E is the variance component and ratio to be pooled.

RESULTS

Data structure and summary statistics for reproductive traits are presented in Table 1. Number of animals in the dataset were 1169, while those with records were 1145. However, animals that showed no records were 24, with 518 sires showing known grandsires. Consequently, dams with progeny were 113. The overall mean of LSB was 10.83 piglets, NPBA was 9.41±2.76 piglets, LSW was 8.72 piglets, and IFI was 147.79 days, respectively.

Table 4.1 Data structure and summary statistics for studied reproductive traits.

Number of animals in the dataset	Number of animals with records		Number of animals without records	Sires with known grandsire	Dams with progeny
1169	1145		24	518	113
	LSB	**NPBA**	**LSW**	**IFI**	

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XIV, Issue XI, November 2025

Mean	10.83	9.41	8.72	147.79
Standard deviation	2.79	2.65	2.50	34.48
Minimum	2	1	1	101
Maximum	19	19	15	282

[a]LSB=Litter size at birth; LSW= Litter size at weaning; NPBA= Number of piglets born alive; IFI= Inter farrowing interval; AFF= Age at first farrowing.

Estimates of genetic (σ_a^2) and phenotypic (σ_p^2) variances and heritability for reproductive traits in sows are presented in Table 2. Genetic variances were LSB (0.10±0.30), NPBA (1.33±1.80), LSW (0.01±0.21) and IFI (23.29±22.71). Phenotypic variances were LSB (7.63±0.33), NPBA (6.67±0.29), LSW (6.03±0.26) and IFI (589.38±23.48). Heritability estimates for reproductive traits were low. The estimate for LSB was 0.014±0.040, NPBA was 0.011±0.039, LSW was 0.001±0.035 and IFI was 0.039±0.038.

Table 2 Traits, variance components and heritability.

Traits	Variance components		Heritability
	σa^2	σp^2	
LSB	0.10±0.03	7.63±0.33	0.014±0.040
NPBA	1.33±1.80	6.67±0.29	0.011±0.039
LSW	0.01±0.21	6.03±0.26	0.001±0.035
IFI	23.28±22.71	589.40±25.48	0.039±0.038

[a] LSB=litter size at birth, NPBA=number of piglets born alive, LSW=litter size at weaning, IFI= inter-farrowing interval. σ^2a= Genetic variance, σ^2p= phenotypic variance.

The high genetic variance observed in IFI suggests that direct selection for this trait could yield significant genetic responses, as genetic variation is the foundation of evolutionary progress (Meryer, 2005; Briggs & Walters, 2016; Dobrzański et al., 2020). However, the small dataset may have inflated these estimates, necessitating cautious interpretation to avoid genetic bias in improvement programs. On the other hand, the low genetic variance in LSB, NPBA, and LSW indicates limited genetic diversity and low response to direct selection for these traits, which reduces the resilience and persistence of the population. Therefore, genetic improvement for these traits may require leveraging information from progeny and ancestors, rather than relying solely on direct selection (Meuwissen et al., 2016; Rauw & Gomez-Raya, 2015; Walsh & Lynch, 2018). Furthermore, higher phenotypic variance compared to genetic variance across traits suggests a substantial influence of environmental factors. Sows should be selected to perform in environments similar to the study region (western region) to mitigate genotype-by-environment interactions, emphasizing the role of management in trait improvement.

The generally low heritability estimates across the traits indicate slow genetic progress for these traits if genetic selection is applied (Reproto, 2020; Samorè & Fontanesi, 2016; Rydhmer, 2000). The heritability of LSW, as low as 1%, underscores that most variability in this trait is environmentally driven, necessitating management-based improvement strategies. Interestingly, heritability estimates appeared to increase from LSB to IFI, except for LSW, highlighting a shift in the influence of genetic factors toward traits associated with farrowing intervals. These findings contrast with reports for other breeds, which often show higher heritability due to the exclusion

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XIV, Issue XI, November 2025

of permanent environmental effects (Hermesch et al., 2001; Ajayi & Akinokun, 2013; Freyer, 2018). High heritability values, such as 0.5, indicate a stronger genetic influence, whereas low values around 0.1 imply environmental dominance (Kavlak & Uimari, 2019; Homma et al., 2021; Poulsen et al., 2020). For traits with low heritability, genetic improvement can be achieved by employing advanced selective breeding methods that integrate multiple sources of information, such as pedigree data, genomic information, and repeated measurements, rather than relying solely on mass selection. By leveraging these combined strategies, the accuracy of selection can be enhanced, even for traits with substantial environmental variability.

