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Evaluation of Phenotypic and Genomic Selection Strategies for Enhancing Genetic Gain in Pig Production

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Abstract- Genetic enhancement is very vital in improving performance, profitability and sustainability in pig production systems. Traditional phenotypic selection has been the basis of pig breeding since the ancient times but its reliance on visible traits, longer generations and weak predictability among young animals restrict its effectiveness. Genomic selection, which involves dense molecular markers to estimate genomic breeding values has developed to be a sophisticated tool that enhances the accuracy of selection and speed up genetic development. This paper contrasts phenotypic selection and genomic selection using simulation-based models which include pseudo-BLUP and genomic prediction algorithms. Findings indicated that genomic selection has much superior accuracy and reduced time to generation that translates to higher yearly genetic advantage of economically significant characteristics. These results support the need to include genomic instruments in current pig breeding initiatives to achieve a higher level of productivity, sustainability and economic reliability.

Keywords: Pigs, Simulations, Genetic Improvement

I. INTRODUCTION

Pig production plays a vital role in global food systems contributing significantly to food security, nutrition and household incomes. The species is valued for its high reproductive rate, rapid growth and impressive feed conversion efficiency making it one of the most economically important livestock enterprises (Nielsen et al., 2018). As consumer demand for high-quality pork continues to rise, improving the genetic potential of pig populations has become increasingly important. Genetic enhancement is particularly critical for traits such as growth rate, litter size, feed utilization efficiency and carcass composition traits directly linked to profitability and competitiveness in the pork value chain (Dekkers, 2012). Historically, genetic improvement programs in pigs have relied heavily on phenotypic selection where candidates are evaluated based on their observable performance and pedigree information. Although this approach has contributed substantially to progress in the swine industry, it presents inherent limitations. Phenotypic selection is often constrained by low selection accuracy among young animals especially for traits that are sex-limited, expensive to measure or expressed late in life (e.g., carcass traits) (Bijma, 2011). These limitations prolong the generation interval and slow the rate of genetic gain. Furthermore, pedigree-based methods rely on expected rather than actual genomic relationships, limiting their ability to capture Mendelian sampling variation (Hayes et al., 2009).

The emergence of genomic technologies has transformed animal breeding by allowing direct examination of genome-wide DNA markers. Genomic selection, which uses dense SNP markers to estimate genomic estimated breeding values (GEBVs), enables more accurate and earlier selection of breeding candidates. This approach captures actual genetic relationships and Mendelian sampling differences with high precision significantly increasing selection accuracy (Meuwissen, Hayes, & Goddard, 2001). Genomic selection is particularly advantageous for traits with low heritability. Traits expressed late in life or those that cannot be measured on selection candidates such as carcass quality (Wolc et al., 2016).The method has already demonstrated remarkable success across livestock species. In dairy cattle, genomic selection has doubled the rate of genetic gain and shortened generation intervals (Garcia-Ruiz et al., 2016). Similar improvements have been reported in sheep, goats and swine where genomic prediction enhances efficiency and profitability (Saintilan et al., 2013). However, the magnitude of its advantage varies across populations, breeding goals, trait architectures and production systems necessitating comparative evaluation. In response to these challenges and opportunities, this study simulates and compares phenotypic and genomic selection strategies for key economic traits in pig production. By examining growth performance, reproductive traits, feed efficiency and carcass characteristics, the study provides empirical insights into the relative effectiveness and long-term economic impact of adopting genomic selection in pig breeding programs.

II. MATERIALS AND METHODS

Study Design

In this research, a simulation model was used to compare phenotypic and genomic selection in a closed pig population across several generations. The comparisons of selection strategies under simulation conditions allow a comprehensive comparison of the strategies without long-term field experiments which are limited by time and resources.

Population Structure

The simulated population consisted of 1,000 base-generation pigs which represent a realistic nucleus breeding population. Out of this, 50 sires and 300 dams got selected to develop breeding groups. Evaluation of the population was done across 10 generations. The traits that were taken were; average daily gain (ADG), feed conversion ratio (FCR), litter size at birth (LSB) and back fat thickness (BF). The traits were chosen in terms of their economic value and reflection of growth, reproductive and carcass performance.

