Proceedings
Beef Improvement Federation
43rd Annual Research Symposium and Annual Meeting

June 1-4, 2011
Montana State University
Bozeman, Montana

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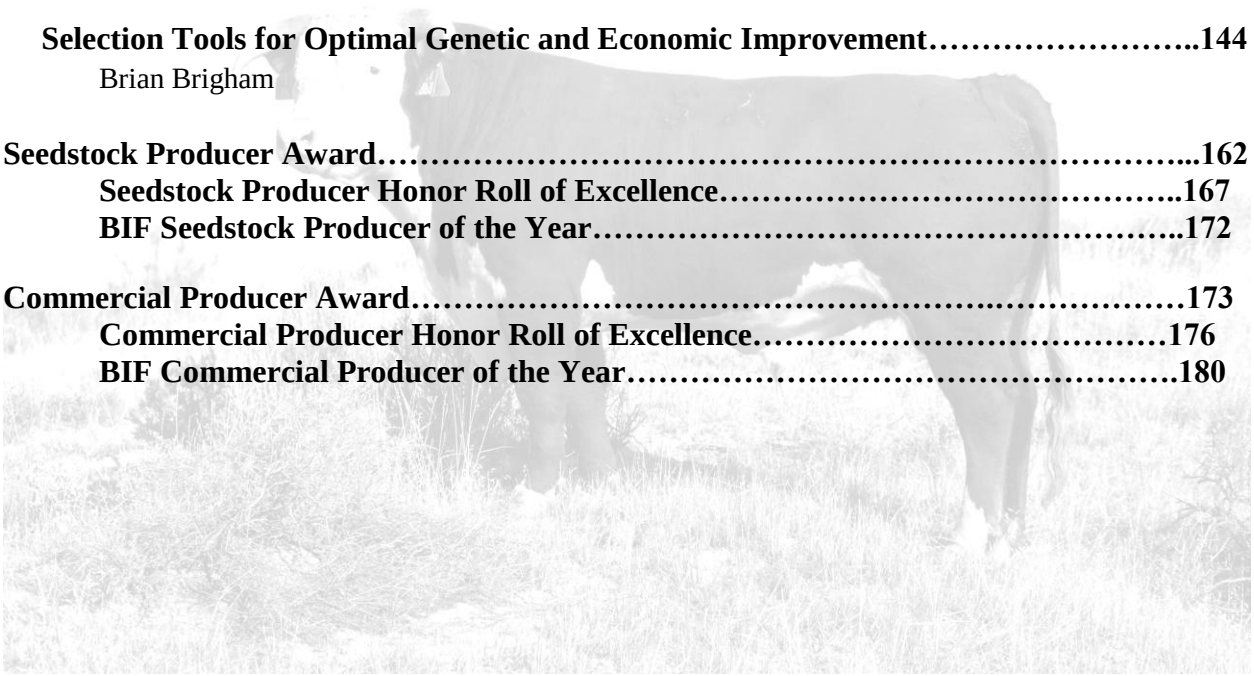

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Beef Improvement Federation

43rd Annual Research Symposium and Annual Meeting
Student Union Building, Montana State University
Bozeman, Montana
June 1-4, 2011

Wednesday June 1

Noon - 5:00PM	Early Registration
5:00PM – 7:00PM	Opening Reception
7:00PM – 9:30PM	**NAAB Symposium**
	Welcome to Montana, Bill Donald, President of National Cattlemen's Beef Association (via video)
	Genetic Improvement from AI and Synchronization—Everybody Wins! Mike Tess, Packhorse Services, LLC and John Paterson, Montana State University
	They Call Me Dr. Discard - Clif Marshall, VP Production, Select Sires/NAAB

Thursday June 2

7:00 AM	Registration
8:00–10:30 AM	**General Session I: Role of Genetic Evaluation Technology in Enhancing Global Competitiveness** – Chair: Jeff Jacobsen, Dean of Agriculture MSU
8:10 – 8:45 AM	**The Role of Genetic Evaluation Technology in Enhancing Global Competitiveness** Scott Newman, Genus, PLC, Hendersonville, TN
8:45 – 9:20 AM	**Role of Genetic Evaluation Technology in Enhancing Global Competitiveness** Robert Williams, Director of Breed Improvement and Foreign Marketing, American International Charolais Assn., Kansas City, MO
9:20 – 9:55 AM	**An AI industry perspective on the role of genetic evaluation technology in enhancing global competitiveness** Willie Altenburg, Associate Vice President-Beef Marketing, Genex Cooperative, Inc., Shawano, WI
10:00 – 10:30 AM	Break
10:30 – 11:20 AM	**General Session II: Genetics in Improving Animal Health** – Chair: Mark Jutila, Veterinary Molecular Biology Department, Montana State University
10:30 – 10:55 AM	**Evidence of genetic variability in cattle health traits: Opportunities for improvement** R. Mark Enns, Colorado State University, Fort Collins

11:05 – 11:30 **Integrating animal genomics with animal health: Genetics of vaccine response in cattle**
Michael Gonda, Department of Animal and Range Sciences, South Dakota State University, Brookings

11:30 – 11:55 **Environmental and management factors influencing BVDV antibody levels and response to vaccination in weanling calves**
E.D. Downey, Animal Science Department, Iowa State University, Ames

12:10 – 2:30 PM **Beef Improvement Federation Awards Luncheon I:** Commercial Producer of the Year, Baker Scholarship Award, Roy Wallace Award, Ambassador Awards, BIF Continuing Service Awards, Graduate Fellowship Recipient Recognition

2:30 – 5:30 PM **Concurrent Committee Meetings (Technical Sessions)**

Advancements in Cowherd Efficiency & Advancements in Selection Decisions - Chairman: Mark Enns, Colorado State University

Application of genetic strategies to utilize reproductive records from cattle populations
Tara McDaneld, USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE

Goals and objects for a five year national research and extension project to improve feed efficiency in beef cattle
Dorian Garrick, Iowa State University, Ames

Feeding behavior as indicator traits for genetic evaluation of feed intake
Gordon Carstens, Texas A&M University, College Station

Fertility in beef cows
Tom Geary, USDA-ARS Fort Keogh Livestock and Range Research Laboratory, Miles City, MT

Live Animal, Carcass and Endpoint - Chairman: Robert Williams, AICA

Hair Coat Shedding in Angus Cows
Joe Cassady - North Carolina State University, Raleigh, NC

Temperament assessment provides insight into future health and growth performance of beef cattle
Rhonda Vann - Mississippi Agriculture and Forestry Experiment Station-Brown Loam Experiment Station, Mississippi State University

Beef Cattle Breeding in Ireland – data collection through an integrated database
Brian Wickham - ICBF & Sheep Ireland Highfield House, Shinagh, Bandon Co. Cork.

From field data to Expected Progeny Differences... EPD calculation in cowboy language
Wade Shafer - American Simmental Association, Bozeman, MT

6:30 PM on **Best of Bozeman – Food and Entertainment**
@ Emerson Center for the Arts and Culture, 111 South Grand Ave.

Friday June 3

7:00 AM	Registration
8:00 – 10:30 AM	**General Session III: New Traits in National Cattle Evaluation** – Chair: Kathy Creighton-Smith, Montana Angus Association
8:00 – 8:10 AM	Welcome President Cruzado, Montana State University
8:10 – 8:45 AM	**Measuring feed efficiency in beef cattle - minimizing inputs across the whole production chain** Stephen S. Moore, University of Alberta, Canada
8:45 – 9:20 AM	**Selecting for female fertility: What can be learned from the dairy experience** Christian Maltecca, Animal Science Department North Carolina State University, Raleigh.
9:20 – 9:55 AM	**What weighting should be given to BRD resistance in selection decisions?** Alison Van Eenennaam, Animal Science Department, University of California, Davis.
10:00 – 10:30 AM	Break
10:30 – 11:30 AM	**General Session IV: A toolbox full of genetic prediction tools – is profit in there, too?** – Moderator: Dan Moser, Kansas State University Panelists: Lauren Hyde (American Simmental Association), Steve Radakovich (Radakovich Cattle Co.), Doug Frank (ABS Global)
11:30 – noon	**Business Meeting**
12:10 – 2:30 PM	**Beef Improvement Federation Awards Luncheon II:** Seedstock Producer of the Year Award, Pioneer Award, President's Address, International Guest Recognition, 2012 BIF Conference Invitation
2:30 – 5:30 PM	**Concurrent Committee Meetings (Technical Sessions)**

Advancements in Genetic Prediction - Chairman: Mark Thallman, USDA-ARS

Improving our genetic prediction of female reproduction
David Johnston, University of New England, NSW Australia

Challenges and Opportunities in Genetic Evaluations Incorporating Genomics
Steve Kachman, University of Nebraska, Lincoln

How Should We be Predicting Breed Differences in Multibreed Genetic Evaluation?
Larry Kuehn, USDA-ARS U.S. Meat Animal Research Center, Clay Center, NE

The New Infrastructure for Beef Cattle Breeding in Ireland
Brian Wickham, ICBF & Sheep Ireland Highfield House, Shinagh, Bandon Co. Cork.

Advancements in Emerging Technologies - Chairman: Jack Ward, American Hereford Association

Integrating molecular data into NCE: expectations, benefits, and needs
Matt Spangler, University of Nebraska, Lincoln
DNA pooling as a low-cost method to detect important genomic regions for difficult traits in beef cattle
Larry Kuehn, USDA-ARS U.S. Meat Animal Research Center, Clay Center, NE
Pathways to genomic analysis of heifer puberty and pregnancy
Warren Snelling, USDA-ARS U.S. Meat Animal Research Center, Clay Center, NE
An Australian approach for incorporating genotypes in genetic evaluation
David Johnston, University of New England, NSW Australia

Advancements in Producer Applications - Chairman: Jane Parish, Extension Beef Cattle Specialist, Mississippi State University

Delivering Specialized Education to Seedstock Producers
Michelle F. Elmore - Extension Animal Scientist, Beef Cattle Improvement, Alabama Cooperative Extension System
The Economic Value of Residual Feed Intake at Bull Sales
Dr. John Paterson - Extension Beef Cattle Specialist, Montana State University

Saturday June 4

Tour #1

- Midland Bull Test, Columbus, MT http://www.midlandbulltest.com/
- Genex Hawkeye West, Genex Cooperative, Inc. Billings, MT
- Holden Ranch Red Angus, Reedpoint, MT

Tour #2

- Sitz Angus Ranch, Harrison, MT http://www.sitzangus.com/
- Virginia City, MT http://www.virginiacitymt.com
- 5L Red Angus, Sheridan, MT http://www.5lredangus.com/
- Cooper Hereford Ranch, Willow Creek, MT http://www.cooperherefords.com

The Role of Genetic Evaluation Technology in Enhancing Global Competitiveness

Scott Newman

Genus, PLC, Hendersonville, TN 37075

Introduction

When we talk about global competitiveness or even just competitiveness in general, what exactly do we mean, and once defined, how do we relate this to genetic evaluation? Here are some beef and dairy examples to help us better understand:

> "The mission of the National Beef Cattle Evaluation Consortium will be to develop and implement improved methodologies and technologies for genetic evaluation of beef cattle to maximize the impact genetic programs have on the economic viability, *international competitiveness*, and sustainability of U.S. beef cattle producers."[1]

> "…Our objectives will be to: Establish and coordinate, with industry partners, the priorities for genetic evaluation of U.S. beef cattle in order to position the U.S. as a leader in this area thereby increasing the *global competitiveness* of the U.S. beef industry;…"[1]

> "…Finally, continued development of national sire selection indexes for lifetime economic merit is essential for US dairy breeders to *compete globally* in the economic production of dairy products. Such efforts are also essential to ensuring a plentiful supply of affordable dairy products for the US consumer."[2]

> "…Improve decision-making on public policy related to productivity and *global competitiveness* of the U.S. agricultural production system. Adoption of improved integrated livestock grazing management systems could improve the economic condition of livestock operators and their associated communities and land ecological conditions."[3]

Note that the fourth quote has nothing to do with genetic evaluation *per se*, but it does provide a further clue to what we mean by global competitiveness - the ability of industries to utilize technology to make money by reducing input costs and/or increasing output. The idea is that genetic change is accomplished by selecting candidates based on an index composed of EPD of economically relevant traits (ERT) weighted by marginal economic values identified by sound breeding objectives that take into account traits most closely associated with income and expense, and to do so more effectively than competitors do nationally and internationally. If we can accomplish this process, then we have the potential to produce a globally competitive product. Genetic evaluation becomes the engine to drive this process.

At its most basic, genetic evaluation is accomplished through computer services processing pedigree information and performance records for one or more traits. These records are systematically recorded and submitted by breeders of a particular breed. The choice of traits to

[1] Mission and objectives of the National Beef Cattle Evaluation Consortium (NBCEC). http://www.reeis.usda.gov/web/crisprojectpages/195268.html

[2] Statement of issues and justification S-284: Genetic Selection and Crossbreeding to Enhance Reproduction and Survival of Dairy Cattle. http://nimss.umd.edu/homepages/home.cfm?trackID=2354

[3] Statement of issues and justification WERA1002: Managed Grazing Systems for the Intermountain West. http://nimss.umd.edu/homepages/home.cfm?trackID=1235

measure and record involves some collective judgment about what traits are economically relevant, and what traits can be routinely measured in the breeders' operations (Harris and Newman, 1994). Genetic evaluation is simply the analysis of that data using some defined statistical model(s) to arrive at estimates of the genetic merit of animals in the population. The output from a genetic evaluation is, in the case of beef cattle, an Expected Progeny Difference, or EPD, which measures the difference in performance that is expected from future progeny of a parent. Genetic evaluation procedures that produce EPD for specific performance traits should be considered a means to an end (and not the end). The desired end is an improved economy of producing consumable and desirable livestock products for the benefit of the breeder and the consumer (Garrick and Golden, 2009).

Seedstock producers are in business primarily to make a profit, as are their breeding stock customers, who produce food products. Producer's profits are influenced by consumers' demand for their products. Purchase of breeding stock involves a cost but can provide a positive influence on the functioning of the system by reducing other expenses or increasing income from output, or both. The producer will be motivated to pay more for breeding stock if given assurance that profit will increase because of these increased costs. Products sold to earn income for a breeder are primarily breeding stock (or alternatively semen). Efforts to improve the value of this product (and thus the income earned) are likely to add expenses due to the extra labor of recording data, registration and computer charges, marketing of intact animals for slaughter, and so on. The breeder will be motivated if given assurance that greater income will adequately cover these increased expenses (Harris and Newman, 1994; Harris 1998).

To summarize, genetic evaluation makes genetic improvement possible. It provides the capability to benchmark individuals within a breed, or possibly different breeds. It is a means whereby the joint investment in recording and selection can be converted to market advantage. It is possible to maximize returns in this process by recording the right traits, and make sensible use of indexing, selection and mating. To maximize the quantity and quality of data recorded so that genetic evaluation can be used most efficiently to add value a well-defined breeding structure is of fundamental importance.

Industry structures for genetic improvement

It is often useful to display the structure of a breeding program in terms of a pyramid, which also helps to reflect the size of each tier. A pyramid characteristic of pig and poultry breeding structures is composed of three tiers that direct genetic improvement (Dekkers et al., 2011). Actual genetic improvement takes place at the top of the pyramid (nucleus), followed by the multiplication of that genetic improvement to produce large numbers of purebred and/or crossbred females, which are sold to commercial farms for the production of finishing, or market pigs. From a beef industry perspective breeders who generate sires to produce sires (SS path) and dams who produce sires (DS path) are effectively the nucleus breeders.

Genetic improvement is disseminated down the pyramid, which introduces a time delay, or genetic lag (e.g., Guy and Smith, 1981). Genetic lag in pig breeding programs can range from three to five years. However, using sires at lower tiers that come directly from the nucleus allows the breeder to reduce this delay time. This allows the collection of commercial (crossbred) information for use in genetic evaluation, which helps reduce the effects of genotype x environment interaction, and aids in increasing the accuracy of genetic evaluation through the addition of crossbred relatives' records.

An alternative to the pig or poultry breeding pyramid would be that of dairy cattle, which possesses a so-called *open* nucleus structure, where animals (in this case female) from lower tiers

can be brought into an upper tier by generating sons that are chosen as if they were bred in the nucleus.

Understanding the genetic structure of breeding populations helps to understand how genetic improvement is disseminated, and to identify ways to reduce genetic lag. The US beef industry does have a nucleus-multiplier-commercial structure, although not as clearly delineated as other livestock industries. Márquez and Garrick (2007, 2010) quantified the pathways of selection (sires to produce sires, SS; sires to produce dams, SD; dams to produce sires, DS; dams to produce dams, DD) in the American Red Angus database. Only 1,271 herds (30% of the total) produced SS, and only 153 of those (3.6% of all herds in the pedigree) produced 50% of the SS animals that appeared in the pedigree.

In general, an industry is at a greater advantage when genetic improvement can be concentrated in superior, or nucleus herds, especially when a breeder must select animals from another herd to introduce outside genetics with greater confidence and without loss in overall genetic superiority (Harris, 1998). How many US beef breeds can identify with confidence the nucleus and multipliers herds, or at least define a breeding structure? Do we know magnitude of genetic lag in our breeds? These are fundamental questions because they can influence the adoption of technology and determine how and where investments in technology should be made for the greatest benefit.

Uptake of genetic evaluation in the US beef industry

I have not been able to quantify the percentage of US seedstock producers who utilize genetic evaluation; it is likely not as high as it could be. Therefore, it is not apparent how well the US industry is doing in applying genetic evaluation. Some reasons for this might include:

1. The amount and quality of recording per animal or per herd varies widely. This will mean that EPD and index accuracy (if used) will vary widely among selection candidates and reduce the power of selection
2. There are opportunity costs generated when genetic evaluation is not based on sensible indexes (or indexes are not used)
3. From a simple perusal of genetic trends there is no suggestion that the US is making significantly faster progress for individual traits (or indexes) than major competitors

The question arises as to how breeders see genetic evaluation. Is it a vehicle for accelerated wealth creation, or a hurdle adding costs with little benefit? This in part reflects imperfections in the market as well as the time it takes to learn effective use of the technology. It is safe to say that the pig industry has embraced genetic evaluation as an integral step in turning recording effort into profit.

Information nucleus schemes

Genetic evaluation is a tool that converts data into information. This information forms the basis of genetic gain. The value generated by genetic evaluation depends on the information content of the dataset relevant to the breeding objective, and the effectiveness of selection. The information content is a function of the amount, quality and cost to obtain performance data. As pointed out earlier, nucleus structures are very efficient in doing this. Provided sire sampling is done wisely, they influence the entire breeding and production system.

The challenge is then to explore ways of getting the most useful data possible for a breed. A structured progeny test, called an Information Nucleus (IN; Banks, 2006, 2011), allows a breed to collect data on hard to measure traits without which its capacity for progress is greatly restricted.

There are number of traits influencing the beef supply chain that are either very expensive to measure (e.g., feed intake), or are recorded at phases and locations other than the seedstock herd (e.g., eating quality), or which take a long time to record (e.g., fertility and longevity). A breeding program that does not capture data on eating quality for example, cannot manage that trait set, let alone make genetic improvement.

The IN structure has three key elements:

1. Use of young, elite sires from diverse genetic backgrounds;
    a. Sires are progeny tested across a range of environments and for as many traits as can be measured
    b. Sires are genotyped for available markers, panels, or whole genome scans, so that the most relevant and reliable estimates of marker effects are obtained

Information Nuclei have been implemented in the Australian Sheep and Dairy industries, and recently in beef (Banks, 2011). Five Australian beef breeds (Brahman, Charolais, Hereford, Limousin, Angus) have had three or more sire intakes in their first cohort and involve recording a comprehensive set of growth, carcass, reproduction (male and female), eating quality, and docility traits.

The IN provides a way for breeds to identify and concentrate performance recording that will provide a clearer path for dissemination. When breeders and producers have relevant information about genetic merit, their combined responses could lead to faster genetic improvement for traits that drive profit. As mentioned previously, with value-based marketing, the services delivered to buyers and sellers must deliver value, so the market for services becomes more efficient as well.

A short section on indexing

I would be remiss if I did not make mention of the use of indexing in genetic improvement programs in beef cattle (or of any livestock species). It would seem logical that the ability to develop and use a selection index (Hazel, 1943; MacNeil, 2005) as part of the genetic improvement process would greatly benefit the speed at which genetic improvement in profitability can be made and also further focus attention on the importance of economically relevant traits. Garrick and Golden (2009) provide reasons why the classic Hazel approach can be difficult to implement (e.g., lack of covariances between ERT and indicator traits, lack of motivation to calculate marginal economic values, lack of industry promotion of the value proposition associated with genetic improvement). However, solutions exist to make indexing accessible. For example, MacNeil and Matjuda (2007) reported on an aggregated simulation model used to estimate marginal economic values for specialized sire lines but can also be used for more general scenarios. Through the NBCEC, Garrick (2005) developed an alternative approach using the concept of selection by simulation. Phenotypes are predicted based on current performance levels and then used to predict costs and revenue. This allows the producer to model alternative selection scenarios from a variety of breed databases[4]. Having the ability to access a common breed database would aid in the incorporation of heterosis and across-breed EPD. Some US beef breed associations do provide the ability to rank animals on a variety of indexes, but I have not been able to ascertain if these indexes are being used for animal selection and how they are being used as part of a genetic improvement program.

Closing comments

[4] See http://ert.agsci.colostate.edu/ or http://dss.ansci.iastate.edu/.

For the past ten years, I have applied a great deal of my knowledge of genetics and animal breeding to the pig, but I have never forgotten my roots – the Australian and U.S. beef industries. While I have not spent a great deal of time discussing specific aspects of how genetic improvement is made in the pig industry, much of what I have written about global competitiveness and genetic evaluation in cattle underpins what I have learned in pigs.

1. The pyramid structure for genetic improvement is very well defined. Genetic improvement takes place in PIC's nucleus farms.
    a. Genetic improvement is disseminated through well-defined tiers in the pyramid
    b. A large amount of information is collected on nucleus animals. The important point is that *every animal is recorded.*
    c. Semen from young nucleus boars is used in commercial farms so we can collect both purebred and crossbred data simultaneously so the crossbred information can be used in genetic evaluation to increase accuracy of breeding value estimation. This also helps reduce genetic lag.
        i. The crossbred data collected includes carcass, reproduction and mortality information.
    d. We also collect an enormous amount of SNP data for use in genetic evaluation.
2. All lines have distinct selection indexes
    a. While some pre-test culling occurs for certain defects, selection decisions are based on index selection *only.*
3. All of our mating decisions are accomplished with mate selection (Newman et al., 2009; Kinghorn 2011). Mate selection allows us to balance diversity (rate of change in inbreeding) with response to selection.

It is not my intention to recommend that you all become pig breeders. However, I do believe that there are lessons the beef industry can learn from pig breeders to make structured genetic improvement:

1. It is imperative that the major cattle breeds define their breeding structures and implement an Information Nucleus scheme. Among other opportunities will be greater prospects for data collection associated with hard to measure traits and also clarity in the application of genomic information as part of the genetic evaluation scheme.
    a. Decision support modeling could form the basis of a more flexible path to selection index use and also provide breeders a better feeling of controlling their own destiny, as they would have the ability to assign proper emphasis on traits of economic importance for their circumstances.
2. Utilization of genomic information of whatever form, by anyone, will depend on having relevant phenotype data with which to calibrate marker tools, whether they are individual markers or QTL, panels or whole genome scans.
3. Since breeding objectives target commercial performance, there should be a concerted effort to collect half-sib commercial and crossbred information (e.g., carcass data) to provide a basis for crossbred EPD estimation.
4. A unified database would provide the ability for higher accuracy across-breed EPD, efficient utilization of commercial/crossbred information, and also provide better decision support capabilities.
5. Implementation of a mate selection process will allow additional power to the breeding program. Mate selection will allow, for example, pre-culling of animals; consideration of a wide range of outside sires to help increase gains, lower inbreeding levels, and provide connections to outside seedstock sources that will result in better gains in the longer term, and the ability to make herd size variable by factoring in the cost of maintaining breeding

females. This can provide a path to a controlled reduction of herd size through periods of drought or financial hardship, with parallel accommodation of concerns about genetic gains.

Independent of species, to be globally competitive, we must be able to maximize the quality and quantity of data relevant to the breeding objectives we have defined per dollar invested, and then utilize the results of our genetic evaluation effectively to add value for our customers.

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Role of Genetic Evaluation Technology in Enhancing Global Competitiveness

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Introduction

Livestock producers seek to use the genetic variation which exists between animals for making directional changes in their herds and breeds for selected traits of interest. When selection decisions are made there are expectations of a response to those selections. Going back in history there are key events; the importation of beef genetics, establishment of research, education and extension programs, the beef cattle performance revolution and the printing of the first Sire Summaries which all have had a profound impact on the U.S. beef population increasing value and production.

Since the Spaniards first introduced cattle to the new world through the great cattle drives of the late 1800s beef has become a major economic business in the U. S. As America became settled and our economy grew, ranching became a way of life. Regardless if genetics move from one breeder to another or across continents there is an anticipation of adding value, increasing output and/or creating efficiencies of the nations beef herd. This transfer of genetics wasn't only about serving domestic demand for beef but also enhancing our competitiveness in a global economy.

Given the U.N. has projected the world's population to reach 9 billion people by the year 2050 which has lead to the call for food production around the world to double by the year 2050 (Green, 2009) increasing production levels and efficiencies are a growing concern. Additionally, meat is demanding an increasing share of the global market as diets in developing countries are changing and as incomes rise (FAO, 2002). Although global competition has intensified for the growing international demand for beef, opportunities exist for U.S. producers to capitalize.

American beef producers historically have responded aggressively to an increasing demand for our product with increased production levels and improved efficiencies. While current beef cow inventories have returned to levels of the 1950s beef production has more than doubled (USDA, 2011) over the same period of time.

While much of the improvements in productivity can be traced to the migration of genetics, it has been the last 30-40 years that our increased focus on performance and genetics has been responsible for significant gains as well. Many of our successes can be traced to work done within the framework of the Beef Improvement Federation.

While research is continuing here in the U.S. we should be concerned about the funding for such research. We have not always enjoyed the abundances in this country as we do today. Our system of research, education and extension should be credited for much or our standard of living and our abundance of affordable and healthy foods.

We can trace the roots of our current system of research, education and extension back to 1903 when Seaman Knapp arrived in east Texas to talk to the local farmers. Knapp identified Walter C. Porter of Terrell, Texas to set aside a small part of his farm as a demonstration farm using new technologies to grow cotton. Because of the success of this first step the U.S.D.A. Cooperative Extension Service was formed and by 1920 there were seven thousand federal extension agents, working in almost every county in the nation, and by 1930 they had set up more than seven

hundred and fifty thousand demonstration farms. (Gawande, 2009) However, investments in public agricultural research have slowed since 1980 (Pardey et al., 2006) placing research stations and our land grant universities under growing budget constraints. During this same period of time the private sector has increased research and development significantly faster than the public sector (Huffman et al., 2011).

Genetic evaluations have played a significant role in the improvement of beef cattle in the United States for many characteristics. Genetic trend tables, readily available on association websites, are a testament to our success domestically and have also helped establish the U.S. as a leading genetic source. This is particularly evident in a 2007 report prepared for Meat and Livestock Australia which showed consistent trends for breeds in the USA and Canada for reduced birth weight and stronger trends for yearling weight (McDonald, 2007).

As the international community continues to develop stronger objective based performance and genetic improvement programs the intensity of identifying superior genetics may expand across borders beyond current levels for those breeds and breeders who can better characterize their populations for important traits. As I commented in the opening paragraph there is an expectation of response to imported genetics. This question has been addressed by joint international research projects which have shown when using current genetic evaluation methodology, sires ranked similarly across countries and within regions of the United States (de Mattos et al., 2000; Donoghue and Bertrand, 2004) which has lead to a greater interest for international evaluations.

The production of international genetic evaluations can provide improved marketing opportunities for genetics with increased accuracy, increase confidence of selection across international borders and accelerate genetic progress given the benefits of the larger pedigree and performance information that is made available. However, international evaluations are not without their problems given the timing of data collection, production sales and marketing competition.

Challenges Faced by Beef Breed Associations

Both, the U.S. beef cow inventory and U.S. breed registries reached their peaks in the 1970s with breed associations recording record numbers of animals. However, a decline in the U.S. beef cow inventory (USDA, 2011) has created a shrinking demand for seedstock bulls since 1975. In fact the industry today needs approximately 400,000 fewer bulls than it did in 1974-75. The decreasing size of commercial beef cow numbers is the direct cause for a loss of approximately 430,000 registrations for U.S. beef breed associations over the same period of time (NPLC, 2010). This loss of registration numbers continues to strain association budgets for research and development as well as other services.

Beef breed associations have benefited greatly from the research and development from USDA ARS and land grant universities among others. However, development of new technology often takes a building-block approach where new discoveries are based on earlier discoveries and increased knowledge. We are a witness to this today as genomic enhanced selection continues to improve and the optimism that it will play a larger role in the genetic characterization of our cattle. The question whether to use genomic information will be replaced by how to use it efficiently (Misztal et al., 2010).

Historically in the United States genetic evaluation services have been provided by a few land grant universities. However over the course of the last several years genetic evaluations have moved in house for some breeds (Angus and Simmental) while others have contracted with service providers other than the traditional land grant universities. This change was necessitated

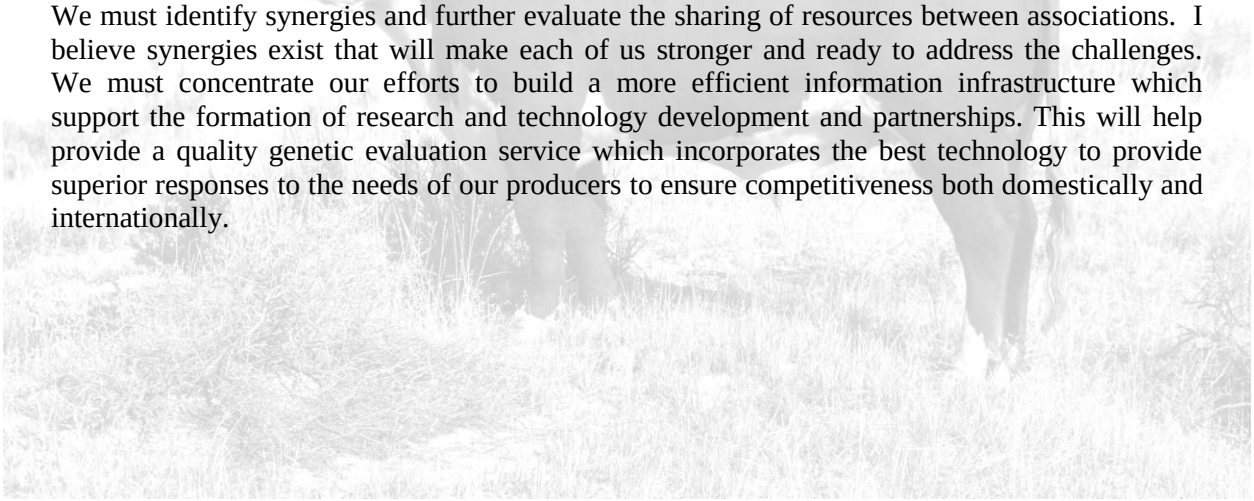
as land grant university budgets became strained and an increasing need and desire to focus more efforts on improving genetic evaluation models. This transition has not been without its bumps and bruises as we have moved forward.

Our transition is far from complete, however. Today we spend more time trying to access, prepare and manipulate data sources and less time modeling data and applying expertise to improve and expand evaluations. The challenge is compounded further as the amount of data and complexity of problems increase. Additionally, new technology will offer more computing options and new genetic tools for traits which historically have been difficult to characterize in our populations.

The current system of "islands of data" is inefficient and inhibits active associations from moving forward in an efficient way. We need to begin capturing data more efficiently which can benefit the building of resource populations for research and development of genomic tools. The current situation is that we have multiple and disparate sets of data that are intended to represent the same or similar concepts.

The cornerstone for our success the last 30-40 years has been the collection of quality phenotypic data which has allowed our producers to capitalize on research/technology transfer programs for genetic improvement. This will continue to be important or research into genomic markers may have little if any impact. The old adage "genetic evaluations are only as good as our data" will continue to be true and will be important information as the expansion of genomic data will require large volumes of phenotypic data and will be required to update existing marker effects (Funk, 2009).

We must identify synergies and further evaluate the sharing of resources between associations. I believe synergies exist that will make each of us stronger and ready to address the challenges. We must concentrate our efforts to build a more efficient information infrastructure which support the formation of research and technology development and partnerships. This will help provide a quality genetic evaluation service which incorporates the best technology to provide superior responses to the needs of our producers to ensure competitiveness both domestically and internationally.



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Evidence of genetic variability in cattle health traits: Opportunities for improvement

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Introduction

From the perspective of today's society, animal health is synonymous with animal welfare and any mention of a sick animal conjures up a negative perception in conjunction with factory farm. To those of us actually in the beef industry, animal health is also synonymous with animal welfare and we continually strive to improve the welfare of our cattle.

Improved health reduces costs associated with treatment, reduces mortality losses, and eliminates the reduced levels of performance typically associated with sick cattle. While management decisions can clearly reduce incidence of disease, there are typically costs associated with those management procedures. Historically, management of disease focused on modifying the animals' environment through vaccination, low stress handling, and through the treatment of clinically ill animals with little attention given to the potential for genetic improvement of health-related traits. Much of this is likely due to one of the greatest weaknesses in current national cattle evaluation--a lack of tools upon which to make these selection decisions. In turn, that lack of tools likely springs from difficulty in identifying the economically relevant traits related to animal health. The term "health" includes a vast array of potential traits for selection.

The Challenge

At a rudimentary level, health traits, as related specifically to "disease" fall into three general categories. The first group contains those diseases that are the result of a defect in the individual's genetic composition such as osteopretrosis, Arthrogryposis Multiplex , fawn calf, tibial hemimelia, etc. The second class contains those diseases associated with non-transmittable environmental challenges such as fescue toxicity, facial eczema, or high-altitude (brisket) disease. One could class these traits as more directly related to adaptability or as being environmentally induced. The final class represents those diseases related to some specific disease vector or pathogen whether it be bacterial, viral or parasitic in nature. From this point forward we will refer to these as pathogen-associated. All three of these categories likely offer the opportunity to capitalize on genetic improvement.

As recent experience in the beef industry would show, there is clear opportunity to eliminate genetic-caused disease from populations through the use of gene marker tests. These tests have been very successful in identifying animals carrying a specific deleterious recessive gene. This process alone is evidence of our potential to improve health traits, at least in the first category. The remaining two classifications are more challenging. In field data, there are often issues related to the accuracy of diagnoses, to the utility of data collected across production environments, and to concerns relative to differences in pathogen exposure.

The Process

As with any new trait that becomes a candidate for genetic evaluation and selection, there is a process that must be completed prior to developing selection tools. First the economically relevant traits and potential indicator traits must be identified. For instance, before the theory behind calculating heifer pregnancy EPD was developed, background research showed that

yearling scrotal circumference in bulls was related to age of puberty in their daughters with the logic being younger age of puberty should result in higher heifer conception rates. Subsequently, scrotal circumference was shown to have a genetic component, or put another way, it was shown to have a heritability greater than zero. As with any trait we wish to improve, health traits must be shown to be under some degree of genetic control. Put another way, there must be genetic variability in the population we are selecting from. Without that genetic control there is no opportunity for genetic improvement. Often the difficulty lies in identifying the appropriate phenotype or outcome to collect in order to meet our goals. We believe this is especially true of health traits.

Once the appropriate traits are identified the challenge becomes collecting field data in sufficient quantities to develop a genetic evaluation. Field data would ideally be collected on the economically relevant trait itself, but barring that, highly related indicator traits could be used. This process is similar to the development and use of ultrasound data on breeding animals for prediction of carcass merit in their slaughter progeny. Ideally we would collect carcass data on every animal for use in genetic evaluation, but that is problematic. To overcome this issue, ultrasound was introduced.

In the absence of the adequate field data, an alternative is the development of DNA marker tests that explain significant amounts of variability in the traits of interest. This development often requires extensive research populations of highly phenotyped individuals along with sufficient validation populations, but once successfully developed DNA marker test results can be used to facilitate delivery of EPD to producers for selection.

In summary the process followed in new trait development is to

1. Identify the appropriate economically relevant traits and associated indicator traits
2. Develop methods for sufficient collection of field data to determine if genetic variability exists in the traits (and if alternative measures such as DNA marker tests could be developed)
3. Based on the results of #2 continue to collect appropriate data
4. Use the information collected in #3 to begin to release selection tools for use by breeders in selecting for improved animal health.

With that as the process, let's examine the opportunities for genetic improvement in health traits given current research. The discussion will evaluate health traits for both an environmentally induced disease and a pathogen induced disease.

Environmentally Induced Disease

What are the opportunities for genetic improvement of environmentally induced disease using the above process? To examine this we will use high-altitude disease commonly referred to as brisket disease as the template. Historically this disease manifested itself in cattle in environments above 5500 feet of elevation. The disease manifests itself with a swollen brisket area, reduced appetite, reduced thriftiness (poor doing) and eventual death. Physiologically, the disease is the result of lower concentrations of oxygen at higher elevations. In that low oxygen environment, the heart responds vigorously by forcing blood through the pulmonary system in turn forcing fluid out of the circulatory system resulting in the swollen brisket.

Here, the economically relevant trait would be resistance to brisket disease or survival at higher altitudes. In extensive range environments typical at these elevations, precise identification of afflicted animals is often problematic and collection of data is difficult. In the absence of that data, an indicator trait for brisket disease was developed—pulmonary artery pressure (PAP) based on evidence that animals diagnosed with brisket had elevated PAP. Subsequent research showed that PAP was heritable (.46; Enns et al., 1992) and should respond to selection. In 1992, the first expected progeny differences for PAP were calculated and used in selection of breeding stock at the Tybar Ranch near Carbondale, CO. The trend in PAP since 1992 has been consistently downward (favorable) since that time (Figure 1) resulting in a reduction in lost performance and mortalities.

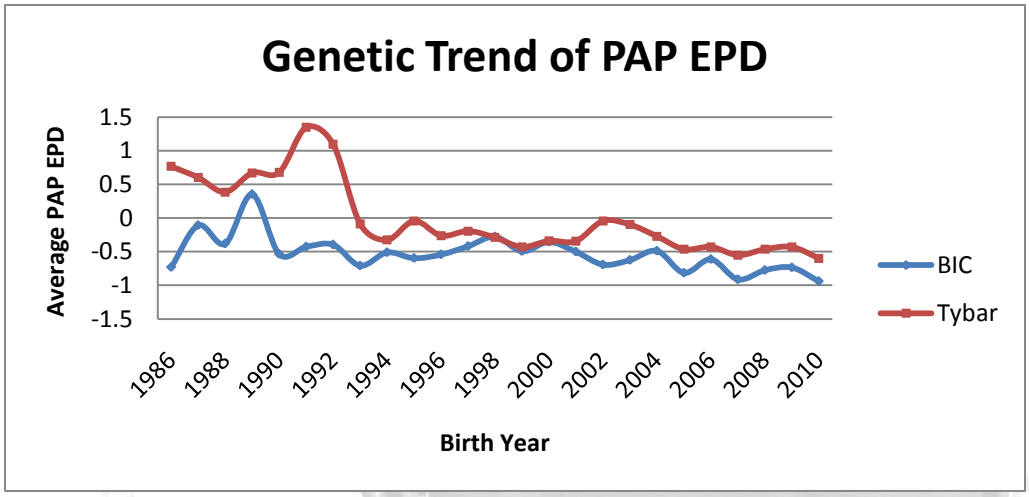

Figure 1. Genetic trend in pulmonary artery pressure at the Tybar Ranch (Tybar) and the CSU John E. Rouse Beef Improvement Center (BIC) since selection with EPD began in 1992 (Tybar) and 2002 (BIC).

The Colorado State University Beef Improvement Center near Saratoga, WY has used EPDs in their selection program since 2006 with a similar favorable response, albeit slower. The reduced rate of progress is a result of the use of the facility as a test herd for evaluating for sires from elevations below 5500 feet.

The limitation of the PAP test is that animals are required to reside above 5500 feet for at least 30 days before the test is performed. This requirement limits the quantity of data that can ultimately be collected and costs other than the cost of data collection itself often preclude testing of animals whose native environment was less than 5500 feet of elevation. This limitation is not uncommon as one of the difficulties often associated with environmental health challenges—often, as in this case, the animals must be in that environment to determine susceptibility to the specific environmentally induced disease. This limitation illustrates the need to develop appropriate indicator traits genetically correlated to the traits of interest and/or to develop genetic marker panels explaining sufficient genetic differences in susceptibility. DNA marker tests would allow for screening of animals from lower elevations to identify those most likely to produce progeny adapted to high elevations.

Pathogen-Associated Disease

The class of animal health traits associated with pathogens pose similar difficulties for genetic improvement. The challenge lies in identifying the economically relevant traits, associated

indicator traits, available data, and DNA marker tests to enable the implementation of genetic evaluation.

Collection of field data for pathogen-associated diseases is especially problematic as there are typically concerns with whether animals were equally exposed to the disease causing pathogen and therefore had the opportunity to fully express genetic differences. Additionally, questions often arise as to whether animals were correctly diagnosed, the severity of the disease, and appropriate causative pathogens identified.

Given these difficulties, initial selection of disease traits for development of genetic predictions should address those of highest economic importance. Estimates suggest prevention and treatment of disease in the feedlot costs the industry in excess of $3 billion (Griffin, 1997). More specifically, with Bovine Respiratory Disease Complex has been shown to be increasing in prevalence and is responsible for a large portion of these costs (Loneragan, et al. 2001; Callan and Garry, 2008). Besides these costs associated with its prevention and treatment, BRDC has also been associated with decreased feedlot and carcass performance (e.g. Schneider et al., 2009; Snowder et al., 2006 and 2007). As such, BRDC, has become a high priority for development of tools for genetic improvement

Given the economic importance of BRDC to the cattle industry, Colorado State University in conjunction with Pfizer Animal Genetics and JBS Five River's Cattle Feeding developed a research project to identify selection tools aimed at reducing the incidence of this disease. This project illustrates both the potential for genetic improvement of pathogen-associated disease and the difficulties associated with collecting field data on disease traits.

The project was conducted over 2 years with 1551 steers fed in year 1 and 1319 fed in year two of the study. Animals exhibiting clinical signs of BRDC as determined by commercial feedlot personnel were treated following feedlot protocols and classed as positive for BRDC. Treatments for other feedlot diseases such as pinkeye and bloat were also recorded. Sires of calves were identified with DNA markers and that parentage information was subsequently used to estimate heritability.

BRDC treatment rates were 45% and 7.1%, in year 1 and 2, respectively illustrating the difficulties associated with collection of field data given variable rates in incidence across contemporary groups.

Even with the contemporary group differences present in this study, the probability that animals were treated for BRDC was 17% heritable based on BRDC treatment records in this population and the probability that an individual was treated for **any** health related problem as 24% heritable. "Any" treatment would include treatments for foot rot, pink eye, bloat, etc. To put these values in perspective, the heritability of heifer pregnancy is often in this range as is the heritability of milk production in a number of beef cattle breeds. While not high, both would indicate that there is genetic variability associated with pathogen-associated disease traits.

Collection of treatment data on sire-identified feedlot cattle on a large scale would likely be problematic so our approach has been a two-pronged effort by both evaluating potential indicator traits and determining if DNA marker tests could be developed to predict susceptibility to BRDC.

Conclusion

In each of the three categories of health-related traits there is evidence for genetic control. In two of the three categories, selection tools have been successfully developed and marked genetic progress made. In the category of pathogen-associated disease, while genetic variability exists,

developing data collection systems and DNA marker tests will be critical to the delivery of selection tools to the beef industry.

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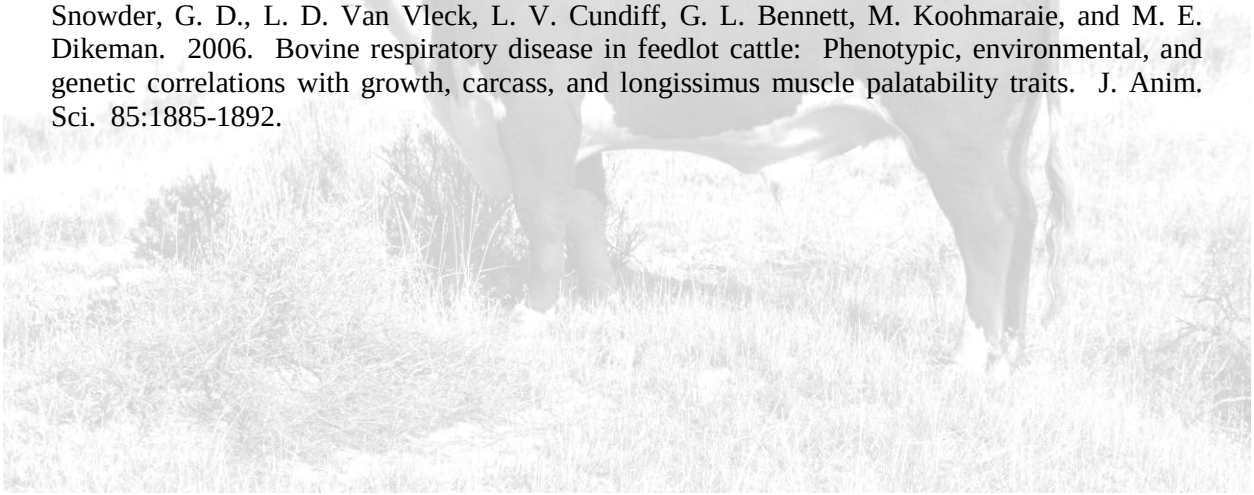

Integrating animal genomics with animal health: Genetics of vaccine response in cattle

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Introduction

Beef cattle breeders have successfully developed EPDs for a large number of traits, including average daily gain, carcass merit, stayability, calving ease, and feed efficiency. Despite these successes, a genetic prediction for animal health in beef cattle remains elusive. The reasons why a genetic prediction for animal health has not been developed are 1) limited recording and availability of phenotypic records on disease incidence to breed associations and 2) low heritability of disease traits. In spite of these challenges, several quantitative trait loci (QTL) associated with disease susceptibility have been mapped for pinkeye (Casas and Stone, 2006), Johne's disease (albeit in dairy breeds only) (Settles et al., 2009; Gonda et al., 2007), Bovine Respiratory Disease (Neibergs et al., 2011), and trypanosomiasis (Hanotte et al., 2003). Disease phenotypes in these studies have often been categorically defined: "healthy" or "non-infected" vs. "sick" or "infected". These QTL mapping studies have been valuable for unraveling the genetic architecture of disease susceptibility in cattle.

