Genomics and the beef industry: Missing links

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Abstract

Genomic selection has become pervasive across all animal breeding programs. In the beef industry, genotyping a non-parent animal is equivalent to that animal having already produced approximately 5 to 25 offspring, depending on the trait. Although this increase in information can greatly increase the rate of genetic gain, if utilized, the benefit of genomic information could be multiplied if it were to be used throughout all sectors of the beef industry. This would ideally require a data feedback loop whereby commercial-level phenotypes were used in genetic evaluation and prediction of genetic merit to inform management decisions of commercial animals. The decisions made could be enhanced using sophisticated software to contemplate genetics, environment, management, and societal demands many of which manifest into economic constraints. The objective of this paper is to briefly summarize the current state of genomic selection and to propose a path forward relative to a more comprehensive use of genetic information throughout the beef industry.

Key words: bovine, beef, genomics

Résumé

La sélection génomique est devenue omniprésente dans tous les programmes de reproduction animale. Dans l'industrie bovine, le génotypage d'un animal non-parent équivaut à une production approximative par cet animal de 5 à 25 descendants selon l'attribut. Bien que cette augmentation de l'information puisse grandement accroitre le taux de gain génétique si on l'utilise, le bénéfice de l'information génomique pourrait être multiplié si elle était utilisée systématiquement dans tous les secteurs de l'industrie bovine. Ceci demanderait idéalement une boucle de rétroaction où les phénotypes au plan commercial seraient utilisés pour l'évaluation génétique et la prédiction du mérite génétique afin d'éclairer les décisions de gestion des animaux commerciaux. Les décisions prises pourraient être améliorées en utilisant des logiciels de pointe pour prendre en compte la génétique, l'environnement, la gestion et les exigences sociétales dont plusieurs se manifestent sous la forme de contrainte économique. L'objectif de cette présentation est de faire un bref survol de l'état actuel de la sélection génomique et de proposer une démarche favorisant un recours plus systématique à l'information génétique dans tous les secteurs de l'industrie bovine.

Introduction

Genomic selection has become a reality for all major US beef cattle breeds. This has enabled more accurate expected progeny differences (EPD) and, if utilized, would be expected to increase the rate of genetic gain. Although genetic decisions, and the accumulation of genetic merit, that take place in the seedstock sector do flow to the commercial cow-calf, backgrounding, feedlot, packing, retail, and consumer segments of the beef industry, the genetics are "masked" due to industry segmentation. Consequently, more informed management and purchasing decisions conditioned on genetic background become challenging if not impossible. Moreover, a feedback loop of preferences and data to accommodate changes given preferences to the seedstock sector is generally not possible, creating partial disconnect between commercial level profitability and consumer satisfaction with genetic selection decisions.

There is also a growing sense of 'information overload' such that seedstock suppliers and their direct clientele are confronted with a growing number of EPD from which to make decisions. Given more than 1 trait impacts profitability, multiple-trait selection is necessary. The most desirable method of practicing multiple-trait selection is by using a selection index.[2] However, current economic selection indexes provided by beef breed organizations would benefit from the inclusion of additional EPD for economically relevant traits (ERT). Simplifying these decisions, with net profit of the commercial industry as the goal, and including data from outside of the seedstock sector are critical objectives that must be solved in order to create a sustainable beef industry.

Genomic Selection

The methods for including genomic information into EPD have changed over the past decade. The method first used by the American Angus Association (AAA) was first proposed by Kachman[3] and used by MacNeil et al[6] in their prototype evaluation. This became known as the 'correlated trait approach' and assumed that the linear combination of the 50,000 (50K) DNA marker genotypes known as the Molecular Breeding Value (MBV) could be fitted as a correlated indicator trait in existing multiple-trait models. The majority of breeds that followed implemented a blending (indexing) approach whereby the MBV and EPD were indexed together to produce a 'genomically enhanced' EPD (GE-EPD). Both of these methods were essentially variations on the same two-step theme: estimate the SNP effects using a large data set of genotyped and phenotyped animals from the same 'breed' to train the MBV and then fit them into genetic evaluation.

