

ANIMAL SCIENCE

Title: Optimizing Selection on Major Genes in Swine - NPB #98-062

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ABSTRACT

Current advances in molecular genetics are leading to the discovery of individual genes for traits of economic importance (major genes or marked QTL). Examples are the halothane gene, the ESR gene and the RN gene. The use of such genes in selection has the potential to substantially enhance rates of genetic improvement, especially for traits with low heritability (e.g. litter size) and traits that are difficult to measure (e.g. meat quality). Identified major genes or markers can be powerful tools that will enhance rates of genetic improvement if they are used properly. At the same time, however, improper use of these powerful selection tools can result in undesirable effects and in less than optimal genetic improvement. Guidelines and strategies on how to best incorporate major genes in selection programs are needed. The aim of this research was to develop such strategies.

To this end, methods were developed to optimize simultaneous selection on a major gene and as well as other (unidentified) genes that affect the trait, through a selection index of major genotype and regular EBV. The latter is derived from phenotype and estimates the value of all the other genes that affect the trait. Index selection strategies were compared to other selection strategies, including a two-stage selection strategy in which selection was first on the major gene and secondly on EBV among selected individuals with the poorest major genotype. As an example, results were applied to selection for litter size using the estrogen receptor gene (ESR). Results showed that, although the two-stage selection strategy led to the fastest fixation of ESR, it resulted in less response in litter size than index selection strategies. This was caused by the lower response in the other (unidentified) genes that contribute to litter size with two-stage selection. These results clearly showed the importance of balancing emphasis on the major gene against emphasis on the other genes that affect the trait through a selection index. Results also showed that response to selection can be further enhanced by optimizing the emphasis on the major gene in the index through the methods developed in this study. Although further work is needed to fine-tune the optimal strategies, their application will ensure that greatest benefit is obtained from the information obtained from molecular genetics.

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