Table 3 Genetic (below the diagonal) and phenotypic (above the diagonal) correlations of reproductive traits studied.

Traits[d]	LSB	NPBA	LSW	IFI
LSB	**1**	0.810±0.011	0.655±0.018	0.019±0.031
NPBA	0.227	**1**	0.821±0.010	0.004±0.031
LSW	-0.555	-0.924	**1**	0.034±0.031
IFI	0.865	-0.283	-0.079	**1**

[c]Standard errors after the ± sign [d]LSB=litter size at birth; NPBA=number of piglets born alive; LSW= litter size at weaning; IFI=, inter-farrowing interval

There was a positive genetic correlation between NPBA and LSB (0.227) and between IFI and LSB (0.865). Conversely, negative genetic correlations were observed between LSW and LSB (-0.555), LSW and NPBA (-0.924), and IFI and NPBA (-0.283).Phenotypic correlation estimates showed strong positive relationships between LSB and NPBA (0.810 ± 0.011), LSB and LSW (0.655 ± 0.018), and NPBA and LSW (0.821 ± 0.010). However, low positive phenotypic correlations were noted between LSB and IFI (0.019 ± 0.031), NPBA and IFI (0.004 ± 0.031), and LSW and IFI (0.034 ± 0.031).

The genetic correlations observed among reproductive traits highlight complex relationships. Negative genetic correlations between traits such as LSB and LSW, and NPBA and LSW, indicate that improving one trait could adversely affect the other, presenting challenges for breeding programs (Serão et al., 2014; Yu et al., 2022; Lee et al., 2015). In contrast, positive correlations, such as between LSB and NPBA, suggest opportunities for multi-trait breeding strategies. The low negative genetic correlation between LSW and IFI implies that improving litter size at weaning could slightly reduce inter-farrowing intervals. However, the strong negative correlation between NPBA and IFI suggests that increasing the number of piglets born alive may significantly shorten the inter-farrowing interval, offering potential for reproductive efficiency. NPBA emerges as a promising reproductive trait for breeding improvement due to its favorable correlations with other traits.

CONCLUSION

The low genetic variance compared to phenotypic variance across traits indicates a strong influence of environmental factors on reproductive traits, limiting the genetic contribution to variability. The very low heritability values with high standard errors highlight the limited potential for genetic improvement through selection and emphasize the use of other sources of information like progeny and ancestors. The genetic correlations with both positive and negative relationships, suggesting the need for careful, balanced selection to avoid unfavorable genetic trade-offs between traits. Strong positive phenotypic correlations between traits like LSB and NPBA suggest shared environmental influences, underscoring the importance of improved management for overall reproductive performance.

The low genetic variance compared to phenotypic variance across traits indicates a strong influence of environmental factors on reproductive traits, limiting the genetic contribution to variability. The very low

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XIV, Issue XI, November 2025

heritability values with high standard errors highlight the limited potential for genetic improvement through selection and emphasize the use of other sources of information like progeny and ancestors.. The genetic correlations with both positive and negative relationships, suggesting the need for careful, balanced selection to avoid unfavorable genetic trade-offs between traits. Strong positive phenotypic correlations between traits like LSB and NPBA (0.810) suggest shared environmental influences, underscoring the importance of improved management for overall reproductive performancethe low genetic variance compared to phenotypic variance across traits indicates a strong influence of environmental factors on reproductive traits, limiting the genetic contribution to variability. The very low heritability values with high standard errors highlight the limited potential for genetic improvement through selection and emphasize the use of other sources of information like progeny and ancestors.. The genetic correlations with both positive and negative relationships, suggesting the need for careful, balanced selection to avoid unfavorable genetic trade-offs between traits. Strong positive phenotypic correlations between traits like LSB and NPBA (0.810) suggest shared environmental influences, underscoring the importance of improved management for overall reproductive performanceThe strong direct relationship between litter size at birth (LSB) and litter size at weaning (LSW) is highly significant. Larger litter sizes at birth in all the herds generally resulted in a larger number of piglets at weaning. Effective management of larger litters requires proper resource allocation, including adequate nutrition, space, and healthcare (Maes et al., 2020), to support the survival and growth of all piglets. This was observed in herd 1, where feeding was conducted twice daily and records were kept up to date. Thekkoot et al. (2016), in agreement with this study, in their research on parameter estimation of reproductive traits, suggest that traits associated with lactation in sows have a sizable genetic component and show potential for genetic improvement.The strong direct relationship between litter size at birth (LSB) and litter size at weaning (LSW) is highly significant. Larger litter sizes at birth in all the herds generally resulted in a larger number of piglets at weaning. Effective management of larger litters requires proper resource allocation, including adequate nutrition, space, and healthcare (Maes et al., 2020), to support the survival and growth of all piglets. This was observed in herd 1, where feeding was conducted twice daily and records were kept up to date. Thekkoot et al. (2016), in agreement with this study, in their research on parameter estimation of reproductive traits, suggest that traits associated with lactation in sows have a sizable genetic component and show potential for genetic improvement.

