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Genetic correlations between growth traits measured in a nucleus population and the survival of their progeny in commercial herds

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Introduction

Genetic improvement programs in swine are typically structured around nucleus populations, where selection candidates are intensively recorded for growth, efficiency, and carcass traits, while commercial populations are used to evaluate robustness and survival under production conditions. Understanding the genetic relationships between traits measured in these two environments is essential to ensure that selection in the nucleus translates into improved performance in commercial herds. Unfavourable genetic associations between growth and survival could compromise robustness and increase mortality if not properly accounted for in breeding objectives (Lozada-Soto *et al*., 2022). However, few studies have examined the genetic links between growth traits in nucleus populations and survival outcomes in commercial crossbred progeny, despite the economic and welfare importance of survival.

A 3 % change in preweaning mortality has an economic impact equivalent to a 1 % change in postweaning mortality (Harper and Bunter, 2024). Preweaning mortality remains high, accounting for 10 – 20 % of live-born piglets, with 80 % of deaths occurring within the first 72 h of life (Kirkden *et al*., 2013). The lack of universally agreed upon measures of piglet viability complicates accurate prediction of survival and the effectiveness of management interventions (Tucker *et al*., 2021).

Additive genetic variation for preweaning survival is sufficient for improvement through breeding, although selection is challenging due to the binary nature of the trait and high environmental variance (Knol *et al*., 2002). Estimates of heritability for survival traits are generally low, indicating that direct genetic improvement through selection on survival could be challenging. However, because growth traits typically show higher heritability and favourable (albeit moderate) genetic correlations with survival, they can be exploited as correlated selection criteria to achieve indirect genetic gains in survival (Su *et al*., 2008; Kapell *et al*., 2011).

The aim of this study was to estimate genetic correlations between growth traits and survival in a nucleus Duroc population and survival recorded in a commercial crossbred population. Growth traits were recorded on growing boars and gilts, undergoing performance test in the nucleus farms of the AcuFast breeding program (purebred population: PB). Survival was recorded in a commercial test herd, where crossbred sows are mated to selected purebred Duroc boars. The resulting crossbred progeny was then tested under commercial conditions (crossbred population: CB).

Materials & Methods

Data. Data used in this study came from an existing database at AcuFast LLC (Navasota, Texas, USA), therefore ethical authorisation was not needed for this study. The PB data came from the AcuFast nucleus flow, and which included a total of 86, 851 Duroc individuals. For these animals records included birth weight (BWp), weaning weight (WW), on-test weight (ONTW) as well as off-test weight (OFTW), back-fat depth (BF), loin eye area (LEA) and intra-muscular fat (IMF), were available. test weight (OFTW), back-fat depth (BF), loin eye area (LEA) and intra-muscular fat (IMF). All phenotypic records included the corresponding

date of measurement. In addition, measures of pre-weaning growth (PWG), nursery growth (NADG) and finisher growth were calculated (FADG).
The CB data came from the AcuFast commercial test herd and included a total of 298,489 individuals. For these animals, records of birth weight (BWc), birth date and mortality date were available. These were used to calculate survival at 5, 30 and 150 days of life (SVd5, SVd30 and SVd150, respectively). Provided birth and mortality dates for each animal, SVd5 was assigned '1' if the mortality age was larger than 5, '0' otherwise. SVd30 and SVd150 were determined likewise.
All individuals had full pedigree information, traced back to 10 generations. The two sets of records were linked by 425 common sires, which had progeny records for both CB and PB traits and were genotyped using a custom 70k AcuFast BeadChip.

Statistical methods. The statistical models used included several fixed and random effects, in agreement with the routine genetic evaluations for these traits. For PB traits, these were:

$$\mathbf{y} = u + \mathbf{X}\mathrm{b} + \mathbf{Z_l}\mathrm{l} + \mathbf{Z_p}\mathrm{p} + \mathbf{Z_s}\mathbf{s} + \mathbf{e} \quad (1)$$