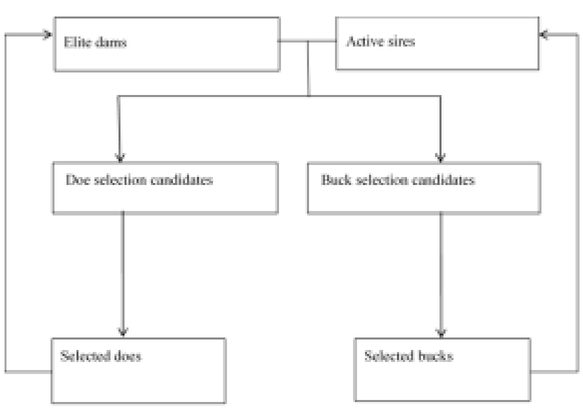


Figure 1: Simulation Workflow for Phenotypic and Genomic Selection.

Evaluation Criteria

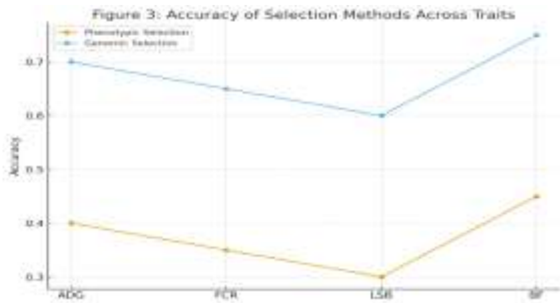
Comparison between selection strategies was made in terms of accuracy of predicted breeding value, generation interval, genetic gain per generation, annual genetic gain and change in genetic variance over time. The chief measure of overall breeding efficiency was the annual genetic gain. Phenotypic selection was based on observable traits and pedigree data to predict breeding value, which was a pseudo BLUP animal model with selAction software. In this scheme, the animals chosen were only after demonstrating certain characteristics of interest like the rate of growth or carcass structure. This requirement resulted in long generation intervals because animals could not produce performance data until they had reached maturity. The accuracy of phenotypic selection was limited by the number of records available, environmental variation and the low heritability of some traits such as reproduction. As a result, selection decisions were often delayed and less precise particularly in young replacement animals.

Genomic selection adapted genome-wide SNP markers to forecast genomic estimated breeding values (GEBVs) in all the candidates upon birth. Since genomic prediction is a better indicator of within-family variation compared to phenotypic or pedigree-based models, the accuracy of selection was increased significantly. Genomic selection also allowed for earlier selection of breeding candidates reducing the generation interval by nearly half.

III. RESULTS

Selection Accuracy

The findings indicated that phenotypic selection was significantly more accurate compared to genomic selection in all the traits as indicated in figure 3. The values of accuracy were between 0.70 and 0.75 in phenotypic selection and between 0.40 as 0.45 in genomic selection. This was particularly enhanced on low-heritability and late-expressed traits including litter size and carcass quality.



Generation Interval (L)

Phenotypic selection resulted in long generation intervals of 1.5–2.0 years due to the need for performance records before selection decisions could be made. In contrast, genomic selection reduced the generation interval to 0.8–1.0 years by enabling early selection at weaning. This reduction contributed significantly to the overall increase in annual genetic gain.

Genetic Gain (ΔG)

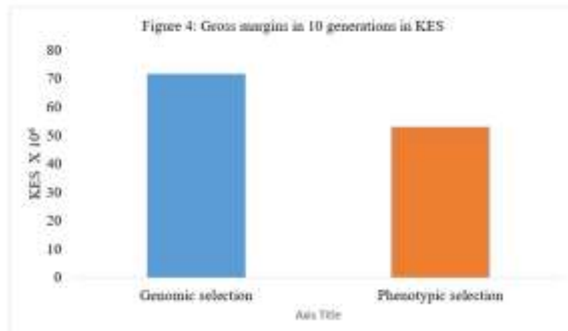
Genomic selection consistently produced higher genetic gains across all traits. The relative improvement over phenotypic selection was +55%, +25%, +40% and +40% for ADG, FCR, LSB and BF, respectively. These results demonstrate the potential of genomic tools to accelerate the improvement of key economic traits as shown in Table 1

Table 1: Genetic Gains

Trait	Phenotypic Selection	Genomic Selection	% Genetic gain
ADG	+70 g/day	+108.5 g/day	+55%
FCR	–0.12	–0.15	+25%
LSB	+0.50 piglets	+0.70 piglets	+40%
BF	–0.80 mm	–1.12 mm	+40%