ACKNOWLEDGMENT

The authors acknowledge Maseno University for availing facilities for this research and the pig producers in western Kenya who volunteered their data for this study.

Conflict of Interest

The authors declare no conflict of interest.

Data availability statement

The data that support the findings of this study is available from the corresponding author upon reasonable request

REFERENCES

1. Ajayi, B., & Akinokun, J. (2013). Evaluation of some litter traits and heritability estimates of Nigerian Indigenous pigs. International Journal of Applied Agriculture and Apiculture Research, 9(1–2), 113–119.
2. Alves, K., Schenkel, F. S., Brito, L. F., & Robinson, A. (2018). Estimation of direct and maternal genetic parameters for individual birth weight, weaning weight, and probe weight in Yorkshire and Landrace pigs. Journal of Animal Science, 96(7), 2567–2578.
3. Blanford, J. I., Blanford, S., Crane, R. G., Mann, M. E., Paaijmans, K. P., Schreiber, K. V., & Thomas, M. B. (2013). Implications of temperature variation for malaria parasite development across Africa. Scientific Reports, 3(1), 1–11.
4. Briggs, D., & Walters, S. M. (2016). Plant variation and evolution. Cambridge University Press.

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XIV, Issue XI, November 2025

5. Chaudhary, R. (2017). GENETIC EVALUATION FOR TRAITS OF ECONOMIC IMPORTANCE USING PEDIGREE INFORMATION AND SNP MARKERS IN CROSSBRED PIGS.
6. de Oliveira, L. F., Lopes, P. S., Dias, L. C. C. M., e Silva, L. M. D., Silva, H. T., Guimarães, S. E. F., Marques, D. B. D., da Silva, D. A., & Veroneze, R. (2023). Estimation of genetic parameters and inbreeding depression in Piau pig breed. Tropical Animal Health and Production, 55(1), 14.
7. Dieguez, D. G. (2020). Genomic selection accounting for non-additive genetic effects in pig and corn crossbreeding schemes.
8. Do, D. N., & Haja, N. K. (2018). Genetic factors affecting feed efficiency, feeding behaviour and related traits in pigs University of Denmark, Denmark. In Achieving sustainable production of pig meat Volume 2 (pp. 97–118). Burleigh Dodds Science Publishing.
9. Do, D. N., Strathe, A. B., Ostersen, T., Pant, S. D., & Kadarmideen, H. N. (2014). Genome-wide association and pathway analysis of feed efficiency in pigs reveal candidate genes and pathways for residual feed intake. Frontiers in Genetics, 5, 307.
10. Dobrzański, J., Mulder, H. A., Knol, E. F., Szwaczkowski, T., & Sell-Kubiak, E. (2020). Estimation of litter size variability phenotypes in Large White sows. Journal of Animal Breeding and Genetics, 137(6), 559–570.
11. Duenk, P., Bijma, P., Wientjes, Y. C., & Calus, M. P. (2020). Predicting the purebred-crossbred genetic correlation from genetic variances within, and covariance between parental lines. 130–130.
12. Fangmann, A. M. (2018). Genomic and conventional evaluations for fertility traits in pigs.