where y is the vector of phenotypic measures, u was the intercept, $\mathbf{X}$ and b were incidence matrix and vector of solutions for the fixed effects (birth sow parity, sex, contemporary group, age at the corresponding stage), $\mathbf{Z_l}$ and l were the incidence matrix and vector of solutions for the litter random permanent environmental effect, $\mathbf{Z_p}$ and p were the incidence matrix and vector of solutions for the pen environmental effect (for off-test traits only), $\mathbf{Z_s}$ and $\mathbf{s}$ are the incidence matrix and vector of solutions for the sire additive genetic effect, $\mathbf{e}$ was the random residual.
For CB traits, these were:

$$\mathbf{y} = u + \mathbf{X}\mathrm{b} + \mathbf{Z_l}\mathrm{l} + \mathbf{Z_a}\mathrm{a} + \mathbf{e} \quad (2)$$

where y was the vector of phenotypic measures, u was the intercept, $\mathbf{X}$ and b were incidence matrix and vector of solutions for the fixed effects (dam line, sow parity, litter size, sex, cross-fostering indicator, contemporary group), $\mathbf{Z_l}$ and l were the incidence matrix and vector of solutions for the litter random permanent environmental effect, $\mathbf{Z_s}$ and s were the incidence matrix and vector of solutions for the sire additive genetic effect, $\mathbf{e}$ was the random residual.
Variance components and genetic correlations were estimated using bivariate models implemented in a Single-Step GBLUP approach, using Gibbs sampling using the BLUPf90 family of programs (Aguilar *et al*., 2019). Chains were run for a total of 120, 000 iterations, with 20, 000 samples burn-in and a thinning every 20 samples. Convergence was assessed by visual inspection of the trace models.

Results

Descriptive statistics for the traits studied are reported in Table 1. Here, the two populations showed a 0.216 kgs difference in birthweight, the only trait being measured in both PB and CB. The CB population is showing a slightly smaller value (1.495 vs 1.711), probably because of large litter size given by the maternal dam lines.
Genetic correlation estimates are reported in Table 2. Here, the posterior mean and 95 % empirical confidence intervals are reported as estimate and uncertainty, respectively.
Results showed a strong, positive genetic correlation ($r_g = 0.728$) for birth weight measured in the two populations. The correlation between CB birth weight and the other PB growth traits dissipated progressively with increasing age at recording of PB traits (from 0.446 to 0.029). The genetic correlations between CB survival with early-life PB growth were positive but not significant, becoming null with later-life PB traits. Significant, unfavourable correlations for the CB survival traits were reported only for IMF. However, moderate and favourable correlations ($r_g > 0.2$) were found between SVd150 and NADG and ONTW.

Table 1. Descriptive statistics (mean and SD) for traits[1] recorded in the purebred nucleus population (PB) and crossbred commercial population (CB).

Trait	Unit	Mean	SD
Purebred population traits[2]			
BWp	kg	1.71	0.33
WWt	kg	6.04	1.41
PWG	kg	4.33	1.26
NADG	kg/d	0.50	0.09
ONTW	kg	41.45	7.72
OFTW	kg	111.63	13.51
FADG	kg/d	0.97	0.14
BF	cm	1.84	0.44
LEA	cm^2	50.24	6.61
Intramuscular Fat (IMF)	%	2.23	0.78
Crossbred population traits[3]			
BWc	kg	1.49	0.40
SVd5	Surv/Total[4]	0.93	.
SVd30	Surv/Total[4]	0.84	.
SVd150	Surv/Total[4]	0.75	.

[1]Overall 86, 851 records were available for the traits recorded on purebreds (84, 872 for IMF), while 298, 189 records were available for traits recorded on crossbreds.
[2]Trait measures in the purebred nucleus population: BWp: birthweight; PWG pre-weaning gain, weaning-weight; nursery average daily gain; ONTW: on-test weight; FADG: finisher average daily gain; OFTW: off-test weight; BF: off-test backfat depth; LEA: off-test loin eye area; IMF: off-test intramuscular fat.
[3] Trait measures in the crossbred commercial population: BWc: birthweight; SVd5: survival to day 5; SVd30: survival to day 30; SVd150: survival to day 150.
[4]Survival is measured as the proportion of survived individuals until the day of life, over the total piglets alive at 24 hours after birth.

Table 2. Genetic correlation estimates (with 95% confidence intervals between parenthesis) between the traits measured in the purebred nucleus population[1] (in rows) and the traits measured in the crossbred commercial population[2] (in columns).