The main limitation with these studies is that the "healthy" or "non-infected" animals are assumed to be resistant to the disease. However, animals may be "non-infected" because they are 1) truly resistant to the disease, 2) not exposed to the pathogen that causes the disease, or 3) the diagnostic test result for infection was a false-negative, i.e., the animal was classified as non-infected when the animal was truly infected with the pathogen. Incorrectly classifying susceptible animals (i.e., infected) as resistant to disease (i.e., non-infected) results in lower heritabilities and decreased power for mapping disease loci.

An alternative phenotype for disease resistance is measurement of immune response to commercially available vaccines. When vaccinated, animals exhibit different immune responses; some animals mount a strong response to the vaccine, while other animals mount a weak response or do not respond to the vaccine at all. Can we increase the percentage of animals that mount a strong immune response to vaccination and thus would be better protected from disease? Traditionally, researchers have focused on improving vaccine response by developing more effective vaccines that protect a larger percentage of a herd. As a complementary approach, could we select for animals that respond more robustly to currently available vaccines? This approach would circumvent the limitation of incomplete disease exposure; all animals would be vaccinated with the same vaccine, thus ensuring uniform exposure. In addition to genetic selection for stronger vaccine response, identification of genes affecting vaccine response variation will also help vaccine manufacturers design more better vaccines.

My hypothesis was that vaccine response in cattle is a heritable trait and we can identify DNA markers associated with vaccine response. These DNA markers could then be used to develop a DNA test for vaccine response. Towards this goal, this paper reports completion of three objectives regarding Bovine Viral Diarrhea Virus (BVDV) vaccine response.

1. Comparison of three measures of the humoral response to BVDV vaccination: a) enzyme-linked immunosorbent assay (ELISA), b) serum neutralization (SN)-1, and c) SN-2.

2. Test whether sire of the calf was associated with BVDV vaccine response. If sire of the calf was associated with vaccine response, then this result would strongly suggest a genetic component to BVDV vaccine response variation in cattle.

3. Test whether a polymorphism in the leptin gene was associated with BVDV vaccine response. The leptin gene is involved in pathways that affect the immune response. This leptin polymorphism has also been associated with carcass and growth traits; if this polymorphism is associated with immune response, then producers could inadvertently be selecting for less immunity when selecting on this leptin polymorphism.

Materials & Methods

Experiment One: This experiment was designed to answer objective one. We collected 406 sera or plasma samples from 193 Angus or Angus-influenced calves that had been vaccinated for BVDV with either Bovi-Shield GOLD 5 (Pfizer, Inc.) or Onset 5 (Intervet). Sera and plasma samples were collected at the time of vaccination and 15-30 days post-vaccination. Calves were raised at the South Dakota State University (SDSU) Cow-calf Teaching and Research Unit (Brookings, SD) or the SDSU Cow Camp (Miller, SD). Calves had not previously been vaccinated for BVDV, although dams had been vaccinated.

Antibodies to BVDV were measured in sera and plasma by 1) BVDV-specific ELISA (Idexx Inc.), 2) SN-1, and 3) SN-2. The ELISA measures total BVDV antibodies regardless of whether antibodies can protect the calf from infection. The SN measures only BVDV-1 (SN-1) or BVDV-2 (SN-2) antibodies that can protect the calf from infection. The SN tests were completed by the Animal Disease & Research Diagnostic Laboratory at SDSU. The correlation between the ELISA, SN-1, and SN-2 was measured with a Spearman correlation coefficient.

Experiment Two: This experiment was designed to answer objectives two and three. Angus and Angus-influenced calves (n = 267) were sampled from three herds: 1) SDSU Cow-calf Teaching and Research Unit (Brookings, SD), 2) SDSU Cow Camp (Miller, SD), and 3) SDSU Antelope Research Station (Buffalo, SD). Calves were vaccinated with Pyramid-5, which includes BVDV-1 and BVDV-2, at 1-8 months of age. Calves had not previously been vaccinated for BVDV, although dams had been vaccinated. Blood samples were collected at the time of vaccination and 21-28 days post-vaccination.

The blood sample at time of vaccination was used for three purposes: 1) DNA isolation, 2) measurement of baseline BVDV antibodies present in blood at time of vaccination, and 3) identification of calves persistently infected (PI) with BVDV. Regarding purpose 2, calves would have absorbed BVDV antibodies from colostrum that could still be detected in the calves' blood. Regarding purpose 3, if a PI calf was identified, all of the calves in the same contemporary group would likely have been exposed to BVDV prior to vaccination and we would need to remove this group from the study. The post-vaccination blood sample was used to measure BVDV-specific antibodies circulating in blood post-vaccination. The BVDV antibodies were measured with a BVDV-specific ELISA (Idexx).

Vaccine response was measured by subtracting BVDV antibodies present at time of vaccination from BVDV antibodies present post-vaccination. At the SDSU Antelope Research Herd, sire of the calf was determined by parentage testing (GeneSeek, Lincoln, NE). At the other herds, dams were artificially inseminated and sire of the calf was determined by herd records. The leptin polymorphism was genotyped as described previously (Buchanan et al., 2002). Vaccine response was regressed on sire of the calf and leptin genotype, with covariate age at vaccination and fixed effects herd and gender also included in the linear model.

Results & Discussion

Objective 1: The ELISA was significantly, positively correlated ($P < 0.0001$) with SN-1 ($\rho = 0.809$) and SN-2 ($\rho = 0.638$).

As shown below (**Table 1**), ELISA S/P ratios are positively correlated with SN titers and can thus be used as an indicator trait for SN titers. The relationship between ELISA and SN is linear when titers are > 1:64. However, the relationship between ELISA and SN is not linear when titers are low. Still, low SN titers are indicative of low ELISA S/P ratios and we should be able to use the ELISA as an indicator trait for SN titers even at low antibody levels.

Table 1. Comparison of SN-1 and SN-2 titers with mean ELISA sample-to-positive (S/P) ratios.

SN Type 1		SN Type 2	
SN 1 Titers	μ ELISA S/P (± SD)	SN 2 Titers	μ ELISA S/P (± SD)
< 1:8	0.286 (± 0.271)	< 1:8	0.339 (± 0.298)
1:8	0.361 (± 0.263)	1:8	0.430 (± 0.253)
1:16	0.324 (± 0.166)	1:16	0.423 (± 0.263)
1:32	0.472 (± 0.208)	1:32	0.566 (± 0.333)
1:64	0.484 (± 0.242)	1:64	0.667 (± 0.430)
1:128	0.631 (± 0.254)	1:128	0.980 (± 0.536)
1:256	0.933 (± 0.475)	1:256	1.001 (± 0.592)
1:512	1.151 (± 0.454)	1:512	1.255 (± 0.577)
1:1024	1.388 (± 0.392)	1:1024	1.410 (± 0.506)
1:2048	1.563 (± 0.353)	1:2048	1.552 (± 0.465)
1:4096	1.797 (± 0.489)	1:4096	1.780 (± 0.411)
1:8192	2.084 (± 0.314)	1:8192	1.883 (± 0.793)

Objectives 2-3: No PI BVDV calves were found. Sire of the calf was significantly associated with vaccine response ($P < 0.05$). Because vaccine response was heritable for other vaccines in cattle (O'Neill et al., 2006) and in humans (Kimman et al., 2007), these results strongly suggest that BVDV vaccine response is heritable in cattle. Therefore, it should be possible to identify DNA markers associated with BVDV vaccine response which can be used for genetic selection. We chose not to estimate heritability for BVDV vaccine response with this data because the estimate would not be precise given the small number of calves in the study.

The leptin polymorphism was not associated with BVDV vaccine response ($P = 0.26$). Selecting for favorable leptin alleles should have no impact on humoral BVDV vaccine response.

Implications

This study is the first step towards development of a DNA test for vaccine response that producers could use to select for healthier cattle. With the development of dense single-nucleotide polymorphism genotyping panels (e.g., 850K SNP, 50K SNP), the number of DNA markers found to be associated with economically important traits should increase substantially throughout this decade. For animal health traits, the limiting factor will now be collection of a sufficient number of phenotypes on animal health that can be used for DNA testing. For this reason, development of a DNA test for vaccine response will be a long and laborious process. Additionally, many questions remain unanswered:

1. What is the genetic correlation between vaccine response and disease susceptibility?

2. How should vaccine response be measured? Should we focus on measures of the humoral (antibody) immune response, the cell-mediated immune response, or both?

3. What is the genetic correlation between vaccine response and other economically important traits?

4. Which DNA markers are associated with vaccine response? After discovery, these associations will need to be confirmed in an independent gene mapping population before use.

5. How can we best transition from discovery of DNA markers associated with animal health to implementation of a tool useful for producers for making selection decisions?

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Environmental and management factors influencing BVDV antibody levels and response to vaccination in weanling calves

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Summary

Vaccination has many benefits for disease prevention and overall health status of animals. Not all animals respond equally to vaccinations. A number of factors can be shown to influence a young animal's response to vaccination. Calves with more maternal antibodies at the time of vaccination have poorer immune response. The level of maternal antibodies at the time of vaccination is influenced by the amount of passive immunity transfer obtained via colostrum in the first 24 hours and the subsequent loss of maternal antibodies over the period up until vaccination. Younger dams appear to supply fewer passive antibodies to their calves and these maternal antibodies from younger dams appear to degrade at a faster rate than those from older dams. The level of response achieved in vaccinated calves varies by calving season. Vaccination during periods of high stress, such as weaning, has shown negative impacts on response. Further, calf age impacted the ability of a calf to mount an antibody response. Calves needed to be at least 130 days of age to elicit a positive response to vaccination. Collectively, these data suggest ranchers may be able to improve the value of vaccination by avoiding this activity at weaning and by consideration of the age of the dams, and the age of the calves at vaccination.

Introduction

Bovine Respiratory Disease: Bovine respiratory disease (BRD) has the greatest incidence among feedlot diseases and has the largest negative economic impact, with an estimated cost of $750 million annually, to the feedlot industry (Holland et al., 2010). It has been characterized as a complex disease that involves environment, stress, and infectious pathogens (Step et al., 2009). The viral agents most often associated with BRD are bovine viral diarrhea virus (BVDV), bovine respiratory syncytial virus (BRSV), bovine infectious rhinotrachetious (BIR), and parainfluenza 3 (PI_3) (Salt et al., 2007). BRD is seldom caused solely by a viral pathogen, but most often is the result of a secondary bacterial infection, which resulted due to a weakened immune system as a consequence of the viral pathogen infection (Salt et al., 2007).

Vaccination: Vaccination is currently used as a primary method for prevention of respiratory disease. Vaccination has been shown to improve animal health and productivity by reducing disease incidence as animals move through production phases. Optimization of vaccination protocols to decrease disease prevalence provides an opportunity to reduce these losses. It has been shown that vaccination of weaned cattle prior to arrival into the feedlot can prevent infectious diseases that may lead to the onset of BRD (Kirkpatrick et al., 2008). While the practice of vaccination has been adopted in many production systems, a protective response from the vaccines is still necessary for disease prevention.

Maternal Antibodies: Newborn calves passively acquire antibodies from their dams via consumption of colostrum immediately after birth. However, factors such as dam age, quality and quantity of colostrum, and timeliness of colostrum consumption may influence the amount of maternally derived antibodies present in the circulatory system of a calf. As a calf's immune system is not fully developed at birth, maternal antibodies are important for prevention of disease, such as infection of BVDV shortly after birth. However, passively acquired antibodies have been shown to block the ability of the calves' immune system to mount an antibody response to

vaccination, and therefore may need to have decreased to a sufficiently low level in order for calves to respond to vaccines (Menanteau-Horta et al., 1985). There is a period of vulnerability, during the period that maternal antibodies have regressed up until the time vaccination has induced a sufficient level of protection. This vulnerability period impacts a manager's decision about when to vaccinate calves to elicit a protective response (Endsley et al., 2003). Therefore, the age of dam, total passive immunity transferred, and the maternal antibody decline rate may be important factors to consider when developing a vaccination protocol.

Stress: There have been a number of studies that have shown that stress has deleterious effects on antibody development, growth performance, and carcass quality in calves (Niekamp et al., 2007; Richeson et al., 2008; Salak-Johnson, 2007; Step et al., 2008). Some high stress periods have been identified as weaning, transportation, de-horning, castration, bunk breaking, and commingling (Elenkov, 2002). Weaning has often been incorporated with vaccination to reduce labor needs. However, this may have detrimental effects on an animal's ability to respond to vaccinations. Therefore, minimizing stress at the time of vaccination may likely give the best return on vaccine use. However, this may not always be a viable management option.

Vaccination of cattle has been considered a standard management procedure for disease prevention, and remains one of the most effective methods for disease prevention. There are environmental and genetic factors that contribute to an animal's ability to respond; both are of interest for improved immune response (O'Neill et al., 2006; Richeson et al., 2008). There are management factors that can be controlled by producers such as, but not limited to, induced stress, calf age at vaccination, and animal nutrition, which can enhance or impede the vaccine response of calves (Bagley, 2001). While vaccination is a disease prevention method, animals must develop a protective response from the vaccine in order to actively protect against pathogens. The goal of this project was to develop vaccination management recommendations, which increase the effectiveness of vaccinations. In this study, weanling calves were evaluated to identify factors that effect maternal antibody transfer and persistence in the calf along with environmental factors that impact an animal's ability to respond to vaccination.

Materials and Methods

Sample Collection: To evaluate response to BVDV type II vaccination, data and serum samples were collected from 1,012 purebred American Angus calves from the Iowa State University breeding project at the ISU McNay Research and Demonstration farm. Calves were born in 2007, 2008, and 2009 with 334, 354, and 324 calves born in each year, respectively. The cow herd was managed in two calving seasons with 380 calves born in the fall season and 632 calves in the spring season. Animals were vaccinated using a standard two-shot protocol, with shots administered approximately three weeks apart, as suggested by the vaccine manufacturer. All calves in this study were vaccinated with the recommended 2cc dose of Pfizer Bovisheild Gold-5®. In addition to response to BVDV II vaccination evaluation, the effect of wean stress on the ability of calves to respond to vaccination was incorporated. Approximately half of the calves in each year/season were weaned at initial vaccination and the other half of the calves were weaned at booster vaccination, with 512 and 500 animals being weaned in each group, respectively (**Figure 1**). To evaluate antibody levels and response measurements, serum samples were collected at four time points. The first sample was collected three weeks prior to the initial vaccination (**pre-vaccination**) to quantify the level of maternal antibodies present in the calves and enable assessment of maternal antibody loss over a period of time prior to vaccination. Three other samples were collected: just prior to the initial vaccination (**initial**); at booster vaccination (**booster**); and three weeks post booster vaccination (**final**) (**Figure 1**). Serum was analyzed using a viral neutralization assay to quantify BVDV II neutralizing antibodies. These neutralizing

antibodies were the BVDV II specific antibodies that were present in the serum that were capable of attaching to the virus and preventing infection, this was done using a serial dilution of individual calf's serum. The highest dilution of serum that carried enough antibodies to protect against the virus was reported as a titer score. The higher the titer score the higher the level of antibodies present in the serum of a calf, which should equate to an increased protection against viral infection.

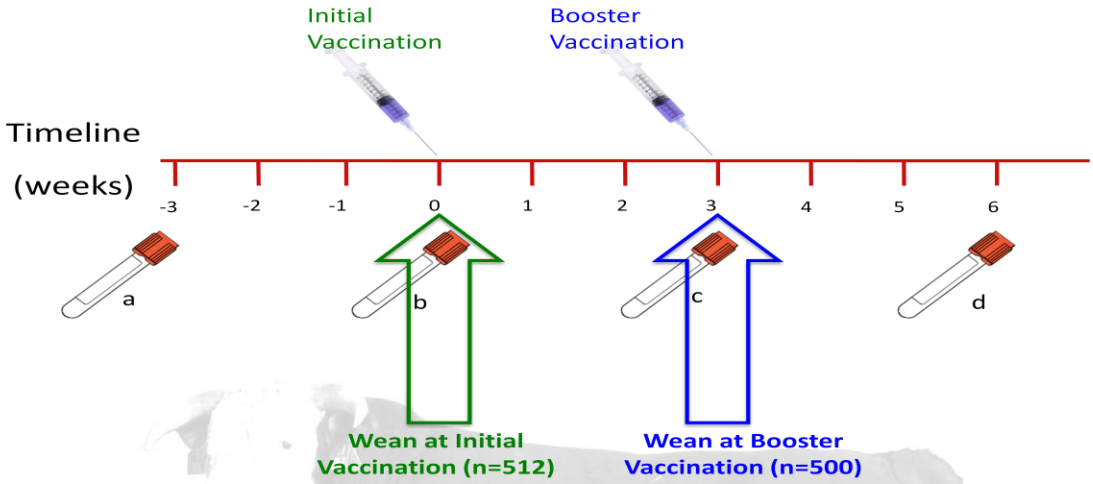

Figure 1. Diagram of serum sample collection, vaccination timing, and weaning timing. The syringes at week 0 and 3 indicate time when vaccine was administered to calves. The collection tubes indicate the four serum collection time points. **a**) Pre-vaccination antibody level (n=615). **b**) Antibody level at initiation of the vaccination protocol (n=1,012). **c**) Antibody level in calves 3 weeks after the initial vaccination (n=1,012), i.e., response to initial vaccination and at booster. **d**) Final antibody level achieved following the 2-shot protocol (n=1,012). The green arrow indicates that half (n=512) of the calves were weaned at initial vaccination. The blue arrow indicates the time of weaning for the second half (n=500) of the calves.

Variable Calculations: Pre-vaccination and initial titer levels were used to evaluate maternal antibody transfer and rate of maternal antibody regression. Initial titer was used with pre-vaccination titer to determine the **rate of maternal antibody decline** (**Figure 2**). Maternal antibody decline was calculated as the difference between initial and pre-vaccination titers divided by the number of days between the two samples.

Final titer was used to evaluate total antibody development of the animal three weeks post booster vaccination (end of the vaccination protocol). Three response variables were also evaluated: **response to initial vaccination**, **response to booster vaccination**, and **overall response**. Response to initial vaccination was calculated as the difference between the booster and initial titers. Response to booster vaccination was calculated as the difference between final and booster titers. Overall response was calculated as the difference between initial and final titers (**Figure 2**).

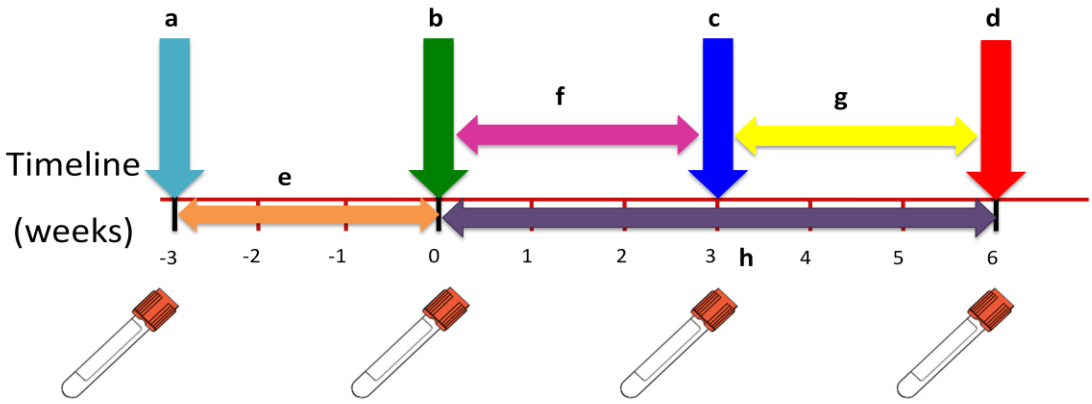

Figure 2. Collection tubes represent the times of serum collections and therefore the titers at these points. The arrows indicate the evaluated variables, a) pre-vaccination titer level, b) initial titer, c) booster titer, d) final titer, e) decline of maternal antibodies, f) response to initial vaccination, g) response to booster vaccination, h) overall response.

Results

Environmental Factors: Effects of: dam age, calf age, circulation of maternal antibodies, year by season, time of wean stress, and gender were evaluated for their influence on antibody levels and response to vaccination variables. Calf gender was not found to influence antibody levels or affect overall response to vaccination. However, there was a significant difference seen in year by season groups.

Means and Correlations: Pre-vaccination and initial serum antibody levels were evaluated for age of dam effects, specifically for differences in maternal antibody transfer. Additionally, rate of decline of maternal antibody decline was evaluated on dams of different ages. **Table 1** has the observed means with standard deviations for titer score (base 2 log), calf age (days), and weight (lbs) for the four collection time points (pre-vaccination, initial, booster, and final). These means are then broken down by season, as seasonal differences have been observed.

Table 1. Means for titer level, calf age, and calf weight at four serum collection time points, which were collected ~21 days apart. Data are also reported by calving season, spring or fall.

Collection Time	N	Titer Score (base 2 log)	SD	Age (days)	SD	Weight (lbs)	SD
Pre-vaccination	615	4.36	±2.24	99.1	±26.6	276	±67.5
Initial	1,012	3.05	±2.25	133	±30.4	327	±84.6
Booster	1,012	2.56	±1.86	154	±30.7	376	±92.9
Final	1,012	4.01	±1.84	176	±29.5	426	±96.1
Spring-born							
Pre-vaccination	303	2.86	±1.57	115	±21.7	292	±72.6
Initial	632	2.03	±1.83	149	±24.5	359	±80.9
Booster	632	1.81	±1.50	170	±25.4	406	±95.6
Final	632	4.28	±2.06	191	±25.5	456	±98.5
Fall-born							
Pre-vaccination	312	5.82	±1.78	83.7	±21.4	261	±58.0
Initial	380	4.74	±1.82	107	±19.5	272	±58.1
Booster	380	3.80	±1.73	128	±17.9	327	±62.8
Final	380	3.56	±1.30	152	±17.1	377	±67.6

Calf age (days), age of dam (years), and weight (lbs) were correlated with pre-vaccination, initial and final antibody levels to evaluate their relationships. Calf age had a higher correlation with pre-vaccination and initial antibody level than did calf weight (**Table 2**). Thus, calf age may be the more informative indicator of maternal antibody levels in the calf's circulatory system. Additionally, age of dam was also highly correlated with both pre-vaccination and initial antibody levels. Therefore, there may be differences in maternal contributions depending on the age of the dam.

Table 2. Correlations for pre-vaccination, initial, and final antibody (titer) levels with calf age, dam age, or calf weight.

Collection Titer	Pre-vaccination	Initial	Final
Calf Age	-0.626	-0.621	0.315
Age of Dam	0.602	0.531	-0.063
Weight	-0.230	-0.363	0.266

Maternal Antibody Acquisition and Decline: Pre-vaccination and initial antibody levels were representative of the amount of passive antibodies that were acquired by calves. It is expected that this passively acquired immunity will erode over time. By including calf age as a covariate for pre-vaccination or initial titers, a generalized rate of maternal antibody decline was estimated and the level of maternal antibody transferred at birth was then estimated. The general maternal antibody decline can be seen in **Figure 3**, as there is a decline between pre-vaccination and initial antibody levels.

Pre-vaccination and initial antibody levels, after correction for calf age, were significantly influenced by dam age (**Figure 3**). There was a significant difference in the transfer of passive immunity for each dam age group for two to five year old dams, but once cows reach five years of age there were no further differences in the amount of maternal antibodies transferred to the calf (see **Figure 3**). The improvement in passive antibody transfer seen across dam age could be due to differences in colostrum quality and quantity that was available to calves and timeliness of colostrum intake by calves (i.e. how quickly the dam mothered up the calf to nurse).

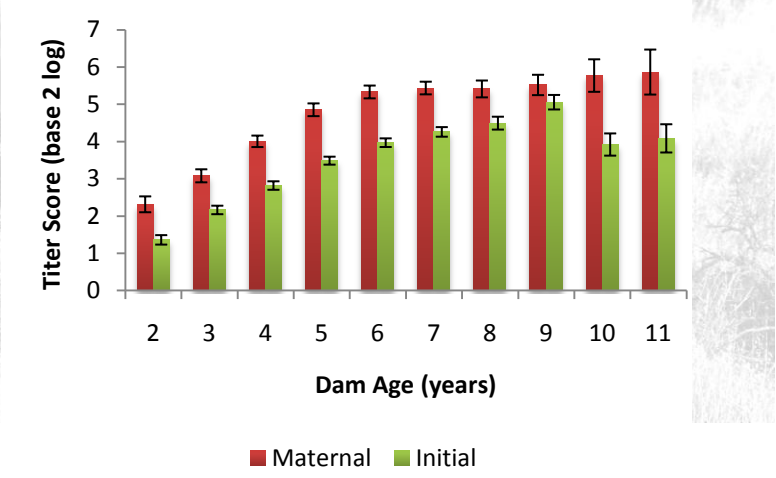

Figure 3. LSMean titer scores for dam age for pre-vaccination and initial antibody levels.

Differences in animal specific maternal antibody decline rate were evaluated by age of dams in this population. The rate of maternal antibody decline in calves from younger cows was faster than the rate of decline observed in calves from older dams when year by season, age of dam, calf age, and pre-vaccination titers were accounted for (**Table 3**).

Recognizing that two-year old dams have transferred fewer maternal antibodies to their offspring, their calves would potentially reach negligible levels of maternal antibody at a younger age and therefore be vulnerable to a natural infection at a younger age than calves from older dams. Thus, calves from younger dams may need to be vaccinated at a younger age to provide them with adequate protection against viral infection.

Table 3. LSMean for rate of decline of maternal antibodies by age of dam. Estimates with different superscript (a,b,c) are significantly different at P<0.05.

Dam Age (years)	Titer Decline Rate (Titer/day)
2	-0.061 (±0.006)^{bc}
3	-0.051 (±0.005)^{bc}
4	-0.045 (±0.004)^{ab}
5	-0.046 (±0.005)^{bc}
6	-0.033 (±0.005)^{ab}
7	-0.023 (±0.005)^{a}
8	-0.022 (±0.006)^{a}
9	-0.036 (±0.008)^{ab}
10	-0.045 (±0.012)^{ab}
11	-0.023 (±0.017)^{ab}

Maternal Antibody Interference: Maternal antibodies serve protective roles in young calves with immature immune systems, but high levels of maternal antibodies at the time of vaccination can impede the development of the specific immune system in calves.

Figure 4 displays mean antibody level (titers) by age of dam across the four collection time points (pre-vaccination, initial, booster, and final antibody levels). Calves from younger dams had lower maternal antibody levels at pre-vaccination. High maternal antibody levels can block/inhibit the immune systems ability to respond to vaccination. Maternal antibodies present at the time of vaccination were shown to inhibit overall response to vaccination by -1.2 titer scores for every 1-point titer increase in circulating maternal antibodies at initial vaccination. Therefore, at day 0, when calves were administered the initial vaccine, those calves that were

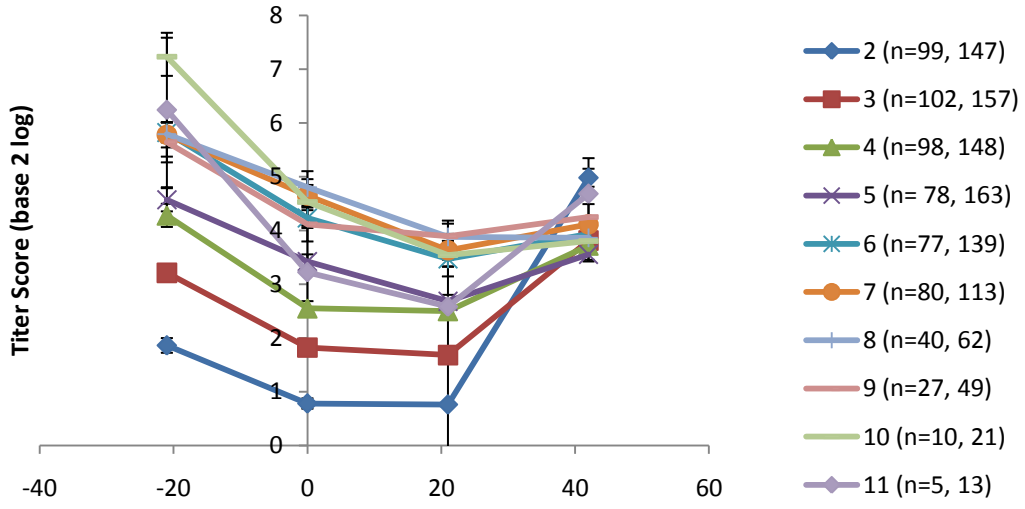

Figure 4. Average antibody level (titer scores) for the four collection time points (-21, 0, 21, and 42 days) by dam age (2 through 11 year old dams). Number of calves for each dam age is listed in parentheses following the dam age label, with sample number at pre-vaccination followed by the number of calves for the three subsequent collection time points.

from younger dams had lower initial titer scores and were more likely to develop and antibody response to vaccination; thus, enabling those calves to show a greater overall response to vaccination.

Calf Age: Beyond age of dam, calf age also significantly affected pre-vaccination and initial antibody levels. To look at the age affects on antibody level over time, calves were grouped by age in 21-day intervals (**Figure 5**). Not surprisingly, younger calves tended to have higher initial antibody levels compared to older calves, while older calves had a higher antibody level at the final response and had a greater overall response to vaccination (see **Figure 5**). The ability of older calves to mount a high overall response may be explained by the removal of more maternal antibodies that could inhibit a response to vaccines. These results indicate that vaccinating calves at an older age will allow them to mount a larger positive response to vaccination.

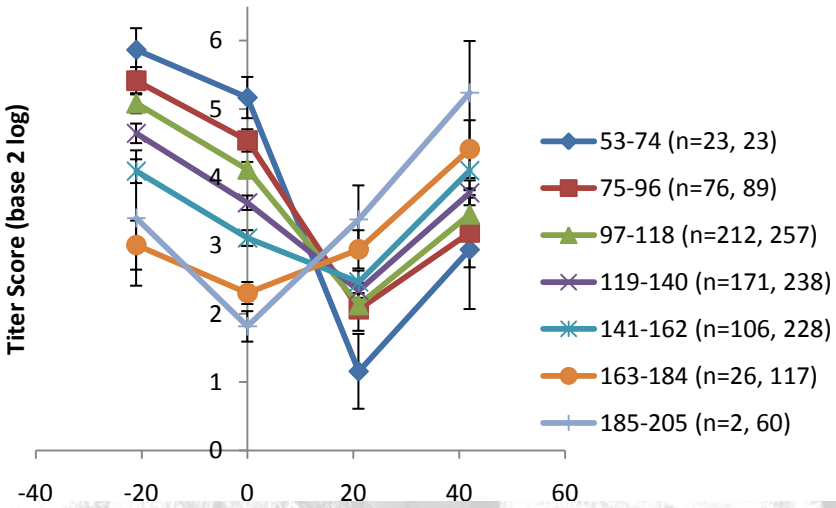

Figure 5. LSMean for calves grouped by 21-day intervals by age for maternal, initial, booster, and final antibody titer comparison, with the sample number listed by maternal titer, initial titer. The older calves show less circulating maternal antibodies at the beginning of the vaccination protocol and higher final response to vaccinations.

As another method to evaluate the effect of calf age on time vaccination, calves were separated into non-responders, low responders, and high responders. The LSMeans for age at initial vaccination for these response groups were then estimated (**Table 4**). Non-responder calves had a negative or zero overall response, with titers less than zero. Low responder calves had overall

Table 4. LSMean for age at vaccination by response to vaccination group: non-responders, low responders, and high responders. Superscripts indicate significant differences in ages at $P<0.05$. Year by season has been accounted for in the age at vaccination mean.

Response Group	Age at Vaccination (days)	Mean Overall Response (base 2 log)
Non-Responders	123.1 (±0.856)[a]	-1.776 (±0.987)
Low Responders	129.5 (±1.089)[b]	1.680 (±1.217)
High Responders	135.5 (±1.445)[c]	5.981 (±1.217)

response titers from zero to five; and high responders were calves that had overall response titers (antibody levels) of five or more. Forty-nine percent of the calves were classified as non-responders, 28% were classified as at low responders, and 23% were classified as high responders. There were significant differences by response group in their ages at vaccination. In this study, the calves that achieved a response to the vaccination were approximately 130 days old at the time of the initial vaccination vs. 123 days old for.

Weaning Stress Interference: Periods of high stress are known to suppress the immune system and thereby increase the risk of disease during these elevated stress periods (Salak-Johnson, 2007). Weaning has been identified as a high stress period in cattle that could affect the immune response (Niekamp et al., 2007). This immune suppression, caused from weaned calves, affects antibody response in vaccinated cattle. Therefore, vaccination of calves in a stress free environment would be the ideal management practice. However, in many commercial operations, this is not a practical management option and weaning and vaccination occur simultaneously. Therefore, it has been shown that timing of weaning can have significant effects on an animal's ability to respond (**Figure 6**; Niekamp et al., 2007). This effect of wean-stress timing was evaluated for the three response variables. Two wean-stress times were identified, weaning at the initial vaccination and weaning at the booster vaccination, as these may be typical management practices applied in production settings. **Figure 6** illustrates the effects of these two wean-stress periods. Once year and season differences are accounted for, animals weaned at the initial vaccination elicited a higher overall response than calves weaned at the booster vaccination. Therefore, if a high stress activity, such as weaning, was implemented at time of vaccination, there is a greater overall response from those calves that experienced the stress at the initial vaccination.

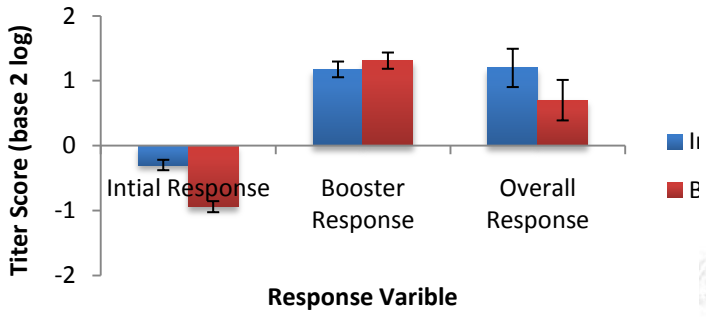

Figure 6. LSMean titer scores for the two weanstress periods for initial response, booster response and overall response. Animals weaned at initial vaccination elicit a greater response to vaccination than animals weaned at booster vaccinations.

Conclusion

Timing of vaccination is very important in order to induce a protective antibody response in weanling calves. Optimal timing of vaccination is influenced by both age of dam and calf age. Increases were seen in the amount of antibody transfer for each dam age group from two to five year olds, once cows reached five years of age no significant differences in maternal antibody transfer were seen. The rate of maternal antibody decline is also dam age dependent, with younger cows having a faster antibody decline rate. The amount of maternal antibodies transferred and the rate of decline will both influence the optimum calf age for vaccination to enable a positive response. Before a vaccination can have a positive response, maternal antibodies must have declined to a level low enough not to immediately neutralize antigens from vaccines. Therefore, calves from younger dams would be eligible to be vaccinated at a younger age than calves from older cows to avoid periods of infection vulnerability. This age at which to vaccinate calves was also influenced by passively acquired immunity. As maternal antibody level

needs to decline to a sufficiently low level so that an immune response can be elicited response. However, calves need to be vaccinated before they enter into a vulnerable period for infection. Stress can negatively impact immune response to vaccination, however if weaning stress and vaccination occur simultaneously, calves that were weaned at the initial vaccination saw an increased overall response.

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Measuring feed efficiency in beef cattle - minimizing inputs across the whole production chain

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Introduction

The profitability of any enterprise is determined by the difference between the input costs and the revenues from sales. In growing beef cattle the major input cost is that of feed, that may be as much as 70% of the total fixed costs (Herd et al. 2003). Clearly, a reduction in the cost of feed or the amount of feed required to produce a marketable animal is a key determinant of profitability both in the cow-calf sector and in the feedlot. Therefore, there has been a growing interest in feed efficiency particularly in the feedlot sector, made more important by the increasing cost of feed due to a number of factors including the growing biofuels sector.

Traditional measures of feed efficiency have been a simple comparison of the amount of feed consumed compared to the growth achieved by animals, expressed as gain to feed ratio (**G:F**) or the inverse feed conversion ratio (FCR). These measures are relatively easy to measure on individual animals or pens of animals but suffer from a number of issues. The trait is highly correlated with growth and confounded with the maturity patterns of animals (Kennedy et al., 1993; Archer et al., 1999). As a selection tool, G:F has the potential to increase growth rate in young animals. It could also result in substantial increases in mature cow size as well as in the feed intake of the cow herd thereby resulting in negative impacts on the overall production system efficiency (Dickerson, 1978).

An alternative to G:F was proposed by Koch et al. (1963). Residual feed intake (RFI) is the difference between an animal's actual intake and its expected intake based on its body weight and growth rate over a particular period. It has been shown to have great potential as an index of feed efficiency for beef cattle (Archer et al., 1999; Arthur et al., 2001a). The trait is moderately heritable with estimates ranging from 0.16-0.58 (Herd and Bishop, 2000; Crews et al. 2003) and considerable variation within groups of cattle tested has been observed (Herd and Bishop, 2000; Basarab et al. 2003). A great deal of focus has been given to RFI over the last 15 years to evaluate its utility as a breeding or management tool in the beef industry.

Residual Feed Intake and Correlated Traits

Residual feed intake is generally calculated as the difference between the actual Dry Matter Intake (DMI) of each animal and its predicted feed intake, which can be calculated either using a phenotypic regression (RFIp) or genetic regression (RFIg) of on DMI on weight (metabolic body weight) and Average Daily Gain (ADG) (Arthur et al. 2001a,b; Crews 2005). Thus, individual animal feed intake and frequent weight measurements have to be collected in order to estimate RFI, which has made it difficult to estimate RFI on large numbers of animals. Recent technology has improved on this, for example the Growsafe equipment widely used in North America, however the cost of phenotypic measurement remains a hurdle to widespread adoption.

A number of studies have looked at correlated traits, particularly carcass and meat quality, resulting in the finding of a small effect on general fatness (Basarab et al. 2003; Nkrumah, 2007). More recently, difficult-to-measure traits such as bull and cow fertility have been investigated (Basarab personal communication), however to date the investigations are not complete as the

number of animals tested remains low.

Factors Confounding RFI Measurement

More recently, a number of factors including diet, season of testing and animal maturity have been shown to influence RFI estimates in growing beef cattle. Mujibi et al. (2010) reported seasonality effects on feed intake and efficiency. Although correlations were found between feed intake and temperature, wind speed and humidity, the nature and the magnitude of the correlations differed between fall-winter and winter-spring feeding periods. More detailed work is required to better understand these effects.

Durunna et al. (2011) examined the effect of grower versus finisher diet on the ranking of steers when measured for RFI. More than half the steers tested changed their RFI estimate by more than 0.5 Standard Deviations (SD) or 0.20 kg DM d^{-1} when measured on grower and finisher diets sequentially (Figure 1). The rank correlation between the first and the second period in these steers was 0.33 but smaller re-ranking (rank correlation = 0.42-0.44) was seen in the control animals maintained on grower or finisher diets in the two periods and measured for RFI in each period. This suggests other environmental or developmental effects such as animal maturity are in play. Interestingly, much better correlations were seen between RFI measured over the combined testing periods and RFI measured in the second period (Durunna et al., 2011). This might suggest that the accepted testing period of 63-90 days for estimating RFI might be too short, or that testing young animals may not reflect the overall RFI particularly in circumstances where large seasonal effects or different diets come into play.

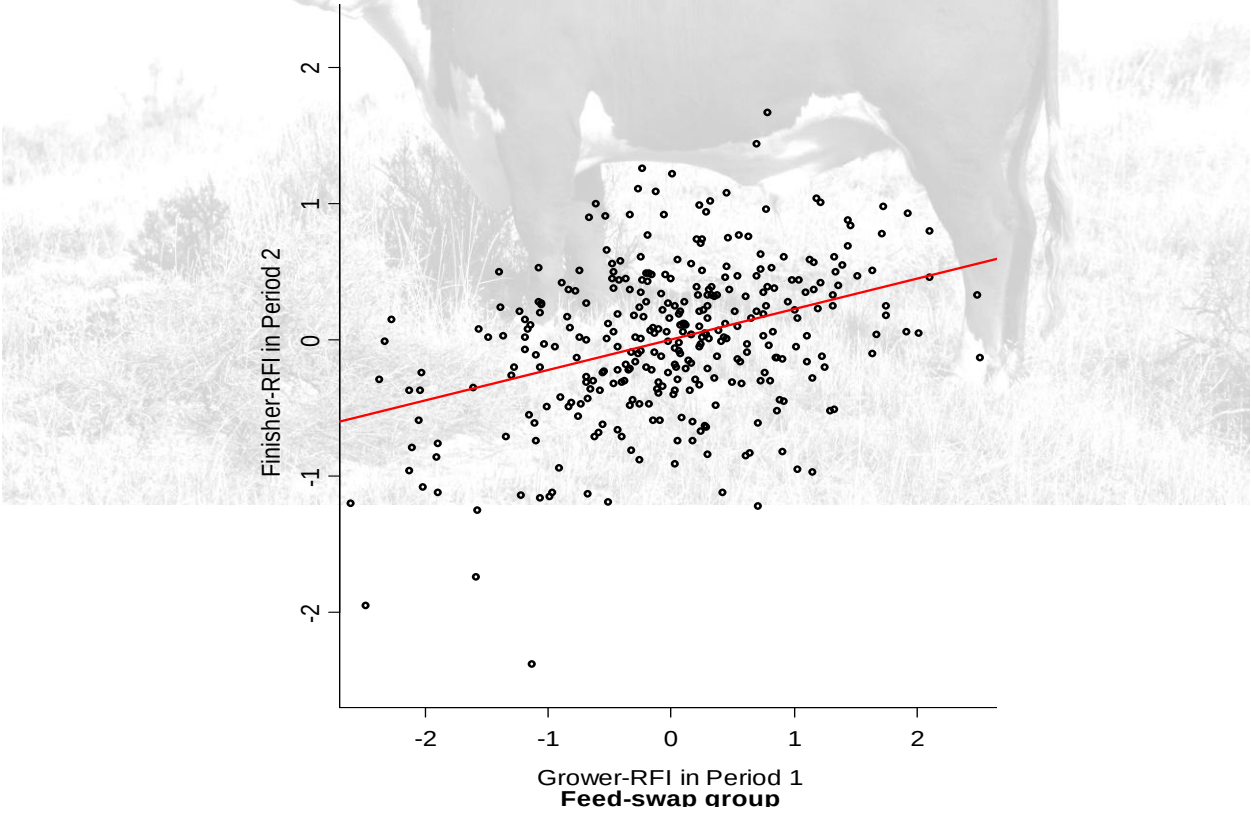

Figure 1. RFI values measured sequentially on grower diet (X-Axis), and finisher Diet (Y-Axis). (Durunna pers. Communication)

Molecular Markers for Feed Intake and Efficiency

The cost and difficulty in measuring RFI makes the trait a strong candidate for marker assisted selection. Clearly if the cost of a gene test is below that of the direct phenotypic measurement and the estimate can be made at an earlier age, selection of breeding animals that are superior for the trait could be greatly enhanced.

A number of studies have attempted to develop marker panels for feed efficiency in cattle (Barendse el al. 2007, Nkrumah et al. 2007a, Sherman et al. 2008, Moore et al. 2009). The common factor with all of these studies is that the markers have generally performed better in the population used in the discovery step than in subsequent populations used to validate the markers. That being said, some markers have been validated biologically across multiple populations and are being sold commercially to cattle producers.

The variability of the amount of the genetic variation explained by any one marker panel across different populations makes it difficult to assess the economic value of the markers in any one circumstance. Certainly, a better estimate of the biological and economic potential of any marker set can be achieved if the application is restricted to a single population or breed (Rolf et al. 2010), but this limits the applicability of the technology in an industry made up of multiple breeds or breed crosses.

The different breeds of cattle have been genetically separated for long enough that trait associated markers that lie somewhat distant along the chromosome to the causal mutation may not tag the advantageous causal allele in all the breeds. In other words when summing up the effect of a marker panel, although each marker may tag a positive effect in the discovery population, in a different population or breed, some markers may now tag a mixture of positive and negative alleles diminishing the overall predictive power of the marker panel overall. In addition, some causal mutations may be invariant in some breeds making a particular marker redundant.

The solution for this is simple, but until recently unachievable. Simply increasing the density of the markers will ensure that a marker close enough to the causal mutation can be found in most if not all breeds. The development of a marker panel with 50,000 Single Nucleotide Polymorphisms (SNPs), the Bov50SNP chip (Matukumalli et al. 2009), meant that at least within breeds it was possible to develop predictive equations for numerous traits (Cole et al. 2009). The Bov50SNP chip however still does not have sufficient density of markers to work across breeds, providing a marker approximately only at 100,000 base pair intervals on each chromosome. Estimates of conservation of chromosome segments known as Linkage Disequilibrium or LD Blocks, would suggest marker densities at least 10 fold higher than this will be required to develop technologies that work across breeds (Gibbs et al. 2009).

Now with the availability of 600,000 and 700,000 SNP panels it is now possible to test this proposition. The issues around equivalence of phenotype discussed above however remain to be resolved.

