

ANIMAL SCIENCE

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

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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.

These research results were submitted in fulfillment of checkoff-funded research projects. This report is published directly as submitted by the project's principal investigator. This report has not been peer-reviewed.

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