Economic Evaluation

Genomic selection led to much long-term profitability than phenotypic selection. Even though the application of genomic tools raised the selection costs by KES 2,700 per candidate, such costs were compensated by the enhanced biological performance. More rapid growth (108.5 g/day compared to 70 g/day on phenotypic or 70 g/day on carrass) and high feed ratio, litter size and carrass characteristics generated an extra KES 1,300 net returns per pig. Genomic selection at the herd level provided KES 11,350 more per sow annually that was equivalent to a 35 percent increase in cumulative profit (KES 18.7 million) over ten generations at a 120 sow breeding unit. These results demonstrate that genomic selection is economically superior and offers significant long-term benefits for pig producers as shown in figure 4.



IV. DISCUSSION

This research study indicates that there is a distinct variation between the phenotypic selection and the genomic selection in their ability to promote genetic gain among pig populations. Genomic selection was always able to outperform phenotypic selection in all simulated breeding programs situations mainly because it was able to raise the level of selection as well as decrease the generation interval. Such findings are in agreement with Hayes et al. (2009) who demonstrated that genomic prediction significantly improves the accuracy of estimated breeding values hence enabling more accurate identification of breeding superior individuals at a very young age. Genomic selection assists breeders to make better decisions by using marker information that captures variation within a family long before the accumulation of phenotypic records eventually resulting in rapid genetic advancement. In phenotypic selection systems, comparatively less genetic gains were witnessed per annum. This is not surprising since phenotypic selection is basically dependent on the observable characteristics that are prone to environmental influences, measurement errors and control inconsistencies. Also, phenotypic recording in pigs is lengthy particularly when the traits to be recorded can only be determined at maturity such as slaughter weight or puberty. This restricts accuracy and intensity of selection. Likewise limitations have been experienced in small ruminant and cattle breeding programs in low-input systems (Kosgey et al., 2006; Ojango et al., 2004) which emphasize that use of phenotypes alone delays genetic improvement particularly on low heritability traits.

The findings also indicate that genomic selection brought about higher cumulative discounted expressions (CDE) as compared to phenotypic selection. This implies that the better animals found in the genome will give a greater contribution to the gene pool in the long term. The rise in CDE is not only an increase in genetic gain but also the more effective spread of better genetics between generations a trend also observed in the nucleus-based breeding programs (Rewe et al., 2004; Rege et al., 2001). The gene-flow model employed in this paper is another confirmation that genomic selection enables rapid turnover in the breeding nucleus that causes higher multiplier effect as better genetics in the nucleus herds are exported to the commercial populations. The results can be economically interpreted meaning that even though genomic selection means more investment in genotyping and data management, the returns will cover the extra costs. Greater genetic gain associated with economic traits including growth rate and slaughter weight resulted in higher gross margins achieved on the strategies of genomic. This is in line with previous research that has explained genomic selection as economical in the long run particularly in species with high reproduction like pigs (Hayes et al., 2009; Peacock, 2005). In contrast, phenotypic selection despite its lower operational costs was less profitable due to slower improvement, delayed turnover of elite stock and the long intervals required to accumulate measurable phenotypes.

Genomic selection was most effective when applied in organized systems that had controlled mating, proper recording of pedigree and systematic distribution of superior stock. This is consistent with the effectiveness of community-based and nucleus breeding programs that have been reported with the small ruminants and other livestock (Wurzinger et al., 2011; Haile et al., 2013). Effective breeding programs are used to make sure that the genetic benefits derived at the nucleus are passed on to commercial herds at maximum national productivity. The results of superiority of genomic selection are an indicator of the transformative nature of genomic tools in the contemporary pig breeding. Nevertheless, genetic selection implementation can be hampered in under-resource environments such as the prohibition of cost and poor laboratory capacity and breeder attendance. Thus, genomic selection is technically superior but it requires the infrastructure and a commitment of stakeholders.

V. CONCLUSION

This research reveals that genomic selection significantly improves genetic gain in pigs relative to the conventional phenotypic selection. Genomic selection maximizes the accuracy of selection and shortens the generation interval speeding up the enhancement of traits of growth, reproduction and carcass which form the core of pig production profitability. It is highly encouraged to adopt the use of genomic tools where available and blended selection methods can be used in smallholder production systems.

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