Conclusion

Selection for feed efficiency measured as RFI is becoming possible for some breeds of beef cattle. The major hurdles remain the cost of collecting the phenotype, ie. individual animal feed intake and weight gain, and the consistency of the phenotype measured considering environmental effects such as diet and season and possible confounding effects such as animal maturity.

Marker assisted techniques such as Whole Genome Selection using dense marker panels, or

derived smaller marker panels remains a maturing technology requiring some further validation in terms of the amount of genetic variation tagged in each population and hence the economic value of the marker panels to the producer. Recent advances in DNA marker technology in cattle give cause for optimism that useful marker panels that will have wider applicability across beef cattle breeds or populations are becoming available.

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Selecting for female fertility: What can be learned from the dairy experince

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Introduction

Genetic improvement programs in dairy cattle have until recently focused on increasing net profit by increasing gross income per cow, rather than reducing costs of production [1]. Strong selection pressure on yield traits coupled with management practices aimed at maximizing production may have resulted in undesirable side effects related to decreased fitness [2]. These concerns have been confirmed by work on reproductive efficiency done among others by Lucy [3] and VanRaden et al. [4]. There are strong motives for including reproduction in selective programs, both economical and welfare related [5].

Female fertility cannot be easily defined as a single trait as it comprises different aspects. Some of these aspects are related to the prompt resumption of cyclicity and the showing of recognizable estrous behavior, while others are related to the ability of the cow to become (and remain) pregnant with a limited number of inseminations [6]. In addition, cows should have good calving ability and give birth to viable calves [5].

A relevant body of literature now links selection for production to a loss of reproductive fitness, health, and longevity in several breeds [7], [8], and unsatisfactory reproductive performance is a primary reason for culling for the first three lactation in the USA dairy population [9].

Factors affecting cows' fertility

Several factors are responsible for good (or bad) fertility in cows. Although in the following section we have separated some for sake of simplicity it should be kept in mind that most of these elements are intrinsically related and exert some effect on each other.

Management: Management represents one of the factors with largest effect on female fertility. In a 2009 study Tsuruta and coworkers [10] reported differences in fertility parameters among large and small dairy operations. The authors found an average difference of 7 days in favor of large herds for calving to conception (days open), and days to first second and third service (17, 22, and 24 respectively). In contrast conception rates (overall, at first, second, and third insemination) were higher for smaller herds with advantages of approximately 5% in all cases. The largest influence exerted by management practices on fertility can be linked to the conditioning of cows around parturition. Negative energy balance (NEB) at the beginning of lactation is responsible for an increase in metabolic diseases, reduced immune function, and overall decreases in fertility [11]. Body condition scores (BCS) is the most easily applicable tool to monitor and manage the metabolic status of cows around parturition. Cows with low levels of BCS at parturition suffer from extreme NEB with a reduction of ovulation rate, increased calving to first insemination, and increased calving intervals [12]. Over-conditioned dry cows are more likely to suffer from ketosis and fatty liver, both of which may suppress immunity directly or through an excessive negative energy balance route [13]. Because of these inter-relationships, unfavorable energy balance in the

transition cow regularly results in cascade effects that increase the incidence of infectious diseases, production diseases, and consequently reduce fertility.

Environmental effects: Several environmental components affect female fertility. Among these heat stress is particularly significant. Summer heat stress is a main factor related to low conception rate in high producing dairy herds in warm areas worldwide [14]. Under heat stress, production and fertility decrease and animals have a decreased chance of survival [15]. Ravagnolo and Misztal [16] found for example, correlations between non return rate at 90 day and heat tolerance of -0.95. Furthermore, Garcia-Ispierto et al., [14] found that the likelihood of conception rate for Spanish Holstein Friesians increased significantly by factors of 1.48, 1.47, 1.5, and 1.1 for Temperature Humidity Indexes (THI) classes <70, 71–75, 76–80, and 81–85 on Day 3 before artificial insemination (AI), and by factors of 1.73, 1.53, 1.11, and 1.3 on the insemination day, for THI classes <70, 71–75, 76–80, and 81–85.

Incurrence of diseases: While in most cases disease losses are quantified through their direct costs associated to production loss, increased culling rate and treatment costs, their importance go beyond these direct effects and often involve the costs related to a decrease in fertility.

Mastitis: Mastitis is an inflammation of the mammary gland and is responsible for reduced milk production and milk quality, increased involuntary culling rates, and discarded milk [17]. Cows experiencing clinical mastitis before first postpartum artificial insemination (AI) have a greater days not pregnant (DNP) compared with uninfected cows [18]. Moreover, cows experiencing mastitis between the first AI and pregnancy confirmation have greater services per conception (S/C) and DNP compared with cows without mastitis [18].

Lameness: Lameness can be defined as an abnormal gait due to leg or foot problems [19] and includes several different foot lesions. Lameness has a detrimental effect on herd productivity, second only to mastitis [20]. Negative effects of lameness include a decrease in milk yield [21], [22] and fertility [23] and an increase in risk of culling [24].

Uterine diseases: Uterine diseases are a family of diseases (metritis, endometritis) associated with abnormal post-partum events. These diseases are associated with sub-fertility and infertility and are characterized by longer intervals from calving to first insemination or conception for affected animals, and more cows culled for failure to conceive in a timely manner [25]. As an example, LeBlanc et al. [26] showed that service conception rate was lower for cows with endometritis (29.8% vs. 37.9%), with longer median calving to conception interval (151 vs. 119 days) and with more diseased animals culled for failure to conceive (6.7% vs. 3.8%) than unaffected animals.

Parity: Several authors have reported a general decrease in fertility performance with increase of parity number. VanRaden at al., [4] reported phenotypic trends in days open from first to fifth parity from 1965 to 2000. For the period reported days open increased with parity order, with differences of approximately 20 days between first and fifth lactation. Similar results have been reported for number of inseminations [7], [27], [28].

Production level: High producing cows tend to be less fertile and this prolongs the length of calving interval as well as the rate of involuntary culling [29]. Genetic antagonism between yield and fertility is often indicated as the major factor leading to declines in reproductive performance [30], [31], [32]. This antagonism is related to higher energy utilization from the mammary gland in early lactation to sustain elevated production, leading to an amended hormonal and metabolic profile, which in turn exerts a negative effect on ovulation rates, estrous behavior, and embryo establishment [33]. Low fertility is therefore at least in part a manifestation of the cow's inability

to cope with the metabolic demands of high production.

Breed: Breed is a significant contributor to cow fertility. Campos et al., [34] reported differences in calving to conception and calving interval between Holstein and Jersey cows, with a difference in favor of the Jersey breed of 39 and 19 days for days open and calving interval, respectively. Similarly, Grosshans et al., [35] compared calving to conception and calving intervals between Holstein and Jerseys and found shorter intervals of 5 and 3 days in favor of Jerseys for days open and calving intervals, respectively. Inchaisri et al., [27] estimated the probability of success at first insemination in relationship to the proportion of Holstein or Dutch red and white genes present. Percentages of success ranged from approximately 37% for purebred Holstein to 43% for purebred red and white with a linear increase in success rate as a function of the increase of red and white genes. VanRaden et al., [4] reported values of Daughter Pregnancy Rate for Ayrshire, Brown Swiss, Guernsey, Holstein, Jersey and Milking Shorthorn calculated with a multi-breed animal model. Daughter pregnancy rate is one the measures of fertility reported by the USDA Animal Improvement Program Laboratory (AIPL), and represents the percentage of non-pregnant cows that become pregnant during each 21-day period. The authors reported average predictive transmitting abilities (1/2 of the Estimated Breeding Value) of, -0.5, 0.1, -0.8, -0.2, -0.3, +0.2, for the different breeds, respectively.

Breeding for increased fertility

Traits definition: A univocal definition of fertility is a complicated (and perhaps vane) exercise. Pryce et al., [31] describe fertility as "The accomplishment of pregnancy at the desired time", while Hyppanen and Juga [36] refer to it as "The ability to produce a living offspring during an economically and physiologically approved period". Darwash et al. [37] frame fertility as the "Ability of the animal to conceive and maintain pregnancy if served at the appropriate time in relation to ovulation". Finally, for Groen et al., [6] "Female fertility can be defined as the ability of the cow to return on heat within an acceptable period, to show the heat in a proper manner and to become pregnant with a minimum number of inseminations". Although several authors place more or less emphasis on some specific aspects of fertility, at least two main components can be readily identified [38]:

- ✓ The success at a particular event (insemination, pregnancy)
- ✓ The elapsed time to that particular event

The majority of traits currently measured and employed in selection programs fall in one of these two categories.

- ✓ *Conception rate:* Can be defined as the outcome (success/failure), for every insemination, validated by pregnancy check or calving.
- ✓ *Number of insemination to conception:* Is the number of services needed to achieve pregnancy.
- ✓ *Calving Interval:* Describes the difference, in days, between two subsequent calvings.
- ✓ *Interval from calving to first service:* Is the difference, in days, between calving and the next breeding.
- ✓ *Interval from 1st service to conception:* Is the difference, in days, between first and last service (validated by pregnancy check or subsequent parity)

To these general categories, more specific definitions can be added and additional parameters can be considered. For example, hormonal profiles can be employed in characterizing fertility.

Lamming and Bulman [39] recognized that "Progesterone profiling provides a more objective method for tracking reproductive events in dairy cows" and more recently, work on this area has been presented by Pollot and Coffey [40], and Petersson et al. [41], [42]. Direct measures of fertility are difficult to obtain and data quality is often a challenge. Therefore several correlated traits are often employed as proxy measures of fertility. Several authors have proposed the measure of energy balance as a reliable indicator of the fertility status of individual cows. Energy balance can be monitored directly or through indirect measures. The most widely used measure of energy balance in cows is the Body Condition Score (BCS), although more recently the use of milk parameters such as protein/fat ratio [43] and milk urea has been proposed [44]. A summary of the most common measures of female fertility is reported in Table 1.

Data structure: Several challenges arise from the use of fertility traits related to data quality and availability. Calving interval is the trait most easily measured and is only marginally influenced by data quality when compared to other direct measures of fertility such as conception rate or number of inseminations to conception. However, it is not available for individuals culled before subsequent calving for fertility or other problems, leading to overestimation of reproductive performance. Moreover, calving interval is a late measure of fertility as it is available almost one year after the beginning of estrus activity with a delayed publication of breeding values. Several alternative measures have been proposed as early-recording indicators for fertility [12].

Box 1: The challenges of selecting for fertility traits:

Biological:

- ✓A mixture of traits

Structural and logistics:

- ✓Data Availability
- ✓Data Quality

Modeling:

- ✓Binary/Ordinal
- ✓Unequal variance
- ✓Censoring

Selection:

- ✓Low h^2
- ✓Antagonistic effect on production traits

Non-return rate at 56 days after first service (NR56) is the most widely used trait in genetic improvement of fertility in dairy [45], [8]. An important limitation of this trait is that it considers successful all terminal services without the validation of a subsequent calving date. On the other hand, NR56 provides a fast evaluation for fertility where the subsequent calving has not (yet) occurred.

The use of direct measures of fertility other than calving interval could lead to more timely results in breeding programs, provided that phenotypic data are reliable and that they are modeled correctly. One of the major limitations with fertility traits is that female fertility is not fully represented by a single trait but it is rather a complex of traits including non-normal and categorical traits. Conception rate and the number of inseminations are categorical and highly skewed. The intervals (parturition-first insemination, first insemination-conception, and parturition-conception) are conceptually based on a categorical number of estrus cycles and are again characterized by a highly asymmetrical distribution. Furthermore, not all the cycles lead to an insemination (voluntary waiting period, non observed estruses, health problems, etc.), not all inseminations result in a conception (infertility), and not all conceptions lead to a parturition (abortions), thus confirming the complexity of defining reproduction efficiency.

Finally, the beginning and end of each estrus cycle are not regularly recorded at the population level and insemination and parturition information is sometimes lacking as well (censored data). Modeling the intervals in terms of number of potential 21-d cycles and the use of censored threshold models has been proposed to overcome some of these limitations [46].

Table 1. Fertility traits definition.

Trait	Variable	Definition
Success traits:		
Conception at *x* service	Binary [0/1]	The outcome of an insemination validated by calving data
Non-return at *n* days after *x* service (n=56-60-70-90)	Binary [0/1]	The outcome of an insemination validated by the occurrence of a second breeding within *n* days
Number of insemination to conception	Count [1,2…n]	The number of services needed to achieve pregnancy
Conception rate	Continuous [0…1]	1/INS
Non-return rate at *n* days after *x* service		1/NRn
Interval traits:		
Days from parity to first heat	Continuous (days)	The days from calving to the first observed heat (by farmer)
Voluntary waiting period	Continuous (days)	The number of days intentionally left by the farmer before the re-start of breeding
Days from parity to first service	Continuous (days)	The days from calving to the first service
Days from first service to conception	Continuous (days)	The days from the first to the successful service (or the last service if no calving is available)
Days from parity to conception	Continuous (days)	The days from calving to the successful service (or the last service if no calving is available)
Calving interval, in days	Continuous (days)	The number of days between 2 subsequent calvings
Endocrine measurement traits:		
Interval from calving to 1° luteal activity	Continuous (days)	Interval from calving to first luteal activity (2 subsequent measures of progesterone => 3ng/mL)
Average progesterone level	Continuous (ng/mL)	Expressed in ng/mL (during breeding period)
Cycle length	Continuous (days)	Interovulatory period
Luteal phase length	Continuous (days)	Interluteal period
Number of cycle per lactation	Count [1,2…n]	Derived by luteal activity over time
Delayed ovulation I	Binary [0/1]	The occurrence of a delay for >

Delayed ovulation II	Binary [0/1]	45d postpartum The occurrence of a delay for > 12d between 2 luteal phases
Delayed luteolysis I	Binary [0/1]	Delayed luteolysis during the first cycle with a persistent corpus luteum
Delayed luteolysis II	Binary [0/1]	Delayed luteolysis during subsequent cycles with a persistent corpus luteum
Incidence of silent heats	Binary [0/1]	Combining on-farm-recorded data and progesterone profiles
Days from first heat to first service	Continuous (days)	Combining on-farm-recorded data and progesterone profiles

Another issue concerning genetic aspects of fertility is that variance components might vary across parities. Several authors have reported heritability values estimated across lactations [12], [47], while other studies [45] reported different variance component estimates in the different parities and genetic correlations within the same trait measured on different lactation that were less than unity.

Heritabilities and correlations with other traits: For the reasons explained in the previous section many fertility traits are difficult to handle in parameter estimation and genetic evaluation. Most of the traits are analyzed either through linear or threshold models, although applications of survival analyses are not uncommon [48]. Models employed range from single sire models [49], to random regression animal models [50], single or multiple trait models [51] and with or without the specific modeling of censored data [49]. Whereas model complexity has increased exponentially over the last few years, heritability estimates for fertility remain relatively low, on average below 5%, mainly due to the large influence of management and environmental effects [5], which are not trivial to disentangle when evaluating fertility. A further aspect of heritability of fertility traits is represented by the limitedness of the conventional-recording fertility traits. When we move from conventional traits (e.g. days to first service) to other measures of fertility (e.g. days to first heat) the impact of genetic variance is much higher. Pryce [30] reported an heritability of 0.06 for the days to first service and 0.18 for the days to first heat. The difference between those 2 kind of traits derives by the interaction of other biological traits (e.g. the intensity at first estrous) and farmer decisions (e.g. voluntary waiting period) which can't be extrapolated from conventional recording. Thus, the heritability of fertility is rather higher if we shift to traits which are more representative of the cow physiology. But a national evaluation of fertility has to be based on large scale recording system, and the most of farmer-recorder data might be not reliable. In spite of low heritabilities though the phenotypic variation for most fertility traits is relatively large and provides a favorable opportunity for selection [52]. In the United States, DPR evaluations are available since 2003 and are currently calculated through an all breed animal model [53]. Heritability of DPR is currently estimated at approximately 4%. A summary of estimates of heritability of fertility traits as estimated by different authors is reported in table 2.

A summary of estimates of correlations between fertility traits and milk yield as estimated by different authors is reported in table 3. Correlations between fertility and production traits are generally negative [54], [55], [56], [57], [10], with values ranging between approximately 0.2 and 0.4 and increasing with the number of lactation as a consequence of the increased energy requirements with increased productions.

Table 2. Point estimates of heritability for different traits as reported by different authors

Author	Year	h^2	Trait	Structure
Abdallah and McDaniel.	2000	0.03	Calving to conception	Linear
Hou et al.	1981	0.01-0.21	Calving to first service	Survival
		0.008-0.12	Calving to Conception	Survival
Chang et al.	2004	0.03	Inseminations to Conception	Threshold
		0.04	Calving to conception	Linear
Pryce et al.	2001	0.001	Conception at first service	Linear
		0.18	Days to first observed heat	Linear
		0.06	Days to first service	Linear
Hodel et al.	1995	0.01-0.02	Non return rate 90 days	Linear
		0.02-0.03	Non return rate 90 days	Threshold
Veerkamp et al.	2001	0.07	Days to first service	Linear
		0.03	Calving Interval	Linear
Berry et al.	2003	0.02	Number of Inseminations	Linear
Muir et al.	2004	0.029	Non return rate 56 days	Threshold
González-Recio et al.	2006	0.04	Number of inseminations	Threshold
Wall et al.	2003	0.02	Number of inseminations	Linear
VanRaden et al.	2004	0.04	Pregnancy rate	Linear
Sewalem et al.	2010	0.017	Non return rate 56 days	Linear
		0.08	Calving to first service	Linear
		0.049	Calving to conception	Linear
Jamrozik et al.	2005	0.04	Non return rate 56 days	Linear
		0.09	Calving to first service	Linear
		0.07	Calving to conception	Linear
De Haas et al.	2007	0.08	Days to first insemination	Linear
		0.08	Days from first to last insemination	Linear
		0.04	Calving interval	Linear
		0.01	Number of services per conception	Linear
		0.01	Conception rate to first insemination	Linear
Schneider et al.	2005	0.037-0.056	Hazard of pregnancy	Survival
		0.04	Calving interval	Linear

Table 3. Estimated correlations between different traits and milk yield as reported by different authors.

Author	Year	R_g point estimate	Fertility trait	Production trait
Berger et al.	1981	0.47	Calving to conception	60-d Milk yield
		0.44	Number of inseminations	60-d Milk yield
		0.62	Calving to conception	305-d Milk yield
		0.62	Number of inseminations	305-d Milk yield
Hoekstra et al.	1994	−0.26	Non return rate 56 days	305-d Milk yield
Pryce et al.	1997	−0.19	Conception rate at first service	305-d Milk yield
Dematawewa and Berger	1998	0.55	Calving to conception	305-d Milk yield
		0.53	Number of inseminations	305-d Milk yield
Kadarmideen et al.	2000	0.41	Number of inseminations	305-d Milk yield
		−0.42	Conception rate	305-d Milk yield
Veerkamp et al.	2001	0.48	Number of inseminations	305-d Milk yield
		−0.49	Conception rate at first service	305-d Milk yield
Berry et al.	2003	Negative except in early lactation	Pregnancy rate	Test-day Milk yield
Muir et al.	2004	0.02	Non return rate 56 days	305-d Milk yield
González-Recio et al.	2006	0.63	Calving to conception	305-d Milk yield
		0.23	Number of inseminations	305-d Milk yield

Muir et al. [51] reported genetic correlations among different fertility traits for first lactation Holsteins. In their work, estimated genetic correlation for age at first insemination as heifer and 56 days non return rate as heifer was positive and small (0.08) while genetic correlation between age at first insemination as heifer and 56 days non return rate as cow was negative (−0.20). Non return rate as a heifer and as a first lactation cow were poorly related between themselves (0.22) but unrelated to calving interval. Higher, albeit small, correlations between reproductive performance traits were reported by other authors [58], [32].

De Haas et al., [59] reported correlations between fertility traits and body condition score. Correlation of days to first service with BCS was -0.42, while values of -0.62, -0.53 -0.27 and 0.60 were reported between BCS and days between first and last insemination, calving interval, number of services per conception, and conception rate at first insemination, respectively. Similar results were found by other authors [60], [61] .

Heringstad et al. [62], reported genetic correlations between disease occurrences and fertility traits. Correlation between number of clinical mastitis and services to conception (with censoring) were estimated to be 0.21. Furthermore, estimated correlations of 0.15, 0.07, 0.20, -0.34, 0.13, 0.18 were reported by the same author [63] between clinical mastitis and calving to first insemination interval, clinical mastitis and non return rate at 56 days, between ketosis and calving to first insemination, ketosis and non return rate at 56 days, and between retained placenta and calving to first insemination, and retained placenta and non return rate at 56 days, respectively.

Conclusion

Reproductive performance is a major determinant of farmers' profitability in dairy. Inadequate reproductive performance increases involuntary culling, reduces overall production and lowers calves per cow in a year increasing production costs and ultimately decreasing the farmer's profit. The antagonistic relationship between fertility and production traits is the main cause of the unfavorable trends for fertility when reproductive efficiency parameters are not included in selection programs. Furthermore, even if included in the breeding objective there is still a risk of deterioration of fertility due to low heritability if the emphasis placed on fertility is too little [5]. In spite of its importance fertility presents several challenges. Reproductive efficiency includes different physiological aspects; it's not easily defined, and suffers in some case of lack of reliable information. Reproduction is an economically relevant component of many livestock species. Beef cattle are no exception. Genetic improvement programs for fertility in beef have been hindered by the difficulty of developing reliable systems of data collection for fertility related events. An increasing body of knowledge of fertility in beef cattle is available (see [64] for a review). In addition the experience gained over the last decade by the dairy industry in selecting for increased fertility will represent a potential source of information for the implementation of efficient fertility selection programs in beef cattle. Nonetheless, the incorporation of these traits in beef genetic improvement programs will depend on the identification of suitable field recorded traits, and the consistent compilation of the information collected by the breed associations for its subsequent use [64].

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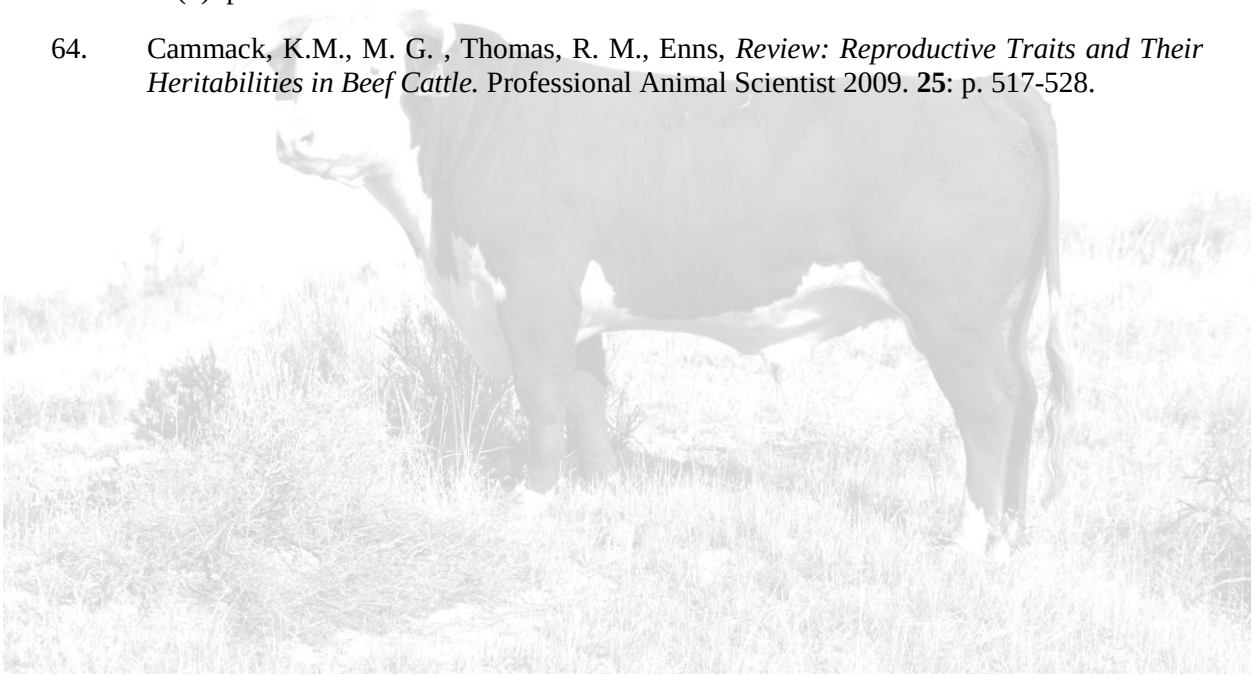

What weighting should be given to BRD resistance in selection decisions?

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Introduction

Multiple-trait selection indexes should include all of the economically-relevant traits that influence the profitability of beef cattle production. They provide an economic evaluation of the genetic differences among sires, and an objective way to determine likely differences in the profitability of progeny from different sires. In contrast to the swine, poultry, sheep, and dairy cattle industries, in which economic indexes are a critical component of selection strategies, the US beef industry has made little use of selection indexes (Garrick and Golden, 2009). Some breed associations have produced and published generalized indexes for their breeders, but details concerning the criteria and relative economic weights are not readily available. Wide disparities in the costs of production and different marketing strategies exist throughout the US, making it unlikely that the economic values used in these generalized indexes are universally applicable. However, correlations among breeding objectives that incorporate local prices conditions are generally quite high, making an approximate index perhaps a preferable option to no index at all.

As DNA testing becomes more comprehensive and encompasses a larger number of traits, it will provide a selection tool for traits where no other information or selection criteria exist. There are many economically-relevant traits in this category including cow and feedlot feed efficiency, and disease resistance (Pollak, 2005). This will enable the development of more comprehensive selection indexes that include all of the economically-relevant traits of relevance to U.S. beef production systems. One of the most important of these is likely to be feedlot health.

Almost all US cattle are finished in feedlots. At any one point in time there are around 13.6 million US cattle on feed, and 26 million head were fed in 2009. In the United States, 1.4% of all feedlot cattle perish before reaching harvest weight and of those, the majority are due to bovine respiratory disease (**BRD**). Indeed, more feedlot cattle die from BRD than all other diseases combined, and this trend is increasing. (Lonergan et al., 2001) Bovine respiratory disease accounts for 29% of all US cattle industry deaths and causes annual losses of more than one million animals and $692 million (National Agricultural Statistics Service 2006).

There is growing interest in selective breeding of domestic livestock for enhanced disease resistance. Disease-resistant animals contribute to sustainability goals in that they have improved health, welfare, and productivity (Stear et al., 2001). Understanding the genetic basis for susceptibility has become an increasingly important target for research, especially with the availability of genome sequence. BRD resistance represents an obvious target for selective breeding programs. However as with any trait selection emphasis needs to be weighted by its effect on profitability relative to other economically-important traits. **The objective of this paper was to calculate the weighting that should be given to selection for BRD resistance in a multi-trait selection index for Angus terminal sires.**

Materials and Methods

Methods were based on those outlined in MacNeil (2005) for the development of breeding objectives for terminal sires in U.S. beef production systems. All herd level economic statistics were modeled for a 1000–cow-calf enterprise and retained ownership was assumed. All progeny of terminal sires were harvested and so no economic value was associated with maternal traits. Only phenotypes for weaning weight, feedlot average daily gain, feed intake, USDA yield grade, marbling score and BRD incidence (%) contributed to the breeding objective. The feedlot phase was divided into three periods. The first period (backgrounding) was terminated at a weight-constant end point of 850 lb. The second (growing) and third (finishing) periods were of 50 and 100 days duration, respectively. The genetic parameter estimates and phenotypic characterization used to develop the terminal sire index were those used to develop the Angus Sire Alliance Index detailed in MacNeil and Herring (2005), although the liveweight and carcass prices were updated in 2008, as detailed in Table 1.

Weaned calf weight (lb)	**$/lb**	**Quality/Yield Grade**	**$/100lb**
< 350	1.21	Prime	28.07
351-400	1.15	High Choice	5.53
401-450	1.09	Choice	0
451-500	1.04	Select	-10.20
501-550	1.01	Standard	-20.20
551-600	0.96		
>600	0.92	Yield Grade 1	3.00
Carcass weight (lb)	**$/100lb**	Yield Grade 2	2.00
Base price	155.95	Yield Grade 3	0.00
<550	-15	Yield Grade 4	-10.20
>950	-15	Yield Grade 5	-20.20

Table 1. Prices, premiums and discounts used in developing the multi-trait selection index for Angus terminal sires.

To parameterize the model to include BRD, the following was assumed: 1) All BRD occurred when calves were moved to the feedlot phase at weaning; 2) the fixed cost of feedlot phase was unchanged; 3) a dead calf incurred no feed costs; 4) there was a 10% mortality from BRD (Holland et al., 2010; Reinhardt et al., 2009) 5) there was a 13% reduction in ADG (1.3 lbs/d) for the first phase of feeding (weaning to 850 lbs; (Holland et al., 2010); 6) final yield grade was reduced by 0.1 (Garcia et al., 2010; Reinhardt et al., 2009); and 7) the cost to diagnose and treat a BRD calf was $44 (Randall Raymond DVM, Simplot Land and Livestock, personal communication).

To obtain the genetic standard deviation for BRD incidence the following calculations were made. The phenotypic variance of the binomial at a mean incidence of 10% was calculated to be p(1-p) = 0.09. A binomial scale heritability of 0.07 (Snowder et al., 2006) was applied to get a genetic variance of 0.0063, or a genetic standard deviation of 0.0794. Transforming from decimal to a percentage resulted in a genetic standard deviation of 7.94.

Economic values were calculated by performing bio-economic simulations using a modified version of the computer software described by MacNeil (1994). The main modification was that harvest phenotypes were generated stochastically, and steers were valued based on a multivariate normal distribution of marbling, yield grade, and carcass weight. In separate simulations, the phenotypes for each of the economically relevant terminal sire traits were changed by one unit. The difference between simulated profit with a phenotype perturbed by one unit and profit in the baseline simulation was taken to be the economic value for that trait (Table 2). The results are

expressed on enterprise basis, rather than per cow exposed or progeny produced. To provide some indicator of the relative magnitude of the economic values, each economic value was multiplied by the corresponding trait genetic standard deviation to give the relative economic value (REV). To simplify trait comparisons, each REV was divided by the REV for the trait with the smallest value (i.e. yield grade in this index), and the absolute value of that calculation is shown as "Relative Importance" in Table 2.

Results

Table 2. Enterprise economic values, relative economic value, and relative importance of economic values for traits in the terminal sire breeding objective.

Trait (unit)	Economic Value ($)	Genetic SD	Relative economic value (REV)	Relative Importance (relative to YG)
BRD incidence (%)	-8424.7	7.94	-66892	37.7
Weaning wt. (lb)	241.4	41.76	10081	5.7
Feed Intake (lb/d)	-5811.8	1.41	-8195	4.6
Feedlot ADG (lb/d)	27654.5	0.24	6637	3.7
Marbling score	8926.0	0.51	4552	2.6
Yield Grade	-5379.2	0.33	-1775	1

Selection index methodology is designed to weight traits by their economic merit. Following Henderson (1963), the appropriate terminal sire selection index weighting for EPDs the economically-relevant traits listed in Table 2 would be the economic value for each trait. The REVs suggest that to maximize the profitability of the commercial production system modeled in this study, BRD incidence should be very heavily emphasized in terminal sire selection, followed by a relatively uniform emphasis on weaning weight, postweaning average daily gain and feed intake, and less emphasis should be placed on marbling score and yield grade.

This emphasizes the economic importance of BRD on feedlot profitability. It should be noted that other potential benefits were not considered in these calculations. These include reduced shedding and transmission of pathogens from resistant hosts, and externalities like improved animal welfare and public support for the decreased use of antibiotics in food animal production.

The values derived in this study were for terminal sire selection. There is a higher relative importance of maternal traits compared to feedlot and carcass traits, when the goal is to produce herd replacements. Melton (1995) suggested that US cow-calf producers keeping replacement heifers and selling calves at weaning should have a relative economic emphasis of 47% on reproduction, 24% on growth, and 30% on carcass traits, whereas producers in an integrated system should have a relative economic emphasis of 31% on reproduction, 29% on production, and 40% on carcass traits. This relative emphasis will depend on how much the value derived from genetic gain in feedlot and carcass traits is shared with the producer in the integrated system.

Discussion

Our preliminary data based on this terminal sire selection index suggest that there would be considerable value associated with the successful development of DNA tests to enable selection for BRD resistance. This index was developed to maximize the profitability of the entire industry as though it were one vertically integrated production system. In reality, even though nearly all US calves go through the feedlot and are sold on a carcass quality basis, most commercial producers market their calves at weaning or shortly thereafter. Ninety percent of US cattle operations (692,050) have fewer than 100 head, and most sell their cattle at auction prior to feedlot entry. Consequently, producer financial returns are tied very closely to the number of calves, a function of reproduction, and less to feedlot performance and health, and even less to carcass traits. To incentivize the inclusion of BRD resistance in selection decisions, a mechanism analogous to a calf preconditioning bonus would be needed to equitably share some of the value derived from reduced feedlot disease incidence and to compensate breeders and producers for reduced selection emphasis on other economically-relevant traits.

There are a number of issues that will need to be addressed in the development of DNA tests for BRD resistance. The first is that disease resistance heritabilities tend to be low, especially under field conditions. There a number of reasons for this including suboptimal diagnosis (e.g. not all sick animals are identified and healthy animals may be incorrectly diagnosed as ill), and some susceptible animals will appear resistant to a disease when in fact they have not been exposed to the disease agent (Bishop and Woolliams, 2010). These factors add environmental noise to field data. Field studies therefore likely underestimate heritability, and thus also undervalue the potential gains that could be made by breeding for disease resistance (Allen et al., 2010).

Evidence that BRD susceptibility/resistance is under genetic control is demonstrated by breed differences in BRD morbidity and mortality, the fact that BRD prevalence in unweaned calves and feedlot cattle is heritable, and the finding of genomic regions that have been shown to be associated or "linked" with BRD incidence. Prior to entry into the feedlot, the incidence of BRD in weaned calves varied by breed from a low of 10% in Angus to a high of 35% in Pinzgauer (Snowder et al., 2006). Mortality also differs by breed, ranging from 0.1% in Braunvieh cattle to 8.9% in Red Poll cattle. Susceptibility differs among various breeds, ranging from 28% in Braunvieh to 73% in Hereford. Heritability estimates also suggest there is a genetic underpinning of the disease. The heritability estimate for feedlot animals was 0.18, when adjusted to an underlying continuous scale (Snowder et al., 2006).

BRD susceptibility is most likely a complex genetic trait governed by the effects of many genes. This suggests a large number of cases and controls will be needed to detect all of these variants and so datasets for disease resistance marker discovery will need to be comprised of observations on several thousands of individuals (Amos et al., 2011).

On the positive side, obtaining markers that track disease resistance loci relies on "linkage disequilibrium" (LD) between DNA makers and the causative loci. Fortunately cattle have long stretches of LD and it is thought that the new generation of high density SNP arrays (e.g. Affymetrix Bovine 650K, Illumina Bovine 770K HD SNP Array) will provide adequate coverage of the bovine genome to track loci that are associated with disease susceptibility (Allen et al., 2010). It is also hoped that these high density arrays will enable the development of tests that can work across multiple-breeds.

With the less dense (i.e. 50,000 SNP) marker panels, a marker associated with a trait in one breed was not associated in the same way in another breed (Figure 1A). The reason for this is that the SNP marker could be located a "long way" from the gene and so in some breeds it was not associated or "linked" with the variant of the gene causing a given phenotype. By increasing the number of SNP markers to > 700,000, markers are more closely spaced and there is a greater likelihood of finding SNPs that are close to the gene (red markers in Figure 1B), and hence the marker will "work" in both breeds.

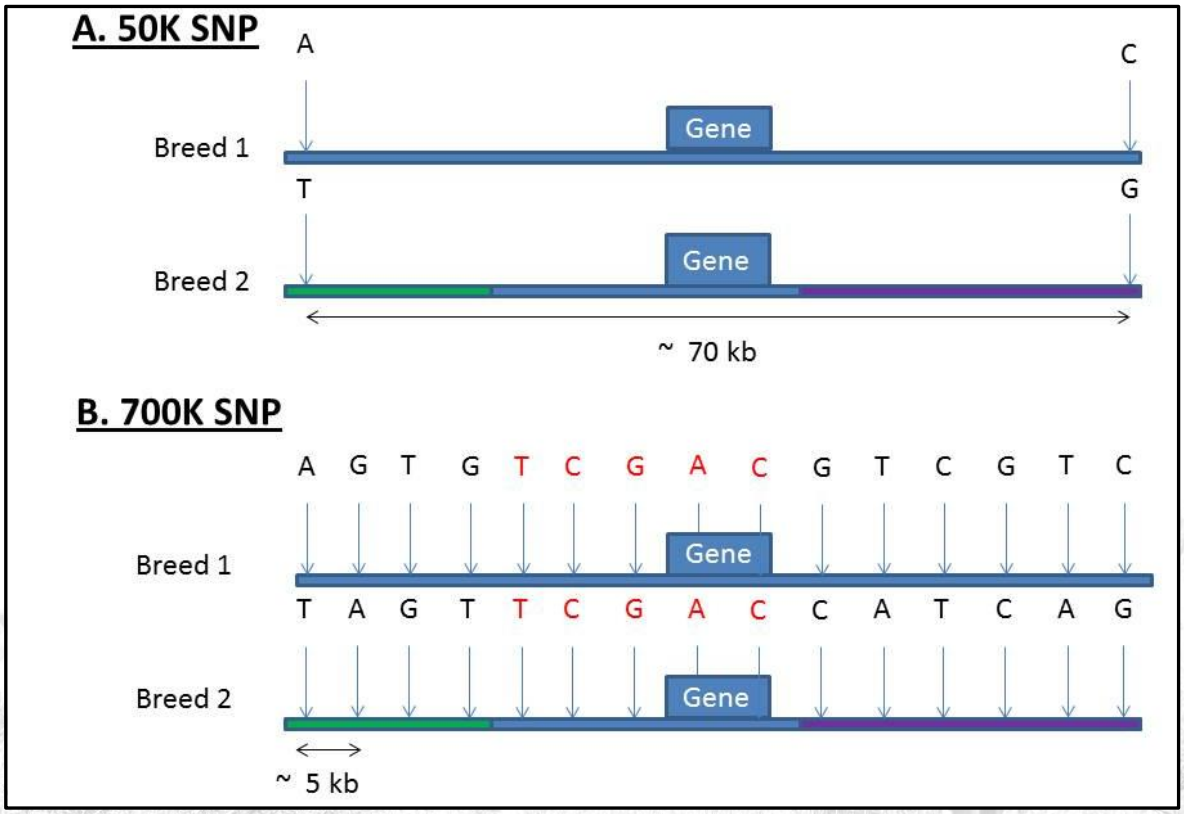

Figure 1. Marker location relative to the gene of interest in two breeds when using (**A**) the 50K SNP marker panel (markers spaced at 70 thousand base pair (70 kb) intervals), or (**B**) the high-density 700K SNP marker panel (markers spaced at approximately 5 thousand base pair (5 kb) intervals).

In cattle it has been estimated that SNPs need to be spaced less than 10 kb apart to show consistent LD phase across breeds (de Roos et al., 2008). These high density bovine marker panels also provide an opportunity for multiple *Bos taurus* breeds to pool information and records. Developing large multi-breed training data sets for disease phenotypes may collectively improve the accuracy of tests for all breeds, more than any single breed can do on its own due to the larger number of combined records. These high density bovine marker panels also provide an opportunity for breeds to pool information and records (Figure 2).

In dairy cattle, selection programs have been developed to take advantage of genetic variability in mastitis resistance, despite the fact that the heritability of clinical mastitis is low and mastitis resistance has an adverse correlation with production traits (Rupp and Boichard, 2003). Likewise chicken breeders have long used breeding to improve resistance to avian lymphoid leucosis

complex and Marek's disease (Stear et al., 2001). Recent developments in molecular genetics and genotyping platforms offer a unique opportunity to use modern genomic tools to manage the future health of beef cattle. Developing large multi-breed training data sets for disease phenotypes may collectively improve the accuracy of tests for all breeds, more than any single breed can do on its own due to the larger number of combined records. Reducing the considerable animal morbidity, mortality and economic losses associated with BRD will require the simultaneous development of DNA tests to enable the selection of resistant animals, and the incorporation of this trait into breeding objectives of relevance to U.S. beef production systems.

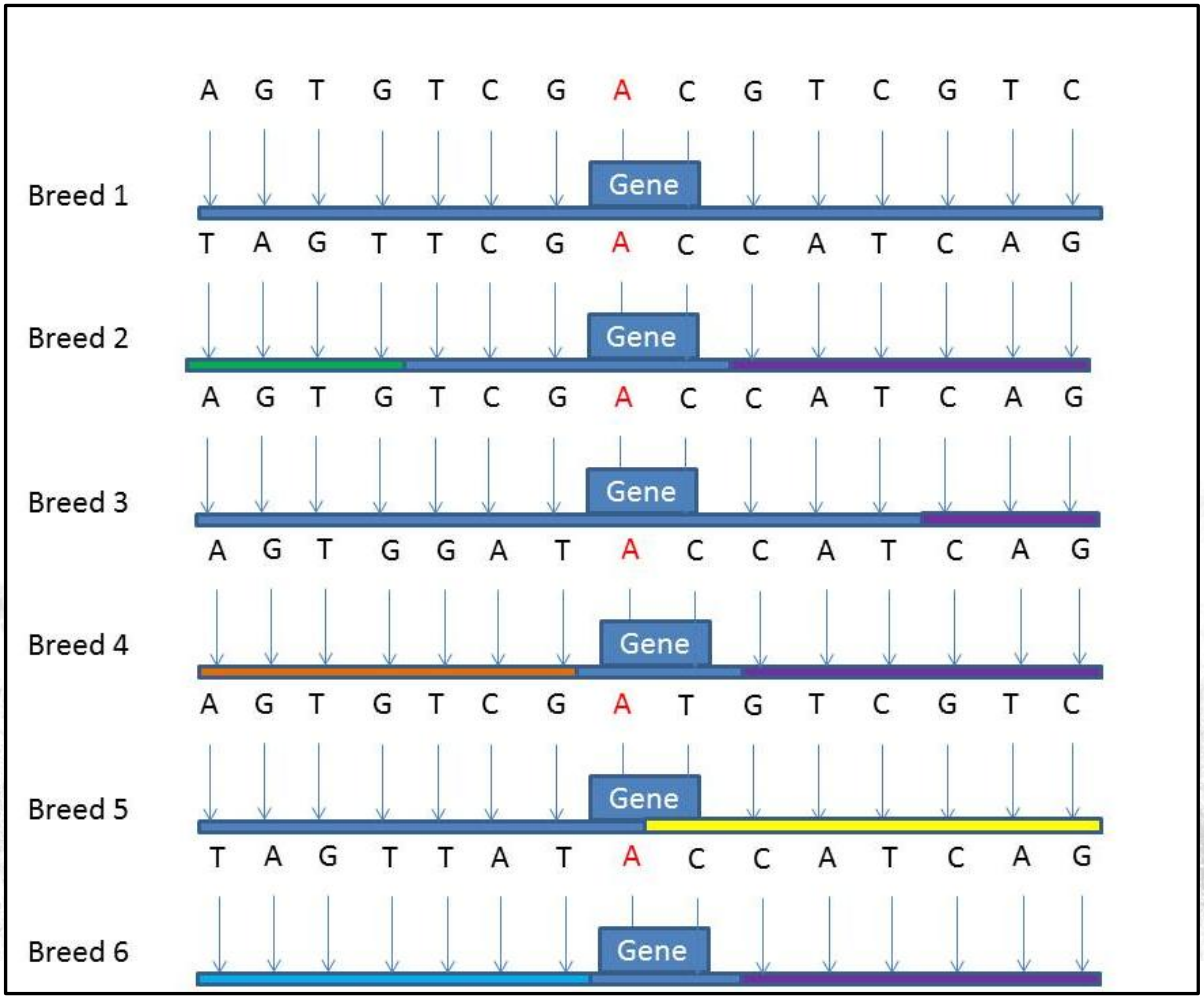

Figure 2. High density SNP marker panels may enable the discovery of the causal mutations underlying genetic variation (i.e. red "A" SNP located in the gene).

"We now stand at a defining moment in the history of agriculture wherein we can use modern genomic tools to subtly influence the future evolution of the animals we have farmed for thousands of years." (Allen et al., 2010)

Acknowledgements

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Hair Coat Shedding in Angus Cows

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Introduction

The principal method for heat dissipation in cattle is evaporation cooling. A bovine animal's success in cooling itself is directly influenced by many factors including humidity, wind speed and physiological factors like respiration rate and activity of sweat glands (Blackshaw and Blackshaw, 1994). As the ambient temperature and humidity exceed the animal's thermal neutral zone, effectiveness of evaporative cooling through sweating and respiration decreases. When humidity is high, water from sweat or even sweat vapor gets trapped in spaces between the hair follicles causing the animal to expend more energy in thermoregulation by increasing its respiration rate and increasing the amount it sweats (Finch, 1985). Cattle with dark, thick, wooly coats are at an extreme disadvantage in hot, humid climates and are at an increased risk of heat stress and dehydration. In the Southeastern region of the United States, where the climate is sub-tropical, it has been observed that cows that fail to shed in a timely manner tend to show more signs of heat stress when compared to slick-coated contemporaries. Signs of heat stress include decreased mobility, decreased appetite, and poorer general health. A common perception among producers in this region is that cows which shed late in the season are inferior dams with poor performing calves. The objective of this study was to (1) adapt a reasonable method to assess hair coat shedding within purebred Angus cattle, (2) determine how much hair coat shedding variation exists among Angus cows, (3) estimate its effects on adjusted 205 d weight (d205wt) and cow's body condition score (BCS).