More recently, beef breed associations implemented 'single-step' genomic evaluations. This eliminated the need to estimate marker effects and develop a prediction equation to be applied to newly genotyped animals and helped to avoid the bias associated with selectively genotyping animals (genotyping only the 'best'). Two methods are currently used; one that uses DNA markers to inform kinship,[5] and another that selects the most informative markers *a priori* and only fits those in the genetic evaluation.[1] Both of these methods have proven to increase the accuracy of EPD and provide less biased estimates than previous 'two-step' methods.

Priority Areas

Despite the tremendous progress that has been made over the past several years relative to genomic selection, challenges still exist.

1) Improve the portability of genomic predictions.

It is well known that the accuracy of genomic predictions erode as the target population becomes more distantly related to the training population. This can occur overtime, but perhaps the larger concern is across differing breeds. Kachman et al clearly illustrated that a 50K-based genomic predictor for weight (either yearling or weaning) that was trained in Angus was not predictive in Red Angus.[4] The issue of robustness, or portability, of genomic predictions across breeds is critical for 3 reasons: 1) not all breeds will have the resources to adequately estimate markers effects for all traits, 2) prediction in non-pedigree commercial populations will remain elusive unless this issue is resolved, and 3) the transfer of genomic information from research settings for novel traits to industry populations will not occur otherwise.

Encouraging results using identified variants from whole genome sequence information that are contained on the new GGP-F250 panel are becoming available.[8] In this paper, Snelling and colleagues reported that 293 variants explained 36% of birth weight genetic variation in the Germ Plasm Evaluation project (GPE) at the US Meat Animal Research Center, and MBV trained using GPE effects had genetic correlations with birth weight in other populations ranging from 0.25 to 0.44. Similar correlations were obtained from a subset of SNP that contained only 11 variants. Genetic correlations between birth weight and genotypes for the single most significant variant in GPE were between 0.17 and 0.34 in the independent populations. Although we have a considerable amount of work yet to do, the incorporation of biological information into our predictions of genetic merit using genomic data seems encouraging.

2) Improve phenotypic data recording for traits that are commercial industry profit drivers.

Although fertility EPD do exist in some form for several beef breed associations, the information content is not sufficient. This is due to a combination of factors including the lowly heritable nature of these traits, and both the quantity and quality of data reported.

There are other traits that are economically relevant to the commercial industry that are either sparsely collected or non-existent in current breed association databases. Included are traits such as disease susceptibility (bovine respiratory disease, pinkeye, etc.), carcass data including primal yields, mature cow weights, male fertility, cow feed intake, and the list could go on. The majority of these phenotypes exist in the commercial sector (cow/calf, feedlot, and packer) and are collected in some form every day. To fully capitalize on genomics, we must exploit the data that exists in our industry and ensure it enters into genetic evaluation. It is obvious that breeds without a solid genetic evaluation foundation cannot make use of genomics, and for many traits of economic importance all breeds fall into this category. Unfortunately, these are the traits for which genomics could help the most—those that are expensive to collect, collected on older animals, or sex-limited.

3) Improve the understanding and utilization of genetic selection tools.

Weaber et al reported that unpaid consultants, such as neighbors or friends, were most frequently (38.9%) identified by respondents as valuable sources of breeding and genetics information followed by veterinarians (29.7%), extension professionals (29.5%), seedstock producers (27.7%), internet search (18.9%), farm supply or feed store staff (18.1%), breed association personnel (14.7%), AI stud personnel (11.7%), popular press sources (9.3%), and paid consultants (2.1%).[11] These results suggest that it is important to educate not only traditional information providers (veterinarians and extension educators), but also commercial producer peers and their seedstock suppliers about genetic and breeding principles, as these entities are often consulted as trusted sources of genetic selection information.[11]