13. Freyer, G. (2018). Maximum number of total born piglets in a parity and individual ranges in litter size expressed as specific characteristics of sows. Journal of Animal Science and Technology, 60, 1–7.
14. Hermesch, S., Luxford, B., & Graser, H.-U. (2001). Genetic parameters for piglet mortality, within litter variation of birth weight, litter size and litter birth weight. 14, 211–214.
15. Herrero-Medrano, J., Mathur, P., Napel, J. ten, Rashidi, H., Alexandri, P., Knol, E., & Mulder, H. (2015). Estimation of genetic parameters and breeding values across challenged environments to select for robust pigs. Journal of Animal Science, 93(4), 1494–1502.
16. Hess, A. S. (2016). Genetic and biological factors influencing host response to porcine reproductive and respiratory syndrome virus in growing pigs.
17. Homma, C., Hirose, K., Ito, T., Kamikawa, M., Toma, S., Nikaido, S., Satoh, M., & Uemoto, Y. (2021). Estimation of genetic parameter for feed efficiency and resilience traits in three pig breeds. Animal, 15(11), 100384.
18. Houaga, I., Mrode, R., Opoola, O., Chagunda, M. G., Mwai, O. A., Rege, J. E., Olori, V. E., Nash, O., Banga, C. B., & Okeno, T. O. (2023). Livestock phenomics and genetic evaluation approaches in Africa: Current state and future perspectives. Frontiers in Genetics, 14, 1115973.
19. Kavlak, A. T., & Uimari, P. (2019). Estimation of heritability of feeding behaviour traits and their correlation with production traits in Finnish Yorkshire pigs. Journal of Animal Breeding and Genetics, 136(6), 484–494.
20. Knap, P. W. (2022). Pig breeding for increased sustainability. In Animal Breeding and Genetics (pp. 139–179). Springer.
21. Knol, E. F., van der Spek, D., & Zak, L. J. (2022). Genetic aspects of piglet survival and related traits: A review. Journal of Animal Science, 100(6), skac190.
22. Lee, J.-H., Song, K.-D., Lee, H.-K., Cho, K.-H., Park, H.-C., & Park, K.-D. (2015). Genetic parameters of reproductive and meat quality traits in Korean Berkshire pigs. Asian-Australasian Journal of Animal Sciences, 28(10), 1388.
23. Lopez, B. I., Kim, T. H., Makumbe, M. T., Song, C. W., & Seo, K. S. (2017). Variance components estimation for farrowing traits of three purebred pigs in Korea. Asian-Australasian Journal of Animal Sciences, 30(9), 1239.
24. Makhanya, L. G. (2018). Phenotypic and reproductive characterisation of kolbroek pigs.
25. Mbuthia, J. M., Rewe, T. O., & Kahi, A. K. (2015). Analysis of pig breeding management and trait preferences in smallholder production systems in Kenya. Animal Genetic Resources/Resources Génétiques Animales/Recursos Genéticos Animales, 56, 111–117.
26. Meuwissen, T., Hayes, B., & Goddard, M. (2016). Genomic selection: A paradigm shift in animal breeding. Animal Frontiers, 6(1), 6–14.
27. Mrode, R., & Pocrnic, I. (2023). Linear Models for the Prediction of the Genetic Merit of Animals. CABI.

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XIV, Issue XI, November 2025