Materials and Methods

Animals: Registered Angus cows (n = 532) were used over a 3-yr period in four different locations for this study. The first location was in Reidsville, NC, where the North Carolina State University historic Angus herd is maintained at the Upper Piedmont Research Station (UPRS) on wild-type endophyte-infected tall fescue pastures. Approximately half of the animals were observed in this location. The remaining cows were distributed over three other locations in Mississippi including Mississippi State, Winona, and Okolona, MS. The cows grazed pastures consisting primarily of mixed warm-season grasses, annual ryegrass, and non-toxic endophyte-infected tall fescue. All cows were between 2 and13 yrs of age with a calving season in NC in late autumn and calving seasons in MS was in the early autumn or late winter/early spring. A summary description of the data is shown in Table 1.

Data: In 2007, 2008, and 2009, beginning the last week in March for 5 mo at approximately 30-d intervals, two trained technicians scored cows on a scale from 1 to 5 (Table 2). A score of 1 represented a slick, summer coat, and 5 represented a thick, winter coat. A score of 3 was halfway shed, while a score of 4 was a cow that started shedding but was not quite half way to a summer coat. A score of 2 was more than halfway shed but not shed slick yet.

Table 1. Description of Data	
Registered Angus Cows	n = 532 (693 obs) , some repeated measures, only cows with calves were included in phenotypic analysis
Age of Cows	2 – 13 yr
Diet	UPRS – Wild-type endophyte-infected tall fescue, MS – warm-season mixed grasses, annual ryegrass, non-toxic endophyte-infected tall fescue
Location	UPRS, MS (3 locations)
Collection of Data	once per month for 5 mo beginning the last week in March over a 3-yr period
Scores	1 (slick) – 5 (full winter coat) scale
Calving Season	UPRS – Late Autumn (Nov – Dec); MS – Early Autumn (Sep – Nov), Late Winter/Early Spring (Jan – Mar)

Table 2. Description of hair coat shedding Scores

Hair Shedding Score	Definition
5	Full winter coat
4	Coat exhibits initial shedding
3	Coat is halfway shed
2	Coat is mostly shed
1	Slick, short summer coat

Cows were then grouped into 5 categories based on the month the cow began to shed her winter coat. A cow was considered to have begun shedding its winter coat when she received a score of 3 or less. Cows that never received a score of 3 or less (n = 13) during the 5 months of observation were small in number and were grouped with cows that shed in July. These categories will be referred to as month of first shedding (MFS).

All cows within the analysis weaned a calf at approximately 6 mo of age. Weaning weights were recorded and submitted to the American Angus Association. An adjusted weaning weight (d205wt) was then calculated by the association adjusting for age of dam, and age of calf to 205 d. In this study, d205wt was considered to be a trait of the cow for both phenotypic and genotypic analysis.

Phenotypic Analysis: The first model tested the association between MFS and d205wt or BCS using the mixed procedure of SAS. Models for d205wt and BCS included fixed effects of yr (3 levels), location (4 levels), sex of the calf (2 levels) and MFS (5 levels) with a random effect of sire of calf (n=86). Sire of calf was included in the model to adjust for any genetic advantage from certain sires. Age of calf and age of cow (2 levels; heifer or cow) were added as a covariate and fixed effect, respectively, for BCS. They were not added to the d205wt model, because the trait already accounted for these factors.

Data were further analyzed by dividing cows into two groups. Cows were considered adapted to the sub-tropical climate when they had an MFS of March, April, or May, while the remaining animals were considered unadapted and undesirable. These two categories are referred to as the adapted score (AS).

The second model was similar to the first model except MFS was replaced with AS. All other effects included in the model were as before.

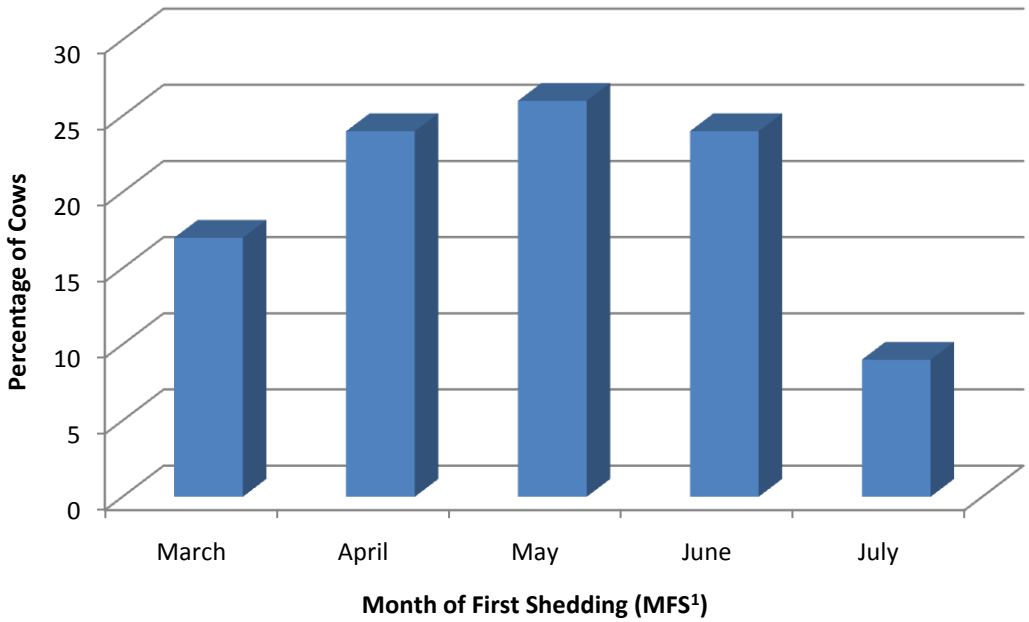
Genetic Analysis: Variance components were estimated for d205wt and AS. Fixed effects included in the model were yr (3 levels), sex of calf (2 levels) and location (4 levels). Random effects of cow and a permanent environmental effect were also included. Variance components were estimated using THRGIBBS2F90 program (Misztal et al., 2002). A single chain consisting of 100,000 iterations was employed, with a burn-in period of 25,000 iterations. Convergence was assessed visually from the trace plot. Inferences on variables were obtained as mean of the respective posterior distributions.

Results

Two technicians collected all shedding scores within each location. Each technician's scores were analyzed separately. It was found that technicians were in agreement in their scoring of the cows (data not shown), and only one technician score was used within each location.

Table 3. LS means of adjusted weaning weights associated with the month the dam begins shedding (MFS)

MFS	d205wt (lbs)	Standard Error
March	597	6.4
April	589	8.8
May	587	7.1
June	578	7.3
July	551	8.8



[1] First month in which a cow received a score of 3 or less using the following scoring system: 5 – Full winter coat, 4 – Coat exhibits initial shedding, 3 – Coat is halfway shed, 2 – Coat is mostly shed, 1 – Slick short summer coat

All effects in the first model were significant ($P < 0.01$) for d205 wt. For BCS, MFS was not significant, therefore BCS was not considered in the rest of the analysis. Least square means of d205wt were calculated for MFS (Table 3). Cows that shed earlier in the year did not differ in their BCS but had calves that were heavier at weaning.

Differences in LS means for MFS (Figure above) were calculated as well (Table 3). Adjusted weaning weight of calves out of cows that had MFS in March, April, and May did not differ from one another. Calves' d205wt out of cows that had MFS in March, April, and May did differ from calves' d205wt out of cows that had MFS in June and July ($P < 0.05$).

The second model takes advantage of this natural grouping found in the data using AS as the effect of interest. All remaining effects were similar to the first model, and all were significant ($P < 0.01$). Least Square means were calculated, and their differences appear in Tables 5 and 6, respectively. Calves from cows that began to shed by the end of May had d205wt at 24 lbs heavier than their contemporaries that were out of cows that began to shed after May.

Table 4. LS means differences of adjusted weaning weights of dams that began shedding in different months

Contrast	Difference	Standard Error	Pr > |t|
March – April	7.9	6.85	0.25
March – May	10.2	7.85	0.19
March – June	19.2	8.52	0.02
March – July	45.9	10.11	0.01
April – May	2.3	7.37	0.75
April – June	11.3	7.91	0.15
April – July	38.0	9.50	0.01
May – June	9.0	6.95	0.20
May – July	38.0	9.50	0.01
June - July	26.7	7.93	0.01

Table 5. LS means of adjusted weaning weights associated with cows that shed by the end of May or after May (AS).

AS	d205wt (lbs)	Standard Error
Shed by May	589	5.6
Shed after May	565	6.8

Table 6. Differences in LS Means of adjusted 205 d weaning weights of dams that began shedding by May vs. after May

Contrast	Difference	Standard Error	Pr > |t|
Shed by May – Shed after May	24.1	6.16	.01

Variance components were estimated for two traits and heritabilities and genetic correlations were calculated (Table 7). Heritabilities of d205wt ($h^2 = 0.27$) and AS ($h^2 = 0.35$) were low to

moderately heritable, and the genetic correlation was moderately strong, negative, and favorable (r_g = -0.50). On average, cows which shed their hair coats by the end of May wean heavier calves than cows who take longer to shed their hair coats.

Table 7. Heritabilities on diagonal and genetic correlation below diagonal

	d205wt	AS
d205wt	0.27	
AS	-0.50	0.35

Discussion

Scoring cattle on a scale of 1 to 5 starting in March provided phenotypic data which adequately described the variation that exists among hair coat shedding in Angus cattle located in the Southeastern region of the United States. Some variation did occur among technicians when scores were 3 or less and between 4 and 5. To decrease the amount of variation that occurred among technicians, scores were grouped into two categories as explained above. Because this scoring system was used over multiple locations and technicians, grouping the shedding scores into these categories led to consistent measurement.

The first model showed that an extended time to shedding in cows resulted in lighter calves at weaning. Although this trend did hold over all 5 months, there was no significant difference between the first three months. For this reason animals were grouped using AS, which in reality is a more realistic approach for implementation. Labor costs and time would prohibit monthly shedding scores to take place in most production settings; however, it has been shown that one score taken at a strategic time is sufficient for capturing the variation that occurs in hair coat shedding. In this sample it was shown that by the end of May animals should be scored to predict calf weaning performance. This time may vary depending on the location, humidity, and overall environment of the herd in question.

Weaning weight is an economically important trait. Angus producers have increased the weaning weights of their calves over the past 40 yr. This study shows that there is a high genetic correlation between weaning weight and hair coat shedding. It would seem reasonable that by default animals will continue to improve in hair coat shedding through correlated selection. Although this does seem plausible, most drive for selection within the Angus breed occurs in cooler, less humid environments. There may be a genotype by environment interaction that is not evident in the more temperate regions where most of the selection occurs. This study provides evidence that certain sires will produce better calves in hot, humid, and otherwise less than ideal environments, but definite conclusions cannot be made until more data are collected in cooler environments with some of the same sire families represented.

It is possible that early hair coat shedding does not necessarily cause heavier d205wt. However, there is evidence that even if early hair coat shedding is not the cause, it is a good indicator of heavier weaning weights. Hair coat shedding has a greater heritability than weaning weight; therefore, by including AS in an index, producers could potentially increase their response to selection of d205wt in sub-tropical climates.

A possible explanation for the relationship between hair coat shedding and weaning weight of calves could be differences in prolactin concentrations. Prolactin has many functions within the cow. One of its functions is associated with lactation (Knight, 2000). Prolactin also influences hair regression regulation (Nixon et al., 2002). Therefore, it could be concluded that hair coat

shedding rate could be an indicator of the amount of prolactin available. When cows are not shedding, it indicates that prolactin levels are low. Low prolactin levels may also affect the amount of milk available for the calf, which would directly affect d205wt.

Hair coat shedding has also been shown to be affected by diet. Toxic wild-type endophyte-infected tall fescue affects prolactin concentrations (Bernard et al., 1993) and hair coat shedding (McClanahan et al., 2008). Based on results of this study, it was concluded that even while all animals are on wild-type endophyte-infected tall fescue there still was variation within the herd. This provides evidence that some sire families are more adapted to this type of environment and they are more productive even when fed a wild-type endophyte-infected tall fescue diet.

Temperature may also play an important role in when cows begin to shed their winter coat. Further analysis will need to be performed to determine how much temperature affects rate of hair coat shedding within these herds.

Continued research will help to completely understand how shedding and productive traits like calf weaning weight are associated. This research does provide evidence that cows that shed late in the season wean lighter calves. Hair coat shedding is a heritable trait and could be altered by selection. Producers within the Southeastern or Southern United States that have observed late hair coat shedding within their herds can select for hair coat shedding earlier in the season. This should result in higher weaning weights, making the cow herd more productive.

Recommendation

Producers seeking to reduce heat stress in their herds related to hair coat shedding should score their cows on a 1 to 5 scale in late May. Cows with hair coat shedding scores of 4 or 5, indicating little or no shedding, should be considered for culling.

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Temperament assessment provides insight into future health and growth performance of beef cattle

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Introduction

Throughout the productive life of beef cattle many stressful events occur (e.g. branding, castration, vaccination and tagging) coupled with weaning, social mixing, and transportation. These stressful events have been reported to induce secretion of several of the prominent stress-related hormones: cortisol, epinephrine, and norepinephrine (Crookshank et al., 1979; Rulofson et al., 1988; Lay et al., 1992; Buckham Sporer et al., 2008). Acute stress is not necessarily detrimental to the health of an animal, and may even be beneficial (Galyean et al., 1999; Dhabhar, 2002; Duff and Galyean, 2007; Sorrells and Sapolsky, 2007). However, chronic stress can negatively impact growth, reproductive function, and immune function (Moberg, 1987; Dobson et al., 2001). Therefore minimizing adverse consequences of multiple stressful incidents as well as identification of animals that may react differently to multiple stressful events may be beneficial to health and growth of beef cattle.

The effect of animal temperament on health and performance is an area of increasing research interest. Specifically in cattle, temperament is defined as the reactivity, or fear response, to humans (Fordyce et al., 1988a). Correlations between temperament and concentrations of stress hormones in cattle have been reported in that more temperamental, or excitable, cattle have greater concentrations of cortisol and epinephrine (Schuehle et al., 2005; King et al., 2006; Curley et al., 2006a, b, 2008). In addition, temperament can have negative impacts on growth (average daily gain), carcass traits, and immune function in cattle with less desirable temperaments (Voisinet et al., 1997; Fell et al., 1999; Oliphint, 2006).

Multiple studies have provided valuable information on the relationships between cattle temperament, transportation, immune challenges, and production traits over the last six years. Temperament assessments of beef cattle can be comprised of several subjective and objective tests; however, our studies have primarily focused on the following three measurements: 1) chute score, 2) pen score, and 3) exit velocity. While chute and pen scores are subjective measures of temperament, exit velocity is an objective measurement that records the rate (m/s) at which cattle exit a working chute (Burrow et al., 1988; Curley et al., 2006a). Pen score (Hammond et al., 1996) is a subjective measurement in which cattle are separated into small groups of three to five and their reactivity to a human observer scored on a scale of 1 (calm, docile, and approachable) to 5 (aggressive, volatile, and crazy). Chute scores reflect the behavior of the animal while confined in a chute and scored on a scale of 1 (calm, no movement) to 5 (rearing, twisting of the body, or violent struggling; Grandin, 1993). Utilization of a temperament score which is the average of exit velocity and pen score provides a combined temperament measurement that encompasses both the subjective and the objective perspectives (Curley et al., 2006a; King et al., 2006). Additionally, temperament is a moderately heritable trait and improvements in overall herd

temperament and production efficiency can be made relatively quickly in a practical production situation.

Results and Discussion

The two measurements used most often for the collaborative research at Texas AgriLife Research and Mississippi State-MAFES-Brown Loam Experiment Station are pen score and exit velocity. Whereas the various methodologies for temperament assessment may measure slightly different aspects of animal behavior, they do relate to one another and, in the case of exit velocity and pen score, to increased circulating glucocorticoids such as cortisol (Curley et al., 2006a, b). Calves that exhibit a greater exit velocity or leave the working chute at a greater speed are usually more temperamental than those calves that leave the working chute at a lesser speed. Additionally, secretion of the stress-related hormones epinephrine and cortisol is exaggerated in the more temperamental calves (Schuehle et al., 2005; Curley et al., 2006a, b, 2008; King et al. 2006). Exit velocity can be measured in cattle of all ages, from 3 weeks of age through maturity, although from a practical production standpoint, and to more accurately predict temperament in calves, it is best for producers to determine exit velocity closer to weaning time (Burdick et al., 2009; 2011a). Cattle can be ranked based on their exit velocity and this can help producers determine which animals are the "flightiest" and therefore provide an objective measurement to determine which animals should be culled due to temperament or assigned to different management groups (e.g. feeder versus retained as a replacement in the breeding herd). Additionally, temperament score is an average of exit velocity and pen score and is the primary measure of temperament assessment in our research group due to the fact that it provides a more accurate assessment of temperament in that it takes into account two aspects of behavior involved in the "flight" or "fight" syndrome.

Human-animal interactions in cattle production commonly occur through handling coupled with various management practices. Animal temperament has been shown to have negative impacts on aspects of both dairy and beef production. Cattle with more excitable temperaments exhibit lower body weight gains (Burrow, 1997; Voisinet et al., 1997), produce tougher meat (King et al., 2006; Voisinet et al., 1997), have inhibited milk production (Drugociu et al., 1977; Breuer et al., 2000), and yield increased amounts of bruise trim due to injuries acquired during transportation (Fordyce et al., 1988). Coupled with the negative effects on growth and carcass traits, temperament can also have negative effects on immune function (Fell et al., 1999; Oliphint, 2006). More specifically, temperamental animals have decreased carcass weight and tenderness, as well as increased carcass pH, and abnormal meat flavor or color (Fordyce et al., 1988b; King et al., 2006). This also renders cattle more susceptible to disease-causing pathogens (Oliphint, 2006). Mississippi cattle producers consigned steers (n=186) and heifers (n=24) to the Farm to Feedlot program in which cattle were evaluated for temperament using chute score, pen score and exit velocity prior to shipment to the feedlot (Vann et al., 2008a). Cattle were evaluated for ADG, treatment costs, net returns and carcass quality. Individual treatment costs increased as pen score and exit velocity increased. As exit velocity increased, final body weight, total gain, and ADG decreased ($P < 0.05$). In addition, as exit velocity increased, net returns decreased along with an increase in the number of days cattle were treated for sickness ($P < 0.07$; Vann et al., 2008a). We concluded that cattle that possess more excitable temperaments have increased treatment costs and lower net profits compared to cattle with calmer temperaments (Vann et al., 2008a). Researchers at Iowa State University reported that not only does cattle disposition influence convenience traits, but disposition also influences feedlot performance and carcass quality (Busby, 2005). All of these factors can lead to an increase in cost to the producer and decreased profitability.

Other stressors that cattle will encounter throughout the different management practices during their lifetime are transportation and commingling. Transportation has been purported to be a stressor in the livestock industry, yet interestingly there have been limited studies in cattle that have demonstrated increases in rectal temperature due to transportation. Tarrant et al. (1992) did not find a change in rectal temperature measured before and after a 24-h transport of Friesian steers. In addition, a shorter 9-h transport of beef bulls did not find a transport-induced difference in rectal temperature, measured using a hand-held digital thermometer (Buckham Sporer et al., 2008). Furthermore, rectal temperatures of bulls in that study were lower 48 h after the initiation of transportation. In contrast, rectal temperature increased in heifers that were transported for 4 h on two consecutive days compared to non-transported controls (Behrends et al., 2009). A recent study reported relationships between temperament and transportation with rectal temperature and serum concentrations of cortisol and epinephrine in bulls with rectal temperature recording devices for continual collection of rectal temperature during transport (Burdick et al., 2010). In this study, temperamental bulls had greater rectal temperature than calm or intermediate bulls ($P < 0.05$). Rectal temperature peaked within 30 min after the onset of transportation with temperamental bulls having greater peak rectal temperatures than calm or intermediate bulls ($P < 0.05$). The lowest mean rectal temperature was reached 400 min after the onset of transportation with calm bulls having lower mean rectal temperatures than intermediate or temperamental bulls ($P < 0.05$). Prior to transportation, temperamental bulls had greater cortisol concentrations than calm bulls ($P < 0.05$) as well as greater concentrations of epinephrine than calm or intermediate bulls ($P < 0.05$). Temperamental bulls also had greater concentrations of cortisol and epinephrine post-transportation than calm bulls ($P < 0.05$; Burdick et al., 2010). Additionally, a subsequent study by Burdick et al. (2011b), suggests that the most stressful part of transportation actually occurred prior to the transport event, and was more closely associated with the sorting and loading process. This study utilized automatic sampling devices (IceSampler™) which provided "real-time" endocrine indices of stress responsiveness during a 4-h transport and these hormonal changes were related to temperament. These studies indicate that temperamental cattle react very differently to varying aspects of management practices and thus that actual human-animal interactions are probably the most stressful events that these animals encounter.

Evaluation of ultrasound body composition traits as affected by temperament, transportation and an immune challenge has also been a focus of our research team. The objective of one research project was to evaluate the combined effects of transportation and animal temperament on real-time ultrasound body composition traits (primarily percentage of intramuscular fat) in Angus crossbred (n=68) and Brahman (n=60) steers (Vann et al., 2008b). Cattle were assigned temperament scores at weaning, as yearlings, and prior to departure to the feedlot and three sets of steers were hauled three distances (644, 809 and 1,236 km) to a feedlot. Breed and distance cattle were hauled affected percentage of intramuscular fat ($P = 0.053$) and rib fat ($P = 0.02$) at feedlot arrival. Angus crossbred steers hauled shorter distances had smaller changes in percent intramuscular fat than Brahman steers ($P < 0.002$). As the distance cattle were hauled increased, the percentage change in intramuscular fat increased (Figure. 1). These results suggest that transportation has negative impacts on body composition traits, specifically intramuscular fat and rib fat. Furthermore, in another study Brahman bulls were evaluated to determine the influence of temperament on ultrasound body composition traits in response to transportation and an endotoxin challenge (Vann et al., 2008b). Based on their temperament score (combination of exit velocity and pen score) the calmest (n=8), intermediate (n=8), and most temperamental bulls (n=8) were transported (770 km) and underwent an endotoxin challenge. Prior to departure and post-endotoxin challenge, ultrasound measurements were collected on the bulls for percent intramuscular fat, ribeye area and rib fat. Rib fat was reduced (average 0.03 ± 0.03 cm) due to transportation for bulls in all temperament classifications ($P < 0.03$). There was a numerical trend for bulls classified as temperamental (-0.15 ± 0.11) to have the smallest decrease in percentage of

intramuscular fat compared with calm (-0.41 ±0.11) or intermediate (-0.43 ± 0.11) bulls due to either transportation or post-endotoxin challenge. Although many of these changes in ultrasound body composition traits are minimal, there are some trends; however, more research needs to be done to further elucidate these changes in body composition traits. Transportation does have negative impacts on body composition traits, especially intramuscular fat in young steers transported to the feedlot or bulls undergoing transport and an immune challenge, however, there is some inference which can be applied to fat cattle that are transported long distances to a harvest facility as they could undergo similar changes in percent intramuscular fat and this could impact carcass quality grade for cattle marketed on a grid system.

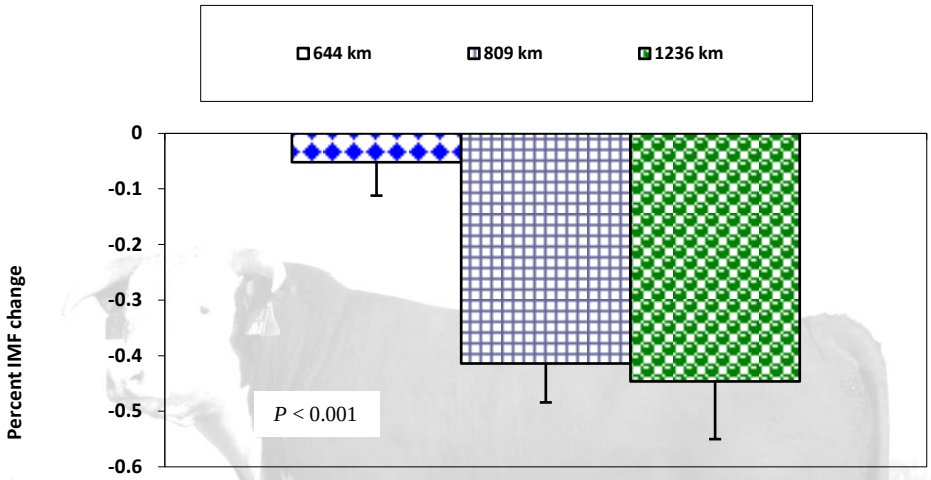

Figure 1. Loss of intramuscular fat (%IMF) was related to travel distance of Angus crossbred and Brahman steers (Vann et al., 2008b).

In summary, there are many methodologies that can be utilized to measure cattle temperament, however; these data suggest that objective measures of temperament assessment may be more useful than subjective methodologies alone. Furthermore, a combined temperament score (an average of subjective and objective measures) provides a more complete assessment due to the fact that it accounts for more than one aspect of cattle behavior. All measures of temperament indicate some adaptation of animals to interactions with humans and management practices. Truly excitable cattle seem to need longer periods of adaptation and are at greater risk for injury to themselves, personnel and equipment in interactions occurring in routine management practices. Not to mention, these more excitable animals have elevated concentrations of stress hormones and catecholamine's throughout their lifetime which negatively impacts growth performance, carcass traits (e.g. quality grade, tenderness, and marbling), and response to vaccination, and immune challenges. In a feedlot atmosphere, these excitable cattle tend to have lower ADG, lower carcass weights, and increased treatment costs due to sickness resulting in lower net profits. Cattle temperament is a moderately heritable trait; thus, identification of these animals in a herd can be utilized to a producer's advantage in that these animals can be marketed or assigned to different management groups (e.g. feeder versus retained as replacements in the breeding herd) which better fits their overall production potential. Future research focus for our team involves more in depth exploration of the interactions of temperament, transportation and immune function as well as cattle feeding behavior and its relationship to overall animal health, productivity, and profitability.

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The new infrastructure for beef cattle breeding in Ireland

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Abstract

Ireland has established an integrated cattle breeding information system to underpin the breeding objectives for beef and dairy breeding in Ireland. This system covers birth & calving, reproduction, growth, carcass and maternal traits. It covers all breeds and crosses, including those with dairy breeds, and meets the information needs of Breed Assns, AI Companies, Breeders and Commercial Producers. Ireland is promoting international collaboration in cattle breeding as part of its strategy to improve the profitability of its beef and dairy industry. Two current initiatives are Interbeef and IGenoP. This paper outlines: the benefits of international collaboration, progress and plans for establishing an international beef genetic evaluation service known as Interbeef, and progress and plans for establishing a database of shared cattle genotypes known as IGenoP.

Introduction

Over the last thirteen years Ireland has established a new infrastructure to facilitate the genetic improvement of both dairy and beef cattle. Prime responsibility for leading the development rests with the Irish Cattle Breeding Federation Society Ltd (ICBF) established in 1998 with the objective of achieving the greatest possible genetic improvement in the national cattle herd for the benefit of Irish farmers, the dairy and beef industries and members. This development has been funded by a unique partnership involving farmers, breeders, service providers, service income and Government.

In this paper we outline the major developments that have taken place in Ireland over the past 13 years and illustrate the impact these have had on the breeding of beef cattle. Our focus is on the developments that have impacted on the availability of data for use in creating information essential for effective cattle breeding decisions. These have included: the formation of ICBF, creation of the ICBF Cattle Breeding Database, implementation of the Animal Events data collection system, the creation of linkages with other data collection systems, and the ICBF Genetic Evaluation system.

Irish Beef Cattle Industry

The Irish cattle industry is based on some 2 million calvings per year with 1.1 million in dairy herds and 0.9 million in suckler herds. The industry involves a large amount of cross-breeding with; 38% of dairy cow calvings to beef sire breeds – mainly Angus & Hereford, and 61% of calvings of suckler cows being to a different beef breed to the breed of the cow. The five main beef breeds are Charolais, Limousin, Simmental, Angus and Hereford.

Of the calves born in suckler herds 22% become herd replacements, 16% are exported live and 62% are slaughtered in Ireland almost exclusively for export as cuts to other EU countries.
The suckler herds are small, averaging some 15 cows, not profitable without state support and include many part-time enterprises.

Formation of ICBF

ICBF was established in 1997 and commenced operations in 1998 with its current structure[i] being finalized in 2000. Its main activities are those associated with: developing the cattle breeding infrastructure in Ireland, operating the cattle breeding database, providing genetic evaluation services, and providing information useful for cattle breeding decisions.

ICBF is owned by the cattle industry with 18% of shares held by each of the Artificial Insemination (AI), Milk Recording (MR) and Herd Book (HB) sectors and the remaining 46% held by the organizations (IFA & ICMSA) representing farmers. The ICBF Board of 16 comprises persons appointed by the shareholders (3 from each of AI, MR and HB, 6 from the farm organizations) and one appointed by the Department of Agriculture Fisheries and Food (DAFF[ii]).

Since its inception, much of ICBF's work has been focused on improving the quantity and quality of data available for cattle breeding. New technologies have been tapped into and business arrangements established, with both shareholders and industry stakeholders alike, with the overall goal of ensuring that Irish farmers have access to high quality information for use in breeding more profitable cattle.

Beef Breeding Objectives & Selection Criteria

A widespread industry consultation supported by extensive research resulted in an agreed breeding objective and selection criteria for beef cattle in Ireland[iii]. The focus of the objective is farm level profitability accounting for the most significant sources of income and cost. Meat income is also considered in the dairy-breeding objective for Ireland. An overall index, the Suckler Beef Value (SBV) is expressed in economic terms (€) and computed from economic sub-indexes for Weanling Export, Beef Carcass, Daughter Fertility and Daughter Milk. These indexes and the evaluations for some of the key component traits are expressed as €uro-Stars on a one to five star scale with each star representing an interval covering 20% of the population. Examples are readily available on the ICBF website[iv].

ICBF provides the genetic evaluation system for both dairy and beef cattle breeding in Ireland. This system operates in close association with the ICBF database. ICBF is a full participant in the activities of Interbull, the international dairy genetic evaluation organization and is currently providing leadership for the establishment of Interbeef.

The genetic evaluation system used by ICBF is an across breed system with a single base for each set of traits. For some traits, eg calving and carcass, the evaluation uses data from dairy and suckler herds and the results are comparable across dairy and beef breeds.
With the establishment of clear and agreed breeding objectives the focus ICBF's efforts have moved to improving the availability of relevant data on those animals that are least prone to biases associated with selective recording and selective treatment. That is, commercial producers.

Creation of the ICBF Cattle Breeding Database

At the time ICBF was formed there were a large number of separate computer systems supporting aspects of cattle breeding in Ireland. Each had its own data collection system and supported the information needs of one or other aspect of the cattle breeding industry. For example, each Herd Book (there were 18 at that time) had their own system, each Milk Recording organization (there

were 8 in 1998) had its own system, and DAFF operated separate systems for genetic evaluations and the official calf registration and cattle movement monitoring system (CMMS). These systems used several different animal identifications and held limited cross-references.

ICBF established its cattle breeding database using the IRIS[v] software system from the Dutch Cattle Breeding organisation NRS. Creating the database involved an enormous effort to: negotiate agreements for the sharing of data, to establish shared data collection systems and to consolidate the existing computer files into a single shared database. The key principles under pinning the agreement between organizations to share data are summarized in table 1.

Table 1. Principles of data and information sharing agreement underpinning ICBF database.

No.	Principle
1	Contributors of data to the creation of the database retain "ownership" and can obtain a copy of their data at any time.
2	All data originating on farm, and known first to the farmer, is captured through "Animal Events" a system controlled by ICBF.
3	ICBF operates an industry wide network of systems to facilitate the electronic sharing of relevant data collected for other purposes. Examples include; inseminations, slaughter data, and sale data.
4	All data in the database is available for research subject to a minimal set of conditions.
5	Genetic evaluations are an integral element of the database.
6	Herd owner's control service provider access to herd and animal data.
7	Service providers have access to data and information systems needed by their particular businesses for those herds that have granted access.
8	HerdPlus® is a service provided by ICBF to the herd owner that facilitates access to all data and information relevant to the herd in the database.
9	Service fees are set on the basis of *User Pays* and *Full Cost Recovery*.

ICBF established a team of information technology developers, supported by a number of contractors, to customize IRIS to meet the needs of the Irish breeding industry. This customization has now reached the point where the ICBF database requires no support from NRS. The ICBF cattle breeding database supports, through the use of a range of new technologies[vi], the information needs of milk recording, herd books, AI organizations and cattle farmers. Farmers are able to access their own data in the database through the web through the HerdPlus® service. Figure 1 illustrates the data sources, information outputs and services that are currently supported by this database.

It is important to note that Genetic Evaluations are a peripheral yet integral element of the ICBF database. All data used in the evaluations is sourced from the database and all results returned to the database from whence they are published and distributed.

Implementation of the Animal Events Data Collection System

The Animal Events (AE) data collection system was developed, as part of the overall database development, to replace the overlapping data collection systems operating in 1998. This system was built to remove duplication in data collection, at farm and organization levels, and to ensure all the data required for cattle breeding and other official purposes was collected efficiently and accurately. The AE system collects data on those cattle breeding events, e.g. calving, birth, identification, mating… which are first known to the farmer. Both paper and electronic systems are supported. The data collected in this way is accessible to those participating organizations that provide cattle breeding services to the herd. The AE system has revolutionized cattle breeding data collection in Ireland.

The ICBF database has been fully operational for dairy, beef, milk recording, beef performance recording, genetic evaluations and herd books since 2005. Some 77,000 herds, with 1.8 million calvings, representing ninety percent of the entire Irish cattle herd, were participating in one or more aspects of the database by the end of 2010.

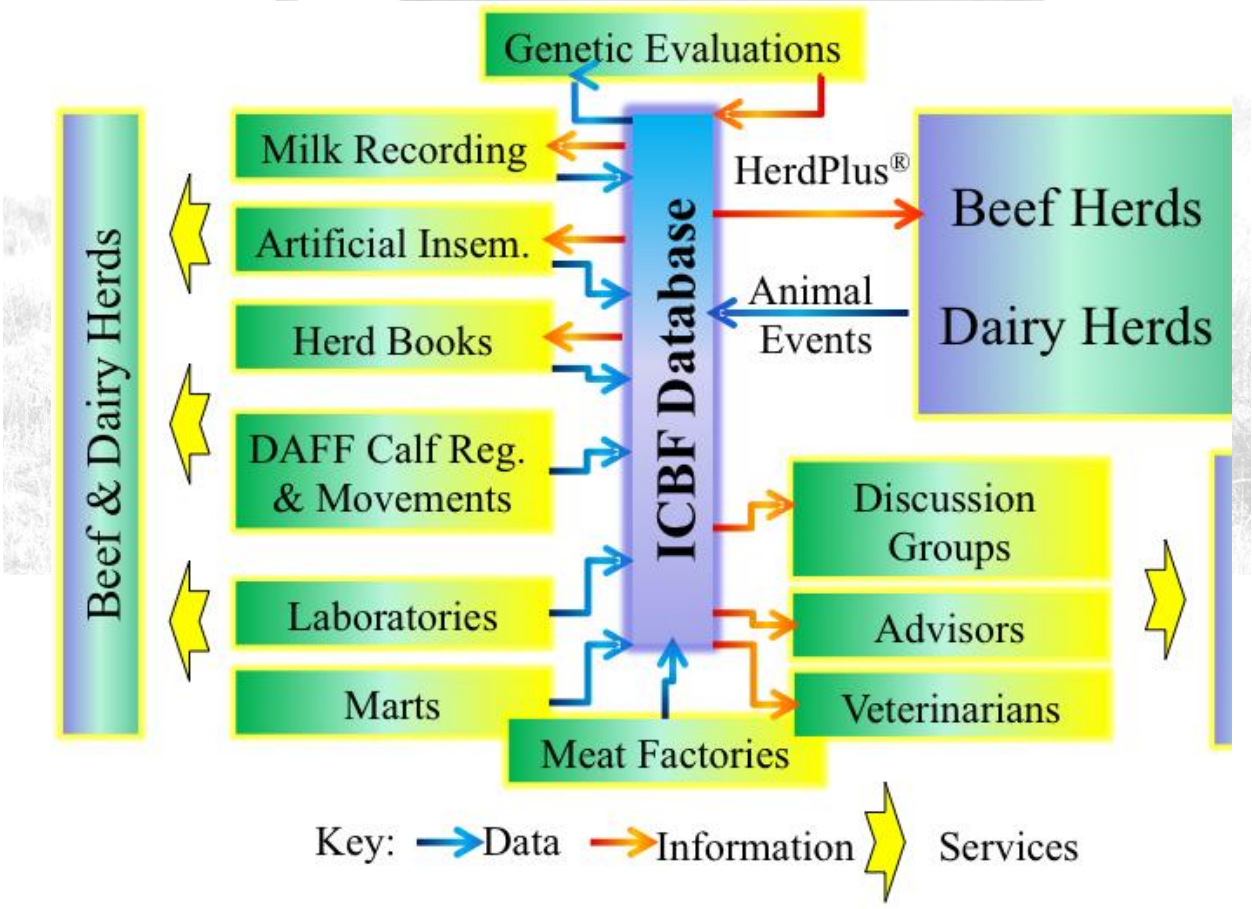

Figure 1. ICBF database showing data sources, information outputs and services to farmers.

LINKAGES WITH OTHER DATA COLLECTION SYSTEMS

The ICBF database has access to data collected by a wide range of organizations for other purposes. The data collected and stored in the ICBF database from these other sources, includes:

- Calf registrations through DAFF – all calves born in Ireland are first registered by DAFF albeit based on data provided by farmers through the AE system, and only then added to the ICBF database. This ensures the official EU identification is available for all calves entering the ICBF database.

- Cattle movements, exports and deaths through CMMS – this eliminates the need for any of the cattle breeding organizations to collect this data. A nightly data feed is provided to ICBF for all movements into or out of herds participating in the database.

- Slaughter data from meat processing plants in Ireland. This includes slaughter date, carcass weight, carcass grade, fat score and, more recently, the two images used in carcass grading.

- Sale data from Marts. This includes dates, weights albeit not always for single animals, and prices.

- Milk records from Milk Recording organizations. The ICBF database is an integral part of the milk recording and result reporting process that operates in Ireland.

- Artificial inseminations recorded by technicians. ICBF has developed a hand-held computer system that links directly to the ICBF database for insemination recording. This system is used by all the main AI field service companies operating in Ireland.

- Linear scoring, dairy and beef, and weight recording services. The same handheld technology used for AI technicians is provided by ICBF for linear scoring and classification services.

These linkages ensure that neither farmers nor organizations are faced with duplicated effort in collecting data that has already been collected for another purpose. The result is a greatly increased availability of data to all participants in the ICBF database.

Animal Welfare, Recording & Breeding Scheme

The Animal Welfare, Recording & Breeding Scheme (AWRBS) was launched in January 2008 by DAFF as a five-year program with the dual objectives of improving animal welfare and improving the scope and quality of data available for beef cattle breeding. Key elements of the scheme included the adoption of best practice animal welfare associated with castration, dehorning and weaning. It was also a requirement of the scheme that ICBF's AE recording system be used for record key events including the sire of calves. In return, the farmer received a payment of, initially €80/cow and more recently, €40/cow. The results of this scheme had a dramatic impact on the availability of sire, calving, weaning and docility data from commercial suckler herds.

Progress

The amount of data collected has risen dramatically as illustrated in table 2. The biggest increase coincides with the introduction of the AWRBS in 2008. The collection of carcass data commenced before 2008 but the advent of the AWRBS has significantly impacted on the number of animals for which the sire is known. This illustrates the benefit and importance of having a database that links animal details recorded at birth with those recorded at slaughter.

Table 2. Progress in data collection. ([1] million, [2] thousand)

Year	Births[1]	Animal events births[1]	Pedigree births[1]	Herds[2]	Carcass - known sire[1]	Carcass – unknown sire[1]	Docility[1]
2003				12	0.010	0.021	0.006
2004	.73	.47	.09	16	0.184	0.307	0.018
2005	.94	.54	.09	22	0.211	0.385	0.021
2006	1.02	.60	.09	29	0.286	0.711	0.016
2007	1.11	.61	.09	33	0.336	0.924	0.014
2008	1.84	1.25	.10	74	0.355	0.944	0.581
2009	1.82	1.31	.10	76	0.422	0.838	0.679
2010	1.79	1.24	.10	77	0.782	0.679	0.696

Interbeef

The Irish beef breeding population encompasses a substantial number of beef breeds. For all of the beef breeds in Ireland there are populations in other countries with larger numbers of recorded animals. The question then is the best strategy for obtaining access to information from these other populations to enable Irish farmers to make well-informed decisions on the importation of genetic material.

We have addressed this question firstly, by establishing a breeding objective for Ireland and an accompanying genetic evaluation system based on Irish data. This system enables us to identify the bloodlines that have performed well under Irish conditions. Secondly, our strategy is to work with other like-minded countries to establish an international network for sharing beef genetic evaluation information. In this respect we have been building on the Interbull model that operates for some 30 countries, six breeds and six trait-sets for dairy cattle.

Our initial work conducted in partnership with other European & Oceanic countries involved research comparing two main strategies:

- MACE which uses the sire evaluation output of national genetic evaluation systems and is the approach used by Interbull for dairy cattle, and
- Phenotypes where the raw performance data is used in a combined multi-trait analysis with each country treated as a different trait. That is, genetic correlations between countries of less than one.

Research by INRA and AGBU demonstrated the practicality and desirability of the latter strategy. That is, a combined analysis of performance data.

Based on these findings Interbeef is now moving to establish a routine international genetic evaluation service for beef breeds and traits. Key elements of the proposal, which has yet to be finalized, are summarized here.

Structure & Operations: Interbeef is a Working Group of ICAR (International Committee of Animal Recording)[vii] and is pursuing five objectives relevant to beef cattle:

a. Provide a forum for sharing knowledge on recording & genetic evaluations.
b. Maintain guidelines & standards for beef cattle performance recording.
c. Conduct international surveys relevant to beef cattle performance recording.
d. Develop international genetic evaluation services.
e. Facilitate the use of genomic selection.

Interbeef is guided by a Steering Committee appointed by the Board of ICAR and includes a geographical and technical spread of enthusiastic supporters. A scientific advisory committee has also been established to give advice on technical issues. The Secretariat is provided by the Interbull Centre based at the Swedish University of Agricultural Science (SLU) in Uppsala. The current annual budget for Interbeef is €100,000 which is currently funded by a number of European beef cattle performance recording and genetic evaluation interests along with a contribution from ICAR.

Participants in Interbeef include Service Users and Research Providers. Services Users are ICAR members who are organisations able to represent, for country, breed & trait combinations: beef performance recording database operations, beef performance & ancestry recording service provider(s) and genetic evaluation service providers. Research Providers are organizations with the knowledge and expertise to assist with achieving the objectives of Interbeef.

Interbeef services are to be based on a Service Agreement which covers; fees, rules for participation, roles & responsibilities, operating procedures, data flows & interfaces, quality control & query support, data protection and methods & models for international genetic evaluations.

The service includes the creation of a database of pedigrees and performance data to be used in research and in the computation of international genetic evaluations for beef breeds and traits. The evaluations are provided to the Service Users for distribution in their respective country-breed-trait-set combination. Interbeef will not be publishing evaluations. That role rests with the Service Users.

Progress: A prototype database has been established and tested for two breeds, six countries and one trait set. Methods for resolving animal identification conflicts have been developed and tested. A multi-trait genetic evaluation system has been developed and tested by INRA, and transferred to the Interbull Centre where it has been implemented using MIX99 software. A call for further data will be issued as soon as the current negotiations on the Interbeef Agreement has been finalized.

Benefits & Costs: The benefits that Interbeef will provide to Service Users include:

- Improved ancestry information – both in terms of accuracy & completeness.
- Improved access to genetic evaluations of animals in other countries.
- Better ability to target selective imports & exports of breeding stock.

- Improved knowledge of beef cattle performance recording and genetic evaluation practices in other countries.
- Improved international collaboration.
- Improved competitiveness of beef production relative to meat production systems based on other species.

The main costs that have been identified for participation in Interbeef include:

- ICAR membership fee - €545/year.
- Service fees which have yet to be finalized.
- Data provision – primarily time of information systems experts.
- Time & travel cost for attending meetings and participating in conferences.

Summary: Interbeef is facilitating the international genetic evaluation of beef breeds & traits. It has considerable potential to increase the accuracy of evaluation for foreign selection candidates. Further information is available on the Interbeef Website – www.interbeef.org.
Ireland is enthusiastically supporting Interbeef because of its potential to improve the profitability of beef production in Ireland through better-informed decisions on selective imports of breeding stock. The main beneficiaries in Ireland are expected to be Irish beef producers.

IGenoP

Ireland, like many other countries and cattle breeding organizations, has identified whole genome assisted selection as potentially a very useful tool in improving the rate of genetic gain, and lowering the cost, for dairy and beef cattle. Again, like many other smaller countries, Ireland has limited capacity to procure training populations of sufficient size with sufficient phenotype data to conduct the research required before genomic selection can be effectively implemented. Part of our strategy to overcome this limitation has been the development of an **i**nternational **geno**type sharing **p**artnership – IGenoP.

Objectives: The primary driver of IGenoP is a set of objectives that enable national or breed specific genetic evaluation service providers to provide a better service to local breeders. The objectives are:

- To increase the accuracy of local genetic evaluations by enabling the use of genomic information.
- To facilitate the local evaluation of selection candidates from other countries for which genomic data is available.
- To ensure local evaluation systems are free from bias due to genomic pre-selection.
- To facilitate an efficient service by local organizations.

Operational Concept: The operational concept is based on a sharing of genotypes that are able to be used by the partners in both research and the provision of evaluations for selection candidates as follows:

- An international collaboration of animal evaluation units to share genotypes.
- Establishment of a database of shared genotypes at the Interbull Centre.
- Use of shared genotypes and phenotypes for training genomic evaluations for each partner.
- Use of shared genotypes, and local SNP estimates, for evaluation of national selection candidates, both local and potential imports.