The traditional vehicle for outreach has been face-to-face delivery of educational and written material. These delivery approaches are generally targeted towards increasing knowledge and awareness. Unfortunately, despite decades of effort using these 2 traditional approaches to outreach, little has been accomplished relative to attitude and behavior changes. Survey results suggest that upwards of 70% of US beef cattle producers in the commercial sector do not utilize genetic merit estimates, EPD, as their primary selection criterion.[11]

In 2009, an integrated effort between the National Beef Cattle Evaluation Consortium (NBCEC), the University of Nebraska, and the 7 largest beef breeds in the US (Angus, Hereford, Red Angus, Charolais, Gelbvieh, Limousin, and Simmental) was initiated in an effort to develop an educational program centered on genomics and to build a resource population for the development and evaluation of genomic predictors and related methodology. These 7 breed associations 'nominated' seedstock producers (n=24) in the Northern

Plains region of the US to participate in the project. Initially, producers agreed to provide hair samples on all 2009-born bull calves. These animals were genotyped with a reduced assay for weaning weight and post-weaning gain. The DNA marker discovery for this reduced assay occurred in the Cycle VII population at US Meat Animal Research Center (USMARC). Given the early focus on weight traits as proof of concept, the project was named the Weight Trait Project (WTP).

The impact of an outreach program is best evaluated by changes in behaviors and practices of targeted producers and the industry at large. Of the 7 beef breeds represented in the integrated project, all have implemented GE-EPD. The WTP arguably aided in developing the framework for these breeds to develop a training population and empowered group of seedstock producers to educate their peers relative to the advantages of genomic selection.

A survey was conducted by Spangler et al to quantify changes in knowledge, practices, and behavior; the survey was sent to participants in the WTP.[10] The 17 respondents indicated that collectively they own 20,125 beef cows. Increases in knowledge were rated from 0 (none) to 4 (significant). Mean survey results were 1.5, 2.8, 2.0, 3.4, 2.4, 2.7, 2.8, and 2.9 for EBV, genomics terminology, parentage verification, marker assisted selection, across-breed genomic predictions, whole genome selection and panel development, test validation, and accuracy improvement of EPD, respectively. Producers indicated adoption of methods to improve the following production practices: making mating decisions (40%), efficient use of DNA technology (75%), and selection (bull buying) decisions (47%). Mean responses for changes in behavior (1 = none; 5 = very likely) were 3.9, 3.8, 4.3, and 4.6 for making more informed selection decisions, better educating their clientele, feeling comfortable with terminology, and desiring to stay abreast of DNA technology, respectively.

Precision Selection

Bull purchasing decisions need to account for differing marketing goals and environmental constraints to improve profitability and sustainability, but these are unique to each herd as producer-specific production goals and inputs vary considerably. To achieve widespread use, a decision support tool that allows a tiered level of input information, with default values which are customizable, from each specific user is required. Such a tool would need to be scalable to ensure that producers with limited knowledge of their resource inputs and those with more detailed levels of prior information could benefit from its use at either level.

The correct choice is conditional on marketing objectives, environmental constraints, and value and number of offspring. Knowledge, *a priori*, of the value of individual bulls available and the value differences amongst them, would greatly enhance the profitability of commercial cow/calf enterprises by allowing selection decisions to focus on what is economically important and what bull price is justified to achieve the subsequent goals for a particular firm given its resource constraints. Current bull purchasing decisions do not appear to use all of the relevant information available.[7,11] The Penton Media survey reveals that producers often incorrectly include an animal's own performance record in selection decisions and trait emphasis is disjoint with production/marketing goals. Without the aid of a decision support tool, commercial beef cattle producers, often without the technical knowledge required, are forced to attempt to combine several disjoined pieces of information (e.g. current herd performance, EPD of potential seedstock, accuracy of EPD, mean breed differences, projected costs and value of production, production environment constraints, etc.) to decide which bull to buy, and to determine the economic value conditional on their own needs.

