Genomic and computing strategies in the optimization of the genetic component of specification beef

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ABSTRACT: Genomics and computing are closely interrelated in beef cattle improvement. Both require the prior definition of breeding objectives, both can be used to carry out genetic evaluations of economically important traits, and both can be used in the development of selection tools for sires and dams. Effective use of both requires accurate specification of the desired product, an optimal production program, and crossbreeding structure. Optimizing the genetic component of production requires information on traits of economic importance, identification and relationships of animals, information on candidate and marker genes, and information on economics. Genomic information can be used for strategies involving identified allele deletions, identified allele introgressions, marker-assisted introgression, and marker-assisted selection. Techniques are being developed to combine genotypic data and quantitative data into genetic evaluations, although more developments are needed to optimize the use of these techniques across the range of beef traits varying in economic importance and cost of measurement. The genetic component of economical production of specified products can be optimized with customized selection programs. An example is presented in which performance levels are predicted from genetic evaluations based on quantitative and genomic information. The implications for selection within a seedstock population are also discussed.

Key Words: Beef Production, Genetic Improvement, Genome Analysis

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Introduction

Recent developments in molecular genetics and computing have provided new opportunities for optimizing the genetic component for efficient beef production. At the same time, there is increasing interest in more exactly specified beef products, as indicated for example in the description of certified beef programs by the USDA (2002).

The objectives of this article are to provide a brief review of new developments in molecular genetics and computing, to discuss the interrelationships of these developments, and to discuss strategies for utilizing these new developments in the context of improving the efficiency of producing a clearly specified beef product.

Specification of the Product and Production Program

The importance of specifying the economic value of the carcass in terms of weight and intramuscular fat when selecting sires has been shown by Wade et al. (2001). In general, specifications could include carcass weight, intramuscular fat, indicators of tenderness, or other criteria as dictated by consumer demand. Many of these are included to varying degrees in certification criteria (USDA, 2002) and may have genetic components.

Discussion of optimizing genetics requires consideration of the production environment (Wilton, 1986; 1990). One major component of the production program is the crossbreeding structure being used, whether a rotational cross, terminal cross, or composite. Expressions of traits at the phenotypic level are clearly dependent on combinations of breeds as well as the genetics of individual animals. Selection objectives in genetic populations (breeds for example) depend on the use of those populations in crossbreeding. Selection objectives for populations used as either terminal or maternal populations in terminal crossing differ from each other and from those for populations used in rotational crossing.

Another major component of the production program is the nutritional regimen. Nutritional effects on carcass traits have been shown by many researchers, such as Mandell and Aalhus (2000). The combined effect of genetics and nutrition is a particularly important con-

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sideration in genetic improvement in situations in which the absolute level of performance of commercial progeny is important, as it is in cases of optimal carcass weight, for example.

Optimization of Genetics

Genetic improvement through selection is dependent on changing allelic frequencies. Changes in allele frequencies can be considered for both simple gene effects and for multiple, or quantitative, gene effects. Genetic improvement through intra- or interlocus allele or gene combination effects involves both measurements of interactions and optimization of heterosis. Overall genetic optimization involves matching genetics with environment, or more specifically, with management, nutrition, and marketing programs, as described by Wilton (1986).

Genomic Strategies

There are two basic strategies for improving the genetics of populations with genes of known location, either identified allele elimination or identified allele introgression. Identified allele elimination is basically the elimination of genetic defects and is important when there is complete dominance of an allele at a locus. Some examples of testing services for cattle are for protoporyphria, bovine leucocyte adhesion deficiency, citrullinaemia, complex vertebral malformation, deficiency of uridine monophosphate, and Pompe's disease (Bova-Can, 2002; ImmGen, 2002). This genomic information makes possible the use of strategies to eliminate or at least reduce heterozygotes for breeding purposes.

Identified allele introgression basically involves increasing the frequency of a desirable allele. One example is the identification of mutations in the myostatin gene (Kambadur et al., 1997) and the association of inactivated myostatin with carcass traits (Casas et al., 1998) and palatability (Wheeler et al., 2001). The strategy suggested by Wheeler et al. (2001), at least within the Piedmontese that they studied, was the use of homozygous inactivated myostatin genotypes as terminal sires to produce heterozygous progeny with improved carcass value. A comprehensive analysis of possible mating systems by Keele and Fahrenkrug (2001) indicated that the most profitable mating system depended on price sensitivity to intramuscular fat level and cost of managing dystocia.

The use of markers for simple gene effects is the same as for the use of identified genes. The RN gene in pigs (Mariani et al., 1996) is a marker for meat quality associated with glycogen metabolism and the elimination of heterozygotes can increase the rate of improvement in meat quality. In beef, a marker for intramuscular fat as associated with thyroglobulin concentrations has been reported (Genetic Solutions, 2001). The success of using this marker has yet to be determined in additional populations.

The use of markers for quantitative traits is receiving considerable attention for marker-assisted selection. A recent example is the search for quantitative trait loci for both growth and carcass composition within cattle segregating alternative forms of the myostatin gene (Casas et al., 2001). This search combines the general concept of identifying markers for economically important traits with the specific concept of identifying these markers within populations segregating for a major gene, a possibility indicated earlier by Hanset (1982). Another interesting example is provided by Echternkamp et al. (2002). Three markers on chromosomes 5 and 7 for ovulation rate and twinning have been identified and used along with measurements of ovulation rate and twinning rates in the genetic evaluation and selection of sires in a project designed to increase twinning rate.

Also, recent announcements concerning the identification of single-nucleotide polymorphisms of a draft of the bovine genome (Adam, 2002) offer possibilities for fine mapping and linking of specific genes with meat quality traits. Considerable research has been done in the area of combining markers with quantitative data to improve the accuracy of estimating breeding values, as reviewed and discussed by Van Arendonk et al. (1999) and Weller (2001). However, examples of applications of markers in genetic improvement of commercial beef cattle populations have not yet been reported.