Operational Prototype: ICBF has established bi-lateral sharing arrangements with a number of countries and organizations. To support this sharing and to test the practicality of the IGenoP concept it has developed a prototype IGenoP database. This database is now operational within

ICBF and is a key element in its routine genomic evaluation service to Irish dairy farmers and the Irish breeding industry. It uses the Interbull ID for animal all identifications and manages all aspects – from locating animals to be genotyped through sample collection, genotyping, genetic evaluation and provision of results to the person seeking the information. The underlying database has the potential to scale-up and is currently supporting the Illumina 3K, 50K and HD genotypes. It also includes a facility for extracting a sub-set of SNP results that are available to the genotyping laboratories for parentage testing and quality control. Our current focus is on improving access for our bi-lateral partners and in facilitating its transfer to Interbull.

Draft Agreement: In anticipation of the transfer of the IGenoP database to the Interbull Centre we have also developed a draft agreement for participation. Some of the key elements of the draft agreement are:

- **Parties:** ICAR, Interbull, Animal Evaluation Units (Contributors) & Laboratories
- **Purpose:** researching, developing and operating genetic evaluation services in the base and scale of a contributor's own country, breed and trait-set combination
- **Decision making:** Interbull Steering Committee, Annual Meeting in accordance with the rules and procedures adopted by ICAR
- **Contributors (AE Units) must:**
    a. Provide all genotypes owned or available to contribute & maintain authorisation(s) for other partners to access these.
    b. Contribute genotypes of bulls (and cows?) exclusively progeny tested in own country.
    c. Provide genomic evaluations in their base and scale on a non-discriminatory basis.
- **Contributors (AE Units) must not:**
    a. Provide genomic evaluations in base & scale of any other partner.
    b. Supply genotypes that they do not own or have the right to supply.
    c. Pass information obtained through IGenoP to third parties.
- **Interbull Centre:**
    a. Securely holds the genotypes in a database and ensures they are available.
    b. Operates a secure website for transfer of genotypes to only those with appropriate authorisation.
    c. Arranges all meetings and provides administrative support.
    d. Determine and collect fees to cover the costs of providing the service.
- **Authorised Laboratory(s) -** Upload genotypes & download parentage SNP's.
- **ICAR:**
    a. Ensures that phenotypic data of relevance to commercial cattle production continues to be collected according to well-defined standards on a worldwide basis.
    b. Provides administrative support by facilitating membership to organisations wishing to become involved as Contributors or Laboratories.

Summary: IGenoP is a service that will enable national Animal Evaluation Units to provide more accurate genomic evaluations for national and international selection candidates.
The prototype established in Ireland has proven the concept.
Interbull working with interested Animal Evaluation Units could have the service available quickly.

SUMMARY

In the last thirteen years the Irish cattle breeding industry has undergone a complete redevelopment of its data gathering and genetic evaluation infrastructure. The key developments include:

- the establishment of ICBF as a working partnership between the organizations involved in Irish cattle breeding,
- the establishment of a shared cattle breeding database,
- the implementation of a data collection and sharing system that eliminates duplication at farm and organization level,
- development of a genetic evaluation system which identifies, on a worldwide basis, those cattle that are most profitable under Irish conditions, and
- supporting and promoting increased international collaboration in beef breeding and genomics.

Irish farmers, research scientists, Herd Books and AI Companies have responded by making good use of the greatly increased amount of information now available. As a result Irish farmers are now able to better exploit the potential of genetics as a tool for improving the profitability of their enterprises.

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iii Breeding objectives for beef cattle in Ireland. P.R. Amer, G. Simm, M.G. Keane, M.G. Diskin, B.W. Wickham. Livestock Production Science 2001 67:223-269.
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vi Cromie A, Wickham B, Coughlan S, & M Burke, 2008. The impact of new technologies on performance recording and genetic evaluation of dairy and beef cattle in Ireland. Proceedings ICAR Biennial Conference, Niagara, June 2008.
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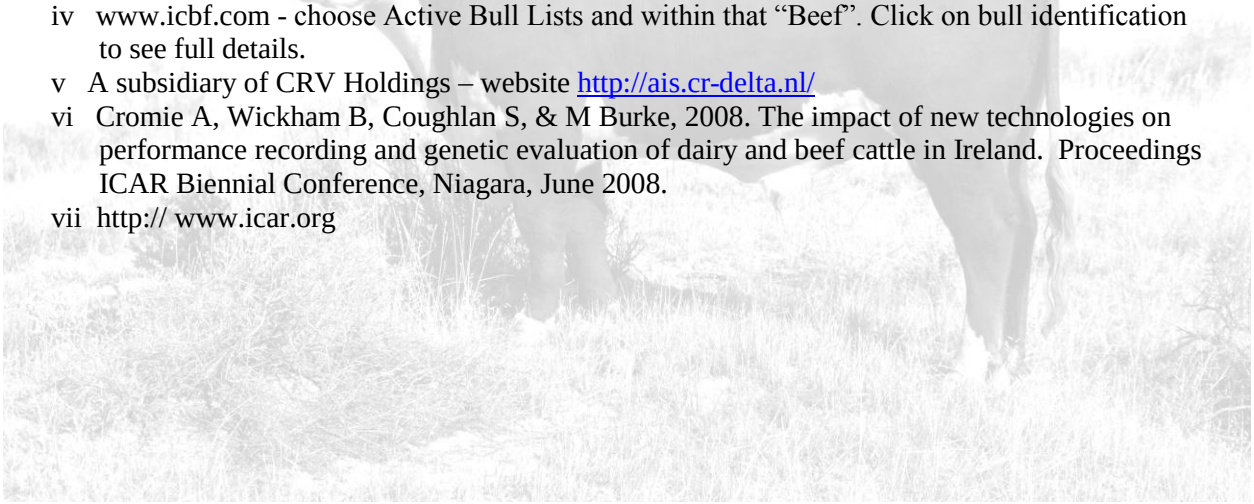

Across-breed EPD tables for the year 2011 adjusted to breed differences for birth year of 2009

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Summary

Factors to adjust the expected progeny differences (EPD) of each of 18 breeds to the base of Angus EPD are reported in the column labeled 6 of Tables 1-7 for birth weight, weaning weight, yearling weight, maternal milk, marbling score, ribeye area, and fat thickness, respectively. An EPD is adjusted to the Angus base by adding the corresponding across-breed adjustment factor in column 6 to the EPD. It is critical that this adjustment be applied only to Spring 2011 EPD. Older or newer EPD may be computed on different bases and, therefore, could produce misleading results. When the base of a breed changes from year to year, its adjustment factor (Column 6) changes in the opposite direction and by about the same amount.

Breed differences are changing over time as breeds put emphasis on different traits and their genetic trends differ accordingly. Therefore, it is necessary to qualify the point in time at which breed differences are represented. Column 5 of Tables 1-7 contains estimates of the differences between the averages of calves of each breed born in year 2009. Any differences (relative to their breed means) in the samples of sires representing those breeds at the U.S. Meat Animal Research Center (USMARC) are adjusted out of these breed difference estimates and the across-breed adjustment factors. The breed difference estimates are reported as progeny differences, e.g., they represent the expected difference in progeny performance of calves sired by average bulls of two different breeds (born in 2009) and out of dams of a third, unrelated breed. In other words, they represent half the differences that would be expected between purebreds of the two breeds.

Introduction

This report is the year 2011 update of estimates of sire breed means from data of the Germplasm Evaluation (GPE) project at USMARC adjusted to a year 2009 basis using EPD from the most recent national cattle evaluations. The 2009 basis year is chosen because yearling records for weight and carcass traits should have been accounted for in EPDs for progeny born in 2009 in the Spring 2011 EPD national genetic evaluations. Factors to adjust Spring 2011 EPD of 18 breeds to a common base were calculated and are reported in Tables 1-3 for birth weight (BWT), weaning weight (WWT), and yearling weight (YWT) and in Table 4 for the maternal milk (MILK) component of maternal weaning weight (MWWT). Tables 5-6 summarize the factors for marbling score (MAR), ribeye area (REA), and fat thickness (FAT).

The across-breed table adjustments apply **only** to EPD for most recent (spring, 2011) national cattle evaluations. Serious errors can occur if the table adjustments are used with earlier EPD which may have been calculated with a different within-breed base.

The following describes the changes that have occurred since the update released in 2010 (Kuehn et al., 2010). The most significant changes continue to relate to the new sampling in the USMARC GPE program. Progeny from 16 of the 18 breeds involved in the across-breed EPD process have been born (approximately 40/yr) and improve the accuracy in predicting the differences between these breeds. These 16 breeds are the breeds that register the most cattle and have national genetic evaluations for production traits. Sires are sampled on a continuous basis (every 2 years). The first progeny of this new sampling

were born in Fall 2007. Adjustment factors for yearling weight and carcass traits were estimated for Santa Gertrudis and Chiangus for the first time last year. Progeny number increased for each of these breeds by approximately 35%. As numbers of bulls sampled and numbers of progeny born for these two breeds are smaller than for other breeds, their factors are the most susceptible to year-to-year changes as more progeny are produced. Maternal milk for these breeds will also be reported in future iterations of this report as daughters from these matings begin to have calves of their own. Chiangus in particular had relatively large changes in their USMARC breed of sire estimates (labeled column 3 in Tables 2 and 3) for weaning or yearling weights or both compared to last year.

Changes in national cattle evaluation can also cause across breed adjustment factors to change relative to previous years. Both Braunvieh and Chiangus had a base shift in their EPDs this year relative to the EPDs used in Kuehn et al. (2010). These changes primarily cause the adjustment (labeled column 6; Tables 1-7) factors for these breeds. Changes to sire breed differences (labeled column5) occur due to changes the mean EPDs of sires sampled for GPE relative to the breed average and due to changes in the sire breed solution (labeled column 3). Changes in the mean EPD of traits in Angus (to which every breed of sire solution difference is deviated from) can also cause changes in the sire bred differences reported. Most changes compared to Kuehn et al. (2010) were relatively minor in this year's update.

Materials and Methods

All calculations were as outlined in the 2010 BIF Guidelines. The basic steps were given by Notter and Cundiff (1991) with refinements by Núñez-Dominguez et al. (1993), Cundiff (1993, 1994), Barkhouse et al. (1994, 1995), Van Vleck and Cundiff (1997–2006), and Kuehn et al. (2007-2010). Estimates of variance components, regression coefficients, and breed effects were obtained using the MTDFREML package (Boldman et al., 1995). All breed solutions are reported as differences from Angus. The table values of adjustment factors to add to within-breed EPD are relative to Angus.

Models for Analysis of USMARC Records: An animal model with breed effects represented as genetic groups was fitted to the GPE data set (Arnold et al., 1992; Westell et al., 1988). In the analysis, all AI sires (sires used via artificial insemination) were assigned a genetic group according to their breed of origin. Due to lack of pedigree, dams mated to the AI sires and natural service bulls mated to F_1 females were also assigned to separate genetic groups (i.e., Hereford dams were assigned to different genetic groups than Hereford AI sires). Cows from Hereford selection lines (Koch et al., 1994) were used in Cycle IV of GPE and assigned into their own genetic groups. Through Cycle VIII, most dams were from Hereford, Angus, or MARCIII (1/4 Angus, 1/4 Hereford, 1/4 Pinzgauer, 1/4 Red Poll) composite lines. In order to be considered in the analysis, sires had to have an EPD for the trait of interest. All AI sires were considered unrelated for the analysis in order to adjust resulting genetic group effects by the average EPD of the sires.

Fixed effects in the models for BWT, WWT (205-d), and YWT (365-d) included breed (fit as genetic groups) and maternal breed (WWT only), year and season of birth by GPE cycle by age of dam (2, 3, 4, 5-9, >10 yr) combination (204), sex (heifer, bull, steer; steers were combined with bulls for BWT), a covariate for heterosis, and a covariate for day of year at birth of calf. Models for WWT also included a fixed covariate for maternal heterosis. Random effects included animal and residual error except for the analysis of WWT which also included a random maternal genetic effect and a random permanent environmental effect.

For the carcass traits (MAR, REA, and FAT), breed (fit as genetic groups), sex (heifer, steer) and slaughter date (224) were included in the model as fixed effects. Fixed covariates included slaughter age and heterosis. Random effects were animal and residual error. To be included, breeds had to report carcass EPD on a carcass basis using age-adjusted endpoints, as suggested in the 2010 BIF Guidelines.

The covariates for heterosis were calculated as the expected breed heterozygosity for each animal based on the percentage of each breed of that animal's parents. In other words, it is the probability that, at any location in the genome, the animal's two alleles originated from two different breeds. Heterosis is assumed to be proportional to breed heterozygosity. For the purpose of heterosis calculation, AI and dam breeds were assumed to be the same breed and Red Angus was assumed the same breed as Angus. For purposes of heterosis calculation, composite breeds were considered according to nominal breed composition. For example, Brangus (3/8 Brahman, 5/8 Angus) × Angus is expected to have 3/8 as much heterosis as Brangus × Hereford.

Variance components were estimated with a derivative-free REML algorithm with genetic group solutions obtained at convergence. Differences between resulting genetic group solutions for AI sire breeds were divided by two to represent the USMARC breed of sire effects in Tables 1-7. Resulting breed differences were adjusted to current breed EPD levels by accounting for the average EPD of the AI sires of progeny/grandprogeny, etc. with records. Average AI sire EPD were calculated as a weighted average AI sire EPD from the most recent within breed genetic evaluation. The weighting factor was the sum of relationship coefficients between an individual sire and all progeny with performance data for the trait of interest relative to all other sires in that breed.

For all traits, regression coefficients of progeny performance on EPD of sire for each trait were calculated using an animal model with EPD sires excluded from the pedigree. Genetic groups were assigned in place of sires in their progeny pedigree records. Each sire EPD was 'dropped' down the pedigree and reduced by ½ depending on the number of generations each calf was removed from an EPD sire. In addition to regression coefficients for the EPDs of AI sires, models included the same fixed effects described previously. Pooled regression coefficients, and regression coefficients by sire breed were obtained. These regression coefficients are monitored as accuracy checks and for possible genetic by environment interactions. The pooled regression coefficients were used as described in the next section to adjust for differences in management at USMARC as compared to seedstock production (e.g., YWT of males at USMARC are primarily on a slaughter steer basis, while in seedstock field data they are primarily on a breeding bull basis). For carcass traits, MAR, REA, and FAT, regressions were considered too variable and too far removed from 1.00. Therefore, the regressions were assumed to be 1.00 until more data is added to reduce the impact of sampling errors on prediction of these regressions. However, the resulting regressions are still summarized.

Records from the USMARC GPE Project are not used in calculation of within-breed EPD by the breed associations. This is critical to maintain the integrity of the regression coefficient. If USMARC records were included in the EPD calculations, the regressions would be biased upward.

Adjustment of USMARC Solutions: The calculations of across-breed adjustment factors rely on breed solutions from analysis of records at USMARC and on averages of within-breed EPD from the breed associations. The basic calculations for all traits are as follows:

USMARC breed of sire solution (1/2 breed solution) for breed i (USMARC (i)) converted to an industry scale (divided by b) and adjusted for genetic trend (as if breed average bulls born in the base year had been used rather than the bulls actually sampled):

$$M_i = \text{USMARC (i)}/b + [\text{EPD(i)}_{YY} - \text{EPD(i)}_{USMARC}].$$

Breed Table Factor (A_i) to add to the EPD for a bull of breed i:

$$A_i = (M_i - M_x) - (\text{EPD(i)}_{YY} - \text{EPD(x)}_{YY}).$$

where,

USMARC(i) is solution for effect of sire breed i from analysis of USMARC data,

$EPD(i)_{YY}$ is the average within-breed 2011 EPD for breed i for animals born in the base year (YY, which is two years before the update; e.g., YY = 2009 for the 2011 update),

$EPD(i)_{USMARC}$ is the weighted (by total relationship of descendants with records at USMARC) average of 2011 EPD of bulls of breed i having descendants with records at USMARC,
b is the pooled coefficient of regression of progeny performance at USMARC on EPD of sire (for 2009: 1.15, 0.86, 1.04, and 1.17 BWT, WWT, YWT, and MILK, respectively; 1.00 was applied to MAR, REA, and FAT data),
i denotes sire breed i, and
x denotes the base breed, which is Angus in this report.

Results

Heterosis: Heterosis was included in the statistical model as a covariate for all traits. Maternal heterosis was also fit as a covariate in the analysis of weaning weight. Resulting estimates were 1.58 lb, 12.75 lb, 17.16 lb, 0.030 marbling score units (i.e. 4.00 = Sl^{00}, 5.00 = Sm^{00}), 0.27 in^2, and 0.039 in for BWT, WWT, YWT, MAR, REA, and FAT respectively. These estimates are interpreted as the amount by which the performance of an F_1 is expected to exceed that of its parental breeds. The estimate of maternal heterosis for WWT was 16.59 lb.

Across-breed adjustment factors: Tables 1, 2, and 3 (for BWT, WWT, and YWT) summarize the data from, and results of, USMARC analyses to estimate breed of sire differences on a 2009 birth year basis. The column labeled 6 of each table corresponds to the Across-breed EPD Adjustment Factor for that trait. Table 4 summarizes the analysis of MILK. Tables 5, 6, and 7 summarize data from the carcass analyses (MAR, REA, FAT). Because of the accuracy of sire carcass EPDs and the greatest percentage of data being added to carcass traits, sire effects and adjustment factors are more likely to change for carcass traits in the future.

Column 5 of each table represents the best estimates of sire breed differences for calves born in 2009 on an industry scale. These breed difference estimates are reported as progeny differences, e.g., they represent the expected difference in progeny performance of calves sired by average bulls (born in 2009) of two different breeds and out of dams of a third, unrelated breed. Thus, they represent half the difference expected between purebreds of the respective breeds.

In each table, breed of sire differences were added to the raw mean of Angus-sired progeny born 2006 through 2010 at USMARC (Column 4) to make these differences more interpretable to producers on scales they are accustomed to.

Across-breed EPD Adjustment Factor Example: Adjustment factors can be applied to compare the genetic potential of sires from different breeds. Suppose the EPD for weaning weight for a Limousin bull is +42.1 (which is below the year 2009 average of 42.9 for Limousin) and for a Hereford bull is +44.0 (which is above the year 2009 average of 43.0 for Hereford). The across-breed adjustment factors in the last column of Table 1 are -1.5 for Hereford and 0.9 for Limousin. Then the adjusted EPD for the Limousin bull is 42.1 + 0.9) = 43.0 and for the Hereford bull is 44.0 + (-1.5) = 42.5. The expected weaning weight difference when both are mated to another breed of cow, e.g., Angus, would be 43.0 – 42.5 = 0.5 lb. The differences in true breeding value between two bulls with similar within-breed EPDs

are primarily due to differences in the genetic base from which those within-breed EPDs are computed.

Birth Weight: The range in estimated breed of sire differences for BWT ranged from 0.3 lb for Red Angus to 7.1 lb for Charolais and 11.3 lb for Brahman. Angus continued to have the lowest estimated sire effect for birth weight (Table 1, column 5). The relatively heavy birth weights of Brahman-sired progeny would be expected to be offset by favorable maternal effects reducing birth weight if progeny were from Brahman or Brahman cross dams which would be an important consideration in crossbreeding programs involving Brahman cross females. Changes in breed of sire effects were generally small, less than 1 lb for all breeds relative to last year's update (Kuehn et al., 2010).

Weaning Weight: Breed effects on weaning weight remained fairly similar to last year for most breeds—all of the 17 sire breed differences were within 10 lb of the values in Kuehn et al. (2010). The average Chiangus sire breed effect was predicted 9.3 lb lighter than reported in Kuehn et al. (2010) relative to Angus. In this update, Chiangus were predicted to be 28.5 lb lighter than Angus as a sire breed; last year Chiangus were predicted to be 19.2 lb less than Angus. Sire breed effects of Braunvieh were 8.3 lb less than last year, likely due to increased sampling of sires and increases in their progeny at USMARC relative to last year. Braunvieh effects seem to be more affected by sampling since their reintroduction into the GPE project in 2007 as their sire breed mean increased by ~8 in last year's update relative to Kuehn et al. (2009). Further sampling and increases in Braunvieh-sired progeny should stabilize these year-to-year changes.

Yearling Weight: Genetic trends for yearling weight in Angus continued to increase at a rate faster than that of other breeds (from 81.5 lb average EPD in 2010 to 83 in 2011). Consequently, all breed differences relative to Angus (Table 3, column 5) decrease by at least 1.5 relative to Angus before adjustments for their own breed effect and genetic trend. Most breed of sire effect changes were relatively small (less than 10 lb) relative to Kuehn et al. (2011). The only exception was Chiangus which decreased in its sire difference relative to Angus by 13.4 lb. This was only the second year Chaingus-sired progeny were used to predict yearling weight differences; 50% more Chiangus-sired progeny were added relative to last year. Hence, their estimated breed solution from USMARC (Table 3, column 3) is still highly variable relative to most of the other breeds.

Maternal Milk: The changes from last year for milk for the current base year (Table 4, column 5) were again generally small. Differences may be more substantial in the future as more heifers from the most recent GPE sampling of bulls reach calving age. The genetic trend for milk for Angus, like that for yearling weight, has been steep relative to breeds such as Simmental and Gelbvieh. Thus sire breed differences between Simmental or Gelbvieh and Angus are relatively small compared to estimates 15 to 30 years ago.

Marbling: Marbling score was estimated to be highest in Angus (Table 5, column 5) with Red Angus being the most similar (~0.4 score units lower) of recently sampled breeds. Continental breeds were estimated to be one-half to a full marbling score lower than Angus with the exception of Salers. Progeny from Hereford sires were predicted to have the lowest marbling score relative to other British breeds.

Ribeye Area: Continental breeds had higher ribeye area estimates relative to the British breeds (Table 6, column 5) as would be expected. The estimates of sire breed differences were similar to last year for almost all breeds.

Fat Thickness: Progeny of Continental breeds had 0.1 to 0.2 in less fat at slaughter than British breeds (Table 7, Column 5). All other breeds were leaner than Angus. Charolais, Salers, Maine Anjou, and Simmental were predicted to be the leanest breeds among the 12 breeds analyzed for carcass traits. Limousin was not included in the FAT analysis because they do not report an EPD for FAT. Changes in

breed of sire effects relative to Angus were all minor compared to the previous year (Kuehn et al., 2010) except for Braunvieh whose breed mean EPD changed relative to last year's analysis by a significant amount (increased by over 0.1 in). This base change actually occurred in 2010 but was not input correctly in Kuehn et al (2010).

Accuracies and Variance Components: Table 8 summarizes the average Beef Improvement Federation (BIF) accuracy for bulls with progeny at USMARC weighted appropriately by average relationship to animals with phenotypic records. South Devon bulls had relatively small accuracy for all traits as did Hereford and Brahman bulls. Charolais and Gelbvieh bulls had low accuracy for yearling weight and milk. Accuracies for carcass traits, as expected, were considerably lower than accuracies for growth traits in general. The sires sampled recently in the GPE program have generally been higher accuracy sires, so the average accuracies should continue to increase over the next several years.

Table 9 reports the estimates of variance components from the animal models that were used to obtain breed of sire and breed of MGS solutions. Heritability estimates for BWT, WWT, YWT, and MILK were 0.58, 0.18, 0.46, and 0.16, respectively. Heritability estimates for MAR, REA, and FAT were 0.45, 0.47, and 0.40, respectively.

Regression Coefficients: Table 10 updates the coefficients of regression of records of USMARC progeny on sire EPD for BWT, WWT, and YWT which have theoretical expected values of 1.00. The standard errors of the specific breed regression coefficients are large relative to the regression coefficients. Large differences from the theoretical regressions, however, may indicate problems with genetic evaluations, identification, or sampling. The pooled (overall) regression coefficients of 1.15 for BWT, 0.86 for WWT, and 1.04 for YWT were used to adjust breed of sire solutions to the base year of 2009. These regression coefficients are reasonably close to expected values of 1.0. Deviations from 1.00 are believed to be due to scaling differences between performance of progeny in the USMARC herd and of progeny in herds contributing to the national genetic evaluations of the 18 breeds. Breed differences calculated from the USMARC data are divided by these regression coefficients to put them on an industry scale. A regression greater than one suggests that variation at USMARC is greater than the industry average, while a regression less than one suggests that variation at USMARC is less than the industry average. Reasons for differences in scale can be rationalized. For instance, cattle, especially steers, are fed at higher energy rations than some seedstock animals in the industry. Also, in several recent years, calves have been weaned earlier than 205 d at USMARC, likely reducing the variation in weaning weight of USMARC calves relative to the industry.

The coefficients of regression for MILK are also shown in Table 10. Several sire (MGS) breeds have regression coefficients considerably different from the theoretical expected value of 1.00 for MILK. Standard errors, however, for the regression coefficients by breed are large except for Angus and Hereford. The pooled regression coefficient of 1.17 for MILK is reasonably close to the expected regression coefficient of 1.00.

Regression coefficients derived from regression of USMARC steer progeny records on sire EPD for MAR, REA, and FAT are shown in Table 11. Each of these coefficients has a theoretical expected value of 1.00. Compared to growth trait regression coefficients, the standard errors even on the pooled estimates are high, though they have decreased from the previous year. Each coefficient deviates from the expected value of 1.00 more than the growth trait coefficients with the exception of REA. Therefore, the theoretical estimate of 1.00 was used to derive breed of sire differences and EPD adjustment factors. The pooled regression estimates would cause USMARC differences to be larger on an industry scale for MAR and smaller on an industry scale for FAT. These regressions will change considerably in upcoming across-breed analyses as more data is added to the GPE program and new sires from most of these breeds are sampled.

Prediction Error Variance of Across-Breed EPD: Prediction error variances were not included in the report due to a larger number of tables included with the addition of carcass traits. These tables did not change substantially from those reported in previous proceedings (Kuehn et al., 2007; available online at http://www.beefimprovement.org/proceedings.html). An updated set of tables is available on request (Larry.Kuehn@ars.usda.gov).

Implications

Bulls of different breeds can be compared on a common EPD scale by adding the appropriate across-breed adjustment factor to EPD produced in the most recent genetic evaluations for each of the 18 breeds. The across-breed EPD are most useful to commercial producers purchasing bulls of two or more breeds to use in systematic crossbreeding programs. Uniformity in across-breed EPD should be emphasized for rotational crossing. Divergence in across-breed EPD for direct weaning weight and yearling weight should be emphasized in selection of bulls for terminal crossing. Divergence favoring lighter birth weight may be helpful in selection of bulls for use on first calf heifers. Accuracy of across-breed EPD depends primarily upon the accuracy of the within-breed EPD of individual bulls being compared.

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Table 1. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2009 base and factors to adjust within breed EPD to an Angus equivalent – BIRTH WEIGHT (lb)

	Number		Ave. Base EPD		Breed Soln at USMARC	BY 2009 Sire Breed	BY 2009 Sire Breed	Factor to adjust EPD
			Breed	USMARC				
	AI	Direct	2009	Bulls	(vs Ang)	Average	Difference[a]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	126	1680	2.0	1.8	0.0	91.8	0.0	0.0
Hereford	131	2117	3.6	2.2	3.7	96.2	4.4	2.8
Red Angus	37	512	0.0	-1.1	-0.8	92.1	0.3	2.3
Shorthorn	43	337	2.4	1.4	6.4	98.1	6.3	5.9
South Devon	15	153	2.8	1.9	5.0	96.8	5.0	4.2
Beefmaster	34	267	0.4	1.1	7.0	97.0	5.2	6.8
Brahman	49	589	1.9	0.6	11.8	103.1	11.3	11.4
Brangus	33	261	0.8	1.1	4.0	94.7	2.9	4.1
Santa Gertrudis	19	148	0.5	1.1	8.1	98.1	6.3	7.8
Braunvieh	29	339	-0.1	0.6	5.2	95.4	3.6	5.7
Charolais	95	968	0.6	0.3	8.1	98.9	7.1	8.5
Chiangus	17	159	2.1	2.7	5.2	95.5	3.7	3.6
Gelbvieh	66	879	1.3	1.1	3.6	94.9	3.1	3.8
Limousin	59	942	1.8	1.0	3.2	95.2	3.4	3.6
Maine Anjou	37	330	1.9	4.2	7.7	96.0	4.2	4.3
Salers	46	323	1.8	2.6	3.1	93.6	1.8	2.0
Simmental	66	918	0.9	2.0	5.7	95.5	3.7	4.8
Tarentaise	7	199	1.9	1.9	2.1	93.5	1.7	1.8

Calculations:

(4) = (3) / b + [(1) – (2)] + (Recent Raw Angus Mean: 91.6 lb) with b = 1.11

(5) = (4) – (4, Angus)

(6) = (5) – (5, Angus) – [(1) – (1, Angus)]

[a]The breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 2. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2009 base and factors to adjust within breed EPD to an Angus equivalent – WEANING WEIGHT (lb)

	Number		Ave. Base EPD		Breed Soln at USMARC	BY 2009 Sire Breed	BY 2009 Sire Breed	Factor to adjust EPD
			Breed	USMARC				
	AI	Direct	2009	Bulls	(vs Ang)	Average	Difference[a]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	125	1543	46.0	25.6	0.0	594.9	0.0	0.0
Hereford	129	1959	43.0	25.4	-1.4	590.4	-4.5	-1.5
Red Angus	37	497	30.9	25.6	-1.3	578.3	-16.6	-1.5
Shorthorn	43	322	15.3	12.5	4.0	582.0	-12.8	17.9
South Devon	15	134	41.4	23.4	1.3	594.1	-0.8	3.8
Beefmaster	34	260	9.0	14.6	21.8	594.3	-0.6	36.4
Brahman	49	507	14.8	7.1	18.8	604.1	9.2	40.4
Brangus	33	252	22.6	22.4	10.0	586.4	-8.5	14.9
Santa Gertrudis	19	142	4.0	8.8	15.0	587.1	-7.8	34.2
Braunvieh	29	321	6.2	5.0	-1.9	573.5	-21.3	18.5
Charolais	94	872	24.2	12.5	23.2	613.2	18.3	40.1
Chiangus	17	150	32.0	37.1	-2.6	566.3	-28.5	-14.5
Gelbvieh	66	825	41.0	33.6	10.2	593.8	-1.1	3.9
Limousin	59	863	42.9	27.5	2.3	592.6	-2.2	0.9
Maine Anjou	37	305	39.7	41.5	5.2	578.8	-16.1	-9.8
Salers	46	307	40.2	31.5	4.8	588.8	-6.1	-0.3
Simmental	65	835	32.1	25.7	22.3	606.9	12.0	25.9
Tarentaise	7	191	16.0	-5.6	1.3	597.6	2.8	32.8

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 574.5 lb) with b = 0.84

(5) = (4) – (4, Angus)

(6) = (5) – (5, Angus) – [(1) – (1, Angus)]

[a]The breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 3. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2009 base and factors to adjust within breed EPD to an Angus equivalent – YEARLING WEIGHT (lb)

	Number		Ave. Base EPD		Breed Soln at USMARC	BY 2009 Sire Breed	BY 2009 Sire Breed	Factor to adjust EPD
			Breed	USMARC				
	AI	Direct	2009	Bulls	(vs Ang)	Average	Difference[a]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	122	1412	83.0	47.8	0.0	1031.3	0.0	0.0
Hereford	125	1822	71.0	42.8	-23.0	1002.2	-29.1	-17.1
Red Angus	36	453	58.2	46.9	-10.0	997.8	-33.5	-8.7
Shorthorn	42	286	24.8	20.1	14.6	1014.8	-16.5	41.7
South Devon	15	134	77.3	50.3	-2.5	1020.7	-10.6	-4.9
Beefmaster	25	164	14.0	22.9	13.6	1000.2	-31.1	37.9
Brahman	43	434	23.8	11.7	-32.9	976.6	-54.7	4.5
Brangus	24	161	44.8	40.9	7.4	1007.1	-24.2	14.0
Santa Gertrudis	15	115	5.0	10.5	-13.0	978.1	-53.2	24.8
Braunvieh	21	289	12.2	11.1	-14.7	983.1	-48.2	22.6
Charolais	89	782	42.3	24.1	26.2	1039.5	8.2	48.9
Chiangus	14	123	59.5	66.5	-15.8	973.9	-57.4	-33.9
Gelbvieh	63	779	75.0	60.6	2.4	1012.8	-18.4	-10.4
Limousin	53	803	80.2	56.4	-23.7	997.2	-34.1	-31.3
Maine Anjou	34	280	78.1	84.2	8.3	997.9	-33.4	-28.5
Salers	44	280	77.4	60.5	2.2	1015.1	-16.1	-10.5
Simmental	62	737	57.9	47.4	25.1	1030.7	-0.6	24.5
Tarentaise	7	189	28.6	-3.6	-30.1	999.4	-31.9	22.5

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 996.1 lb) with b = 1.06

(5) = (4) – (4, Angus)

(6) = (5) – (5, Angus) – [(1) – (1, Angus)]

[a]The breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 4. Breed of maternal grandsire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2009 base and factors to adjust within breed EPD to an Angus equivalent – MILK (lb)

	Number			Ave. Base EPD		Breed Soln at USMARC	BY 2009 Sire Breed	BY 2009 Sire Breed	Factor to adjust EPD
	AI	Direct	Direct	Breed 2009	USMARC Bulls	(vs Ang)	Average	Difference[a]	To Angus
Breed	Sires	Gpr	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	104	2748	559	22.0	11.4	0.0	585.1	0.0	0.0
Hereford	112	3526	747	17.0	8.7	-25.1	561.4	-23.7	-18.7
Red Angus	25	537	127	16.7	13.0	0.2	578.3	-6.8	-1.5
Shorthorn	31	277	82	2.3	5.0	15.5	585.1	-0.1	19.6
South Devon	14	373	70	22.8	19.2	2.4	580.2	-5.0	-5.8
Beefmaster	20	271	52	2.0	-1.6	-12.2	567.7	-17.4	2.6
Brahman	36	778	186	6.3	4.3	16.8	590.9	5.7	21.4
Brangus	19	249	43	10.7	4.3	-6.8	575.1	-10.0	1.3
Braunvieh	15	555	105	0.4	-0.8	20.8	593.5	8.4	30.0
Charolais	69	1286	264	6.4	3.4	-3.9	574.1	-11.0	4.6
Gelbvieh	51	1261	267	18.0	17.2	18.7	591.3	6.2	10.2
Limousin	45	1415	284	20.9	18.3	-7.6	570.6	-14.5	-13.4
Maine Anjou	25	540	98	19.5	24.0	10.4	578.9	-6.2	-3.7
Salers	35	373	100	19.5	22.1	13.2	583.1	-2.0	0.5
Simmental	49	1396	271	3.6	7.3	13.1	582.0	-3.1	15.3
Tarentaise	6	367	80	0.6	5.3	18.6	585.7	0.5	21.9

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 574.5lb) with b = 1.20

(5) = (4) – (4, Angus)

(6) = (5) – (5, Angus) – [(1) – (1, Angus)]

[a]The breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 5. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2009 base and factors to adjust within breed EPD to an Angus equivalent – MARBLING (marbling score units[a])

	Number		Ave. Base EPD		Breed Soln	BY 2009	BY 2009	Factor to
			Breed	USMARC	at USMARC	Sire Breed	Sire Breed	adjust EPD
	AI	Direct	2009	Bulls	(vs Ang)	Average	Difference[b]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	104	621	0.43	0.19	0.00	5.80	0.00	0.00
Hereford	121	838	0.04	-0.01	-0.51	5.09	-0.71	-0.32
Red Angus	35	142	0.07	0.15	-0.04	5.44	-0.36	0.00
Shorthorn	41	152	-0.02	0.01	-0.27	5.25	-0.55	-0.10
South Devon	13	49	0.30	-0.10	-0.20	5.76	-0.05	0.08
Santa Gertrudis	13	52	0.00	-0.02	-0.86	4.73	-1.07	-0.64
Braunvieh	21	139	0.12	0.00	-0.45	5.24	-0.56	-0.25
Charolais	36	157	0.01	-0.05	-0.64	4.98	-0.82	-0.40
Chiangus	14	57	0.09	0.01	-0.56	5.08	-0.72	-0.38
Limousin	51	301	-0.04	-0.08	-0.96	4.64	-1.16	-0.69
Maine Anjou	31	138	0.20	0.13	-0.83	4.80	-1.00	-0.77
Salers	40	132	0.10	-0.34	-0.66	5.34	-0.46	-0.13
Simmental	59	324	0.15	0.07	-0.63	5.01	-0.79	-0.51

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 5.56) with b = 1.00

(5) = (4) – (4, Angus)

(6) = (5) – (5, Angus) – [(1) – (1, Angus)]

[a]4.00 = Sl^{00}, 5.00 = Sm^{00}

[b]The breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 6. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2009 base and factors to adjust within breed EPD to an Angus equivalent – RIBEYE AREA (in^2)

	Number		Ave. Base EPD		Breed Soln	BY 2009	BY 2009	Factor to
			Breed	USMARC	at USMARC	Sire Breed	Sire Breed	adjust EPD
	AI	Direct	2009	Bulls	(vs Ang)	Average	Difference[a]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	104	622	0.21	0.05	0.00	12.77	0.00	0.00
Hereford	121	838	0.22	-0.04	-0.17	12.70	-0.06	-0.07
Red Angus	35	142	0.07	-0.16	-0.33	12.51	-0.26	-0.12
Shorthorn	41	152	0.07	0.01	0.20	12.87	0.10	0.24
South Devon	13	49	0.21	0.21	0.29	12.90	0.13	0.13
Santa Gertrudis	13	53	0.00	-0.03	-0.26	12.38	-0.39	-0.18
Braunvieh	21	139	0.10	0.02	0.89	13.58	0.81	0.92
Charolais	36	158	0.18	0.09	0.91	13.61	0.84	0.87
Chiangus	14	58	0.02	0.07	0.60	13.16	0.40	0.59
Limousin	51	302	0.49	0.27	1.27	14.10	1.34	1.06
Maine Anjou	31	138	0.15	0.15	1.05	13.66	0.90	0.96
Salers	40	133	0.03	0.03	0.79	13.40	0.63	0.81
Simmental	59	325	0.10	-0.05	0.85	13.61	0.84	0.95

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 12.61 in^2) with b = 1.00

(5) = (4) – (4, Angus)

(6) = (5) – (5, Angus) – [(1) – (1, Angus)]

[a]The breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 7. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2009 base and factors to adjust within breed EPD to an Angus equivalent – FAT THICKNESS (in)

	Number		Ave. Base EPD		Breed Soln	BY 2009	BY 2009	Factor to
			Breed	USMARC	at USMARC	Sire Breed	Sire Breed	adjust EPD
	AI	Direct	2009	Bulls	(vs Ang)	Average	Difference[a]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	104	622	0.012	0.002	0.000	0.578	0.000	0.000
Hereford	121	838	0.002	-0.003	-0.056	0.517	-0.061	-0.051
Red Angus	35	142	-0.034	-0.010	-0.050	0.494	-0.084	-0.038
Shorthorn	41	152	-0.010	0.000	-0.153	0.405	-0.173	-0.151
South Devon	13	49	0.010	0.008	-0.107	0.463	-0.115	-0.113
Santa Gertrudis	13	53	0.000	0.002	-0.146	0.420	-0.158	-0.146
Braunvieh	21	139	0.115	-0.012	-0.185	0.510	-0.068	-0.171
Charolais	36	158	-0.001	-0.001	-0.225	0.343	-0.235	-0.222
Chiangus	14	58	0.010	0.009	-0.165	0.404	-0.174	-0.172
Maine Anjou	31	138	0.000	-0.016	-0.226	0.358	-0.221	-0.209
Salers	40	133	0.000	-0.004	-0.223	0.349	-0.229	-0.217
Simmental	59	325	0.015	0.011	-0.210	0.363	-0.215	-0.218

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 0.568 in) with b = 1.00

(5) = (4) – (4, Angus)

(6) = (5) – (5, Angus) – [(1) – (1, Angus)]

[a]The breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

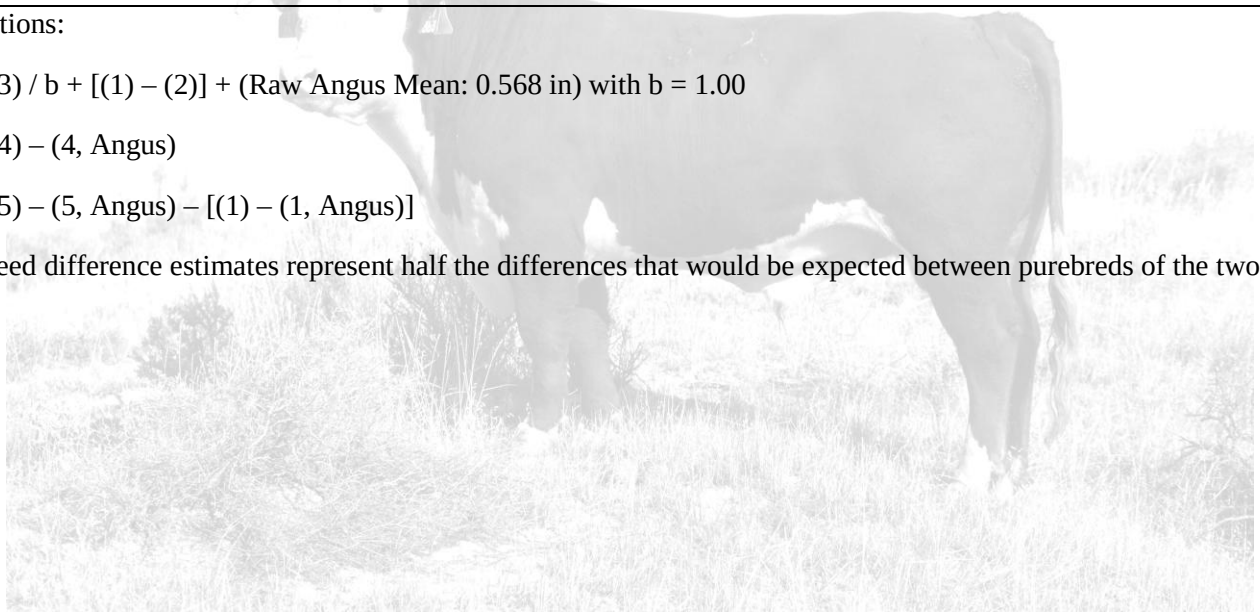

Table 8. Mean weighted[a] accuracies for birth weight (BWT), weaning weight (WWT), yearling weight (YWT), maternal weaning weight (MWWT), milk (MILK), marbling (MAR), ribeye area (REA), and fat thickness (FAT) for bulls used at USMARC

Breed	BWT	WWT	YWT	MILK	MAR	REA	FAT
Angus	0.78	0.75	0.69	0.66	0.50	0.49	0.47
Hereford	0.63	0.59	0.59	0.53	0.23	0.37	0.27
Red Angus	0.91	0.90	0.90	0.88	0.70	0.68	0.79
Shorthorn	0.80	0.79	0.73	0.76	0.61	0.59	0.54
South Devon	0.37	0.41	0.37	0.44	0.02	0.05	0.05
Beefmaster	0.86	0.89	0.86	0.75			
Brahman	0.65	0.66	0.59	0.57			
Brangus	0.87	0.81	0.79	0.68			
Santa Gertrudis	0.87	0.84	0.77		0.32	0.52	0.44
Braunvieh	0.85	0.86	0.83	0.79	0.46	0.28	0.48
Charolais	0.78	0.72	0.62	0.63	0.47	0.50	0.44
Chiangus	0.82	0.79	0.79		0.54	0.53	0.58
Gelbvieh	0.81	0.75	0.61	0.63			
Limousin	0.92	0.89	0.83	0.85	0.73	0.73	
Maine Anjou	0.77	0.76	0.76	0.75	0.35	0.34	0.35
Salers	0.83	0.82	0.76	0.82	0.21	0.26	0.29
Simmental	0.94	0.94	0.94	0.93	0.80	0.80	0.80
Tarentaise	0.96	0.95	0.95	0.94			

[a]Weighted by relationship to phenotyped animals at USMARC for BWT, WWT, YWT, MAR, REA, and FAT and by relationship to daughters with phenotyped progeny MILK.