28. Mugalavai, E. M., Kipkorir, E. C., Raes, D., & Rao, M. S. (2008). Analysis of rainfall onset, cessation and length of growing season for western Kenya. Agricultural and Forest Meteorology, 148(6–7), 1123–1135.
29. Mujibi, F. D., Okoth, E., Cheruiyot, E. K., Onzere, C., Bishop, R. P., Fèvre, E. M., Thomas, L., Masembe, C., Plastow, G., & Rothschild, M. (2018). Genetic diversity, breed composition and admixture of Kenyan domestic pigs. PLoS One, 13(1), e0190080.
30. Muthui, J. N. (2019). Influence of nutrition and value chain governance on enterprise performance in smallholder pig production in Kenya.
31. Okayo, J., Odera, P., & Oluchiri, S. (2015). Socio-economic characteristics of the community that determine ability to uptake precautionary measures to mitigate flood disaster in Kano Plains, Kisumu County, Kenya. Geoenvironmental Disasters, 2. https://doi.org/10.1186/s40677-015-0034-5
32. Poulsen, B. G., Ask, B., Nielsen, H. M., Ostersen, T., & Christensen, O. F. (2020). Prediction of genetic merit for growth rate in pigs using animal models with indirect genetic effects and genomic information. Genetics Selection Evolution, 52(1), 58.
33. Rauw, W. M., & Gomez-Raya, L. (2015). Genotype by environment interaction and breeding for robustness in livestock. Frontiers in Genetics, 6, 310.
34. Reproto, R. O. (2020). Genetic selection and advances in swine breeding: A review of its impact on sow's reproductive traits. Int. J. Res, 7, 41–52.
35. Rochus, C., Groenen, M., Bink, M., Huisman, A., Lopes, M., Knol, E., Ducro, B., Bijma, P., & Mulder, H. (2020). Estimating mutation rate and characterising de novo mutations in pigs. 84–84.
36. Rydhmer, L. (2000). Genetics of sow reproduction, including puberty, oestrus, pregnancy, farrowing and lactation. Livestock Production Science, 66(1), 1–12.
37. Samorè, A. B., & Fontanesi, L. (2016). Genomic selection in pigs: State of the art and perspectives. Italian Journal of Animal Science, 15(2), 211–232.
38. Sell-Kubiak, E., Duijvesteijn, N., Lopes, M., Janss, L., Knol, E., Bijma, P., & Mulder, H. (2015). Genome-wide association study reveals novel loci for litter size and its variability in a Large White pig population. BMC Genomics, 16, 1–13.
39. Sell-Kubiak, E., Wang, S., Knol, E., & Mulder, H. (2015a). Genetic analysis of within-litter variation in piglets' birth weight using genomic or pedigree relationship matrices. Journal of Animal Science, 93(4), 1471–1480.
40. Sell-Kubiak, E., Wang, S., Knol, E., & Mulder, H. (2015b). Genetic analysis of within-litter variation in piglets' birth weight using genomic or pedigree relationship matrices. Journal of Animal Science, 93(4), 1471–1480.
41. Serão, N., Matika, O., Kemp, R., Harding, J., Bishop, S., Plastow, G., & Dekkers, J. (2014). Genetic analysis of reproductive traits and antibody response in a PRRS outbreak herd. Journal of Animal Science, 92(7), 2905–2921.
42. Thekkoot, D., Kemp, R., Rothschild, M., Plastow, G., & Dekkers, J. (2016). Estimation of genetic parameters for traits associated with reproduction, lactation, and efficiency in sows. Journal of Animal Science, 94(11), 4516–4529.
43. Ume, S., Onwujiariri, E., & Nnadozie, A. (2020). Pig farmers' socioeconomic characteristics as determinant to pig production and profitability in the tropics. International Journal of Research and Review, 7(4), 394–405.
44. Walsh, B., & Lynch, M. (2018). Evolution and selection of quantitative traits. Oxford University Press.
45. Yu, G., Wang, C., & Wang, Y. (2022). Genetic parameter analysis of reproductive traits in Large White pigs. Animal Bioscience, 35(11), 1649.

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XIV, Issue XI, November 2025

Figure 1. Heritability Estimates

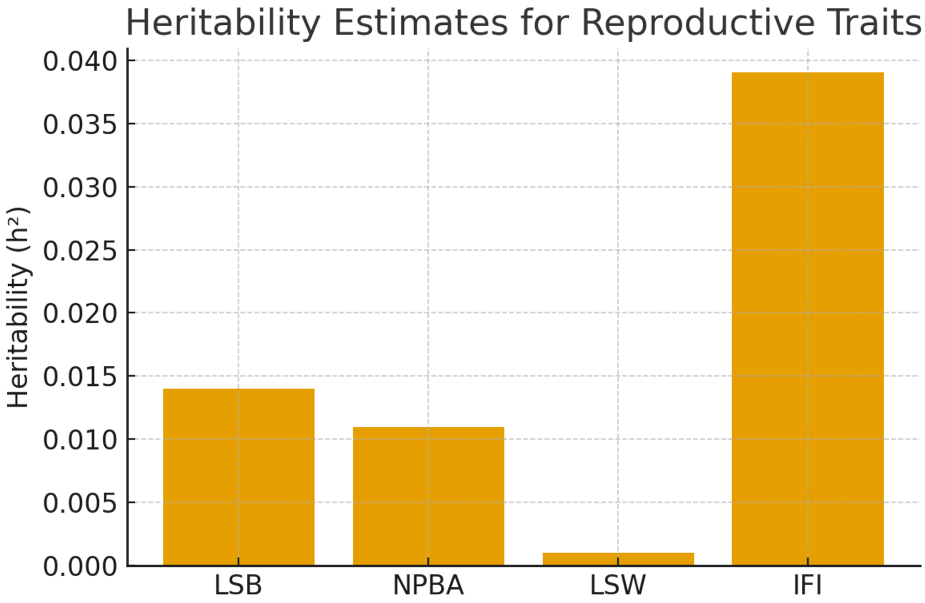

Figure 2. Phenotypic Correlation Heatmap