RESEARCHREPORT
ANIMAL SCIENCE

Title: The economic value of genomic selection to swine breeding herds **- NPB #11-017 revised**

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Industry Summary

Many swine breeding organizations are in the early stages of the decision making or implementation process regarding incorporation of genome-enabled selection into a breeding program. However, little if any published knowledge exists relating the cost:benefit from genomic selection. This project determined the costs associated with genome-enabled selection as it applies to the swine breeding industry. Placing economic value(s) on genome-enabled selection, will allow researchers to know what aspects of genomic selection must be improved in order to make it profitable or more enticing for use by swine breeders. This will guide future research projects, so that their focus is on improving the economic value of genome-enabled selection. Genomic selection is of little benefit to swine breeders if it is too costly to implement and / or insufficient improvement in genetic gain per generation results from its implementation such that swine breeders and ultimately commercial pork producers do not achieve sufficient return on investment.

To date, there have been studies demonstrating the use of genome-enabled selection within the overall swine breeding selection program. However, little or no scientific literature conveying the related economic considerations for genomic selection has been published. This is an important missing piece of knowledge. As technology improves, the cost of genotyping will continue to decrease, and it is likely that more swine breeders will have the ability to take advantage of genome-enabled selection. This research will allow producers to assess the costs associated with genome-enabled selection to determine the potential for a sufficient return on investment from using genome-enabled selection in a breeding program.

The objective of this study was to develop a tool to determine the cost structure associated with incorporating genome-enabled selection into commercial breeding programs. Assuming 1000 sow nucleus populations for both maternal line genetic programs and genotyping all male and female selection candidates at low density and all animals used for breeding at high density, it was determined that genome-enabled selection costs would be approximately $0.08 per weaned pig in the commercial production system assuming that the boars produced in the nucleus are used at capacity. For a 600 sow terminal line nucleus herd and genotyping only male selection candidates at a low density, the cost per weaned pig in the commercial herd was determined to be $0.05. This means that $0.21 per weaned pig from boars produced in the nucleus would need to be added to the genetic merit value for each market pig in order to break even on the added expense when genome-enabled selection is utilized at the nucleus herd of the breeding pyramid.

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Using genomic information to determine an animal's genetic merit at the molecular level can improve estimated breeding value (EBV) accuracy when compared to an EBV based solely on phenotypic records. However, genome-enabled selection is expensive and the increased genetic improvement rate must be large enough to offset the costs associated with incorporating genome-enabled selection into a breeding program. A flexible spreadsheet tool developed from this work can be utilized to estimate the returns needed to recover additional costs associated with genome-enabled selection by modifying the input values such as herd size and genotyping strategy to represent the specific design of any breeding and production system.

- A flexible spread sheet that can be used to determine the total costs associated with genomic selection was developed.
- The spreadsheet can be used by genetic suppliers as well as commercial producers to determine cost effectiveness of genomic selection as is relates to their swine production system
- Given a current rate of genetic gain, the proportional improvement in rate of genetic gain necessary to make genomic selection profitable was determined.

Scientific Abstract

The objective of this study was to develop a tool to determine the cost structure associated with incorporating genome-enabled selection into commercial breeding programs. Determining an animal's genetic merit using genome-enabled selection can improve estimated breeding values (EBV) accuracy. Increasing EBV accuracy will increase the rate of genetic gain within the breeding program; however, the magnitude of the accuracy improvement must be large enough to recover the costs associated with implementing genome-enabled selection. One way to reduce the genome-enabled selection costs is to genotype selection candidates using a low density chip and use high density chip genotyping for animals that are used in the nucleus breeding herd. In the present deterministic evaluation, it was assumed that the training data consisted of 2000 animals genotyped at high density. Under the present scenario, the top 5% based on genome-enabled EBV of the boars produced in the nucleus herd was assumed to be used as nucleus replacements in the maternal and terminal lines, and the top 60% of boars produced from the terminal line were used in the commercial production system. It was assumed that a 1000 sow nucleus population formed the basis for the maternal line's genetic program and genotyping all male and female selection candidates at low density and all animals used for breeding at high density, it was determined that genome-enabled selection costs would be approximately $0.08 per weaned pig in the commercial production system assuming that the boars produced in the nucleus are used at capacity. Similarly, for a 600 sow terminal line nucleus herd and genotyping only male selection candidates with the low density panel, the cost per weaned pig in the commercial herd was determined to be $0.05. This means that $0.21 per weaned pig produced at the commercial level that are sired by boars obtained from the nucleus herd breeding program needs to be added to the genetic merit value in order to break even on the additional cost required when genome-enabled selection is utilized. A flexible spreadsheet tool developed from this work can be utilized to estimate the returns needed to recover additional costs associated with genome-enabled selection by modifying the input values such as herd size and genotyping strategy to represent the specific design of any breeding and production system.