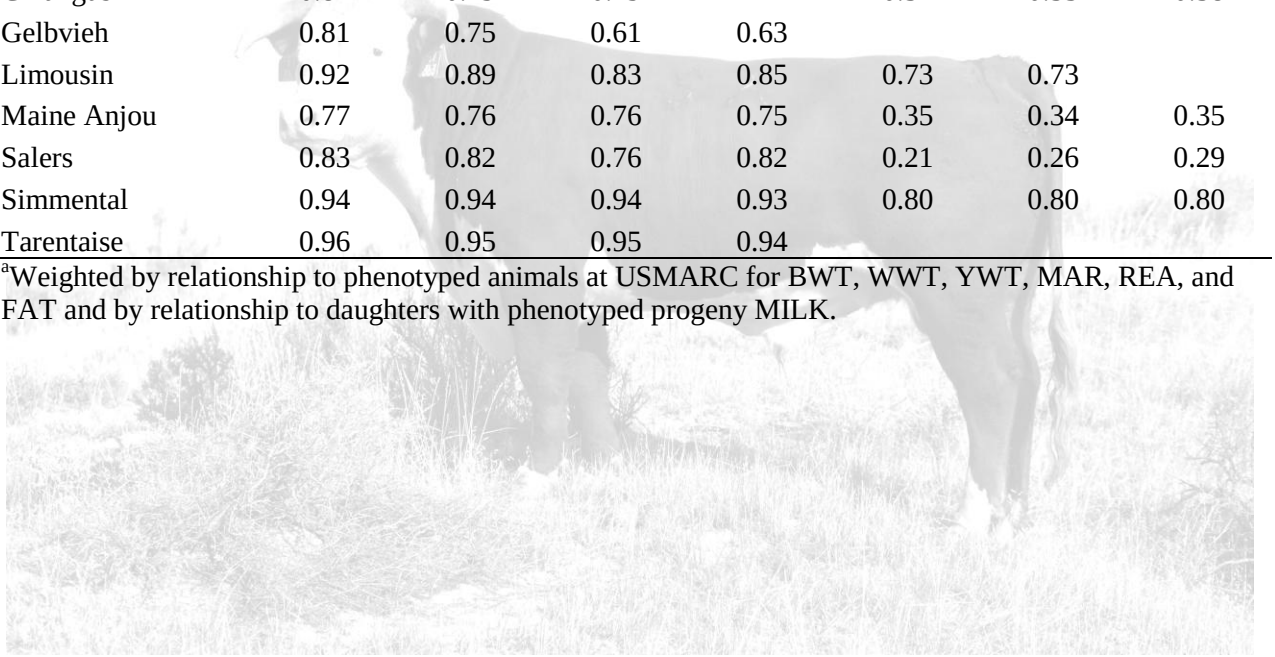

Table 9. Estimates of variance components (lb^2) for birth weight (BWT), weaning weight (WWT), yearling weight (YWT), and maternal weaning weight (MWWT) and for marbling (MAR; marbling score $units^2$), ribeye area (REA; in^4), and fat thickness (FAT; in^2) from mixed model analyses

		Direct	
Analysis Direct	BWT	WWT[a]	YWT
Animal within breed (19 breeds)	70.58	477.83	3576.92
Maternal genetic within breed (17 breeds)		431.22	
Maternal permanent environment		681.53	
Residual	51.40	1207.02	4166.21

Carcass Direct	MAR	REA	FAT
Animal within breed (12-13 breeds)	0.255	0.636	0.0098
Residual	0.318	0.729	0.0148

[a]Direct maternal covariance for weaning weight was -88.59 lb^2

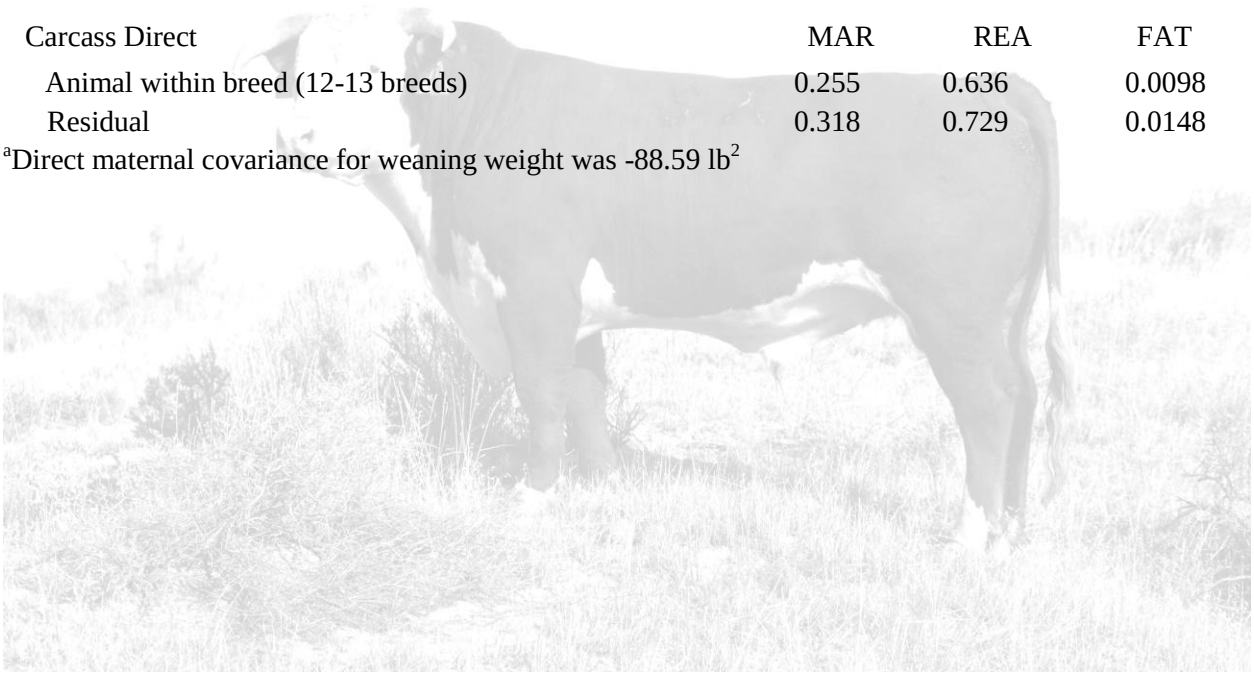

Table 10. Pooled and within-breed regression coefficients (lb/lb) for weights at birth (BWT), 205 days (WWT), and 365 days (YWT) of F_1 progeny and for calf weights (205 d) of F_1 dams (MILK) on sire expected progeny difference and by sire breed

	BWT	WWT	YWT	MILK
Pooled	1.15 ± 0.04	0.86 ± 0.04	1.04 ± 0.04	1.17 ± 0.09
Sire breed				
Angus	1.04 ± 0.10	0.83 ± 0.08	1.21 ± 0.08	1.14 ± 0.16
Hereford	1.18 ± 0.07	0.76 ± 0.05	1.03 ± 0.06	1.08 ± 0.16
Red Angus	1.06 ± 0.15	0.72 ± 0.16	0.56 ± 0.18	1.59 ± 0.34
Shorthorn	0.69 ± 0.28	0.79 ± 0.24	0.81 ± 0.29	0.95 ± 0.93
South Devon	-0.28 ± 0.64	0.02 ± 0.56	0.01 ± 0.47	-0.22 ± 1.54
Beefmaster	2.01 ± 0.45	1.19 ± 0.31	1.07 ± 0.49	3.94 ± 0.72
Brahman	2.18 ± 0.22	1.02 ± 0.21	1.21 ± 0.24	0.34 ± 0.51
Brangus	1.71 ± 0.32	0.45 ± 0.31	0.79 ± 0.43	0.45 ± 0.77
Santa Gertrudis	5.70 ± 1.29	1.44 ± 0.39	-0.02 ± 0.44	
Braunvieh	1.12 ± 0.30	1.39 ± 0.31	1.45 ± 0.39	2.99 ± 1.06
Charolais	1.09 ± 0.13	0.95 ± 0.12	0.77 ± 0.13	1.16 ± 0.30
Chiangus	1.91 ± 0.41	0.73 ± 0.35	0.64 ± 0.49	
Gelbvieh	1.00 ± 0.14	0.96 ± 0.17	1.13 ± 0.17	1.32 ± 0.46
Limousin	0.85 ± 0.11	0.98 ± 0.10	1.14 ± 0.13	1.45 ± 0.29
Maine Anjou	1.51 ± 0.27	0.56 ± 0.27	0.59 ± 0.35	1.07 ± 0.52
Salers	1.32 ± 0.28	0.91 ± 0.34	0.46 ± 0.32	1.75 ± 0.51
Simmental	1.16 ± 0.17	1.52 ± 0.15	1.34 ± 0.14	0.75 ± 0.39
Tarentaise	1.51 ± 1.36	0.70 ± 0.61	1.49 ± 0.82	1.00 ± 0.93

Table 11. Pooled and within-breed regression coefficients marbling (MAR; score/score), ribeye area (REA; in^2/in^2), and fat thickness (FAT; in/in) of F_1 progeny on sire expected progeny difference and by sire breed

	MAR	REA	FAT
Pooled	0.62 ± 0.06	0.98 ± 0.08	1.24 ± 0.11
Sire breed			
Angus	0.97 ± 0.11	0.94 ± 0.20	1.42 ± 0.18
Hereford	0.43 ± 0.19	0.58 ± 0.16	0.95 ± 0.21
Red Angus	1.06 ± 0.23	1.61 ± 0.33	0.85 ± 0.53
Shorthorn	1.81 ± 0.36	0.79 ± 0.68	2.33 ± 0.59
South Devon	-0.29 ± 0.62	1.66 ± 3.17	5.53 ± 4.58
Santa Gertrudis	-0.95 ± 1.64	0.92 ± 0.66	1.29 ± 0.73
Braunvieh	4.35 ± 1.68	1.32 ± 0.71	0.15 ± 0.39
Charolais	1.03 ± 0.32	1.58 ± 0.33	1.93 ± 0.59
Chiangus	0.65 ± 0.28	-0.06 ± 0.54	-0.76 ± 0.93
Limousin	1.18 ± 0.43	1.43 ± 0.21	
Maine Anjou	0.49 ± 0.83	-0.74 ± 0.65	1.34 ± 0.83
Salers	0.03 ± 0.10	3.20 ± 0.91	1.03 ± 0.93
Simmental	0.56 ± 0.18	0.59 ± 0.19	1.83 ± 0.45

Mean EPDs reported by different breeds

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Expected progeny differences (EPDs) have been the primary tool for genetic improvement of beef cattle for over 40 years beginning with evaluations of growth traits. Since that time EPDs have been added for several other production traits such as calving ease, stayability, and carcass merit and conformation. Most recently, several breed associations have derived economic indices from their EPDs to increase profit under different management and breeding systems.

It is useful for producers to compare the EPDs of potential breeding animals with their breed average. The current EPDs from the most recent genetic evaluations of 25 breeds are presented in this report. Mean EPDs for growth traits are shown in Table 1 (25 breeds), for other production traits in Table 2 (15 breeds), and for carcass and composition traits in Table 3 (20 breeds). Several breeds also have EPDs that are unique to their breed; these EPDs are presented in Table 4.

Average EPDs should only be used to determine the genetic merit of an animal relative to its breed average. To compare animals of different breeds, across breed adjustment factors should be added to animals' EPDs for their respective breeds (see Across-breed EPD Tables reported by Kuehn et al. in these proceedings).

This list is likely incomplete; evaluations for some breeds are not widely reported. If you see a breed missing and would like to report the average EPDs for that breed, please contact Larry (Larry.Kuehn@ars.usda.gov) or Mark (Mark.Thallman@ars.usda.gov).

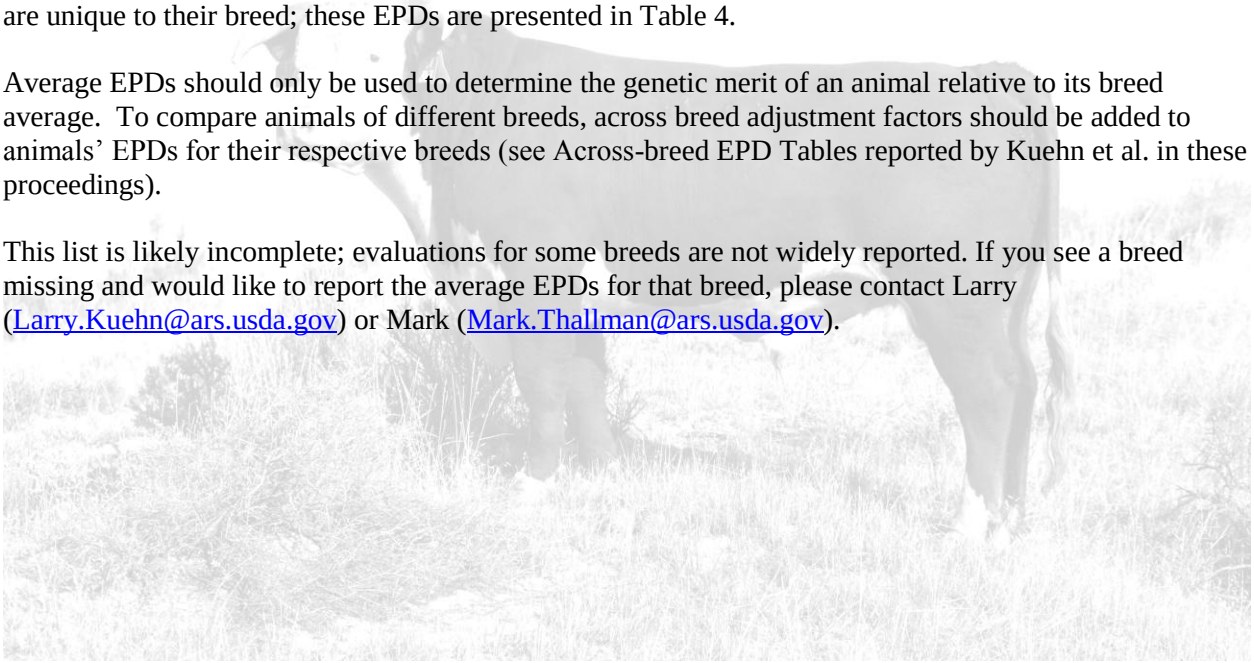

Table 1. Birth year 2009 average EPDs from 2011 evaluations for growth traits

Breed	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)	Maternal Milk (lb)	Total Maternal (lb)
Angus	2.0	46	83	22	
Black Hereford	3.1	42	65.1	13.8	34.8
Hereford	3.6	43	71	17	38
Murray Grey	3.4	20	31	4	14
Red Angus	0.0	30.9	58.2	16.7	
Red Poll	1.7	15	24	7	
Shorthorn	2.4	15.3	24.8	2.3	10
South Devon	2.8	41.4	77.3	22.8	43.5
Beefmaster	0.4	9	14	2	
Braford	1.0	9	13	2	7
Brahman	1.9	14.8	23.8	6.3	
Brangus	-.77	22.6	44.8	10.7	22.1
Red Brangus	1.5	12.7	20.1	5.7	12.1
Santa Gertrudis	0.5	4.0	5.0	0.0	2.0
Senepol	0.9	7.7	10.4	4.2	8.0
Simbrah	2.6	28.3	46.3	2.3	16.5
Braunvieh	-0.11	6.2	12.2	0.4	3.5
Charolais	0.6	24.2	42.3	6.4	18.5
Chianina	2.1	32.0	59.5	12.1	28.1
Gelbvieh	1.3	41	75	18	38
Limousin	1.8	42.9	80.2	20.9	
Maine-Anjou	1.9	39.7	78.1	19.5	39.3
Salers	1.8	40.2	77.4	19.5	39.6
Simmental	0.9	32.1	57.9	3.6	19.7
Tarentaise	1.9	16	28.6	0.6	

Table 2. Birth year 2009 average EPDs from 2011 evaluations for other production traits

Breed	Calving Ease Direct (%)	Calving Ease Maternal (%)	Scrotal Circumference (cm)	Docility Score	Mature Weight (lb)	Stayability (%)
Angus	5	7	0.42	9.5	31	
Hereford	0.3	0.7	0.7			
Murray Grey	-0.7	-0.2	0.10		47	
Red Angus	5.4	3.3				9.0
Shorthorn	-1.7	-1.7				
South Devon			0.1	0.0		
Beefmaster			0.2			
Brangus			0.69			
Braunvieh	-0.05	-1.25				
Charolais	2.8	3.5	0.59			
Gelbvieh	105	104	0.4			4
Limousin	7.7	4.1	0.4	16.6		18.4
Salers	0.2	0.3	0.3	8.0		22.7
Simmental	7.0	3.0				17.8
Tarentaise	-1.2	0.6				

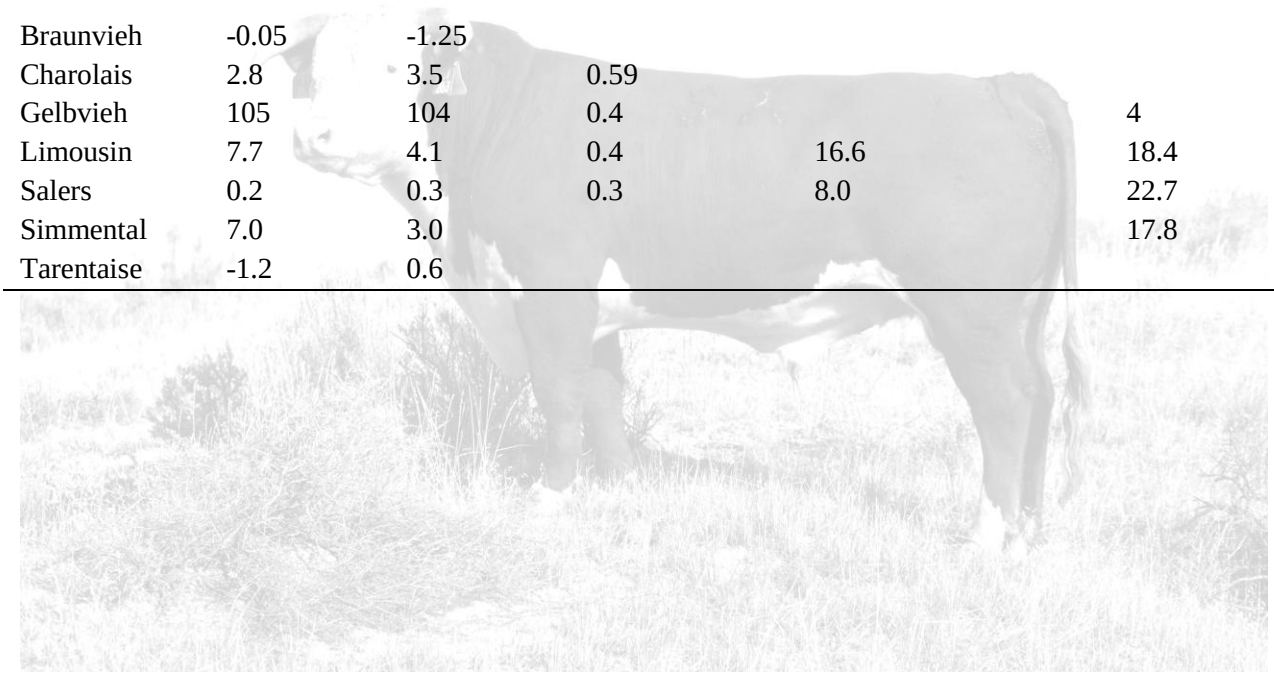

Table 3. Birth year 2009 average EPDs from 2011 evaluations for carcass and composition traits

				Carcass				
Breed	Carcass Wt (lb)	Retail Product (%)	Yield Grade	Marbling Score	Ribeye Area (in^2)	Fat Thickness (in)	Rump fat (in)	WBSF (lb)
Angus	15.0			0.43	0.21	0.012		
Hereford				0.04	0.22	0.002		
Murray Grey	27	0.3		0.0	0.09	0.00	-0.01	
Red Angus	35.5		-0.003	0.07	0.07	-0.034		
Shorthorn	4.9			-0.02	0.07	-0.01		
South Devon	25.0	0.8		0.3	0.21	0.01		
Beefmaster				0.00[a]	0.03[a]	0.000[a]	0.00[a]	
Braford	6			0.01	0.06	0.002		
Brahman	5.2	0.01		-0.01	0.04	-0.002		0.0
Brangus	0.7			0.04[b]	0.37[b]	0.00[b]		
Santa Gertrudis	0.0			0.00	0.00	0.00		
Simbrah	-6.3		0.06	-0.01	-0.2	0.01		-0.03
Braunvieh	0.1			0.12	0.01	0.115		
Charolais	14.1			0.01	0.18	-0.001		
Chianina	-1.2	-0.20		0.09	0.02	0.01		
Gelbvieh	8.3[c]			-0.03[c]	0.10[c]			
Limousin	19.4		-0.08	-0.04	0.49			
Maine-Anjou	-0.1	0.29		0.20	0.15	0.00		
Salers	20.0	0.0		0.1	0.03	0.00		
Simmental	-1.7		-0.001	0.15	0.10	0.15		-0.30

[a]Derived using ultrasound measures and reported on an ultrasound scale (IMF% instead of marbling score)

[b]Reported on an ultrasound scale (IMF% instead of marbling score) but calculated using ultrasound and carcass data in a multi-trait model

[c]Adjusted to a fat-constant endpoint

Table 4. Birth year 2009 average EPDs from 2011 evaluations for other traits unique to individual breeds

Angus	Residual Average Daily Gain (lb)	Mature Height (in)	Yearling Height (in)	Cow Energy Value ($)	Weaned Calf Value ($)	Feedlot Value ($)	Grid Value ($)	Beef Value ($)
	.13	0.4	0.35	1.41	25.50	24.61	24.53	46.23

Hereford	Baldy Maternal Index ($)	Brahman Influence Index ($)	Certified Hereford Beef Index ($)	Calving Ease Index ($)
	15	14	18	14

Red Angus	Heifer Pregnancy (%)	Mature Cow Maintenance (Mcal/mo)
	7.5	4.1

Gelbvieh	Feedlot Merit ($)	Carcass Value ($)	Gestation Length (d)	Days to Finish (d)
	8.82	6.74	-1.4	3.5

Limousin	Mainstream Terminal Index ($)
	42.5

Simmental	All Purpose Index ($)	Terminal Index ($)	Simbrah	All Purpose Index ($)	Terminal Index ($)
	104.6	62.5		75	47

Murray Grey	600-d wt (lb)	Gestational length (d)	Days to calving (d)
	45	-0.1	-0.6

Integrating molecular data into NCE: expectations, benefits, and needs

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Introduction

Genomic information, in the form of Single Nucleotide Polymorphisms, holds the promise to not only increase the accuracy of Expected Progeny Differences (EPD) but also add new and "novel" traits to our suite of traits included in National Cattle Evaluations (NCE). For the most part, genomic information for complex traits (those controlled by many genes) is available to producers in a disjoined context in that it is not seamlessly integrated into EPD estimations and is published separately from EPD. Understanding the benefits of the inclusion of genomic information into EPD first requires knowledge of the differences between an EPD and the results of genomic test (called Molecular Breeding Values or MBV). An EPD is half of the summation of all the independent additive gene effects that cause variation in a given trait (half because each animal only passes on half of their alleles at random). However, with an EPD the specific sources of variation are unknown and for some traits the collection of phenotypes is either cost prohibitive (i.e. tenderness) or it takes a long time to observe a record (i.e. stayability). A MBV, on the other hand, is the summation of the additive SNP effects (multiplied by the number of copies of a given SNP allele) that have been shown through association studies to explain variation in a given trait. SNP are not genes, but serve as markers. The benefit is that DNA, and thus MBV, can be garnered early in life regardless of the trait.

The Value of Improving Accuracy

Several advancements in this technology have occurred with regard to complex traits (i.e. production, carcass, and reproduction traits) including the number of markers included in a given panel, reporting styles of the results, the number of traits for which a diagnostic test exists, and recently, the inclusion of this information for the first time in National Cattle Evaluation (NCE) in the Angus breed.

The promise of the inclusion of marker information into EPD calculations holds three primary benefits:

1. Increased accuracy for young animals (i.e. yearling bulls), which is particularly beneficial when selecting on traits that are measured late in life (e.g., stayability)
2. Shortened generation intervals
3. EPD values for novel traits (i.e. efficiency, end-product healthfulness, disease susceptibility) that may have, at best, sparse collection of phenotypes

The uncertainty surrounding early predictions of genetic merit arise as a result of Mendelian sampling. Every animal is passed a random sample of alleles from each parent, half coming from the dam and half from the sire. We have an estimate of the average effect of what was passed from parent(s) to offspring in the form of pedigree estimates, but the certainty with which we know this estimate is correct (i.e., the accuracy) is low. As more information is collected, such as an individual's own record and data from progeny, accuracy increases. For lowly heritable traits like measures of reproduction, it can take a considerable number of offspring to reach high BIF accuracy levels, given that the BIF scale is more conservative than true accuracy (r) as illustrated in Table 1. To calculate r in the context of progeny test sires the following equation can be used where *n* is the number of progeny:

$$r = \sqrt{\frac{nh^2}{4 + (n-1)h^2}}$$

To convert BIF accuracy to true accuracy (r) the following equation can be used:

$$r = \sqrt{1-(1-BIF)^2}$$

Table 1. Approximate number of progeny needed to reach accuracy levels (true (r) and the BIF standard) for three heritabilities (h^2).

Accuracy		Heritability Levels		
r	BIF	h^2 (0.1)	h^2 (0.3)	h^2 (0.5)
0.1	0.01	1	1	1
0.2	0.02	2	1	1
0.3	0.05	4	2	1
0.4	0.08	8	3	2
0.5	0.13	13	5	3
0.6	0.2	22	7	4
0.7	0.29	38	12	7
0.8	0.4	70	22	13
0.9	0.56	167	53	30
0.999	0.99	3800	1225	700

One primary benefit of molecular information is that it can be garnered much earlier in life (before a phenotypic record can be collected). This knowledge can, in part, reveal a portion of the black box that is Mendelian sampling in young animals. This results in higher accuracy values for young animals, which potentially increases the use of these younger animals in seedstock systems, thus decreasing the generation interval. The equation below predicts the rate of genetic change per year and is dependent on selection intensity, the accuracy of selection, genetic variation, and the length of the generation interval. From this it is apparent that if the generation interval is decreased and /or accuracy is increased this will lead to faster genetic change.

$$\frac{[(\text{Accuracy of Selection}) * (\text{Selection Intensity}) * (\text{Genetic Standard Deviation})]}{\text{Generation Interval}}$$

However, the magnitude of these benefits will depend on the proportion of variation explained by a given marker panel. Without the seamless integration of this technology into EPD calculations, we find ourselves in the current context of being faced with two disjoined pieces of information: traditional EPD and marker panel results. In this scenario, it is impossible to directly compare EPD to marker panel

results. This is because the molecular scores only explain a portion of the additive genetic variation. Further, some of the marker panel results have a metric of accuracy associated with them. At the current time, this metric is not directly comparable to the Beef Improvement Federation (BIF) accuracy value associated with EPD simply due to differences in the way they are computed. Table 2 shows the relationship between the genetic correlation (true accuracy), %GV and BIF accuracy.

Table 2. The relationship between true accuracy (r), proportion of genetic variation explained (%GV), and Beef Improvement Federation (BIF) accuracy.

r	%GV	BIF
0.1	1	0.005
0.2	4	0.020
0.3	9	0.046
0.4	16	0.083
0.5	25	0.132
0.6	36	0.200
0.7	49	0.286

In contrast to the thought process of DNA marker panel results being a separate and disjoined piece of information, these test results should be thought of as a potentially useful indicator that is correlated to the trait of interest. As such, the MBV can be included in NCE as a correlated trait following methods of Kachman (2008). Other methods have been proposed including using large (50,000+) SNP panels to form a genomic relationship matrix that could allow for known relationships between animals based on genotypes across SNP loci. Combining these sources of information, molecular tools and traditional EPD, has the potential to allow for the benefits of increased accuracy and increased rate of genetic change as discussed earlier.

MacNeil et al. (2010) utilized Angus field data to look at the potential benefits of including both ultrasound records and MBV for marbling as correlated traits in the evaluation of carcass marbling score. MacNeil and colleagues used a 114 SNP marker panel that was developed using 445 Angus animals and calculated to have a genetic correlation (r) of 0.37 with marbling (i.e. the test explained $(0.37)^2 = 0.137$ or 13.7% the additive genetic variation). For animals with no ultrasound record or progeny data, the marker information improved the BIF accuracy of the Angus marbling EPD from 0.07 to 0.13. Assuming a heritability of 0.3 for marbling, a BIF accuracy of 0.13 is equivalent to having approximately 5 progeny carcass records on a young animal or an ultrasound record on the individual itself. In this particular study, both ultrasound records and MBV were found to be beneficial indicators of carcass marbling. The genetic correlation between MBV and ultrasound was found to be 0.80. Since the initiation of MA-EPD by AAA, the SNP panel has evolved and now accounts for 42% of the GV for marbling. The amount of information provided by genomics to NCE will continually change as new products enter the market place and SNP panels are retrained overtime.

Figures 1 and 2 illustrate the benefits of including a MBV into EPD (or EBV which is twice the value of an EPD) accuracy (on the BIF scale) when the MBV explains 10 or 40% of the genetic variation (GV), which is synonymous with R^2 values of 0.1, and 0.4. The darker portion of the bars shows the EPD accuracy before the inclusion of genomic information and the lighter colored portion shows the increase in accuracy after the inclusion of the MBV into the EPD calculation. As the %GV increases, the increase in EPD accuracy becomes larger. Additionally, lower accuracy animals benefit more from the inclusion of genomic information and the benefits decline as the EPD accuracy increases. Regardless of the %GV assumed here, the benefits of including genomic information into EPD dissipate when EPD accuracy is between 0.6 and 0.7. On the other hand, when %GV is 40 an animal with 0 accuracy could go to over 0.2 accuracy with genomic information alone. From table 1, this would be the same as having approximately

4 progeny for a highly heritable trait or 7 progeny for a moderately heritable trait.

Figure 1. Increase in accuracy from integrating genomic information that explains 10% of the genetic variation into Estimated Breeding Values (EBV).

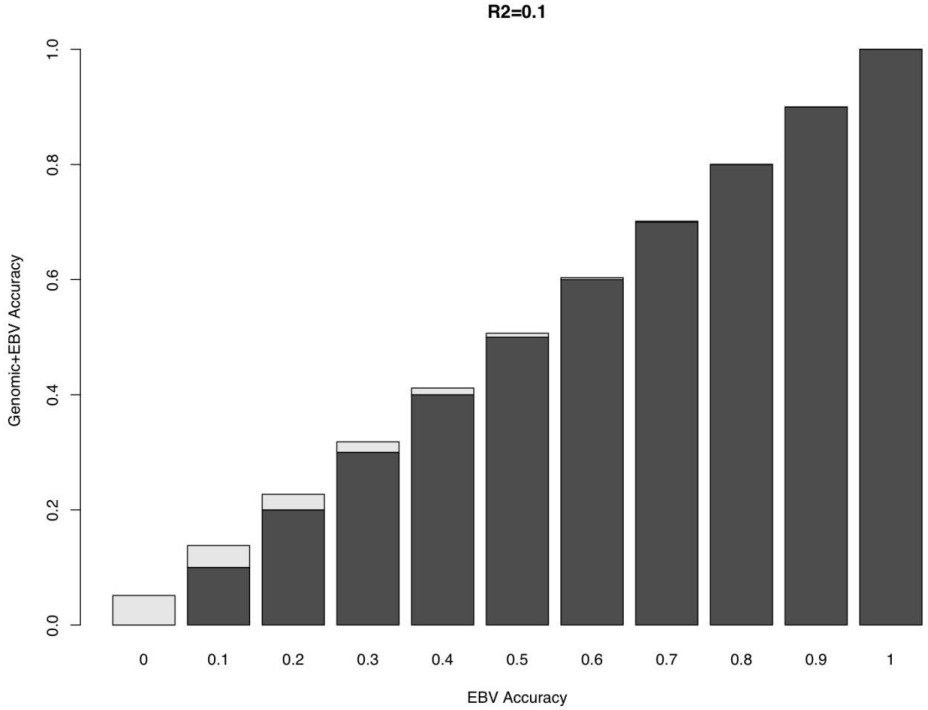
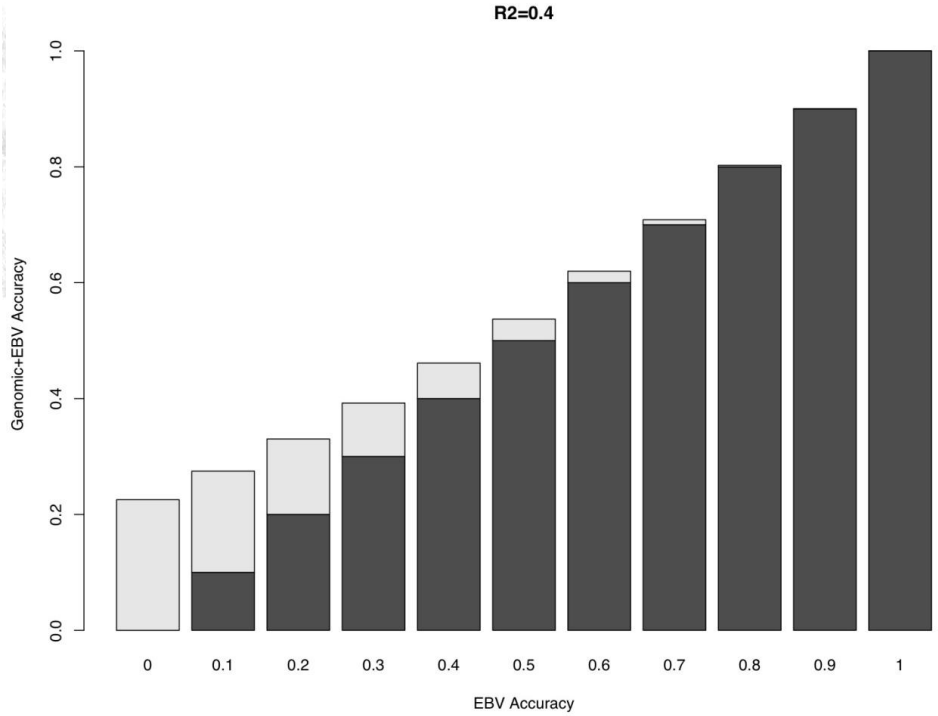


Figure 2. Increase in accuracy from integrating genomic information that explains 40% of the genetic variation into Estimated Breeding Values (EBV).



It is important to understand some limitations in the current application of Marker Assisted Selection. For instance, current marker panels are likely to work best in the populations where discovery occurred, but will potentially decrease in predictive power as the target population becomes more genetically distant from the discovery population (de Roos et al., 2008). The same erosion in accuracy is likely to occur overtime as well (i.e. over generations if panels are not retrained).

Discovery	Target	
Angus	Angus	Closest relationship
Angus	Charolais	↓
Angus	*Bos indicus*	Most distant relationship

In order to investigate the robustness of SNP predictions across breeds, a unified research and outreach project (called the Weight Trait Project; Spangler et al., 2011) was initiated utilizing both industry and academic/ARS resources. Weaning weight records (n=3,328) of calves from the US Meat Animal Research Center (USMARC) were used in the selection of SNP from the Bovine SNP50 associated with adjusted weaning weight. The total pedigree included 5,222 animals. Of the 3,328 calves in the training population, the average breed contributions were 26% Angus, 19% Hereford, and 6.5% each of Red Angus, Simmental, Charolais, Limousin, and Gelbvieh.

Breed associations representing the seven breeds (Table 2) in the USMARC Cycle VII population identified seedstock producers in the region surrounding USMARC to provide DNA samples (tail hair) from calves born in 2009 and their dams. A reduced panel of 192 SNP was constructed based on the most significant SNP from the USMARC association analysis with the addition of 192 SNP from IGENITY® (96 trained on yearling weight in an Angus population and the other 96 from the IGENITY parentage panel). In total, the reduced panel consisted of 384 SNP. IGENITY® served as the genetic service provider partner in this project and genotyped animals with the reduced panel. After editing SNP based on deviation from Hardy-Weinberg Equilibrium and call rates, a total of 159 of the diagnostic SNP (non parentage) were used in the analysis. The genotype data had an average call rate of 85.2% (11.3-100%). Bull calves (n=3,500) from the twenty collaborating herds were genotyped with the reduced panel and MBV were calculated based on prediction equations derived at USMARC for weaning weight (WW) and post weaning gain (PWG). Data including a four-generation pedigree, adjusted weaning weight phenotypes, and pedigree index EPD were obtained from the respective breed associations for each herd in the project. MBV were fit as a correlated trait in both two- and three-trait animal models. Contemporary group effects included herd and sex of calf. Weaning weight was fit with both a direct and maternal component while MBV were assumed to have only a direct genetic component.

Given the partial nature of the genotypes produced by the WTP due to the newness of the genotyping platform used at that time, methodology was developed to account for partial genotypes in the analysis (Kachman et al., 2011). For animal a the proportion, Pa, of the complete genotype (CG) MBV variance accounted for by partial genotypes (PG) is the ratio of the variances calculated by summing over the partial and the complete set of markers. Similarly, the genetic covariance between a trait and PG MBV is also proportional to Pa. The proportion of CG covariance between animals a and b with PG was assumed to be proportional to PaPb. The PG model for the MBV of animal a, scales the CG genetic effect by Pa and adds a missing genotype effect with variance Pa(1-Pa) times the CG genetic variance.

Genetic parameters for weaning weight (direct) and MBV by breed are summarized in Table 3 both before and after accounting for partial genotypes in the analysis. In general, the heritability estimates for WW direct were within expected ranges except for Simmental, which is likely due to the data structure of the Simmental herds in this study. In general, the genetic correlations are low to moderate with relatively

large standard errors. The number of markers used in the current panel might explain the less than desirable performance. Given these correlations, the proportion of genetic variation for weaning weight explained by the panel (r_g^2) ranged from 0 to 7.8% before accounting for PG and 0.09 to 14.44% after. One possible reason for the range in genetic correlations among breeds is that the associations between markers and growth traits are more breed-specific than had been hoped.

Table 3. Heritabilities (SE) by breed for weaning weight (direct) and molecular breeding values (MBV) for weaning weight (WW) direct both Before and After accounting for partial genotypes.

	Heritability	Heritability Molecular Breeding Value		Genetic Correlation	
Breed	Weaning Weight	Before	After	Before	After
Angus	0.23±0.02	0.87±0.16	0.75±0.12	0.00±0.10	0.15±0.11
Red Angus	0.24±0.03	0.67±0.16	0.89±0.14	0.10±0.10	0.14±0.11
Charolais	0.12±0.03	0.33±0.16	0.47±0.18	0.28±0.15	0.38±0.16
Gelbvieh	0.22±0.02	0.64±0.18	0.62±0.16	0.25±0.13	0.26±0.14
Hereford	0.14±0.04	0.83±0.15	0.96±0.14	0.20±0.20	0.25±0.21
Limousin	0.27±0.02	0.60±0.19	---	0.24±0.12	---
Simmental	0.75±0.03	0.61±0.16	0.73±0.16	0.05±0.08	0.03±0.09

Summary

It is likely that the list of genetic selection tools will continue to expand in the short-term as this arena is far from stagnant. Although the goal is the consolidation of information into one of two basic forms, EPD and economic index values, the industry has witnessed several intermediate steps in an effort to quickly commercialize technology that has created confusion. Integrated projects such as the WTP that engage researchers, extension personnel, producers, and breed associations are critical to the further development and employment of genomic selection tools. The WTP has created a vast resource that continues to grow in order to investigate the plethora of questions that still exist related to the use of this technology.

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Genomic Selection: Delivering on the Promise

Megan M. Rolf, University of Missouri

Introduction

I'm still waiting for my hover car. I don't have a "food-o-matic" robot to serve me a steak dinner with the press of a button, and I don't have a robot named Rosie to perform my housekeeping duties. That's what the *Jetsons*, and other pop culture media promised when many of us were growing up: technology that would enhance our everyday lives in the 21st century. While we might not have advanced to the extent promised by the *Jetsons,* rapid advancements in technology have provided a multitude of promising opportunities for cattle producers. Artificial insemination, embryo transfer, and national cattle evaluation have undeniably revolutionized cattle production. A new technology, genomic selection, promises to bring about the most revolutionary changes to date. But after ten years of hypothesizing and research, and a year after the first breed association's implementation of genomic selection, has it delivered on its promises?

Genotype information was first introduced into selection decisions via an approach known as marker assisted selection (MAS). MAS involves genotyping a small number of markers that detect the effects of one or two genes and using these genotypes to inform selection decisions. Marker assisted management works in a similar fashion, except that the marker information is used to more efficiently manage groups of animals using the premise that a small number of genes each have a large effect on a trait. For example, it could be used to increase gain and determine optimal endpoints for cattle in the feedyard. Conversely, genomic selection involves the simultaneous selection for all of the genes in the genome which affect an economically important trait using very high-density panels of single nucleotide polymorphism (SNP) markers. The approach was first introduced by Meuwissen *et al*. (2001) and has the advantage over marker assisted selection in that it explains more of the genetic variance in a trait than do the small number of markers used for MAS when making selection decisions.

Genomic selection can be performed utilizing many different genotyping technologies and breeding program designs, but has the potential to revolutionize selection in the beef industry by decreasing generation interval, increasing selection intensity, and providing more accurate information on the genetic merit of an animal. These advancements could not come at a better time. The United Nations Food and Agriculture Organization (UNFAO, 2011) estimates that the world population will be 9.1 billion by the year 2015, which will increase the worldwide demand for food by 70%. Only about

20% more land in developing countries is arable (UNFAO 2011) and there are limits on fresh water resources, which means that much of the necessary increase in food production will have to come from technological advancements. Additionally, as more countries make the transition to developed nations, the demand for beef and other meat products will increase. Beef cattle are in a position to provide a quality source of protein by utilizing feedstuffs not consumed by humans and land that is unsuitable for crop production. Technological advancements, including genomic selection, have the potential to transform beef cattle production by making cattle more efficient and productive while satisfying increased food demands.

Review of Literature

National Cattle Evaluation

The first U.S. National Cattle Evaluation was performed in 1974 (Willham 1993). Current standards for National Cattle Evaluation (NCE) are based on Henderson's mixed model equations (i.e., Henderson, 1975) which incorporate performance measures on the individual animal, its progeny, and its relatives into one easy to use metric for selection decisions. These equations center around the pedigree relationships described between all of these animals. Wright (1922; 1934) defined a method to compute the kinship relationships between pairs of animals using path coefficients. This method was used for 30-40 years (VanVleck, 2007) until the tabular method was developed (Cruden 1949; Emik and Terrill 1949). It is important to note that these values are based on the average

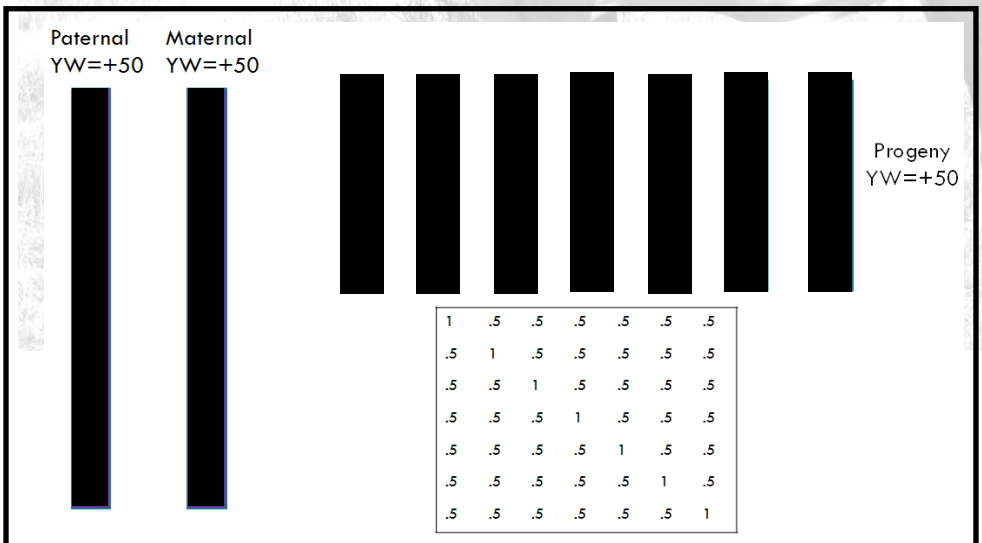

Figure 1: Hypothetical chromosomes inherited from both the sire and dam (larger chromosomes, left) to their progeny (smaller chromosomes, right). All off-diagonal elements of the NRM would be identical for a set of full sibs (bottom). Black color indicates that average performance is expected (YW EPD of +50 lbs) based on the parent average EPD ([Paternal YW EPD + Maternal YW EPD]/2) calculated before performance data are recorded on the set of full sibs.

relationships between a group of animals as defined by the probability that alleles are identical by descent. For example, we would expect that ½ of the genetic material would be shared between full siblings and ¼ would be shared between half siblings. If we were to form a numerator relationship matrix (NRM) between a set of full siblings, all of the pairwise relationships between them would be 0.5 (See Figure 1). These relationships are assembled into a NRM, such as the one shown in Figure 1, which contains the pairwise relationships and inbreeding coefficients for every animal within a population of interest. All of the phenotypic data and realtionships are combined into an analysis that provides a best linear unbiased prediction (BLUP) of the genetic merit of a group of animals which are published by breed associations as expected progeny differences (EPDs).

Before performance data are recorded on an animal, it is assumed that the animal received an average sample of genes from its parents (see equation below).

$$PA\ EPD_{\ progeny} = \frac{1}{2} EPD_{sire} + \frac{1}{2} EPD_{dam}$$

In actuality, an animal may receive a better than average or worse than average sample of genes from its parents due to the random assortment of chromosomes into gametes. This sampling of genes is referred to as the Mendelian sampling term (φ) and describes the deviation from an average sample of genes (see equation below).

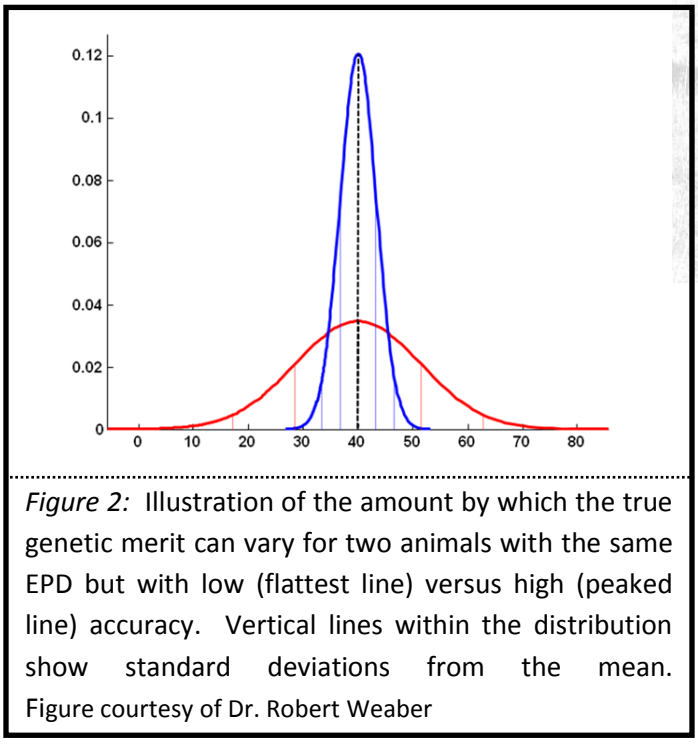

Figure 2: Illustration of the amount by which the true genetic merit can vary for two animals with the same EPD but with low (flattest line) versus high (peaked line) accuracy. Vertical lines within the distribution show standard deviations from the mean. Figure courtesy of Dr. Robert Weaber

$$PA\ EPD_{\ progeny} = \frac{1}{2} EPD_{sire} + \frac{1}{2} EPD_{dam} + \varphi$$

When increasing amounts of phenotypic data on the individual and its progeny are recorded, the Mendelian sampling term can be more precisely estimated, and we have more confidence that the EPD prediction is close to the true breeding value of the animal. This is published by the industry as an accuracy value which increases as the amount of available data increases. Figure 2 shows how the EPD accuracies reflect confidence in the estimation of the true genetic merit of an

animal. Consider two sires with a YW EPD of +40 lbs. EPDs with a low accuracy could change (either for the better or worse) more significantly than high accuracy EPDs as more data is recorded. Producers seldom are disappointed to discover than an animal they have selected for breeding is actually significantly better than they predicted based upon its EPD, but the converse is certainly not the case.

