



Genomics in the United States beef industry[☆]



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ABSTRACT

While genetic evaluation systems which combine performance records and pedigree data have been utilized in the beef industry for over four decades, the incorporation of genomic information into genetic evaluation, and the effective implementation of genomic tools within the industry is relatively novel. Genomic technologies have been effectively deployed in the dairy, swine, and poultry industries; however, the beef industry possesses unique challenges for technology transfer. In this paper, we discuss the current limitations of genomic technologies and hindrances to the transfer of these technologies to the beef industry, while also considering opportunities for improved genomic and epigenomic tools needed to surmount barriers to technology adoption.

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1. Introduction

Beef producers have initiated the adoption of genomic technologies. With the seemingly continuous discovery of novel recessive genetic defects in a diverse spectrum of cattle

breeds, many producers now utilize available genetic tests to identify carriers. Because carriers of known defects are severely discounted in the registered sector, perhaps overly so, the value of genetic testing is clear to bull breeders. Likewise, breed associations value and appreciate simple genomic technologies such as testing to verify parentage, fostering opportunities for seedstock and commercial producers to benefit from these applications. For example, it is well known that in multiple sire mating programs that some bulls will repeatedly sire significantly more calves than do their pasture mates (Drake et al., 2011). The use of parentage testing can identify which bulls disproportionately affect profitability through siring the greatest number of market calves and replacement heifers and which bulls should be sold without impacting reproductive rates. Establishment of pedigree relationships among the progeny also adds considerable value to the performance records collected in multi-sire mated herds for use in genetic evaluation. It is plausible that the employment of

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technologies such as these will continue to increase, becoming as commonplace as vaccination programs.

The use and interpretation of results from genomic testing is often situation-dependent and can vary in different traits and populations. In this article, we will discuss implementation and potential for future applications of genomics in the U.S. beef industry within the context of within-breed application for National Cattle Evaluation (NCE) traits, within breed application for non-NCE traits, and across breed applications for genomics data.

2. Genomic approaches for quantitative traits

There are several examples of single-gene (coat color, horned/polled, genetic defects) or parentage tests which can significantly impact a producer's profit. On the other hand, when causal mutations underlying polygenic traits are not assayed, the cost of genotyping high-density assays, which may have limited predictive power in terms of both traits and populations, creates a challenge to technology transfer, especially for selection and management of commercial cattle. Technology users within the U.S. beef industry covet simple "silver bullet" solutions which genomics can currently provide only for simply-inherited traits or straightforward problems such as parentage verification. For quantitative traits, the solutions are generally complex and suffer from limitations including cost and population specificity. Additional impediments that are specific to the U.S. beef industry are the lack of a profit motive on the part of many small-scale producers who represent approximately 25% of cow ownership (McGrann, 2012) and a lack of transmission of appropriate economic signals from retailers, packers, feedlots and background/stocker operations to breeders due to the fragmented ownership of cattle during their life cycle. While some beef producers can effectively use genomic technologies to increase profit, technology adoption is currently considerably less than in the competing meat industries (Hayes et al., 2013; Newman, 2013; Fulton, 2012).

Providers of currently commercialized tests for quantitative traits return molecular estimates of breeding value or scores/rankings based on their marker tests to either the producer, the breed association, or, often, both. Some breed associations have also negotiated agreements with the service providers to include the receipt of raw genotypes. The Beef Improvement Federation's guidelines dictate that the use of genomic information on quantitative traits be within the context of the generation of genomic-enhanced expected progeny differences (EPDs) which integrate performance, pedigree and genomic data. This approach works well for seedstock cattle and for traits which are commonly included in NCE. However, producers are often confused when they receive both genomic-enhanced EPDs from breed associations and molecular estimates of breeding value or scores/rankings from genotyping service providers which suggest different genetic merits for a trait. For this reason, some breed associations only report genomic-enhanced EPDs, and not the molecular breeding values. Additional problems have arisen as breed associations have experimented with different

methods for integrating genomic data into their genetic evaluation systems to produce genomic-enhanced EPDs. For example, because prediction equations are currently limited to a single breed, a population of animals from that respective breed must be used in the training set to generate molecular breeding values. Those prediction equations are then utilized in the entire population, including those animals represented in the training population, which results in the double counting of data on some animals. This situation can lead to an artificial increase in accuracy; however, the best method to avoid this problem is not clear. Many training populations are small and consist of the most influential animals within a breed. When the animal's owners have paid for genotyping, they expect access to genomic-enhanced EPDs on those animals, and excluding their genomic data from the full evaluation to avoid double counting is problematic. The need to retrain prediction equations results in an ever-expanding training population size, which underscores the necessity of developing a solution to this problem. Additionally, it is widely accepted that the degree of relationship between the training and implementation population influences the accuracy of prediction, and there remains a significant opportunity to explore weighting of genomic data in the analysis to account for these pedigree relationships. Lastly, when genotype information is included in genetic evaluation, the data storage requirements, especially with raw genotypes, are greatly increased. Paired with the need to alter National Cattle Evaluation procedures at each respective breed association to accommodate the molecular data, these necessary changes can pose a challenge to the adoption of this technology within the industry.

To this point, no U.S. beef breed association has implemented the procedures adopted by the U.S. dairy industry, which uses genotype information to generate genomic relationships between animals, largely because raw genotypes have only recently become available to the associations. Rather, the U.S. beef breed associations have adopted one of three approaches to produce genomic-enhanced EPDs: (1) a selection index which weights pedigree-based and molecular EPDs based on the predictive ability of the genomic test, (2) a multivariate analysis in which the molecular EPD is treated as a correlated trait (Kachman, 2008), or (3) an analysis in which the molecular EPD is treated as an external EPD (Quaas and Zhang, 2006; Henderson, 1975). Each approach has advantages and disadvantages; and the selection of method has been primarily predicated on the types of available data (i.e., complete genotype information versus calculated molecular estimates of breeding value) and the flexibility of software used to perform genetic evaluation. Each approach has different advantages including the ability to include an individual accuracy for each genomic test (external EPD), the ability for information to filter through the pedigree to non-genotyped animals to increase the accuracy of genomic-enhanced EPDs for related animals (correlated trait), and possessing readily-available data for retraining that is independent of currently implemented genomic technologies (indexing). However, none of these approaches are optimal, and the ultimate solution to this

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