

Costs of Implementing Genome-enabled Selection in Swine

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Summary and Implications

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. 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.

Introduction

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. 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 on animals and their relatives to determine the expected genetic potential for all animals. This method only uses recorded performance values for traits measured without any additional molecular information that could be used. 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. 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 as breeders in the nucleus herd.

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 the commercial animals and the terminal contributes 50%. Each maternal line nucleus was assumed to have 1,000 sows and 600 sows in the terminal nucleus. All three lines must be selected for improved performance at the commercial level, and thus, EBVs must be estimated for each line.

It was assumed that the training data consisted of 2,000 animals genotyped at high density. In both maternal lines, 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. Only male selection candidates were genotyped for the terminal line and selected boars were re-genotyped at high density.

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. All boars utilized were assumed to be used to maximum capacity.

Results and Discussion

It was determined that genome-enabled selection cost would be approximately \$0.08 per weaned pig in the commercial production system. 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 genetic merit of each market pig in order to break even on the cost of genome-enabled selection. Whether or not this is achievable depends on the improvement in rate of genetic gain that can be expected from genome-enabled selection compared to traditional BLUP selection.

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.