Introduction

The common method to estimate breeding values and rank animals based on genetic merit is known as traditional BLUP (best linear unbiased prediction) selection. This method relies on phenotypic information measured directly on selection candidates and their relatives to determine the expected genetic potential (commonly referred to as an EBV) for all animals. This method only uses recorded performance values for traits measured without including any additional molecular information that could be used.

With advances in molecular technology or new biological tools, researchers have established ways to incorporate variation at the very basic DNA level into breeding programs. When breeders incorporate the variation in the DNA, called genomic information, into a selection strategy, it is known as genome-enabled selection. For genome-enabled selection, a tissue or blood sample is collected and used to obtain genetic information for each animal. The genetic information from an individual animal's sample is decoded or sequenced to determine the specific genetic code at certain points along the entire DNA sequence. This information, specifically the areas where the sequence is different at a single location (called single nucleotide polymorphism, or SNP, which simply means at a single point there are differences in the DNA code) can be used to enhance traditional breeding value estimation. Determining an animal's genetic merit at the molecular level will improve estimated breeding value (EBV) accuracy.

The objective of this study was to develop a tool to determine the cost structure associated with incorporating genome-enabled selection into commercial breeding programs. Determining an animal's genetic merit using genome-enabled selection can improve the accuracy of estimated breeding values (EBV); however, this improved accuracy must be large enough to recover the costs associated with implementing genome-enabled selection. Utilizing the low density marker panel can be an effective method of reducing genotyping costs once the training data set has been established. The method of inferring high density genotypes from a low density panel is known as imputation.

Objectives

The objective of this project is to determine the cost of genome-enabled selection as it relates to genetic improvement in the swine industry. This project resulted in a spreadsheet that can be utilized to calculate the cost differential from using genome-enabled selection versus traditional selection. As a result of the spreadsheet developed, swine breeders can determine the breakeven price for adding genome-enabled selection to a breeding program and this can be used to avoid an unprofitable investment. With the knowledge of the required economic benefits to make genome-enabled selection profitable, producers can make more informed decisions about the practicality of genome-enabled selection. Before genome-enabled selection becomes widely used, it must be shown that there is potential for economic benefits over traditional selection methods.

Materials and Methods

Most commercial animals are the offspring from a mating between a female that is a cross between two maternal lines and a male that is from a terminal line. Therefore, each of the two maternal lines contributes 25% of the genetic material to commercial animals and the terminal contributes 50%. One maternal line is typically derived from a Landrace population, while the other maternal is typically derived from a Large White population. The terminal line is derived from a Duroc population. All three lines must be selected for improved performance at the commercial level, and thus, EBVs must be estimated for each line. The terminal line is typically selected based on a terminal sire index that consists of growth and carcass traits. The maternal lines are often selected based on a maternal line index that is comprised of the terminal traits as well as reproductive traits.

Genotyping costs were assumed to be $115.00 and $55.00 for the high and low density panels, respectively. This cost includes the cost of the genotyping and all other costs associated with collection, storage, shipping, etc. For all 3 lines, it was assumed that the training data consisted of 2,000 animals genotyped at high density. A training population is needed to determine population haplotypes so that imputation can be used to infer genotypes from a low density marker panel.

