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Effects of boar number and genomic selection on genetic gain and variance of response across replicates using simulation

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Introduction

Effective population size (Ne) is a fundamental parameter in animal breeding programs that influences both genetic gain and long-term genetic diversity (Falconer and Mackay, 1996). Smaller Ne values are often the product of higher selection intensities, leading to greater short-term genetic progress. However, lower Ne also increases genetic drift and inbreeding rates, resulting in higher variance in genetic gain across replicates in simulation and lower long-term sustainability (Pook *et al.*, 2026). The advent of genomic selection (GS) has revolutionized animal breeding by enabling more accurate prediction of breeding values (Meuwissen *et al.*, 2001). While GS has been shown to accelerate genetic gain, its interaction with Ne in terms of both expected response and variation of response remains important to investigate. This study employed breeding program simulation to evaluate the effects of varying numbers of selected boars (and consequently Ne) and genomic selection on genetic gain and variance in mean true breeding values (TBV) across replicates in a simulated swine breeding program. The main objective was to determine how the number of boars per generation and GS jointly affect genetic gain and variance of response across replicates in a simulated swine breeding program.

Materials & Methods

Simulation Design. All simulations were conducted using AlphaSimR (Gaynor *et al.*, 2021), an R package for stochastic simulation of breeding programs. A swine breeding program was simulated over 10 generations, with 3 generations of random selection to build a training dataset followed by 7 generations of index selection. Each scenario was replicated 50 times. The number of male parents (boars) selected per generation was varied at four levels: 5, 13, 27, or 60 boars. The female population was held constant at 300 sows per generation. These boar numbers corresponded to target effective population sizes (Ne) of 20, 50, 100, and 200, calculated using the formula $Ne = (4 \times N_m \times N_f) / (N_m + N_f)$ (Falconer and Mackay, 1996). All scenarios used the same founder population. Mating was random among selected individuals. Litter size was set to six offspring per mating per generation. Five economically important traits were simulated: number weaned (NW), early average daily gain (eADG, g/d), testing average daily gain (ADG, g/d), feed conversion ratio (FCR, feed/gain), and backfat thickness at off-test (BF, mm). All offspring received phenotypes for eADG, ADG, and BF. Only male offspring recorded phenotypes for FCR. These traits were combined into a selection index representing a typical maternal breeding objective based on values from Amer *et al.* (2014). Selection was based on either traditional pedigree-based estimated breeding values (EBVs; without GS scenarios: S1-4) or genomic EBV (GEBV) predictions using MiXBLUP software (with GS scenarios: S5-8), resulting in eight total scenarios (4 boar levels × 2 GS strategies). Genomic selection utilized single nucleotide polymorphism (SNP) markers combined with pedigree relationships through single-step GBLUP (Legarra et al, 2014).

Statistical Analysis. Genetic gain was assessed using mean TBV at generation 10, and variance in response was evaluated using standard deviation (SD) and coefficient of variation (CV) across the 50 replicates per scenario. Due to strong tendency for GS to increase genetic

gain, using CV was more appropriate to capture variance in response at generation 10. A general linear model was utilized with boar number and genomic selection as fixed effects:

$$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \epsilon_{ijk}$$

where y_{ijk} is the mean TBV at generation 10 for replicate k in boar level i and GS level j, α_i is the effect of the boar number per generation (4 levels), β_j is the effect of GS (2 levels), and $(\alpha\beta)_{ij}$ is their interaction. Post-hoc pairwise comparisons were conducted using Tukey's honestly significant difference (HSD) test. Analyses were performed in R version 4.4.2 using the *car* and *emmeans* packages (R Core Team, 2024).

Results

Genetic Gain at Generation 10. Mean TBV at generation 10 ranged from 555 (60 boars, no GS) to 708 (5 boars, with GS) for the index (Table 1, Figure 1). The two-way ANOVA revealed highly significant main effects of both boar number ($p < 0.001$) and genomic selection ($p < 0.001$), with a small but significant interaction effect ($p = 0.02$). Tukey adjusted pairwise contrasts of EMMeans for boar number of 5, 13 and 27 were not statistically different from one another. The contrast of EMMean values for genomic selection on the index was highly significant ($p < 0.001$) with the benefit of GS remaining relatively consistent across scenarios (approximately 10-19% improvement). Similar patterns of boar number and GS effects were observed across all component traits, although direction of selection by trait can flip which scenario made more genetic progress (Figure 1). The main effect of GS was significant for every trait besides BF, while the main effect of boar number was significant for 3 out of 5 traits.