The principles of genetic evaluation allow the simultaneous selection for all of the genetic variation underlying a trait, but does require extensive phenotypic records and multiple pedigreed generations of animals for maximum benefit. This framework, paired with standardized data collection procedures (BIF 2010), will continue to serve as the foundation of genetic evaluation for the forseeable future due to its ease of use and producer familiarity.

Genomic Technologies

Genetic marker technologies have been evolving over the last three decades beginning with restriction fragment length polymorphisms (RFLPs) to microsatellites (short stretches of tandem repeats in the DNA), and now, SNPs. SNPs are single base changes in the DNA (for example, an adenine substituted for a cytosine at a specific position along a chromosome, or an A -> C SNP). The first large SNP panel to be commercialized was a 10K SNP chip from Affymetrix (The Bovine HapMap Consortium, 2009). The density of this panel was insufficient to perform genomic selection (GS) or association analyses (such as the one shown in Figure 3). The Illumina BovineSNP50 chip was developed (Van Tassell *et al*. 2008) to provide genotypes on ~50,000 SNPs per animal (Matukumalli *et al*. 2009). Since its introduction, this assay has become the

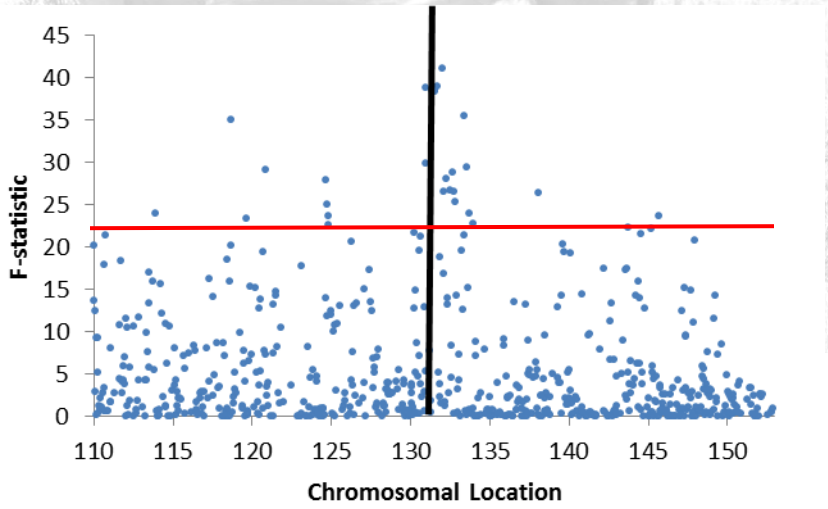

Figure 3: Association analysis showing multiple SNP associations with a single QTL peak. Each dot represents the significance of an individual marker with the phenotype of interest. The horizontal line denotes the significance threshold (genome-wide p<0.05) determined by permutation analysis (n=10,000).

international standard for GS and association analyses in cattle. New assays from Affymetrix and Illumina have just been introduced that will provide from ~640,000-778,000 SNP genotypes per animal. The increased density in these panels will be most useful in across-breed applications of GS.

Most of the SNPs assayed on these platforms are mutations that are likely not causal for phenotypic variation among animals for economically relevant traits. There are millions of SNPs within the bovine genome and those appearing on these assays were selected to be evenly spaced throughout the genome and to be variable within as many breeds as possible. If we assume that there is a single causal mutation located at ~132.0 Mb on the chromosome shown in Figure 3 (vertical black line) we see that multiple SNPs close to the causal mutation (~131.5 to 132.5 Mb) provide statistical evidence for its presence by exceeding the significance threshold set for the analysis (horizontal line at an F of ~23). We see evidence for several SNPs being associated with the causal mutation rather than a single marker because all of these SNPs are in linkage disequilibrium (LD) with the mutation, which allows us to model its effect without actually knowing the identity of the actual mutation. This region has historically been called a quantitative trait loci (QTL) and the region would be a good candidate for further sequencing and analysis to find a causal mutation. If it could be located, the causal mutation would be an excellent candidate for marker assisted selection (MAS).

Marker Assisted Selection

The sequencing of the bovine genome (The Bovine Genome Sequencing and Analysis Consortium 2009; Zimin *et al*. 2009) and the subsequent technologies and knowledge derived from that endeavor have allowed the use of molecular genetic and genomic tools in beef cattle selection decisions. One of these is marker assisted selection, which involves the use of one or a few markers to aid in making selection decisions. This type of approach works best for mutations that cause disease or for qualitative traits which are influenced by one or a small number of genes, such as horned/polled, coat color or double muscling. Because this approach evaluates only the alleles present at a small number of loci, it neglects trait-associated variation of small effect, making it most suitable for Mendelian traits and diseases. If all variation within complex traits was known, then marker assisted selection could be used to select for those traits which are influenced by many genes. However, finding causal mutations in the DNA sequence has proved to be very difficult and only a handful of these mutations in cattle have been described to date (i.e. F94L mutation, Grobet *et al*. 1998; doubling muscling, Grobet *et al*. 1997 and McPherron and Lee 1997). Indeed, some mutations have been

mapped to areas of the genome and subsequently investigated for over a decade and the mutation has not been located (Georges *et al*. 1993, Brenneman *et al*. 1995).

Genomic Selection

GS was first proposed by Meuwissen *et al*. (2001) and involves using dense panels of markers spread throughout the genome to predict genetic merit. As long as an assay exists to genotype sufficient numbers of SNPs, this approach is feasible, as SNPs can be detected approximately every 714 bases in *Bos taurus* cattle (as measured in Angus and Holstein) and about every 285 bases in *Bos indicus* cattle (as measured in Brahman; Bovine HapMap Consortium, 2009), which is well within the range of LD in beef cattle (McKay *et al*. 2007). Ideally, each mutation in the genome that produces an effect on a

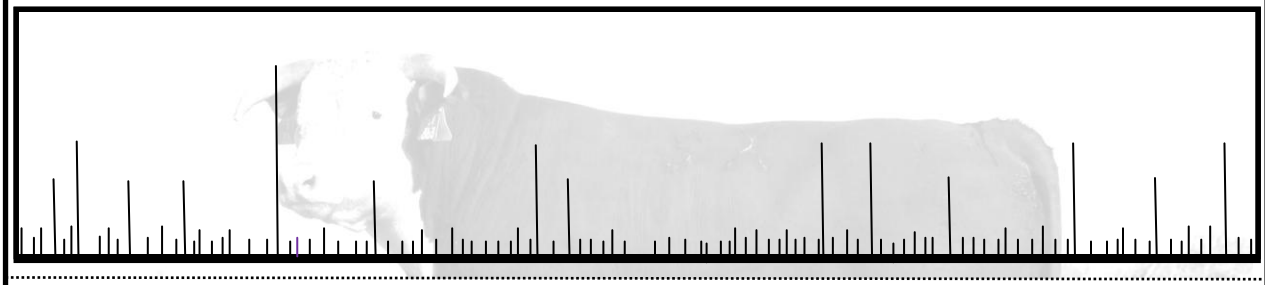

Figure 4: Pictorial representation of the bovine genome. Each vertical line represents a causal mutation with an effect on a phenotype of interest. The size of the line corresponds to the size of the allele substitution effect on phenotype.

trait of interest (vertical lines in Figure 4) would be known and the effects across the entire genome could be summed and the true breeding value of the animal would be known with an accuracy of 1. However, very few causal mutations are known, so we must instead model (estimate) the effects of each mutation using genetic markers, in this case SNPs. The principles of GS require large numbers of markers so that, theoretically, at least one marker should be in linkage disequilibrium (LD) with every mutation that results in a phenotypic effect (lines in Figure 4). This enables simultaneous selection for all variation underlying a trait without knowing the causal mutations at each locus (Hayes *et al*. 2009). This is particularly important, because most economically important traits in the beef industry are quantitative, not qualitative. Quantitative traits are influenced by many, possibly hundreds or thousands, of genes within the genome. Approaches such as MAS are not very effective for these types of traits because they do not explain sufficiently large amounts of genetic variation to be useful in selection decisions. Picture the genome as a giant ruler with uneven measurements (Figure 4). Each of these lines represents a mutation with an effect on phenotype, for example, yearling weight. The height

of the peak represents the size of the underlying allele substituion effect on phenotype. As with most quantitative traits, there are many very small peaks, or small effects on phenotype, while there may be a small number of mutations with larger effects. To accurately predict phenotype, GS would require a marker close to each underyling locus, both small and large effect, shown in Figure 4 to accurately estimate its effect reliably across generations.

Initial GS research was conducted using simulated datasets due to the lack of high-density genotypes in real animal populations. In the cardinal GS paper, Meuwissen *et al*. 2001 simulated a 1000 cM genome with markers occurring every 1 cM and 1 QTL centered between each marker. A haplotype analysis was performed and yielded accuracies of from 0.73 to 0.85. Calus *et al*. (2008) simulated and performed an analysis on a 3 M genome and found that assumptions about QTL location and distribution of effects influenced which model provided the best fit to the data. Many studies have simulated smaller genomes and fewer segregating QTL than are theorized to exist in real-world populations. The end result has been that the computed effects of QTL from simulated data may be substantially larger than for real QTL, which makes their effects easier to accurately predict than may be possible in real-world data (Goddard and Hayes 2007). Due to these factors, GS methods must be tested in real-world populations in which large numbers of animals have high-quality phenotypes and genotypes from high-density SNP assays so that the expected gains in prediction accuracy for real-world situations can be evaluated. Several methods of GS have been proposed, researched, and in some cases, implemented, in both the beef and dairy industries. The following three methods have their own distinct advantages.

Genomic Relationship Matrices

Traditional NCE methods utilize a NRM to describe the expected relationships between animals based on their pedigrees. Genomic relationship matrices (GRMs) use shared genotypes between animals to define their relationships. Several methods have been proposed to generate GRMs that accurately reflect the relationships between animals (i.e., VanRaden 2008, Hayes and Goddard 2008, Legarra *et al*. 2009), but all methods endeavor to more accurately describe the degree of relatedness between animals than the expected relatedness in a NRM. This is achieved by tracking the inheritance of individual genes or alleles within a population (VanRaden *et al*. 2009). To continue with the example shown in Figure 1, consider the mating of two animals with a YW EPD of +50 lbs. (Figure 5) which produces multiple progeny. In a traditional pedigree based analysis, we would assume that all of the relationships between the full sibs would be 0.5 (NRM, bottom left) and they would have a parent

average EPD of +50 lbs. In actuality, because of Mendelian sampling (φ), some of the progeny receive a better than average sampling of their parents genes (chromosomes on the top left) and some progeny receive a worse than average sampling of their parents genes (chromosomes on the top right). As a result of this sampling, some of the progeny are more or less highly related to each other. These slight variations in relationships are captured by the GRM (bottom right) and as a result of this extra information, we can begin to make more accurate transmitting value calculations (i.e., +65 lbs. *vs* +35 lbs.) for the progeny even before phenotypic data have been recorded.

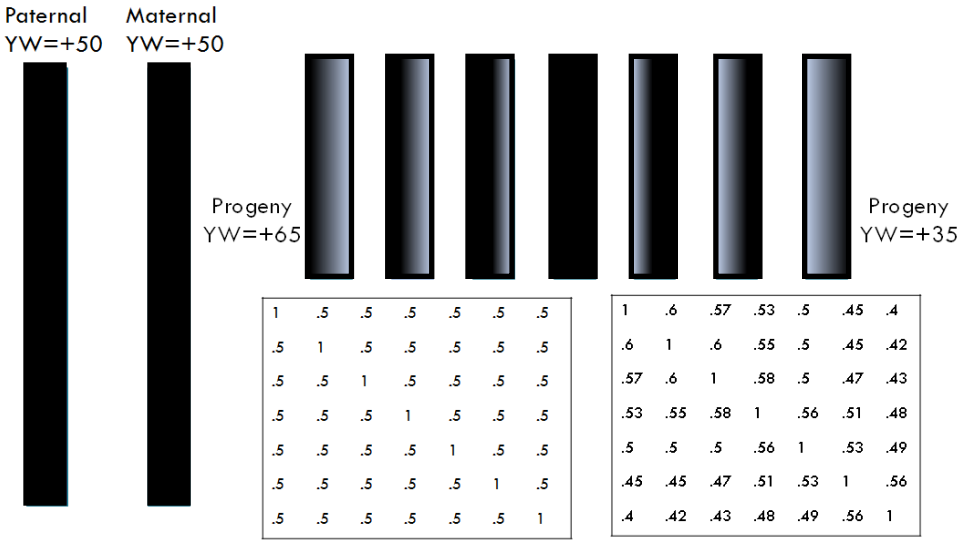

Figure 5: Hypothetical chromosomes being inherited from both the sire and dam (larger chromosomes, left) to their progeny (smaller chromosomes, right). All off-diagonal elements of the NRM would be identical for a set of full sibs (bottom left) but the GRM off-diagonal elements vary according to the segments of chromosome inherited in common from the parents (bottom right). Using this additional information, we can obtain more accurate estimates of the progeny YW EPDs and no longer have to rely on parent average EPDs until performance data is recorded.

Villaneuva *et al*. (2005) suggested that when no QTL have been mapped or no QTL have large effects, using a GRM is a valid method of GS to produce higher EPD accuracies by explaining additive relationships between individuals due to shared markers. Another advantage of this method is that pedigree information is not essential to the majority of these approaches, which means that it is equally applicable to both seedstock and commercial cattle populations. Incorporation of animals with missing or incomplete pedigree data could add information to existing genetic evaluations and allow the capture of additional genetic variation that might otherwise be lost due to drift. Missing and incorrect pedigree information in current NCE systems can be very damaging, and this effect would be mitigated using a

GRM. In fact, incorrect sire information can be more damaging to response to selection than missing sire information, especially when there are small numbers of progeny per sire and/or low trait heritabilities (Sanders *et al*. 2006).

The other limitation of current NRMs is that they can only capture relationships between animals that are identified within the pedigree. This precludes the inclusion of relationships beyond the known pedigree. GRMs can not only bypass errors in pedigree reporting, but can also recover historic relationships that are not accounted for in the known pedigree (Hayes and Goddard 2008). Another attractive feature of using a GRM is that it does not require extensive training and validation datasets. All animals, regardless of their phenotypic status, are included into the GRM and predictions are formed in a single step for all animals.

Harris *et al*. (2008) used a GRM and generated genomic predictions on 4,500 dairy cattle by direct inversion of the mixed model equations (used to calculate EPDs) and found that reliabilities were 0.16 to .33 higher than the parent average breeding value for milk production traits. Rolf *et al*. (2010) used the regression based method defined by VanRaden (2008) to generate a GRM for 698 Angus steers and 1,707 Angus AI bulls. The steers had missing dam pedigree information, but the GRM allowed for the generation of breeding values for all steers and sires. Because of lower than expected heritabilities, accuracies were not as large as in previous studies (0.23 to 0.44). However, this study determined that genetic merit can be predicted in a commercial beef cattle population in the absense of pedigree data where accuracies were equivalent or superior to that of traditional analyses utilizing pedigree data in the same population. Additionally, this study tested the number of markers required to generate an accurate GRM and the similarity of the GRM with the NRM in this population. Approximately 10,000 markers were needed to obtain the best genomic predictions, but the

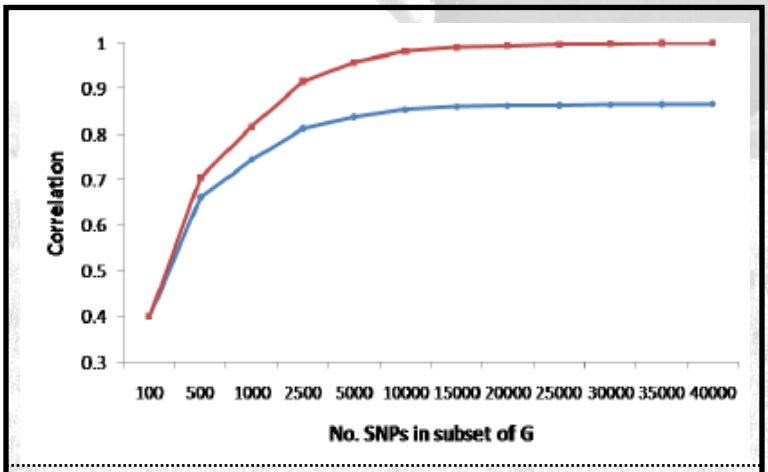

Figure 6: Correlations between GRM estimated from subsets of SNPs (G_n) and the complete dataset of 41,028 SNPs. The top line denotes average correlations between G_n and the full GRM and the bottom line represents correlations between G_n and the NRM (Rolf *et al*. 2010).

correlations between the full GRM and GRM calculated using a reduced set of markers did not drop off dramatically until less than 1,500-2,500 markers were used (See Figure 6).

SNP panels currently, commercialized in the beef industry do not assay sufficient numbers of SNPs to make this approach feasible. However, a 3K assay has been developed by Illumina which contains 2,900 evenly spaced SNPs selected from the BovineSNP50 assay. This panel is being widely used in the US dairy industry to impute 50K genotypes from the reduced 3K marker set. Prediction equations developed using the 50K data can then be used for GS, and accuracy is only reduced to the extent to which error is introduced by the imputation process used to reconstruct the full set of genotypes. In the beef industry, a similar approach could be used if sufficient numbers of animals are genotyped using the 50K assay, or more likely the 3K data could be used to directly generate a GRM.

Estimation of Individual Marker Effects

The general principles of GS dictate that independent, mutually exclusive datasets must be used to test GS prediction models for their efficacy. This necessitates the generation of large "training" populations used to estimate the marker effects which are then used to predict genetic merit in the "validation" population. The validation process is used to determine the extent of the predictive ability of the marker estimates in an independent population. The accuracy of these predictions is determined by the extent of LD between the marker and the causal mutation, the number of animals with phenotypic records available in the training population (Toosi *et al*. 2010), and the extent of relatedness between animals in the training and validation populations. The estimation of marker effects in the training population is essentially the same process that is used in genome-wide association analyses (Legarra *et al*. 2009), and indeed can be used as a simultaneous association analysis by proxy if significance values are not needed. These methods may be the preferred route of implementation of GS when genotyping of all animals is routine (Goddard and Hayes 2007).

Genomic BLUP

Estimation of marker effects using BLUP methodology, also called GBLUP, has become quite popular, as least squares cannot be used due to limits on the number of degrees of freedom in the data. GBLUP assumes that all marker effects are sampled from a normal distribution and have a constant equal variance across all loci. This method can account for stratification due to relationships between animals by incorporation of a NRM (if pedigree is known) or a GRM (if pedigree is unknown). This method is appealing because the only *a priori* required information is the additive genetic variance of

the trait of interest (Hayes *et al*. 2009). Random polygenic effects (often parental average breeding values) can be included in the model to capture genetic variance that is not explained by the markers, such as low-frequency QTL (Hayes *et al*. 2009). These low-frequency QTL are difficult to detect using the common SNPs with a high minor allele frequency (MAF) that are typically found on current SNP panels. It is generally accepted that not all SNPs on a marker panel will be associated with genetic variation for every trait of interest. One drawback of GBLUP is that effects are estimated for all markers and markers that truly have no effect will have small estimated effects, but when these small effects are summed together, they add noise into the genetic predictions (Goddard and Hayes 2007).

Bayesian methods

Evidence suggests that there are a small number of QTL which have large effects on a particular trait and the remaining QTL all have very small effects. Because non-informative markers add noise into the analysis, methods that allow for a prior distribution of effects can be used to better characterize the true distribution of QTL effects across the genome. Bayesian methods are gaining traction because they allow for the inclusion of priors that describe the distribution of marker effects and do not require that all markers be used in genetic prediction. There are too many different types of Bayesian methods found in the literature to allow description here, but they all follow the same general principles. The assumptions made about the data in Bayesian models, such as the proportion of markers that do not have an effect for a certain trait (π), are collectively referred to as priors. The estimated posterior probabilities allow inferences to be made about the data, including genetic variance, heritabilities and marker effects. One fundamental difference between linear and Bayesian models involves the interpretation of the results. Linear models provide a value (a likelihood or p-value, for example) that describes the probability of the data being observed given a specific model. Bayesian analyses provide information on the probability that a certain condition is true (i.e., whether a marker has an effect) given the observed data.

Studies in the literature have provided mixed results on the advantages of Bayesian versus GBLUP analyses. Estimated breeding values on 1,300 Holstein bulls were used by de Roos *et al*. (2007) to compare results from traditional BLUP with their Bayesian model for fat percentage. The accuracy of predicted merit was 0.75 compared to BLUP accuracy of 0.51, which confirmed the advantage of GS methods over BLUP previously shown in simulation studies. Su *et al*. (2009) reported reliabilities from Bayesian estimation methods of 0.49 to 0.73 in cross-validation. On average, reliabilities were 0.13 higher than reliabilities of the parent averages. Hayes *et al*. (2009) found the increase in reliability of

Bayesian methods to be approximately 2-7%. Another study by Harris *et al*. (2008) reported 2-3% greater reliabilities using Bayesian analysis than GBLUP. VanRaden *et al*. (2009) showed that the coefficients of determination for Bayesian predictions were 0.05 to 0.38 greater than parent average predictions. The largest increases in R^2 for that study were were observed for fat percentage, which has a known gene of large efect (*DGAT1*; Grisart *et al*. 2004). Throughout the literature, Bayesian analyses seem to show the largest advantages over GBLUP when generating predictions for a trait with at least one gene of large effect. If all effects are small, Bayesian and GBLUP methods produce similar accuracies.

The Bioinformatics to Implement Genomic Selection Project (http://bigs.ansci.iastate.edu/; Fernando and Garrick 2009) has developed genomic selection software, GenSel, that implements Bayesian methodology for GS through a web interface. The Bayesian methods implemented in GenSel are compared to GBLUP and mixed model analysis incorporating a GRM in Table 1. Briefly, BayesA (Meuwissen *et al*. 2001) includes all markers into the model (π=0) but allows for non-constant marker variances which are estimated individually using Markov Chain Monte Carlo (MCMC) and using a Metropolis-Hastings algorithm. BayesB (Meuwissen *et al*. 2001) allows for a user-assigned value for π and marker variances are also variable. When BayesB is run with π=0, it is equivalent to BayesA. BayesC allows for a user-assigned π, but incorporates a constant variance common to all markers that is subsequently shrunk so that the resulting marker variances appear similar to output from BayesB where π>0. BayesCπ follows the same assumptions of BayesC, except that π is estimated from the data. If a BayesC analysis is run with π=0, all markers are included into the model and variances will remain constant (like GBLUP) because markers cannot be shrunk if there is no sampling of markers in the model. Recently, support for a threshold model was added.

Table 1: Comparison of introduced genomic selection methods

Analysis		Parameter Information			Special Cases
		π	Marker Variance	Training and Validation	
Linear	G-BLUP	N/A	Constant	Yes	
	GRM	N/A	N/A	None	
Non-Linear	BayesA	π=0	Variable	Yes	Equivalent to BayesB when π=0
	BayesB	Variable, user assigned	Variable	Yes	
	BayesC	Variable, user assigned	Constant, except when shrunk	Yes	Similar to GBLUP when π=0
	BayesCπ	Estimated from the data	Constant, except when shrunk	Yes	

Across breed analyses

The scientific literature is replete with studies that examine GS methods within breeds and homogenous populations. This approach is feasible in the dairy industry, where the majority of the cattle in the United States are of the Holstein breed and large DNA and semen repositories exist to archive samples. In the beef industry, these resources do not exist and the breed structure is much more fractured which necessitates the pooling of samples across breeds for analysis (deRoos *et al*. 2009). Some studies have examined the possibility of across breed analyses by training in one breed and predicting in another and achieved poor results (i.e., Harris *et al*. 2008). Patterns of LD tend to vary widely across breeds and influences the ability to detect a QTL with the same SNP across multiple breeds. High levels of LD must exist between the marker and the QTL and the linkage phase must be preserved across all breeds in the analysis (Goddard and Hayes 2007) so that the directionality of the effect is the same. The amount of LD is the limiting factor in the predictive ability of the current 50K chip (Kizilkaya *et al*. 2010). Because SNP allele phase relationships are preserved over approximately 10 kb across different breeds of cattle (The Bovine HapMap Consortium 2009) and haplotypes with strong LD ($r^2 \geq 0.7$) are significantly shorter in admixed and crossbred populations compared with purebred populations (Toosi *et al*. 2010), increased SNP density will probably be required for extensive implementation of across breed GS.

Another consideration in across-breed analyses is the appropriate method to partition the training and validation populations. Kizilkaya *et al*. (2010) showed that training in multibreed populations and predicting in purebreds is less effective than the converse. A study by Toosi *et al*. (2010) suggested that training and testing within the same breed always produces the highest accuracies. However, training and validating in admixed populations performed similarly with regard to accuracies. Training and validation in crossbred populations increased accuracy by 11% compared to training in purebreds and predicting in crossbreds. This indicates that implementation of GS methods in crossbred populations may be feasible. Additionally, these authors noted that a larger sample size may be needed in multi-breed populations to produce comparable accuracies to those achieved in purebred populations due to the fact that a larger number of effects (both breed specific and across-breed effects) need to be estimated. Partitioning of animals to maximize the relationship between the training and validating groups (i.e., placing sires in training and progeny in validation; VanRaden *et al*. 2009), random allocation, and genetic distance between breeds (Toosi *et al*. 2010) have been examined.

Data analysis in five breeds of animals (Angus, Hereford, Charolais, Limousin and Simmental) enrolled in the NCBA Carcass Merit Project (n=3,240) performed using GenSel (BayesCπ) indicated that across-breed GS may be feasible using 50K data. Using random allocation across all breeds, animals were partitioned into training and validation sets that comprised differing percentages of the total data (Figure 7). Because multiple independent samples could be taken from the data for each analysis, 20 bootstraps were performed for each training percentage group. The minimum, mean and maximum realized accuracies (correlation between phenotypes adjusted for fixed effects (p) and the predicted genetic merit ($\hat{g}$) for Warner-Bratzler Shear Force (WBSF) divided by the square root of the heritability) over 20 bootstraps are shown in Figure 7. Training in over 70% of the data tended to result in slightly higher maximum realized accuracies, but allowed sampling effects that resulted in very low minimum correlations. These data indicate that the most effective size for the training set is somewhere between 60-80% of the data which results in a realized accuracy of 0.66-0.69 across all breeds. Accuracies within each breed varied according to number of genotyped animals and the heritability of WBSF within the breed. Models incorporating only the 100 or 200 most informative markers resulted in only small decreases in the accuracy of predicted genetic merit, indicating that there is likely to be significant pedigree relationship between animals in the training and validation populations. The modeling of such linkage effects can be useful to predict rare QTL effects (VanRaden *et al*. 2009) or across breeds where sufficient LD does not exist to precisely predict QTL effects, however these effects will decay more rapidly over time (Habier *et al*. 2007). Nonetheless, these data indicate that across breed applications of 50K data are possible as

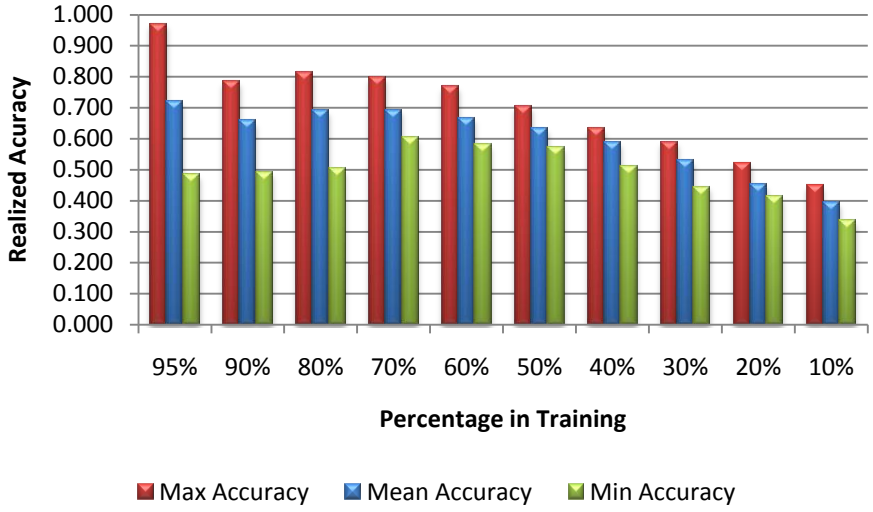

Figure 7: Analysis of WBSF using GenSel BayesCπ. Varying proportions of the data were included in the training and validation populations and animals were randomly allocated to each set across all breeds across 20 bootstraps.

long as the modeling of linkage is recognized. Higher density (such as 800K) data will provide even more opportunities for improvement and for the generation of GS models that will be more stable over many generations.

Incorporation of Molecular Breeding Values into NCE

The previously discussed methods for the implementation of GS are all scientifically feasible and have been shown to be successful in both beef and dairy research populations. However, the marker density required for most of these methods to be successful is not economically sensible for commercialization of the technology to beef cattle producers. The DNA marker panels that have been commercialized in the beef industry to date are small (less than 384 markers per trait) and consist of the SNPs that are deemed to be the most important in research populations for predicting merit for a trait. The results from these panels are typically summarized into a single marker score or molecular breeding value (MBV). These MBVs provide additional information on animals with low EPD accuracies, but do not include information on all of the genetic variation for a trait like an EPD does. The most useful solution is to incorporate the MBVs into existing NCE systems and publish a single value (EPD) which combines both sources of information to enhance the EPD accuracy. Because none of the marker genotypes are available to the breed associations, a method was developed (Kachman 2008) to include MBV information into genomic-enhanced breeding values for the beef industry. The method treats the MBV and the observed phenotype as genetically correlated traits.

The American Angus Association implemented this technology in fall of 2009 into their carcass EPD evaluations in the form of genomic-enhanced EPDs, which are updated weekly. "Genomic-enhanced" EPDs are calculated for nearly 2 million animals for carcass weight, marbling score, ribeye area and fat thickness (Northcutt 2010). This has not only allowed the rapid incorporation of marker panels, carcass phenotypes, and ultrasound data, but also generation of carcass EPDs for dams, which previously had no records, as soon as the MBV is processed for their progeny (Northcutt 2010). Young animals with no ultrasound scan records but with MBVs will achieve EPD accuracies of 0.28 to 0.38 depending on the trait, compared to a parent average EPD with an accuracy of 0.05 for animals without an MBV or scan record (Northcutt 2010). Genomic-enhanced EPDs are now provided for docility, residual gain, and growth traits (birth, yearling, and weaning weight and milk) in addition to the carcass evaluation (AAA, 2011).

Implications

There are many advantages to GS and very few drawbacks other than the need to mitigate expense and develop infrastructure to handle the data. First, effective GS models allow the selection of young animals (even as soon as the embryo stage [Seidel 2009]), which can dramatically shorten generation interval and increases genetic progress (Seidel 2009). It has been estimated that GS could double the rate of response to selection (Schaeffer 2006). Secondly, GS has the ability to increase selection intensity while saving costs. A larger pool of genetically superior animals can be identified earlier in life using EPDs that are more accurate, before the expense of raising the animal to breeding age and the subsequent production of inferior calves. Females typically do not have high accuracy EPDs until very late in life, if at all. Using GS, EPDs for females are just as accurate as for males (VanRaden *et al.* 2009). Due to their large numbers, it is likely that many more genetically superior females exist than superior males, but the only way we can accurately identify them is if large numbers of animals have been genotyped. While this is very relevant for beef producers, this has been particularly vital in the dairy industry, where considerable expense goes into progeny testing elite sires and GS could save approximately 92% of the costs of proving bulls (Schaeffer 2006). While the reduction of costs associated with progeny testing would not be as important in the beef industry, significant opportunity exists to capture additional economic value in many aspects of the food production chain while simultaneously increasing demand for beef by providing a higher quality product. Using WBSF as a test case, a study by Weaber and Lusk (2010) indicates that if bulls in the upper 30% of genetic merit for WBSF are selected each year, feeder cattle profits would increase $9.60/head and $1.23/head for fat cattle within 20 years. The lifetime progeny value for a bull in this pool of candidates would be expected to increase revenues by more than $312 for feeder calves, assuming a productive life of 5 years with 20 progeny sired per year. After 10 years of selection on WBSF, this advantage should exceed $876. The availability of marker data could make possible the advent of tenderness-based marketing programs at both feeder and stocker levels. A genetic improvement program such as this is estimated to produce $7.6 billion in net value (Weaber and Lusk 2010).

Possibly the most important applications of GS in the beef industry are towards traits that are either:

a. Novel – Sufficiently large numbers of phenotypes to perform traditional NCE do not exist and will not likely exist outside of discovery populations for the near future.

b. Measured late in life - By the time sufficient data exists for selection on traits such as stayability and longevity, the animal's productive life is nearing an end.
c. Difficult and/or expensive to record – Traits like feed efficiency and animal health or disease resistance are expensive and/or require specialized equipment to record phenotypes.
d. Collected at harvest – These traits can be collected on progeny after they reach adulthood, however those animal used in breeding herds do not have records for these traits.
e. Sex-Limited – Traits like milk production and scrotal circumference cannot be directly measured in one gender and require progeny records to increase the accuracy of the EPD; however, equal accuracies can be obtained on males and females using GS (VanRaden *et al*. 2009)
f. Have implications in animal welfare –GS may have future implications in animal welfare, where the collection of useful phenotypes would require exposure to disease or invasive techniques (Solberg *et al*. 2009).

Additional merit may be gained in the use of GS for selection on traits with low heritabilities (Figure 8) such as fertility. While improvement of these traits is currently effected through management decisions and breeding schemes such as crossbreeding, GS would more easily allow selection on the

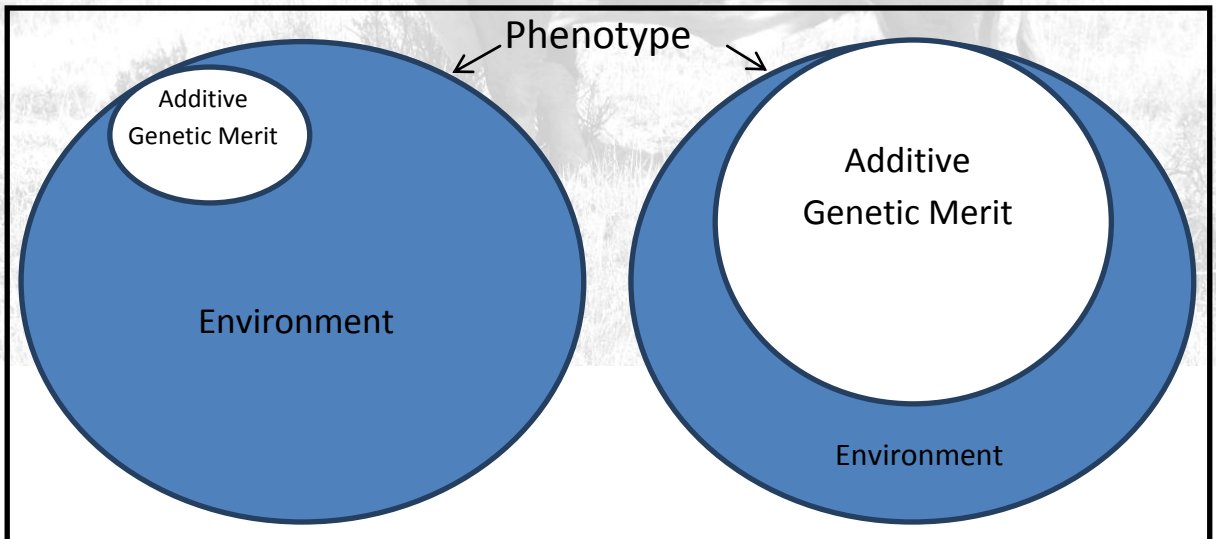

Figure 8: Traits with high heritabilities are largely influenced by the genetic merit of the animal and have less influence from the environment (right). Low heritability traits are largely determined by environmental effects with a smaller proportion from the additive genetic merit (left) and are more likely to be influenced by management decisions.

underlying genetic merit. Increases in additive genetic merit could be paired with better management to make faster gains for lowly heritable traits.

Additional value from genotyping and phenotyping animals can be captured by the generation of large phenotypic and genetic databases (Sosnicki and Newman 2010), especially as it pertains to traits with the previously detailed features . These resources can be utilized for genomic evaluations, validation of DNA markers identified in independent experimental populations, and to test candidate markers for causality (Sosnicki and Newman 2010). As beneficial markers move to fixation in a population due to selection, the accumulation of resources within these databases and the generation of DNA repositories for re-estimation of marker effects will be critical to continued success of GS programs.

Conclusions

The future for genomic technologies seems very bright. Decreases in the cost of whole genome sequencing and new research into epigenetics will provide more opportunities for selection in the beef industry. Unlike the hover car and robotic maid in the *Jetsons*, what was once viewed to be the future in the beef industry is now a reality with the arrival of genomic-enhanced EPDs. GS has the opportunity to provide added value for seedstock and commercial producers and their customers alike. These improvements will be passed along to the consumer and strengthen demand by enhancing the quality of beef products. It may still be too soon to judge the future impacts of GS in the beef industry, but if current research and the success of genomic-enhanced EPDs in the Angus breed are any indication, GS is poised to revolutionize the beef industry.

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Selection Tools for Optimal Genetic and Economic Improvement

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INTRODUCTION

The earliest fossil evidence of human's domestication of animals occurred approximately 14,000 years ago (Davis and Valla, 1978; Leonard et al, 2002). Since that time selection has been imposed upon domesticated animal for beneficial traits and attributes. Through time, selection pressure has progressed from fitness traits and visual appraisal to production traits and underlying genetic merit.

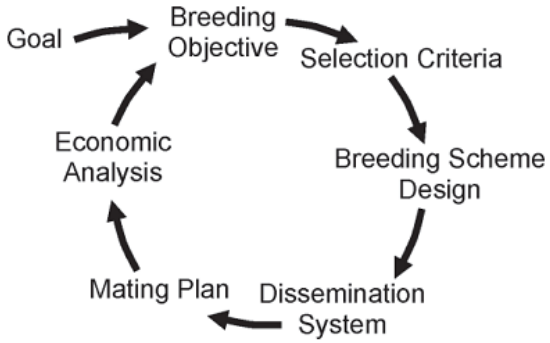
The most common selection tool today comes in the form of expected progeny difference (EPD). The first large scale genetic evaluation to provide producers EPD was published in the early 1970's (American Simmental Association, 1971). Applying the methods of Henderson (1966), national cattle evaluation became possible and revolutionized the way animals could be compared to one another. Over the next forty years advancements have been made in the number of traits evaluated, the number of animals evaluated and ways to use EPD in multiple trait selection.

However this amount of information has made selection a daunting task. Confusion in the definition of an EPD, how to apply the EPD, relationships among EPD are all obstacles producers face when selecting the next generation. Most producers are left with choosing a few EPD to focus on and ignoring the rest. This leads to not using all the information available and taking full advantage of technology. Methods for combining multiple EPD into single a value to capture all the information in a more manageable form has been studied extensively using two primary approaches, selection indices and decision support models.

Review of Literature

Selection for profit: Selecting animals to become the next generation is a decision which carries long term impact. Deciding which animals are the best may be different depending upon the goals or objectives of each individual producer. A guide to navigate the steps required to reach an answer to what is best is illustrated in figure 1 (Harris et al., 1984, Garrick and Golden, 2009). The first step in the process is to identify a goal. A broad definition of this goal may be to remain in business by being profitable.

Figure 2: Logical steps to arrive at selection improvement (Garrick and Golden, 2009, adapted from Harris et al., 1984)



After the goal had been identified, the remainder of the process revolves around what traits are biologically and economically relative to the goal. Assuming profitability is the goal then producing an animal that will net the greatest return within a given production scenario can be considered best. Eleven years ago Golden et al. (2000) introduced the concept of economically relevant traits (ERT) to the industry though the Beef Improvement Federation. Golden's defined ERT as:

> "Economically relevant traits are the traits that directly affect profitability by being associated with a specific cost of production or an income stream. Indicator traits add information to the prediction of economically relevant trait."

In that paper, a distinction was made between two categories of EPD. These two categories were ERT and indicators of ERT. To be an ERT the trait must have a measurable/quantifiable value on financials of production. An indicator trait is one that may be related to an ERT but by itself does not directly affect the revenue stream of enterprise. The list of Golden's proposed traits presented in the article is given in Table 1. Priority of these ERT may be different for each cow-calf enterprise, based upon their particular marketing strategy, genetic strengths of their herd, production environment or economic structure.

The ERT concept has been well received by the industry. To see examples of the adoption of the ERT concept one only needs to look at any breed association sire summary. For example, of the fourteen EPD published by the Red Angus Association of America, eight are directly from Golden's list. The American Angus association embraced the ERT concept as well. Recently, the association stopped the publication of both carcass and ultrasound EPD by evaluating the ultrasound measures as a correlated trait with carcass measures, only publishing the ERT - carcass EPD (MacNeil and Northcutt, 2008).

Over the past twenty years breed associations have gone through a proliferation of EPD. Table 2 shows the comparison of the number of EPD published by select American breed association. Comparing the early 1990's to 2010 sire summaries most associations have increased the number of published EPD

at least 2 fold. Although the many of EPD created have conformed to the ERT definition, methods for multiple trait selection have lacked and breeders have an enormous amount of information available. A look at 2010 sire summaries show the number of EPD published by varying association's ranges from 10 to 16 phenotypic traits (table 2).

Table 1: Proposed economically relevant traits and their indicators relevant to the cow-calf producer (adapted from Golden et al., 2000)

Economically relevant trait	Indicator traits[1]
Sale Weight Weaning Direct Weaning Maternal (Milk) 600 d Direct Carcass Weight Direct Salvage Cow Weight	Birth weight 205 d Weight 365 d Weight Carcass weight Fat Thickness Cull Cow Weight
Probability of Calving Ease	Calving Ease Score Birth weight Gestation Length Pelvic size
Cow Maintenance Feed Requirements	Mature Cow Weight Body Condition Score Milk production Gut Weight
Stayability or Length of Productive Life	Calving Records Days to Calving Calving Interval Milk Production
Heifer Pregnancy Rate	Pregnancy Observations Scrotal Circumference Age of Puberty
Docility	Docility Scores

[1] "Indicators" means traits which are measured to provide information to produce the economically relevant trait EPD. This list contains just the obvious indicators. It is likely that different situations will be able to use other indicators

[2]Sale weight is a category of EPD. Different breeders will have different times at which they believe the future sales will occur for calves resulting from current breeding decisions. Each situation will require the breeder to use only one of the sale weight EPD.

Table 2: Comparison of the number of EPD and Dollar index values published by various breed associations in 1990 versus 2010.

	Published EPD[1]		Published Dollar Index Values[1]	
Breed Association	**1990**	**2010**	**1990**	**2010**
American Angus Association		16	0	7
American Gelbvieh Association	7	13	0	2
American Hereford Association	7	10	0	4
American International Charolais Association	4	11	0	1[2]
American Simmental Association	6	14	0	2
North American Limousin Foundation	4	13	0	1
Red Angus Association of America	4	14	0	0

1- Counts were obtained from respective association sire summaries
2- Terminal Profit Index is a user customizable index program

Selection Index: Selection index, a weighted combination of economic values and selection criteria for multiple trait selection, was first described by Hazel and Lush (1942). The purpose of developing selection indexes was to maximize economic response from multiple-trait selection (Hazel, 1943). Advancing from single trait selection, selection index offers a method for combining multiple pieces of information into a single value to assess genetic and economic merit of an individual simultaneously. This method of combining all traits of the breeding objective into a single value is a more efficient pathway to attain the breeding goal than selecting for multiple traits independently. The formula of selection index presented by (Hazel, 1943) is:

$$I = b_1X_1 + b_2X_2 + \cdots + b_nX_n$$

Where I is the aggregate index value, b are the relative economic values for each trait in the breeding objective and X represents information on individual animals expressed as performance measures or breeding values. As computing technology has evolved the availability and quantity of evaluated traits with EPD has increased. Replacement of phenotypes in the index with EPD also introduces ways to account for other effects such as inbreeding and contemporary group effects. However, as noted by many authors on the subject, EPD may not be available for all ERT so the necessity to estimate correlations and co-variances among these and indicator traits is still necessary (MacNeil et al., 1997; Hazel et al., 1994).

Performance information only makes up half of the selection index equation, economic values still being required. Derivation of economic values has traditionally been accomplished from one of two methods, either though economic simulation (Cartwright, 1970) or the partial derivative of a profit equation (Harris, 1970). These profit equations are typically complex in nature, summarizing all economic facets of a beef production system. These economic values are generally only applicable under

the scenario used in the derivation and can be subject to difference in cost/revenue assumptions as well as genetic level of herds. MacNeil et al. (1997) suggested that given the lengthy generation interval of beef cattle, when deriving these economic values, average prices from a 10 to 15 year period should be used.

The question arises of which traits should be included in the index? There are several approaches to answer this. Ideally the index would include all economically relevant traits (Gjedrem, 1972). However this is seldom possible because the relationships between many of these traits or the economic weights are difficult to derive and apply due to operation specific dependencies. Sivanadian and Smith (1997) showed a diminishing return to adding additional traits if they are highly correlated to other traits or low in heritability.