Developing genome-enabled EBVs requires more time and computing power compared to traditional BLUP EBVs. For this analysis, it was assumed that 8 months was required to analyze the training dataset and develop the program that will be implemented for genetic evaluations. An additional 8 hours will be needed with each weekly evaluation to prepare data and to ensure the program runs without errors. It was assumed that the EBV development and additional work with each weekly evaluation would cost $60.00/hour in wages and benefits. An investment of $50,000 was assumed for computing infrastructure. This cost includes equipment and labor associated with set-up.

Once a training data set has been collected and analyzed, routine genotype collection can be scheduled for selection candidates. The number of selection candidates in a given year that must be genotyped will be determined by the genotyping strategy as well as the number of offspring produced by the nucleus breeding herd on an annual basis. For this analysis, all male and female selection candidates were expected to be genotyped at low density and then all animals used for breeding were re-genotyped at high density in both maternal lines. Only male selection candidates were genotyped for the terminal line and selected boars were re-genotyped at high density.

Each nucleus maternal line (Yorkshire and Landrace) was assumed to have 1,000 sows while there were 600 sows in the nucleus terminal line (Duroc or some other synthetic line). For the maternal lines, it was assumed that, on average, each litter in the nucleus herd consisted of 11 pigs born alive with a 1:1 sex ratio (PigCHAMP, 2012). Each sow was assumed to have 2.3 litters a years, on average (PigCHAMP, 2012). The combined pre-weaning and nursery mortality was assumed to be 12% (PigCHAMP, 2012). These assumptions result in a total of 22,264 animals to be low density genotyped annually in each maternal line. With 5% and 20% selection for males and females (Falconer and Mackay, 1996), respectively, 557 males and 2,226 females will be re-genotyped with the high density panel annually in each maternal line.

The average sow production in the terminal line nucleus herd was assumed to be 10 pigs born alive per litter with a 1:1 sex ratio and 2.1 litters per sow per year (PigCHAMP, 2011). The total mortality through the nursery was assumed to be 12% as for the maternal line. This means that 5,544 male pigs are produced and low density genotyped in the terminal line nucleus herd, annually. Assuming 5% male selection, 277 males would be re-genotyped with a high density panel.

The top 5% based on genome-enabled EBV of the boars produced in the nucleus herd was assumed to be used as nucleus replacements in the maternal and terminal lines. The top 60% of boars were used in the commercial production system for the terminal line. Boars were assumed to produce 25 semen doses weekly with 15% of doses being thrown away due to semen quality issues (Singleton and Flowers). All boars utilized were assumed to be used to maximum capacity meaning that all doses that are not discarded due to semen quality or other issues are used for insemination. This means that 461,282 and 2,756,754 doses were produced from the maternal line boars and terminal line boars, respectively.

The total weaned pigs produced from the semen doses collected was calculated as 1,940,845 and 10,544,584 for the maternal and terminal lines, respectively. This was based on 10% pre-weaning mortality in the commercial herd and an 85% farrowing rate for commercial sows (PigCHAMP, 2012). For the maternal lines, 40% of the gilts developed were assumed to never produce a litter and for the sows that farrowed at least one litter, it was assumed that each sow produced 35 weaned pigs per lifetime, on average (PigCHAMP, 2012).

Results

The total start-up cost was $356,800.00 for both maternal lines and the terminal line. This includes the costs associated with developing the genome-enabled EBVs and the genotyping of the training data set. The annual costs of routine genotyping were $1,545,045.00 and $337,278.00 for the maternal and terminal lines, respectively. Assuming a 3-year planning horizon and a 5% discounting rate (Federal Reserve, 2012), the increased revenue for the maternal and terminal lines must be $1,686,536.32 and $478,769.32, respectively, in order to break even on the increased costs associated with incorporating genomic information into the selection program.

