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Genomic evaluation of sow stayability traits from second to fifth parities in purebred and crossbred pig populations

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Introduction

Longevity in sows is a key trait for the sustainability and efficiency of swine production systems, given its strong association with economic performance and herd productivity. Premature removal of females prevents full recovery of the investments made prior to their productive life, thereby reducing farm profitability (Poulsen *et al.,* 2020). Beyond its economic implications, sow longevity is also closely linked to animal welfare. However, improving sow longevity through genetic selection remains challenging for multiple reasons. For instance, an extended time is required for phenotypic expression of the trait, as sow longevity can only be fully observed after the completion of the sow's reproductive life. To overcome this constraint, traits expressed earlier in the productive cycle have been proposed as proxies to enhance selection efficiency. In this regard, stayability (STAY) indicators based on early parities may increase annual genetic gain and enable the inclusion of phenotypic records from a larger number of animals in the genetic evaluations.

In this context, Tholen *et al.* (1996) introduced alternative definitions of herd retention, namely STAY2, STAY3, and STAY4, which represent survival from the first to the second, third, and fourth parities, respectively. Their results showed an increase in heritability estimates as the parity threshold increased, ranging from 0.05(0.03) for STAY2 to 0.06(0.02) for STAY3 and 0.09(0.02) for STAY4. Bohlouli *et al.* (2023) reported heritability estimates of 0.08(0.03), 0.07(0.02), and 0.05(0.03) for STAY2, STAY3, and STAY4, respectively, highlighting that the trait definition adopted for stayability has a direct impact on the magnitude of heritability and consequently on the expected response to selection. In this study, previously proposed stayability traits were evaluated, and STAY5 was included as an extension of these definitions, which may provide additional insights into sow longevity. The main objectives of this study were to estimate variance components and genetic parameters for stayability traits (STAY2, STAY3, STAY4, and STAY5) in both purebred and crossbred pig populations using threshold models.

Materials & Methods

Phenotypic, Pedigree, and Genotypic Data. The data analyzed in this study were obtained from six herds of purebred Landrace sows and nine herds of Landrace × Large White crossbred sows. The dataset included sows that were removed from the herds due to both voluntary and involuntary culling reasons. The available records comprised individual animal identification, age at first farrowing, dam parity, and the total number of parities completed over the sow's productive life. Stayability was evaluated as a binary trait and represents the sow's ability to remain in the herd until a specific time point. Four definitions of stayability were evaluated: survival up to the second (STAY2), third (STAY3), fourth (STAY4), and fifth (STAY5) parities.

Phenotypic data editing included the removal of data from sows with no recorded farrowing, those with age at first farrowing outside the range of 300 to 500 days, and contemporary

groups, defined as the combination of herd, birth year, and birth season, containing five or fewer animals. Following quality control, the final datasets consisted of 20,905 sows for STAY2 (14,786 purebred and 6,119 crossbred) and 26,441 sows for STAY3 to STAY5 (14,787 purebred and 11,654 crossbred).

The pedigree file initially comprised 5,378,363 animals, with three generations retained. Genotypes were imputed to a 50K single nucleotide polymorphism (SNP) panel for 22,925 animals. Genomic quality control was carried out using the preGSF90 program from the BLUPF90 software suite (Misztal *et al*., 2014). Filters were applied to exclude individuals and SNPs with call rates below 90%, SNPs with a minor allele frequency (MAF) lower than 0.05, and markers located on non-autosomal chromosomes. After filtering, 22,925 genotyped animals and 40,066 SNPs remained for subsequent analyses.

Statistical Analyses. Variance components were estimated using Bayesian methods based on the Gibbs sampler and Markov Chain Monte Carlo (MCMC) algorithm in the GIBBSF90+ software (Misztal *et al*., 2014). Depending on the trait evaluated, MCMC chains ranged from 500,000 to 1,000,000 iterations, with burn-in periods varying from 150,000 to 600,000 iterations and thinning intervals between 10 and 80 to reduce autocorrelation among successive samples. Convergence was evaluated through visual inspection of trace plots and using the Heidelberger and Welch test (Welch and Heidelberger, 1983) and Geweke's test (Geweke, 1992), as implemented in the package "boa—Bayesian Output Analysis" (Smith, 2007). Posterior means of variance components and genetic parameters were obtained using the PostGibbsf90 program (Misztal *et al.,* 2014).

Single-trait threshold animal models were fitted for all stayability traits using the Single-step Genomic REML (ssGREML) method. The analyses were performed under different data scenarios. First, purebred and crossbred sows were evaluated jointly. Subsequently, analyses were conducted separately for purebred and crossbred populations. Binary stayability traits were analyzed using a threshold animal model, defined as:

$$\mathbf{l} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e} \quad (1)$$

where **l** is the vector of stayability liability; **b** is the vector of systematic effects including contemporary group (herd, season, and year of birth), age at first farrowing, dam parity (only for STAY2), and line for the combined analyses of purebred and crossbred sows; **a** is the vector of additive genetic animal effect; **X** and **Z** are the incidence matrices; and **e** is the vector of random residuals.

Results & Discussion

Phenotypic Description of Stayability. A phenotypic characterization of stayability was performed by summarizing the number of sows that successfully remained in the herd versus those removed before achieving the predefined parity thresholds. These distributions are shown in Figure 1a for purebred sows and Figure 1b for crossbred sows. Retention rates declined progressively from STAY2 to STAY5, from 68.02% to 13.23% in purebred sows and from 75.75% to 25.60% in crossbred sows. This pattern is consistent with the cumulative definition of stayability and reflects the progressively higher probability of sow removal as parity advances, as expected.