Table 1: Summary statistics of mean true breeding values (TBV) of the index at generation 10 across 50 replicates by number of boars (based on target Ne) and genomic selection (GS). 300 females per generation.

Boars	Target Ne	GS	Mean	SD	CV (%)
5	20	No	595	72.40	12.2
5	20	Yes	708	88.99	12.6
13	50	No	614	71.69	11.7
13	50	Yes	701	54.30	7.7
27	100	No	599	51.03	8.5
27	100	Yes	684	50.76	7.4
60	200	No	555	43.55	7.9
60	200	Yes	611	36.23	5.9

Variance in Genetic Gain Across Replicates. Standard deviation and CV of the index across replicate decreased as boar number increased (Table 1). For the index, CV values ranged from 5.9% (60 boars, with GS) to 12.6% (5 boars, with GS), with the overall trend of higher relative variability in response for scenarios with fewer boars and without genomic selection. Across the 5 traits, a similar trend emerged (Figure 2). No general trend was observed between with and without GS as number of boars increased. CV showed a steeper decline from 5 to 27 boars, than from 27 to 60 boars.

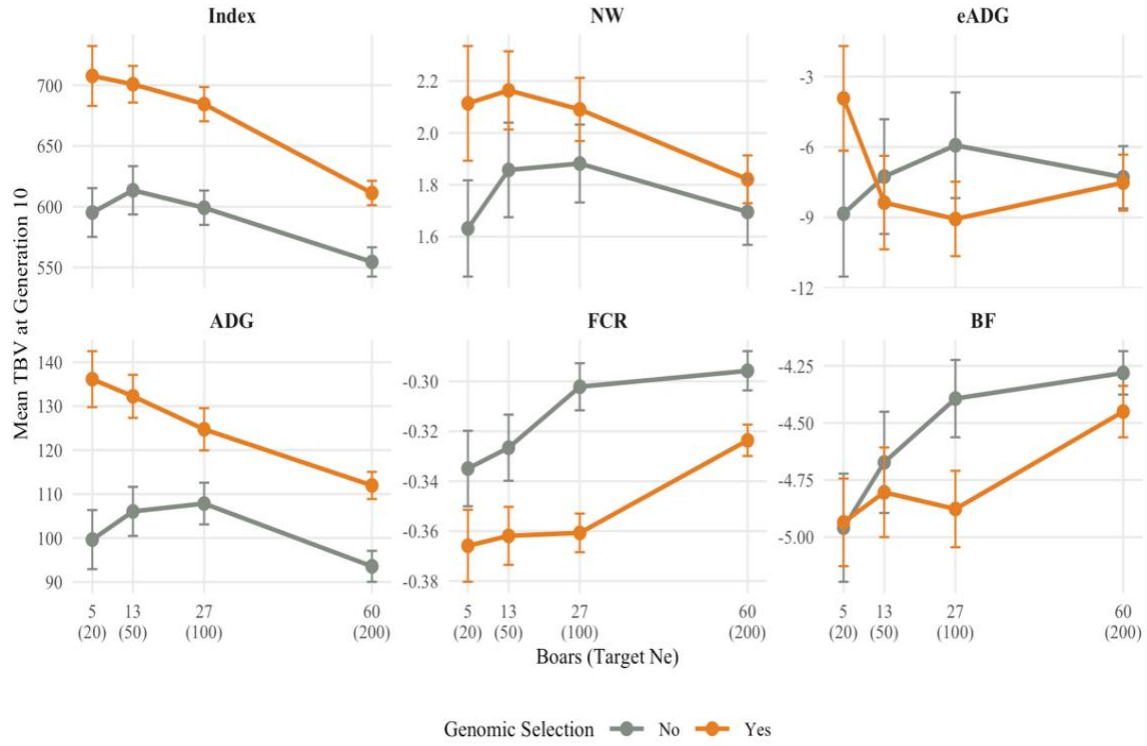

Figure 1: EMMeans of mean true breeding value (TBV) at generation 10 across all traits and replicates (50) by number of boars and genomic selection. Error bars represent 95% confidence intervals. Each panel shows a different trait (Index = selection index; NW = number weaned; eADG = early average daily gain; ADG = test average daily gain; FCR = feed conversion ratio; BF = backfat at off-test). Y-axis scales differ across traits.