Computing Strategies

Developments in computing have been simultaneous with developments in genomics. Computing requirements have increased for merging genomic or marker information with quantitative phenotypic information. New computing possibilities are possible and also needed to obtain more information on phenotypes. Some examples are measurement of carcass traits through video image analysis (Cannell et al., 2002) and feed intake through electronic feeding equipment (Schenkel et al., 2002). Such phenotypic data must be connected to genotypes through pedigree structures and trace-back mechanisms for commercial data. Complete data on traits such as heifer and cow fertility, survival rates of cows, and health of both cows and calves can be obtained only with expanded whole-herd data recording. More automation is still needed for sufficient data to be collected so that more traits can be genetically evaluated or for markers or candidate genes to be identified.

Major developments in computing have taken place in both database management and Internet use. Speed of accessing data and transmitting results makes new approaches in timely genetic evaluation possible. An example of the simultaneous use of extensive databases and Internet use is the development and implementation of a customized sire-selection tool described by Wilton et al. (1998). In this application, net economic values are calculated for the use of sires in a herd with a specified production environment and a specified market. The computing algorithm requires that market prices be stated and that any variations in prices in the product according to yield, quality, or weight be considered. Sensitivity of sire rankings to variation in some of these factors has been shown by Wilton et al. (2002). Computations also require specification of the production environment in terms of crossbreeding system and feeding programs, along with appropriate prices.

Phenotypes to be used to obtain net economic values in this development are predicted from across-breed genetic evaluations (**ABC**), computed as described by Sullivan et al. (1999). Across-breed genetic evaluations for postweaning growth and ultrasonic backfat at end of test are used to predict growth rate of steers in the feedlot and time to market under specified levels of finish as a marketing criterion. Similarly, ABC for intramuscular fat at end of test are used to predict distributions of progeny for marbling score. The ABC for longissimus muscle area are used to predict retail yield of progeny. The ABC for growth rate, ultrasonically measured backfat, and feed intake (individually available through computerized feeding systems) are used to predict feed requirements of progeny in the feedlot. Similar predictions are used for female progeny in the herd, with discounted gene flows to account for expression rates and times. Across-breed evaluations for calving ease are used to predict costs associated with calving difficulties; ABC for direct and maternal weaning weight are used to predict weaning weights of progeny and ABC for growth to predict cow weight. Further refinements could be made by obtaining appropriate data and computing ABC for heifer fertility (Moyer, 2001), cow weight (Mwansa et al., 2002; Rumph et al., 2002), and survival (Snelling et al., 1995; Mwansa et al., 2002).

The endpoint of trait measurement is important in the interpretation and use of ABC in the prediction of progeny performance. For example, reranking of sires for retail yield with a change from a time-constant to a finish-constant basis has been shown by Handley et al. (1996). Fortunately the equivalence of time-constant and finish-constant endpoints as a basis for comparison was shown by Wilton and Goddard (1996) to be valid if time, weight, and finish are considered simultaneously and if production programs are optimized. Consistent time-constant ABC are used in the customized sire selection approach described by Wilton et al. (1998) and are the values used in the discussion to follow.

Net economic values for two bulls assuming two different price grids are given in Table 1, adapted from Wilton et al. (1998), as an example of the importance of customization. The first price grid is primarily based on prices relative to the carcass being a product, with little differentiation in prices for weight and no differentiation in prices for intramuscular fat, and is considered a "commodity" grid. The second price grid is based on greater differentiation of prices of the product based on weight and intramuscular fat and is considered a "quality" grid. In this example, the sire with the higher genetic evaluation for growth has the higher net economic value for the commodity grid, whereas the sire with the higher genetic evaluation for intramuscular fat has the higher net economic value for the quality grid.

The example used is based on choosing sires for specified production programs and market prices and can be repeated for a variety of programs and prices, making customization possible. As such, the example illustrates the use of computing strategies to optimize genetics by matching with the production and marketing environment. Specific levels of traits for individual herds can be obtained by linking to databases on performance measurements of animals in the herd. Choice of sires for use in those herds is made possible through linkage to databases on sires. The customization process described has been adapted for Internet use to provide timely rankings of sires (BIO, 2002).

Combining Genomic and Computing Strategies

Discovery of identifiable genes of economic importance depends on both molecular genetic techniques and measurements of phenotypes, linked by pedigree information. Databases for both genomic and phenotypic information are necessary. Computing strategies are critical for accumulation of phenotypic information on a multitude of traits as well as on pedigree information. Computing strategies are increasingly important for the incorporation of a marker or any genomic information into genetic evaluations. Genetic evaluations based on both quantitative and genomic information can be used in computing strategies to optimize genetics in terms of selection and mating systems for clearly specified products, as well as clearly defined production environments. Additional research is required to develop complete genetic improvement strategies in the beef industry.

Implications

Increases in knowledge of genomics and computing and development of strategies for their combined use can lead to improvements in optimizing the genetic component in the production of desired beef products. More efforts are required in the measurement and re-

Table 1. Net economic values and across-breed comparisons for two bulls for two price grids

	Bull 1	Bull 2
Across-breed comparison		
Postweaning gain, kg	79	13
Backfat depth, mm	0.4	1.0
Intramuscular fat, %	0.1	0.7
Net economic value		
Commodity grid	$3,642	$1,429
Quality grid	$639	$4,327

cording of an expanded range of traits, establishment of databases, improved evaluation techniques incorporating quantitative and genomic information, quantifying of genotype × environment interactions, and cost-effectiveness of the various strategies to make these improvements a reality.

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