It was determined that genome-enabled selection costs would be approximately $0.08 per weaned pig in the commercial production system for each maternal line. This is equivalent to $2.90 increased revenue from nucleus daughters, $3,030.07 per nucleus boar, or $3.66 per semen dose. The cost per weaned pig in the commercial herd was determined to be $0.05 for the terminal line. This is equivalent to $143.93 per nucleus boar of $0.17 per semen dose. This means that $0.21 per weaned pig from boars produced in the nucleus would need to be added to genetic merit of each market pig in order to break even on the cost of genome-enabled selection for all 3 lines. The marketing structure for the genetic supplier will determine how the additional costs associated with genome-enabled selection must be recovered.

The current rate of genetic gain in the nucleus will determine the proportion increase in rate of genetic gain needed to recover the costs of genome-enabled selection. According to the National Swine Registry, the current rate of annual genetic gain for the terminal line index is $0.30, $0.40, and $0.30 per weaned pig for the Duroc, Landrace, and large White populations, respectively (NSR, 2010). The rate of genetic gain for number born alive is 0.08 and 0.07 pigs per year for Landrace and Large White, respectively. Considering that 50% of the terminal line index improvement in the Duroc line would be passed on to the commercial herd, this would mean that a 33% increase in the rate of genetic gain would be needed to recover the costs of genome-enabled selection. The increase in pigs per year must be considered as part of the rate of genetic gain for the maternal lines. Consider this and the fact that 25% of the improvement occurring in each of the 2 maternal lines will be passed on to the commercial animals, 74% and 100% increase in the genetic improvement rate needed for the Landrace and Large White populations, respectively. Figure 1 diagrams the expected improvement in genetic merit at the commercial level.

Another way to recover the costs associated with genome-enabled selection is through obtaining or capturing increased market share. Without increasing the nucleus herd size, the only way to increase the market share is to increase the proportion of male offspring produced in the nucleus herd that are used to produce commercial piglets. Figures 2 and 3 show the relationship between the proportion of nucleus boars used and proportion of improvement in rate of genetic gain for the terminal and maternal lines, respectively. The feasible region, or the region where the costs of genome-enabled selection are recovered is shaded in gray. The gray area not on the break even line indicates a profit is made. Figure 2 assumes that the current rate of genetic gain in the commercial animals was $0.15 per pig from the terminal line. Figure 2 assumes that the current rate of genetic gain in the commercial animals was $0.10 per pig from the maternal line.

Discussion

The expected benefit from genome-enabled selection is improved EBV accuracy (Meuwissen et al., 2001). Due to the direct relationship between accuracy and rate of genetic gain, increasing EBV accuracy will proportionally increase the rate of genetic gain expected given that selection intensity and generation interval remain constant. This increase in accuracy will have to be sufficient enough to recover the added costs associated with using genomic information in the selection program.

Muir (2007) showed that there is potential for increased genetic improvement when using genomic selection in addition to traditional BLUP selection. The added data from genomic information increases breeding value accuracies and therefore increases response to selection. The study also showed that genomic selection could have an advantage over traditional methods when applied to traits that have low heritability and are difficult to measure due to cost of measurement or only being able to measure the trait on certain animals, such as number born alive.

The improved EBV accuracy results from being able to estimate the genetic merit of an animal at an earlier age, potentially before the animal has performance information from the individual itself or its progeny when genomic selection is practiced. When single-step selection is practiced, the improved accuracy comes from better genetic relationship estimates among animals rather using expected genetic relationships based on pedigree information. Genomic information can also be utilized to correct pedigree errors. Using genomic information in this way, not only leads to increased accuracy through genotype data, but traditional BLUP EBVs are improved due to a more correct or more accurate pedigree. Correcting pedigree errors will improve the connectedness of the herd and properly associate relatives' records.

Marker assisted selection has increased genetic improvement from selection for meat quality, net feed intake and pigs born alive compared to the response from BLUP with the largest gap between marker assisted selection and BLUP being for meat quality; however, no genetic improvement was observed for growth when comparing marker assisted and BLUP selection methods (Hayes and Goddard, 2003).