Producers face the problem of obtaining the best bulls for their operation in that given setting. Implicit in this exercise is the need to account for the underlying resource base where the sire's progeny will be utilized. It is worth noting here that 'best' is a relative concept. When accounting for price differentials across bulls, a 'less desirable' bull may become the preferred choice over a 'more desirable' bull if his sale price discount is larger than the differential in value between the 2 bulls. A producer armed with our tool can use the estimates of 'value' on different bulls to identify the relative bargains of bulls that are most under-priced relative to their value.

Conversely, if the spread in bull prices does not sufficiently reflect the differences in economic value of the bulls offered, having good estimates of value should increase profitability of top seedstock producers. Furthermore, customized indices open the opportunity for different customers to rank bulls differently, which would also increase profitability of seedstock producers.

Spangler et al described a USDA-funded grant effort to tackle these issues.[9] The fundamental objective is to develop and provide software that enables beef producers to make more profitable genetic selection decisions, integrating additive and non-additive genetic effects, available resources, and firm-level economics. This requires the integration of several partial solutions, including appropriately weighting selection emphasis on various traits and comparing individuals of different breeds. Specifically, a producer could upload a set of EPD or select individual animals from any collaborating breed association or breeding organization and receive direct comparisons of EPD across these breeds. We further plan to expand the suite of traits that would be included beyond the growth and carcass merit traits that are currently available.

Although the ability to easily compare EPD of animals across breeds for an expanded array of traits is novel, the more germane issue is the economic weighting of these traits conditional on user-defined inputs and marketing goals. Consequently, we will develop a module to apply economic selection indices to AB-EPD and novel traits. The web-based tool proposed by Spangler et al[9] aims to provide profit-based weightings for ERT and thereby rankings of candidate animals for use in the breeding herd.

A Path Forward

The path forward towards greater integration of genetic/genomic tools throughout the beef industry could be reduced to 3 broad, but critical, aims:

1) Increased understanding of genetic selection tools across all sectors.

It is apparent that there is work to be done yet relative to educating both seedstock and commercial cow-calf sectors relative to genetic selection tools. It is also critically important that the feedlot, packing, and retail sectors also again an understanding of fundamental genetic principles such that they are willing to financially reward improved genetic potential and can make use of this information in the management and sale of animals/products.

2) Transfer of data and information across all sectors.

It is impossible to place direct selection pressure on a trait for which no data exists. Although traits such as animal health, components of yield grade, marbling, and dark cutting are recorded daily in the beef industry, virtually none of these data are included into genetic evaluations. This makes improving such traits genetically very challenging. Ideally, data would flow from commercial sectors to genetic evaluation centers (e.g., breed associations) to be included into EPD. In return, genetic predictions of commercial animals could be returned and used to inform management strategies (e.g., diet, vaccine protocol, and market endpoints). This flow of data could be facilitated by genomics. Although pedigree is largely unknown for commercial animals, it can be inferred through genomic information akin to the way that some beef breed organizations use DNA markers to augment pedigree relationships.

3) Development of decision support tools that enable the utilization of dense data towards more profitable decisions (both selection and management).

In addition to the web-based genetic selection tool mentioned herein, additional tools will be needed to help make management decisions considering genetics, management, environment and society, including the interactions between these factors. This is a concept that is called GEMS, representing the main effects and interactions among genetics, environment, management, and society.

Conclusion

Genomic data have positively impacted the beef industry relative to the ability to make accurate genetic selection decisions. The benefit to the commercial industry is currently the mitigation of risk of having made an incorrect bull selection decision. The benefit of genomics could greatly expand to include the ability to manage animals according to genetic backgrounds, somewhat akin to personalized medicine. To achieve this aim requires the sharing of data across sectors, which requires mutual benefit. To fully exploit these data towards more profitable decisions, software will need to be developed to integrate partial solutions to help make decisions.

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