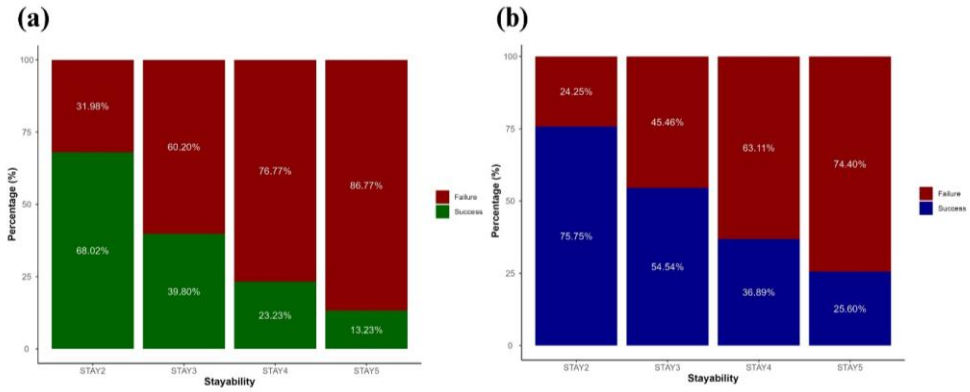

Figure 1. Distribution of stayability across parity thresholds (STAY2–STAY5) in purebred (a) and crossbred (b) sows, expressed as the percentage of successful retention and failure.

Variance Components and Genetic Parameters from the Single-Trait Model. Variance components and genetic parameters for all stayability traits were obtained as posterior means from the Bayesian single-trait analyses. Additive genetic variances, fixed residual variances, heritability estimates, and their corresponding 95% highest posterior density (HPD95) intervals are shown in Table 1. For all models, residual variances were fixed at 1 to ensure identifiability of the parameters. When analyses were performed using the complete dataset, including both purebred and crossbred sows, heritability estimates were generally of moderate magnitude, with slightly higher values observed for later parities, particularly STAY4. The magnitude of these estimates is higher than those reported by Tholen *et al.* (1996) for Australian Landrace and Large White pigs, who used linear models. In that study, heritability estimates ranged from 0.05 for STAY2 to 0.09 for STAY4. Likewise, Bohlouli *et al.* (2023), working with Swabian-Hall Landrace pigs and applying threshold models similar to those used in the present study, reported estimates of 0.08, 0.07, and 0.05 for STAY2, STAY3, and STAY4, respectively. Differences among studies may be attributed to variations in population structure, data size, management conditions, statistical models, or the use of genomic information in the present analyses.

When purebred and crossbred data were analyzed separately, clear differences in genetic variance components were observed. Purebred sows showed higher additive genetic variances and, consequently, higher heritability estimates compared to the combined dataset. In contrast, crossbred sows presented lower additive genetic variances, particularly for early stayability traits, resulting in reduced heritability estimates. The lower heritability observed in crossbred sows, particularly for early stayability traits, may reflect greater environmental influence or more heterogeneous management conditions, which can reduce the proportion of phenotypic variance attributable to additive genetic effects. These findings suggest that the genetic architecture of stayability differs between purebred and crossbred populations, indicating that selection strategies may need to be tailored according to population type. These differences may be influenced by the lower turnover rates in crossbred sows, which allow greater expression of their genetic potential for stayability. Additionally, differences in culling practices between purebred and crossbred populations may also contribute to the observed patterns.

Table 1. Posterior means and 95% highest probability density intervals (HPD95) for direct additive genetic (σ^2_a) and residual (σ^2_e) variances and heritability (h^2) for stayability traits in sows considering both voluntary and involuntary removal reasons.

Purebred + Crossbred								
	STAY2	HPD95	STAY3	HPD95	STAY4	HPD95	STAY5	HPD95
σ^2_a	0.23	0.18-0.29	0.23	0.18-0.29	0.27	0.20-0.33	0.25	0.18-0.32
σ^2_e	1.01	0.98-1.03	1.004	0.98-1.02	1.002	0.98-1.03	1.001	0.98-1.02
h^2	0.19	0.15-0.22	0.19	0.15-0.22	0.21	0.17-0.25	0.20	0.16-0.24
Purebred								
	STAY2	HPD95	STAY3	HPD95	STAY4	HPD95	STAY5	HPD95
σ^2_a	0.28	0.22-0.34	0.30	0.24-0.37	0.34	0.26-0.42	0.32	0.23-0.42
σ^2_e	1.005	0.97-1.04	1.004	0.97-1.04	1.003	0.97-1.03	1.002	0.97-1.03
h^2	0.22	0.18-0.26	0.23	0.19-0.27	0.25	0.21-0.29	0.24	0.19-0.30
Crossbred								
	STAY2	HPD95	STAY3	HPD95	STAY4	HPD95	STAY5	HPD95
σ^2_a	0.09	0.03-0.17	0.15	0.07-0.22	0.23	0.13-0.34	0.29	0.16-0.43
σ^2_e	1.007	0.96-1.06	1.005	0.97-1.04	1.003	0.97-1.04	1.001	0.96-1.03
h^2	0.08	0.03-0.14	0.13	0.07-0.18	0.18	0.12-0.26	0.23	0.15-0.31

STAY2 indicates survival from parity 1 to parity 2, STAY3 from parity 1 to parity 3, STAY4 from parity 1 to parity 4, and STAY5 from parity 1 to parity 5 or later.

Conclusions

The results of this study demonstrate that stayability traits present moderate heritability estimates, indicating meaningful genetic variability and supporting their inclusion in breeding programs aimed at improving sow longevity. The use of early stayability measures, combined with genomic information and threshold models, may represent a feasible strategy to accelerate genetic progress for sow longevity. Overall, these findings contribute to a better understanding of the genetic basis of sow retention and provide relevant insights for the design of selection strategies in pig populations.

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