If genomic information is used alone without phenotypic information, the genetic improvement resulting from selection may not exceed the genetic improvement based on BLUP breeding values (Dekkers, 2007; Muir, 2007). All available phenotypic and genomic information should be incorporated into the EBVs to ensure the most accurate EBV for selection. Genome-enabled selection will not eliminate the need for phenotype collection. Earlier theories associated with the genome-enabled selection suggested that one benefit would be the cost savings associated with reducing or eliminating the collection of phenotypic data; however, due to the decay in accuracy associated with genomic breeding values over generations, genomic breeding values must be re-estimated periodically and phenotypic records will be needed (Jannick, 2010).

The application of genomic breeding values has been investigated for pig populations. Nielson et al. (2010) showed the correlation between genomic breeding values and traditional BLUP breeding values to be 0.62 for the 170 boars used in their data set. Cleveland et al. (2010) reported the accuracy of the genomic breeding value for total pigs born per litter to be between 0.64 and 0.82, depending on the type of training data set used. The authors reported the accuracy of number of stillborns per litter to range from 0.33 to 0.68.

Dekkers (2007) developed a method using selection index theory to calculate the genetic response expected from incorporating genomic selection in a selection index. The method deterministically calculated the genetic response anticipated from using genomic selection with defined genetic parameters. The study showed that, for a trait recorded on both sexes prior to selection, selection based on markers alone can improve response by 8.5% compared to selection based on solely on phenotypic information.

The greatest impact of genome-enabled selection is expected for lowly heritable traits that are hard to measure or measured late in life such as disease resistance, feed efficiency, and longevity. Disease resistance is not easily defined and systematically measured. Feed efficiency is expensive to measure directly, especially on an individual animal basis. Sow longevity is not recorded until the sow is culled from the herd and is a trait that is only measured on females. If traits are not currently measured and recorded, additional costs associated with measuring the novel traits will be connected with genome-enabled selection if these traits are targeted in a selection program. For a novel trait to be incorporated into a selection program, a measureable phenotype associated with the trait must be clearly defined. Depending on the phenotype, there may be a significant cost associated with the infrastructure needed to collect the data.

Using genomic information to determine an animal's genetic merit at the molecular level can improve estimated breeding value (EBV) accuracy when compared to an EBV based solely on phenotypic records. However, genome-enabled selection is expensive and the increase in rate of genetic gain must be large enough to offset the costs associated with incorporating genome-enabled selection into a breeding program. If new technologies, such as sexed semen, were commercially available for the swine industry such that selection intensity would be differentially impacted when using genome-enabled selection compared to traditional BLUP selection, then the potential impact of genomic selection could change relative to BLUP selection. Yet unknown discoveries related to genetic manipulation, reproductive efficiency, and other scientific fields might influence the value of genomic selection in a way that has not been thought of at present. A flexible spreadsheet tool developed from this work can be utilized to estimate the returns needed to recover additional costs associated with genome-enabled selection by modifying the input values such as herd size and genotyping strategy to represent the specific design of any production system.