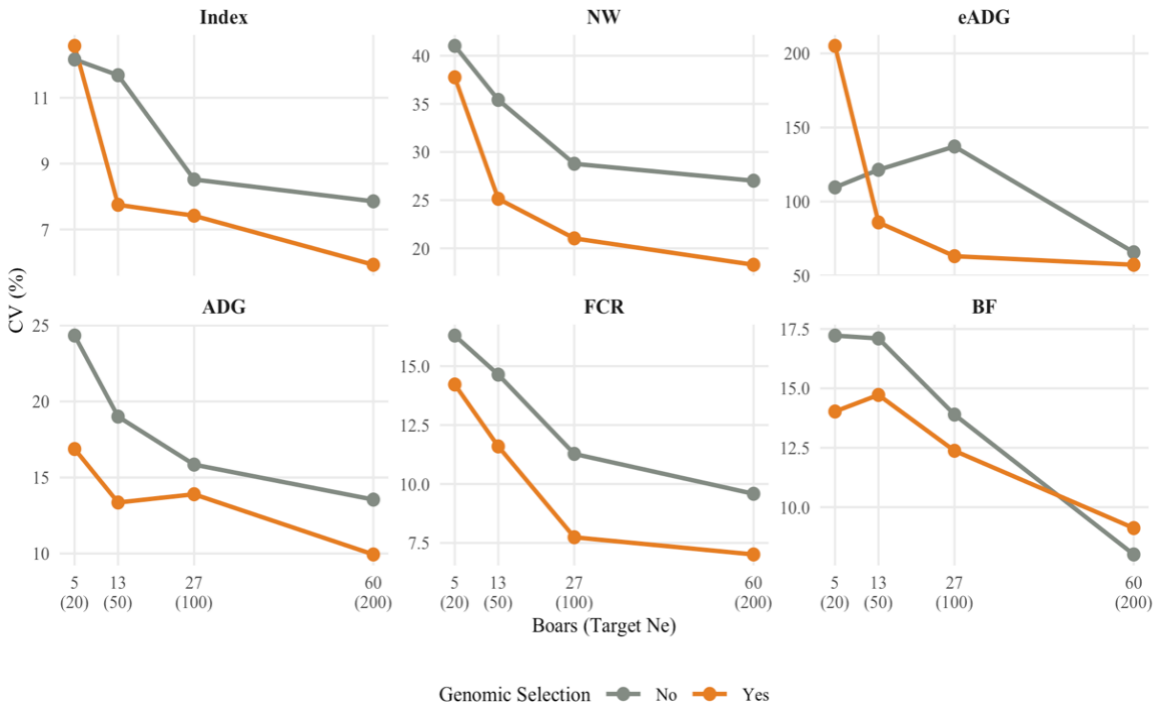

Figure 2: Coefficient of variation (CV) in mean true breeding values (TBV) at generation 10 across 50 replicates for all traits by number of boars and genomic selection. Each panel shows a different trait (Index = selection index; NW = number weaned; eADG = early average daily gain; ADG = test average daily gain; FCR = feed conversion ratio; BF = backfat at off-test). Y-axis scales differ by trait.

Discussion

Stochastic simulation of breeding programs has emerged as a key tool for applied breeders to make key decisions routinely. Historically, these decisions were left to practical constraints (e.g. budget) or deterministic equations (e.g. selection index). Early pilot studies showed dramatic variation in response to selection unexpected by the authors. This research had the background goal of shifting focus from managing a statistic such as ΔF historically done in optimum contribution selection (OCS) and placing more attention on minimizing the variation in response for key traits in their program (e.g. breeding goal traits); along with the main goal of maximizing the average genetic gain expected. Examining and focusing on the variance in response may change key breeding program decisions; given two scenarios with similar expected genetic gain, the CV in response can be ~40% lower (e.g. 5 vs 27 boars without GS). Targets for ΔF may be difficult to set for breeders while variation in response is explicit and easy to interpret from simulation studies.

The current study design shows limited or no advantage to extreme selection intensities, although it is highly dependent on choices such as what generation to stop selection. The choice among these strategies depends on breeding objectives, time horizon, and risk tolerance regarding outcome variability. Limitations of this simulation study include assumptions about population structure, trait architecture, and selection strategies (among many more). Future research should investigate integration of optimal contribution selection methods in combination with different factors studied here.

Conclusions

Boar selection intensity and GS have strong effects on both mean genetic gain and variance in response in both real and simulated swine breeding programs. Lower numbers of selected boars (i.e. higher selection intensity) resulted in higher genetic gain on average but also considerably higher variance in response. Genomic selection enhanced genetic gain by ~10-19% across all selection intensities but did not eliminate the variance at low boar numbers. Breeding programs must carefully balance the trade-off between maximizing short-term genetic progress (favoring 5-13 boars) and maintaining response consistency and long-term sustainability (favoring 27-60 boars).

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