	BWc	SVd5	SVd30	SVd150
BWp	**0.728** **(0.346; 0.891)**	0.082 (-0.378; 0.349)	0.070 (-0.348; 0.313)	-0.029 (-0.389; 0.215)
PWG	0.253 (-0.206; 0.508)	0.108 (-0.379; 0.390)	0.203 (-0.280; 0.455)	0.101 (-0.317; 0.362)
WW	**0.446** **(0.010; 0.657)**	0.145 (-0.379; 0.404)	0.201 (-0.220; 0.436)	0.066 (-0.381; 0.291)
NADG	**0.359** **(0.000; 0.532)**	-0.056 (-0.389; 0.153)	0.044 (-0.286; 0.240)	0.218 (-0.127; 0.399)
ONTW	**0.369** **(0.040; 0.539)**	-0.069 (-0.449; 0.137)	0.049 (-0.301; 0.246)	0.204 (-0.075; 0.367)
FADG	0.171 (-0.097; 0.332)	-0.025 (-0.327; 0.160)	0.010 (-0.291; 0.175)	0.034 (-0.221; 0.197)
OFTW	0.250 (-0.071; 0.418)	-0.074 (-0.370; 0.123)	0.045 (-0.265; 0.216)	0.146 (-0.180; 0.304)
BF	0.097 (-0.196; 0.265)	-0.046 (-0.367; 0.137)	-0.046 (-0.340; 0.129)	-0.058 (-0.309; 0.111)
LEA	0.190 (-0.080; 0.356)	0.039 (-0.270; 0.227)	0.048 (-0.242; 0.218)	-0.025 (-0.283; 0.142)
IMF	0.029 (-0.263; 0.198)	**-0.274** **(-0.548; -0.106)**	**-0.225** **(-0.478; -0.062)**	**-0.235** **(-0.471; -0.088)**

[1]Trait measures in the purebred nucleus population: BWp: birthweight; PWG pre-weaning gain, weaning-weight; nursery average daily gain; ONTW: on-test weight; FADG: finisher average daily gain; OFTW: off-test weight; BF: off-test backfat depth; LEA: off-test loin eye area; IMF: off-test intramuscular fat.
[2] Trait measures in the crossbred commercial population: BWc: birthweight; SVd5: survival to day 5; SVd30: survival to day 30; SVd150: survival to day 150.

Discussion

The dataset used allowed the estimation of the genetic correlations between the two populations. The sire additive genetic effect provided the link between the two populations, since all the individuals with phenotypic records were sired by 425 sires. Shared genetic variation between growth and survival traits is consistent with evidence that survival traits show measurable genetic variation, and that their relationships with underlying traits such as birth weight and other early-life characteristics can support selection response (Knol *et al*., 2022). The results from this study corroborate the shared genetic architecture between CB and PB birth weight. Results suggest a mild link between growth and survival. Generally, the link between these classes of traits is hampered in its estimation due to their nature: only individuals with survival will show full growth recording, in addition to the risk of incorporating preferential treatment in the estimates (Liu *et al*., 2023). This latter could be present when particular care is given to slow-growing diseased animals which promotes both their growth and survival and could be captured as an additive genetic effect if not properly accounted for. This limitation is well documented for survival traits, as selective recording or genotyping of surviving individuals can bias genetic parameter estimates and reduce prediction accuracy, with simulations showing that excluding non-survivors inflates additive genetic variance and underscores the need to account for selection and missing data when evaluating survival-related traits (Liu *et al*., 2023). The use of two separate populations allowed us to overcome this issue.

Albeit mild, the genetic correlations suggest a favourable relationship between growth and survival, which favours the selection for these traits. Estimates are not strong enough to provide a compelling picture for leveraging one of the two sources. This warrants the need of a commercial test herd for the genetic improvement of survival in swine accompanied by direct selection for survival to achieve a meaningful response to selection. This could imply direct measures of growth and survival in both populations.

Conclusions

The present study confirms the possibility of selection for both growth and survival in swine. Genetic progress for growth traits is not expected to be compromised by applying selective pressure for improved survival. This remarks the need of robust, extensive data collection infrastructure for both growth and survival traits.

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