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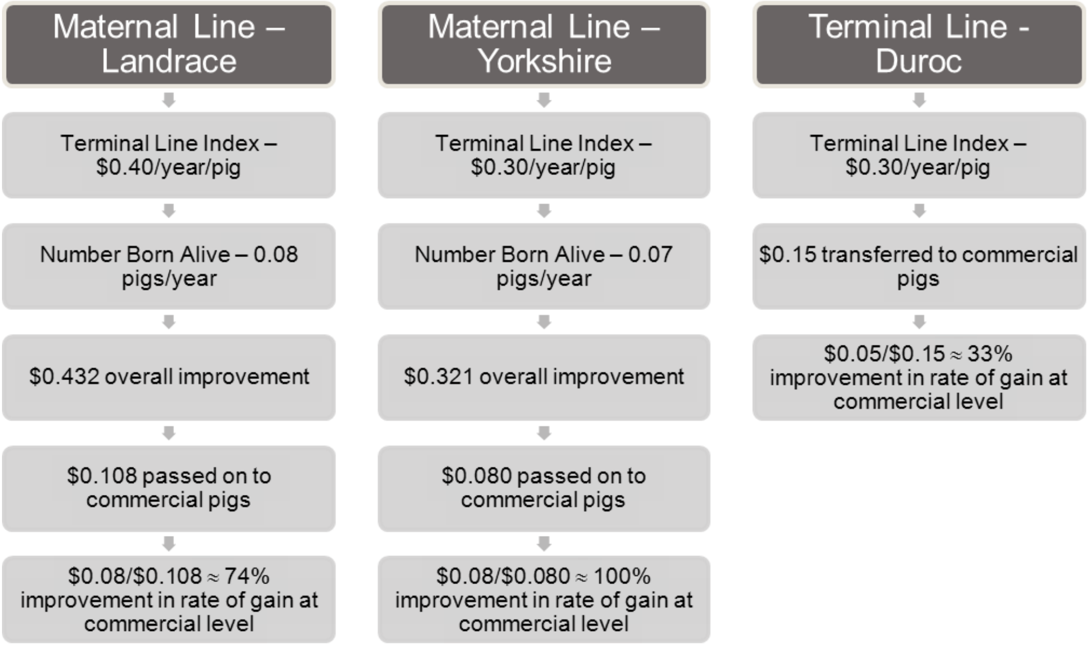
Figure 1. Value of expected improvement in genetic merit at commercial level



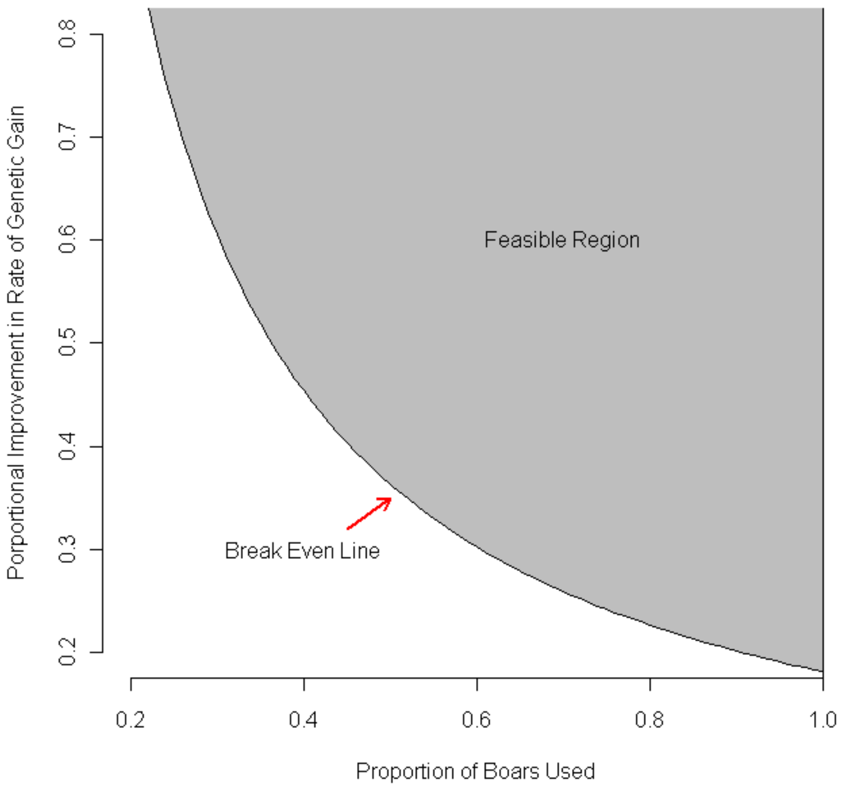


Figure 2: Feasible Region For Terminal Line

Figure 3: Feasible Region For Maternal Line