Index selection has proven successful as reported by MacNeil (2003) who investigated the long term effect of selecting on an index originally proposed by Dickerson et al. (1974). The index consisted of 2 traits, birth weight (BWT) and yearling weight (YWT) using the equation:

$$I = YWT - 3.2 * BWT.$$

Using the index in a research population of composite cattle increased yearling and birth weight 23.2 kg and 1.35 kg respectively after three generations of selection. Correlated responses in other weight traits were also observed. Increases in 200d weight and mature weight were reported to be 10.3 kg and 22.2 kg respectively. Only minor responses in maternal effects were observed. These results illustrate a potential downfall in selection indexes, genetic antagonisms. Using an index which included yearling weight, an economically relevant trait when selling animals at a year of age, selection successfully increased yearling weight. However, if females born under this selection strategy were kept until maturity there would be a potential increase in feed required to maintain these animals due to correlated increases in mature size. While this index was successful in its design, including mature weight in the index as well would have addressed the long term effects on mature weight of female requirements.

Using a more complex selection index, Enns and Nicoll (2008) reported the results of selection for economic return using the traits harvest weight, dressing percentage, net fertility (measured in number of calves weaned) and cow body weight over 17 years. The index originally devised by Morris et al., (1978) and described by Nicoll et al., (1979) was

$$H = 0.53 * HW * D_P * (4.8 * F - 1) + 0.06 * M * D_M$$

Where H was net income per cow lifetime, HW represented harvest weight, D_P and D_M was dressing percentage for progeny and cull cows respectively, M was body weight at disposal and F was calves

weaned per cow exposed. Over the 17 years of selection, response to the index traits was 28.9kg, 2.2kg, -0.595% and 0.021 calves for the traits harvest weight, mature body weight, dressing percentage and calves weaned per cow exposed, respectively. Economically, average returns of an additional $22.87 per year per cow were realized over the life of this study.

Upton et al. (1988) proposed the use of customizable indexes for individual producers. However this is only possible for the largest of producers. The cost associated with the research required to identify which traits to include in the selection as well as the derivation of economic weights for these traits would be too great.

More recently, many breed associations have begun to include generic selection index values in sire summaries. These values, often termed 'dollar value indexes', have proliferated to include maternal, carcass, and growth traits. However details concerning the traits included in these indexes, weighting factors of individual traits and the assumed cost and pricing structure to derive the dollar amounts has not been transparent or detailed (Garrick and Golden, 2009). In order for rankings of 'dollar value indexes' to remain constant, selection objectives, production environment and economic situation must be the same for each user of a generalized selection index. Using such an index to make selection decisions can be risky. If the traits included in these 'black box' indexes are not necessary to achieve the goal or the economic values do not reflect those of the user selection pressure may not be at an optimum (Garrick, 2005). Referring back to table 2, the number of such index values published by breed associations ranges from zero in the Red Angus Association of American sire summary to seven indexes published by the American Angus Association. Most of these indexes fall into the categories of terminal/carcass indexes, feedlot indexes or maternal indexes.

Computer aided beef cattle selection: Using computer modeling to predict future outcomes can be a useful tool to account for production, management and economic changes over long periods of time. Computer simulation has been shown to be advantageous to selection indices because of the ability to parameterize individual management and environmental details (Garrick, 2005). In general there are two types of computer models, simulation models and decision support system (DSS) models. Simulation models tend to be more scientifically targeted, some requiring a vast number of parameters. These complex models attempt to completely describe all variables of a production scenario. Though based on simulation, DSS models may utilize databases to simplify inputs required by the simulation models. Variables that would remain static within an operation over time, such as environment, can be assumed constant as both the baseline and potential simulation would be subject to identical conditions. This allows DSS to focusing primarily on summary of simulation results into fewer outputs.

Simulation models

There have been many simulation models published with the ability to replicate beef production. Perhaps the most often cited and modified simulation model has been the Texas A&M University Cattle Production Systems Model (TAMU) (Tess and Kolstad, 2000a). It has been modified and validated in a variety of environments under varying herd sizes and management practices. First described by Sanders and Cartwright in 1979 (Sanders and Cartwright 1979a, b), the deterministic model simulates levels of performance from specified feed resources and cattle production potentials. Using a monthly time step the model is able to simulate production across years. The model is driven by three primary routines, growth, fertility and death. Simulated animals are classified into groups by age in years, lactation status (monthly basis) and pregnancy status. Calves are classified by age in months and age of dam. All replacements are assumed to be generated within system. Herd dynamics are characterized by simulating growth of individual classes of animals, fertility of females and the loss of animals to either death or sale. Growth of animals is simulated by allocating available feed resources to first meet requirements for survival and physlogical status (gestation, lactation, etc.). Surplus available energy goes into fat deposition. In the event of nutritional deficiencies, production of milk and lean growth is reduced. Fertility is simulated separately for heifers versus cows. Heifers are evaluated for degree of maturity, body condition, weight gain, genetic reproduction potential and this information is then used to determine breeding success. Cows are evaluated for body condition, weight gain, lactational status, postpartum interval and genetic reproduction potential. Death losses are simulated as functions of the time of year, age, body condition and physiological status of animal groups.

Previous to the published description of the TAMU model it had been used several different simulation studies representing different production environments (Davis et al., 1976; Sanders, 1977; Cartwright, 1977; Nelsen et al., 1978; Ordonez, 1978). Environments for these applications ranged from Botswana, Venezuela, Guyana, to central Texas. The authors recommend that due to the complex nature of the model it is best served not as a producer tool but as a research and teaching tool to transmit knowledge back to producers (Sanders and Cartwright, 1979a)

Subsequent modifications to the TAMU model were done by many scientists, changing the environmental, nutrient and predictive capabilities of the original simulation. Notter et al. (1979a) to extend the nutritional equations for a more “complete” modeling of nutrient utilization. These changes included varying digestibility of forage, imposing maximum daily milk intake of suckling calves, introducing a dynamic gut fill parameter, changing limits on dry matter as well as incorporating heterosis values for growth and milk production. Kahn and Spedding (1983) outlined additional modifications

designed for smaller herd sizes of developing countries. Primary changes included; calculating individual animal performance instead of herd-age class group; addition of stochastic events including conception, mortality, and calf sex; variable time steps of 1 to 30d; additional management options of feed supplementation, multi-purpose (dairy, beef and draft) breeds and culling in response to external events; time-scalable output options up to a 10yr in the future; and updated biological functions from recent literature. Subsequent validation of the models output and performance were also published (Notter et al., 1979b; Kahn and Spedding, 1984; and Kahn and Lehrer, 1984).

Building on the modified TAMU model outlined by Notter (1977), Bourdon and Brinks (1987a, b, c) added additional capabilities and changed inputs to represent northern plains range cattle environment. A detailed explanation of changes made to the Notter's version of the TAMU model can be found in Bourdon (1983). In brief, modifications included:

- A dynamic growth curve which used three points in time to simulate growth potential: birth, yearling and mature weight;
- Heterosis values for birth weight as well as growth from birth to maturity and milk production;
- Different calving difficulty equations for heifers versus mixed age cows;
- Cold weather effects on energy requirements;
- Preferential eating habits;
- Body composition of mature cows;
- Herd size scaling to fixed land resources;
- Variable fertility parameters; and
- A separate economic model of biological outputs

These changes were used in subsequent studies of growth and milk production (Bourdon and Brinks, 1979a), fertility traits (Bourdon and Brinks, 1979b) and culling and non-traditional management strategies (Bourdon and Brinks, 1979c).

Perhaps the most complete and complex simulation model, the Colorado Beef Cattle Production Model (CBCPM), integrated beef, forage and rangeland and economic simulation into a single model (Shafer et al., 2005). The beef production was based on the original TAMU model (Sanders and Cartwright, 1979a) and many of the ensuing modifications (Notter, 1977, Bourdon, 1983). Evaluating pre-existing models for each of the non-beef production components added, the Agriculture Research Services Simulation of Production and Utilization of Rangelands (SPUR) model (Wight and Skiles, 1987; Hanson et al., 1992, Baker et al., 1992) was selected as the most robust plant model available and modified to interface with the CBCPM. The General Firm Level Policy Simulation Model (FLIPSIM) (Richardson and Nixon, 1986) was chosen as an economic model that would meet the requirements of the CBCPM. Using more than 200 input variables and 480 total parameters the CBCPM is a highly sophisticated model which requires detailed knowledge to be appropriately applied. Stochastically

simulating growth, fertility, calving, lactation, death, feeding intake and requirements, nutrient partitioning and genetic traits, the CBCPM has the ability to accurately predict production for any herd size using any time step. The success of CBCPM as a research tool is evident in the number of studies completed using its capabilities (Baker, 1991; Baker et al., 1992; Baker et al., 1993; Foy, 1993; Hart et al., 1993; Fioretti, 1994; Rantanen, 1994; Steffens 1994; Enns, 1995; Enns et al., 1996; Hyde and Bourdon, 1998; Doyle, 2000; Teague and Foy, 2002; Shafer, 2003).

Tess and Kolstad (2000a) developed a generalized model of range beef cattle production capable of accounting for diverse genetic types in response to changing forage quality and management strategies. Output of the model is structured in terms of economic performance of the system under different breeding and management strategies. Using a complete and complex set of body composition prediction equations, growth and resulting requirements are predicted deterministically. Forage quality or amount of available nutrients in feedstuffs are input as metabolizable energy, neutral detergent fiber, and crude protein per kilogram dry matter, ruminally degradable protein per kilogram of crude protein. Daily requirement of metabolizable energy becomes a function of daily weight and available feedstuff energy. Although there is the opportunity of parameterize phenotypic weight and gain potential there is no explicate opportunity to account for genetic potential of animals. Stochastically modeling fertility, age of puberty and probability of conception are both used to predict reproduction. Testing this model with two different composite lines cattle, only partial agreement was found between predicted and actual weights (Tess and Kolstad, 2000b). Tess and Kolstad (2000b) concluded it to be necessary to know or have fairly accurate values for crude protein, dry matter digestibility and per animal availability of dry matter (kg) to accurately predict performance.

Decision Support Systems

Decision support systems allow users to interact with a simulation model to achieve some knowledge or summary of results. These systems attempt to mimic a human expert or specialist to answer some specific question, dealing with only a single area and able to give explanation for the reasoning (Lynch et al., 2000). Typical DSS employ a whole system approach where an entire production scheme is modeled from many details but only summarized results are reported back to the user.

Acceptance and usage of DSS in agriculture has been problematic. In a review of attributes necessary for agriculture DSS, Newman et al. (2000) suggests eight reasons for failure of agriculture DSS systems

1. Limited computer ownership among producers
2. Lack of field testing
3. No end user input preceding and during development of DSS
4. DSS complexity and possibly considerable data input
5. No reason seen for changing current management methods
6. Distrust for the output of a DSS because producers do not understand the underlying theories of the model
7. Mismatch of the DSS output with the decision-making style of the producer because the producer's conceptual models are excluded
8. Unclear definition of beneficiaries (e.g., scientists, primary producers, and technology transfer agents)

In the realm of beef cattle breeding, technology acceptance and usage has been slower than that of other livestock industries. This may be due to several reasons, computer usage given the average age of producers as well as lack of transparent systems producers are able understand (Newman et al., 2000). The successes of DSS are dependent on several factors. These include if the system meets the user's needs, commitment of developers, ease of use, and support from management (Newman and Stewart, 1997). Ultimate success of any system depends on a champion to carry the project through and maintain it. Lacking a champion, each system seem relegated to history (MacNeil et al., 1998).

The focus of many DSS for beef cattle has been predicting and comparing different crossbreeding systems or breeds. Some examples of DSS systems that have been developed for beef producers are HotCross (Newman et al., 1997), SIMUMATE (Minyard and Dinkel, 1974), and Decision Evaluator for the Cattle Industry (DECI) (Jenkins and Williams, 1998) and the National Beef Cattle Evaluation Consortium and Colorado State University (NBCEC-CSU) (Brigham, et al., 2004).

HotCross was developed by Newman et al. (1997) to simulate crossbreeding performance in tropical and sub-tropical environments of Northern Australia. Using literature estimates of heat and disease tolerant cross-bred animal's performance, a database was assembled to calculate predicted performance. The user inputs were conceptualized to be as easy as possible for a producer to enter. Inputs include environmental factors, the region of Australia where production will take place, and the level of nutrition available during three defined production phases, breeding/pre-weaning, growing and finishing. Cow herd input consist of breed composition and level of phenotypic production if known. If actual performance figures are unknown these can be populated from the database linked to the system. The predictive portion of the system first calculates performance based solely on the tropical environment, accounting for direct and maternal breed effects and direct and maternal heterosis. This performance prediction is then adjusted by a breed cross specific factors accounting for environmental stressors (region and nutrition). Lastly adjustments for tick, worm and heat stress are factored into the final predication. The output of HotCross is designed to give the user a comparison of different performance potentials of

differing breeds or levels of nutrition. Using the DSS allows producers to compare predicted performance of different potential sire breeds to select one that best fits their expectations and goals.

SIMUMATE (Minyard and Dinkel, 1974) was an early model which was able to compare different crossbreeding systems and different breeds under United States production circumstances. SIMUMATE uses individual management criteria and feed resource parameters as input into the system. Initially the model parameters were gathered from producers either through completion of a survey or through one-on-one interaction with extension agents. These parameters were then sent for analysis and interpretation at South Dakota State University (Newman and Stewart, 1997). SIMUMATE has been updated (MacNeil et al., 1998) and professional assistance is no longer required. Using available feed to scale carrying capacity, ie herd size, based upon predicting energy requirements for maintenance, milk production and weight gain crossbreeding systems could be compared. SIMUMATE has the ability to predict net returns at different endpoints including, weaning, backgrounding, finishing and of the carcass (MacNeil et al., 1998). This DSS has ability to vary both the growth potential and the financial aspects of future production before long term decisions are made. From the output users can rank potential management changes or breed changes in terms of net returns.

The Decision Evaluator for the Cattle Industry (DECI) (Jenkins and Williams, 1998) evolved from the Bourdon and Brinks (1987a) modifications of the Texas A&M University Beef Production. The simulation model was further modified to be used as a dynamic user parameterized DSS (Williams et al., 1992, Williams and Jenkins, 1997). The development goal of the DECI DSS was to provide a tool that allowed comparison of a variety of management choices to current production. Users are taken through stages of production and asked to fill in parameters and management details. DECI is split into five categories, management, feeding, breeding, disposal and financials, with numerous subcategories within each. The herd is modeled using a daily time step, adjusting for weight gain/loss on an individual animal basis. Genetic potential is split into high, medium and low categories. The DECI system predicts a baseline herd from the user inputs and allows changes to be made and compared back to the baseline. Management decisions, such as culling strategies, plane of nutrition, calving season, and heifer replacements are a few examples of predicted output that can be evaluated. The output of the DECI system allows the user to make pair wise comparisons of their baseline herd and potential changes in any variable. The DECI system returns the user both predicted phenotypic averages and dollar figures to help them compare changes in production.

The National Beef Cattle Evaluation Consortium and Colorado State University (NBCEC-CSU) web based DSS, is a tool which allows users to vary phenotypes, management, financial and genetic

potential inputs (Brigham, et al., 2004). Users of the system are able to input their actual production levels and management approaches or use national averages. The NBCEC-CSU DSS is unique in that it is paired with online sire summaries for users to easily search and select individual bulls to simulate matings. A simulated base cow herd is predicted from the user's defined parameters resulting in a current performance level of production which all potential mating are compared to. Matings are simulated to equilibrium between chosen sires and the cow herd resulting in predicted values of a sire's overall genetic effect on the cow herd. The NBCEC-CSU DSS accounts for the entire suite of EPD available and returns a net dollar value of the bull's genetics under the user's production, management, economic and genetic inputs. The background simulation model predicts an age structure, pregnancy rates, growth rates, requirements for energy, calving ease and revenues accounting for base herd and differing sire genetics. Primary differences in revenue come from changes to the number and weight of sale calves and female reproductive ability. The dollar value output presented to the user is similar to a custom index value for the user's unique production circumstances.

Impact to industry and conclusions

Over the past 50 years animal breeding and genetics scientific community has possibility gone too far in making more EPD instead of more useful ways to use EPD. It is possible to make an EPD for any trait that can be measured but a movement to simplify selection and provided more useful tools is needed in the coming generation. Much of our efforts have focused on providing genetic prediction for as many ERT as possible with little emphasis on the economics of production. Suggested by MacNeil et al, (1997) moving from genetic improvement to economic improvement needs to occur to assure profitability. Rather than making EPD for every trait, the relationships and economic impact among traits needs to be addressed and made available for selection. The cost of production has been and will continue to increase and breeders will need to be more efficient and financially driven to remain profitable. Genetic selection tools which meld genetics and economics together are an obvious choice to approach this.

Selection indexes have found a place among EPD suites as an intermediate for producers to select for more economically efficient animal. There is ample proof that selection using indices will result in genetic progress, however lacking customization they may not be the most efficient path to progress. Given that true custom selection indexes will probably never be available to any majority of producers leaves limited appropriate usage. The available index values published by many breed associations are useful but producers must understand and consider the components included in these values. Knowing which traits are included in these and the weighting factors used needs to be transparent to users to avoid

double counting traits if any EPD aside from the indices are used and if economic weights apply in similar magnitude.

Computer models able to simulate beef production have been well documented and validated in literature. However the level of complexity necessary for a simulation model to be robust and accurate is enough to designate them to being useful only in research and development arenas. Given this impediment, a DSS that uses a simulation model in the background maybe a better choice to increase producer acceptance and usage for computer aided selection. In order for any computer program to gain acceptance, a straightforward explanation what it does and how it accomplishes prediction will be necessary. The endless possibilities of differing production environments and management strategies in the beef sector require some type of customizable selection tool to simplify sire selection. The ability of DSS to be customized, simulate all aspects of production and return profit predictions is the best option for assisting producers in the selection maze.

As we approach yet another revolution in genetic prediction, genomic tests and incorporation of genomic information into EPD, new challenges lie ahead of additional information overload and confusion of what to use and how to use it. Advancements in our ability to better evaluate the next generation with higher accuracy using genomic tests is occurring at rate that is difficult to keep up with. An ideal approach to address the new technology and available information may lie in a decision support system that simultaneously accounts for all ERT and combines information into an economic form. Using a simulation model as the engine to power such a DSS and requiring the user to enter only minimum information such a system can remain user friendly yet powerful and robust. Focusing selection on profit through use of all available information will allow producers to make more informed decisions.

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2011 SEEDSTOCK PRODUCER AWARD NOMINEES

Bar T Bar Ranch
Owners/Managers: Bob and Judy Prosser
Winslow, Arizona

The Bar T Bar Ranch has been in Judy's family since the late 1920s. They acquired it in 1990. It encompasses about 326,000 acres of private, state, and forest service lands in northern Arizona between Winslow and Happy Jack. Cattle are raised on the range year-round and are moved to high elevation, Ponderosa-Pine and Pinon-Juniper country in the summer and down to high desert, shrub country in the winter. Annual precipitation averages between 12-18" in the summer country and 5-7" at the winter elevations. The average stocking rate is 1 cow per 160 acres per year. Bar T Bar has a commercial herd of 700-800 cows and a seedstock herd of 400 head. In addition, 500-750 head of yearling heifers are bred for replacement heifers or for sale. The seedstock herd is primarily Balancer®, with some purebred Angus and Gelbvieh. The cow herd calves from March 1 – April 15, with 50 percent of the calves from A.I. sires. They are the 2nd largest breeder of Dams of Merit in the American Gelbvieh Association, and do this in a low rainfall low input environment. The commercial herd calves March 15 – May 15. The Bar T Bar Ranch is proudly nominated by the American Gelbvieh Association.

GV Limousin
Owners: Gene and Virginia Raymond
Managers: Gene Raymond and Arne Hanson
Garnett, Kansas

GV Limousin is a purebred Limousin and Lim-Flex operation in east central Kansas. Owned by Gene and Virginia Raymond, the operation has been producing registered Limousin cattle since 1976, but the operation dates back to the 1950s when Gene first began with a 4-H project. Originally Gene raised and showed polled Hereford cattle and then transitioned over to a commercial operation. GV Limousin was the result of Gene's daughters showing junior projects, when he began to purchase Limousin bulls and since has built his operation to over 400 registered Limousin females. GV Limousin is a split spring/fall calving operation to meet commercial producer's bull demands. In 1991, Gene and Virginia's middle daughter and son-in-law returned to the operation and have been building their own herd of Limousin females. Shortly after they began raising Limousin bulls, GV Limousin began retaining ownership to the rail and realized the breed's advantages. They focus on producing superior genetics that are backed by EPD and carcass data that are demanded by commercial cattlemen. A large percentage of GV Limousin customers are repeat buyers and work with Gene to market their calves. Exceptional customer service and industry leading genetics has been GV Limousin's focus since 1976. The North American Limousin Foundation is proud to nominate GV Limousin.

Jungels Shorthorn Farms
Owners: Dennis, Rita, Derek and Brock Jungels
Kathryn, North Dakota

Jungels Shorthorn Farms (Kathryn, ND) started in 1953 with the purchase of a registered Shorthorn heifer. A herd of registered and commercial cows were maintained until 2000 when son Derek graduated college. At that time, the herd aggressively expanded and began marketing Shorthorn cattle to a more diverse customer base. Intense emphasis was placed on cow fertility. In 2007, Jungels decided to hold their first "Durhams for Denver" Bull Sale. This private treaty bid-off is held annually "In the Yards" and

has grown to become a fixture of the National Western for Shorthorn enthusiasts. The Jungels family currently exhibits and sells 40 head of Shorthorn bulls in Denver in addition to a group of 2-year olds and yearlings marketed directly off the ranch. The 2011 Durhams for Denver Sale marketed bulls from Pennsylvania to California and Texas to North Dakota. Jungels Shorthorn Farms maintains a spring calving herd of 185 head, 100 of which are registered females with the balance of cows being utilized as recipients for a growing ET program. The fall calving herd consists of 80 registered females, with the emphasis on marketing bulls at 18 months of age. Elite females are marketed to purebred operations, with 20-30 heifers retained as replacements. Jungels have more recently added a heifer development segment to the operation in which 100 heifers are purchased, developed, and then mated to Shorthorn bulls. Most of the heifer calves are acquired directly from current bull customers and marketed in bred heifer groups to commercial producers. The American Shorthorn Association is proud to nominate Jungels Shorthorn Farms.

McDonald Farms
Owners: McDonald Family
Manager: Bill McDonald
Blacksburg, Virginia

McDonald Farms is a National Bicentennial Farm that was settled in 1763. It was a self sufficient operation that served as a supply source during the later part of the French and Indian War and the American Revolutionary War. It currently is a diversified livestock operation producing seedstock cattle, sheep, and horses. The forage resources of the farm are utilized through grazing, hay and silage production, with a limited amount of purchased commodities. The seedstock operation consists of 150 female Simmental, Angus, and SimmAngus cattle. The entire herd is spring calving in a 60 day period for cows and 45 days for heifers. McDonald Farms was instrumental in the development of the Southwest Virginia BCIA Bull Testing Program and has evolved to an on-farm "Pick of the Pen" bull sale held annually in April. The McDonalds have always been supportive of Extension and youth livestock programs and have hosted local and state educational programs, field days, and livestock judging team workouts at the farm. Bill has served as a leader in the local and state cattle industry including the board of the National Cattlemen's Beef Association policy division and is currently a board member and serves as the vice-chairman for the American Simmental Association. McDonald Farms is proudly nominated by the Virginia Beef Cattle Improvement Association.

Monogram Farms
Owners: Roland and Doug Preuss & Families
Managers: Roland and Doug Preuss
Terry, Mississippi

Monogram Farms was started by Roland and Doug's father in 1956 with commercial cattle, hogs, and later sheep. The registered Angus herd began as 4-H projects in 1963 by Doug and Roland, who grew the herd over the years to where it numbers 200 head today. Monogram Farms' cow herd is located in Hinds and Lawrence Counties in Mississippi. Performance testing began in 1968 through A.H.I.R. A fall-calving season (September to December) is utilized on 90% of their cow herd with the remaining calving in January and February. Their herd has been closed for 21 years. The majority of their cows trace back to five foundation cows, one of them originating in 1963. Ultrasound was incorporated in 2005. They have participated at bull tests in Mississippi, Texas, and Oklahoma. They have tested bulls at the Hinds Community College Bull Test every year since its inception in the early 1980s. The Mississippi BCIA sales have been a valuable tool in marketing the top bulls from their calf crop. Monogram Farms is the only farm to have participated in nearly every MBCIA bull sale in its 40+ year history and have had some

of the top selling bulls in many of those sales. Cattle are their sole source of income, and they strive to be low input operators. Some practices on the farm are only employed when they have the funds to carry them out. Borrowing money from a bank to make certain expenses is a last resort which they use sparingly. The Mississippi Beef Cattle Improvement Association is proud to nominate Monogram Farms.

Mushrush Red Angus
Owners/Managers: Mushrush Ranches, LLC: partners: Robert & Oma Lou Mushrush, Joe & Connie Mushrush, Daniel & Christine Mushrush
Managing Partner: Joe Mushrush
Strong City, Kansas

Mushrush Red Angus is a family-owned and managed operation located in the heart of the Kansas Flint Hills in Chase County. Literally scattered from one end of the county to the other, Mushrush Red Angus utilizes about 8,000 acres of native tallgrass prairie. While fairly diversified across segments of the cattle industry, the operation is unique in that every endeavor encompasses the use of Red Angus genetics.
The main enterprise consists of 500 registered Red Angus cows split evenly between spring- and fall-calving herds. About 150 bulls are sold yearly in a spring production sale and private treaty sales throughout the year. The target customers are commercial cattle producers. In addition, a bred heifer program has been developed. Between 400 and 500 heifers, sourced from commercial customers using Mushrush genetics, are developed, bred and sold every year. Heifers not meeting the quality of their breeding program, bulls not meeting criteria to be seedstock, and Mushrush Red Angus-sired steers purchased from customers are fed to finish in their on-site 1,000 head feedlot or run through the stocker phase on grass pasture and then put on feed. All fed cattle are sold on a value-based grid to U.S. Premium Beef, with full carcass data collected. Started by Robert and Oma Lou Mushrush in the early 1950s, the operation first accumulated 40 years experience in the commercial cow-calf business. When Joe and Connie Mushrush joined in 1980, the first registered Red Angus cows were added, in addition to an extensive stocker cattle enterprise. The feedlot was added in 1990. This extensive involvement in all segments of the cattle industry has given Mushrush Red Angus a unique insight into the needs of the commercial cattlemen. Mushrush Red Angus is proudly nominated by the Kansas Livestock Association.

Panther Creek Angus
Owners/Managers: Mike and Kati McClelland
Bowen, Illinois

Panther Creek Ranch has been in the purebred seedstock business since 1953 with the purchase by the late Larry McClelland of two purebred Angus heifers. This has resulted in the continual increase of the herd with more rapid expansion over the past several years. Presently, the number of bred females has leveled off at 400, 300 brood cows and 100 bred heifers. There are both fall and spring calving herds consisting of 90 calving in the fall with the remaining 310 in the spring. Panther Creek Ranch comprises a number of locations throughout Hancock and Adams Counties. The total farming enterprise consists of 3,000 acres with 1,400 in row crops and the remaining 1,600 acres in pasture and hay ground. At Panther Creek Ranch, cattle are handled strictly commercial. The cows and heifers must breed, calve, and wean a calf on fescue pasture. Cattle are not pampered and cows are maintained in average condition. Cows that cannot survive under these conditions are soon removed from the herd. Their philosophy is different from almost all other purebred operations. Only the heifers are artificially inseminated. Thus, tremendous emphasis is placed on the bull battery since all cows are bred naturally. The traits emphasized at Panther Creek are similar to what is demanded by commercial producers. Also, emphasis is placed on scrotal circumference and udder conformation along with EPDs that excel in light birth weight, high weaning and yearling weight. Maternal milk is left to fit the fescue environment, and

carcass traits are not ignored, but not overly emphasized. Panther Creek Ranch is a family operation. The patriarch of the Angus operation is the late Larry McClelland who started the Angus herd. Larry passed away in 2004 while mowing pasture on the ranch. His wife, Karol, is still actively involved in the total farming operation by producing noon meals many days and providing guiding advice to the next generation. The Larry McClelland family comprises three children, Mike, Valerie and Vicki. Besides Mike and Kati McClelland and their three children, Bailey, Tristan and Kolby, there is the Peterson family consisting of Steve, Valerie, Shelby and Kayla. In addition, John, Vicki, Kody, and Cole Eilers help out during the annual sale. Kenneth Mowen is also important to the operation as he has been part of Panther Creek for the past 11 years. The University of Illinois Extension and Illinois Beef Association is proud to nominate Panther Creek Angus.

Ridgefield Farm
Owners: Steve and Mary Beth Whitmire
Manager: Nathan Clackum
Brasstown, North Carolina

Ridgefield Farm was founded in 1954 and has been in the same location since that time. The farm consists of 1,023 acres, plus about 600 acres of leased land for additional pasture, hay, and corn, existing in both North Carolina and Georgia. The farm was the 1994 NCBA Environmental Stewardship winner for Region II. The farm began as a commercial cattle operation, and then, from the late 50's until the mid 60's it was run as a Shorthorn operation with about 100 registered cows. In the late 60's a change was made back to a commercial operation. From the late 60's until 1998 about 200 commercial cows of mixed breeding were run, with about 60% being black, with calves sired by Charolais bulls. Calves were sold by video/telephone auction. Upon the death of E.J. Whitmire in 1998 a decision was made to purchase 120 registered Angus cows and to introduce the use of Braunvieh bulls to the commercial herd and to retain ownership of calves to obtain performance data. In 2000, a decision was made to become a seedstock producer of Braunvieh cattle, offering a Progeny Purchase Plan, whereby a contract was provided to bull buyers guaranteeing to purchase the calves sired by Ridgefield Farm bulls, paying them a premium. The calves were then fed out in the Midwest and sold on the grid. In 2008, they made the decision to develop their own branded beef program, establishing Brasstown Beef, which offers a complete line of "Aged, All Natural" beef products. All calves purchased under the Progeny Purchase Plan are now brought to Ridgefield Farm and fed out, harvested and delivered to restaurants, meat markets and grocery stores. Ridgefield Farm is a "Step 4, GAP" rated livestock operation with its Brasstown Beef being sold in Whole Foods Stores and offered on the menu in multiple restaurants on The Biltmore Estate, as well as other fine restaurants in the Asheville and Highlands area of North Carolina and distributed by Sysco and IFC to fine restaurants in the Atlanta area. In addition to all breeding stock being fully tested and ultrasounded, and being evaluated for feed efficiency on Ridgefield's Grow Safe System; a cut of purchased feeder calves, from Ridgefield sires, is also feed efficiency and performance tested in order to close the feedback loop on Ridgefield's genetics. Results of feeding and carcass quality (based upon ultrasound results since there is no USDA grading available), and carcass weights are provided to feeder calf suppliers. Ridgefield Farm runs approximately 125 Registered Braunvieh females, 100 Registered Angus females and 75 Commercial females. The females are all AI'd once, or have embryos implanted, followed by clean up bulls which are left in for sixty days. The goal for calving is from the first of February to the end of March. Bulls are semen checked prior to breeding season and all cows found open upon palpation are sold for slaughter. All bull calves that weigh over 95 pounds are castrated at birth. All heifers with less than 475 pound 205 day weights, and bull calves with less than 550 pound 205 day weights are culled and placed in the Brasstown Beef Program. Ridgefield Farm is proudly nominated by the Georgia Cattlemen's Association and North Carolina Cattlemen's BCIP.

Schuler Red Angus
Owners: Schuler-Olsen Ranches, Inc. and the Darrell Schuler Family
Manager: Butch Schuler
Bridgeport, Nebraska

Located in the panhandle of western Nebraska, Schuler-Olsen Ranches was started by Darrell and Mary Lou Schuler in 1959 with commercial Hereford cattle. A crossbreeding program was implemented in the early 1970's and after witnessing the benefits of heterosis and breed complementarity first-hand, a registered Red Angus herd was started in 1976 to develop seedstock for use on the ranch's commercial cattle and to sell to neighboring operations. The seedstock herd expanded in the 1980's and was improved through artificial insemination, utilization of EPDs and a complete performance testing program. Recognizing the need for identifiable carcass traits, in 1991 Schuler Red Angus began finishing its commercial progeny and collecting carcass data with the assistance of UNL Beef Cattle Specialist, Dr. Ivan Rush. This program expanded to include structured carcass testing, including customer cattle sired by Schuler Red Angus bulls. Over 25% of the Red Angus breed's high accuracy carcass trait sires have been proven by Schuler Red Angus. A composite cowherd was started in 1992 which included Red Angus, Hereford, Gelbvieh, and Simmental genetics. The current ranching operation encompasses 17,000 acres including 2,000 acres of private pasture leases and 1,250 acres of irrigated farm ground. Butch and Susan Schuler and their children Stephanie and David manage the operation today with approximately 1,000 head of spring calving females. The Schuler's hosted their 29th production sale this spring selling 150 registered Red Angus and Schuler Red composite bulls and 20 head of registered Red Angus heifers. Schuler Red Angus is proudly nominated by the Nebraska Cattlemen.

Sunshine Farms
Owners: Tim Minor, Gary Minor, and Jimmy Durbin
Cattle Manager: Jamie McConnell
Genetic and Marketing Manager: Tommy Brown
Clanton, Alabama

Sunshine Farms is part of a family-owned, diversified farming operation, which has been in business for over 50 years near Clanton, Alabama. The farming operation includes the Sim-Angus seedstock division, a large peach production unit to market the famous Chilton County peaches under the Jim Durbin Farms brand, a u-pick strawberry field, a tomato production unit, a timber production unit, a small band of brood mares to produce working ranch horses, and the Mulberry Creek Homestead unit that provides agricultural education for over 1,000 elementary school kids each fall based on corn mazes, a u-pick pumpkin patch and other agricultural product displays. The Sim-Angus seedstock division began in 1993, with the purchase of 30 purebred Angus cows, and has grown to 400 breeding age females. An additional 500 cows, owned by 10 cooperator breeders, are used to produce the 175 bulls marketed through the annual Carcass-Merit Bull Sale held the first Saturday in December and by private treaty. The Sunshine Farms Sim-Angus program is data-driven and maintains complete records for all traits and is recognized as an early pioneer in the use of ultrasound data to improve carcass merit. Sunshine Farms has one of the largest ultrasound databases in the Simmental breed and has tested more young sires in the American Simmental Association's Carcass Merit Program than any other Simmental breeder. Short term goals for Sunshine Farms are to provide genetically superior bulls to commercial bull buyers to optimize profitability. Long term goals are to provide bulls with genetic ability to produce feeder calves with efficient growth in the feedlot and the potential to produce 10% Prime 90% Choice with 100% YG 1 and 2s with carcasses that will provide a product that is tender and acceptable for consumers. The Alabama Beef Cattle Improvement Association is proud to nominate Sunshine Farms.

Seedstock Producer Honor Roll of Excellence

Billy L. Easley	Kentucky	1972
Dale H. Davis	Montana	1972
Elliot Humphrey	Arizona	1972
Harold A. Demorest	Ohio	1972
James D. Bennett	Virginia	1972
Jerry Moore	Ohio	1972
John Crowe	California	1972
Marshall A. Mohler	Indiana	1972
Albert West III	Texas	1973
C. Scott Holden	Montana	1973
Carlton Corbin	Oklahoma	1973
Clyde Barks	North Dakota	1973
Heathman Herefords	Washington	1973
James D. Hemmingsen	Iowa	1973
Messersmith Herefords	Nebraska	1973
Mrs. R. W. Jones, Jr.	Georgia	1973
Raymond Meyer	South Dakota	1973
Robert Miller	Minnesota	1973
William F. Borrow	California	1973
Bert Crame	California	1974
Bert Sackman	North Dakota	1974
Dover Sindelar	Montana	1974
Burwell M. Bates	Oklahoma	1974
Charles Descheemacher	Montana	1974
J. David Nichols	Iowa	1974
Jorgensen Brothers	South Dakota	1974
Marvin Bohmont	Nebraska	1974
Maurice Mitchell	Minnesota	1974
Wilfred Dugan	Missouri	1974
Dale Engler	Kansas	1975
Frank Kubik, Jr.	North Dakota	1975
George Chiga	Oklahoma	1975
Glenn Burrows	New Mexico	1975
Howard Collins	Misouri	1975
Jack Cooper	Montana	1975
Joseph P. Dittmer	Iowa	1975
Leslie J. Holden	Montana	1975
Licking Angus Ranch	Nebraska	1975
Louis Chestnut	Washington	1975
Robert Arbuthnot	Kansas	1975
Robert D. Keefer	Montana	1975
Walter S. Markham	California	1975
Ancel Armstrong	Virginia	1976
Gerhard Mittnes	Kansas	1976
Healey Brothers	Oklahoma	1976
Jackie Davis	California	1976
Jay Pearson	Idaho	1976
L. Dale Porter	Iowa	1976
Lowellyn Tewksbury	North Dakota	1976
M.D. Shepherd	North Dakota	1976
Robert Sallstrom	Minnesota	1976
Sam Friend	Missouri	1976
Stan Lund	Montana	1976
Bill Wolfe	Oregon	1977
Bob Sitz	Montana	1977
Clair Percel	Kansas	1977
Floyd Hawkins	Missouri	1977
Frank Ramackers, Jr.	Nebraska	1977
Glen Burrows	New Mexico	1977
Henry and Jeanette Chitty	New Mexico	1977
Hubert R. Freise	North Dakota	1977
James Volz	Minnesota	1977
Lloyd DeBruycker	North Dakota	1977
Loren Schlipf	Illinois	1977
Marshall A. Mohler	Indiana	1977
Robert Brown	Texas	1977
Tom and Mary Shaw	Idaho	1977
Tom Dashiell	Washington	1977
Wayne Eshelman	Washington	1977
Harold Anderson	South Dakota	1977
WillIiam Borror	California	1977
A.L. Frau		1978
Bill Wolfe	Oregon	1978
Bill Womack, Jr.	Alabama	1978
Buddy Cobb	Montana	1978
Frank Harpster	Missouri	1978
George Becker	North Dakota	1978
Healey Brothers	Oklahoma	1978
Jack Delaney	Minnesota	1978
James D. Bennett	Virginia	1978
Larry Berg	Iowa	1978
Roy Hunst	Pennsylvania	1978
Bill Wolfe	Oregon	1979
Del Krumweid	North Dakota	1979
Floyd Metter	Missouri	1979
Frank & Jim Wilson	South Dakota	1979
Glenn & David Gibb	Illinois	1979
Jack Ragsdale	Kentucky	1979
Jim Wolf	Nebraska	1979
Leo Schuster Family	Minnesota	1979
Peg Allen	Montana	1979
Rex & Joann James	Iowa	1979
Bill Wolfe	Oregon	1980
Blythe Gardner	Utah	1980
Bob Laflin	Kansas	1980
Charlie Richards	Iowa	1980
Donald Barton	Utah	1980
Floyd Dominy	Virginia	1980
Frank Felton	Missouri	1980
Frank Hay	California	1980
James Bryany	Minnesota	1980
John Masters	Kentucky	1980

Mark Keffeler	South Dakota	1980
Paul Mydland	Montana	1980
Richard McLaughlin	Illinois	1980
Richard Tokach	North Dakota	1980
Roy and Don Udelhoven	Wisconsin	1980
Bob & Gloria Thomas	Oregon	1981
Bob Dickinson	Kansas	1981
Clarence Burch	Oklahoma	1981
Clayton Canning	California	1981
Dwight Houff	Virginia	1981
G.W. Cronwell	Iowa	1981
Harold Thompson	Washington	1981
Herman Schaefer	Illinois	1981
J. Morgan Donelson	Missouri	1981
Jack Ragsdale	Kentucky	1981
James Leachman	Montana	1981
Lynn Frey	North Dakota	1981
Myron Autfathr	Minnesota	1981
Roy Beeby	Oklahoma	1981
Russ Denowh	Montana	1981
Bob Thomas	Oregon	1982
Clare Geddes	California	1982
David A. Breiner	Kansas	1982
Frankie Flint	New Mexico	1982
Garold Parks	Iowa	1982
Gary & Gerald Carlson	North Dakota	1982
Harlin Hecht	Minnesota	1982
Howard Krog	Minnesota	1982
Joseph S. Bray	Kentucky	1982
Larry Leonhardt	Montana	1982
Orville Stangl	South Dakota	1982
W.B. Williams	Illinois	1982
William Kottwitz	Missouri	1982
Alex Stauffer	Wisconsin	1983
Bill Borror	California	1983
C. Ancel Armstrong	Kansas	1983
Charles E. Boyd	Kentucky	1983
D. John & Lebert Schultz	Missouri	1983
E.A. Keithley	Missouri	1983
Frank Myatt	Iowa	1983
Harvey Lemmon	Georgia	1983
J. Earl Kindig	Missouri	1983
Jake Larson	North Dakota	1983
John Bruner	South Dakota	1983
Leness Hall	Washington	1983
Ric Hoyt	Oregon	1983
Robert H. Schafer	Minnesota	1983
Russ Pepper	Montana	1983
Stanley Nesemeier	Illinois	1983
A. Harvey Lemmon	Georgia	1984
Charles W. Druin	Kentucky	1984
Clair K. Parcel	Kansas	1984
Donn & Sylvia Mitchell	Canada	1984

Earl Kindig	Virginia	1984
Floyd Richard	North Dakota	1984
Fred H. Johnson	Ohio	1984
Glen Klippenstein	Missouri	1984
Jack Farmer	California	1984
Jerry Chappel	Virginia	1984
Joe C. Powell	North Carolina	1984
John B. Green	Louisiana	1984
Lawrence Meyer	Illinois	1984
Lee Nichols	Iowa	1984
Phillip A. Abrahamson	Minnesota	1984
Ric Hoyt	Oregon	1984
Robert L. Sitz	Montana	1984
Ron Beiber	South Dakota	1984
Arnold Wienk	South Dakota	1985
Bernard F. Pedretti	Wisconsin	1985
David McGehee	Kentucky	1985
Don W. Schoene	Missouri	1985
Earl Schafer	Minnesota	1985
Everett & Ron Batho	Canada	1985
Fred Killam	Illinois	1985
George B. Halternan	West Virginia	1985
Glenn L. Brinkman	Texas	1985
Gordon Booth	Wyoming	1985
J. Newill Miller	Virginia	1985
Marvin Knowles	California	1985
R.C. Price	Alabama	1985
Tom Perrier	Kansas	1985
A. Lloyd Grau	New Mexico	1986
Clarence Vandyke	Montana	1986
Clifford & Bruce Betzold	Illinois	1986
Delton W. Hubert	Kansas	1986
Dick & Ellie Larson	Wisconsin	1986
Evin & Verne Dunn	Canada	1986
Gerald Hoffman	South Dakota	1986
Glenn L. Brinkman	Texas	1986
Henry & Jeanette Chitty	Florida	1986
J.H. Steward/P.C. Morrissey	Pennsylvania	1986
Jack & Gina Chase	Wyoming	1986
John H. Wood	South Carolina	1986
Lawrence H. Graham	Kentucky	1986
Leonard Lodden	North Dakota	1986
Leonard Wulf	Minnesota	1986
Matthew Warren Hall	Alabama	1986
Ralph McDanolds	Virginia	1986
Richard J. Putnam	North Carolina	1986
Roy D. McPhee	California	1986
W.D. Morris/James Pipkin	Missouri	1986
Charles & Wynder Smith	Georgia	1987

Clayton Canning	Canada	1987
Eldon & Richard Wiese	Minnesota	1987
Forrest Byergo	Missouri	1987
Gary Klein	North Dakota	1987
Harold E. Pate	Illinois	1987
Henry Gardiner	Kansas	1987
Ivan & Frank Rincker	Illinois	1987
James Bush	South Dakota	1987
Larry D. Leonhardt	Wyoming	1987
Lyall Edgerton	Canada	1987
R.J. Steward/P.C. Morrisey	Minnesota	1987
Tommy Brandenberger	Texas	1987
Bill Bennett	Washington	1988
Darold Bauman	Wyoming	1988
David and Carol Guilford	Canada	1988
David Luhman	Minnesota	1988
Don and Dian Guilford	Canada	1988
Donn & Sylvia Mitchell	Canada	1988
Douglas D. Bennett	Texas	1988
George Schlickau	Kansas	1988
Gino Pedretti	California	1988
Glenn Debter	Alabama	1988
Hansell Pile	Kentucky	1988
Jay P. Book	Illinois	1988
Kans Ulrich	Canada	1988
Kenneth Gillig	Missouri	1988
Leonard Lorenzen	Oregon	1988
Robert E. Walton	Washington	1988
Scott Burtner	Virginia	1988
WillIowam Glanz	Wyoming	1988
Bob R. Whitmire	Georgia	1989
Donald Fawcett	South Dakota	1989
Ed Albaugh	California	1989
Glynn Debter	Alabama	1989
Harry Airey	Canada	1989
Jack & Nancy Baker	Missouri	1989
Jerry Allen Burner	Virginia	1989
Kenneth D. Lowe	Kentucky	1989
Leonard A. Lorenzen	Oregon	1989
Lester H. Schafer	Minnesota	1989
Lynn Pelton	Kansas	1989
Orrin Hart	Canada	1989
Ron Bowman	North Dakota	1989
Sherm & Charlie Ewing	Canada	1989
Tom Mercer	Wyoming	1989
Bob Thomas Family	Oregon	1990
Boyd Broyles	Kentucky	1990
Charles & Rudy Simpson	Canada	1990
Doug Fraser	Canada	1990
Douglas & Molly Hoff	South Dakota	1990
Dr. Burleigh Anderson	Pennsylvania	1990
Gerhard Gueggenberger	California	1990
John & Chris Oltman	Wisconsin	1990
John Ragsdale	Kentucky	1990
Larry Erahart	Wyoming	1990
Otto & Otis Rincker	Illinois	1990
Paul E. Keffaber	Indiana	1990
Richard Janssen	Kansas	1990
Steven Forrester	Michigan	1990
T.D. & Roger Steele	Virginia	1990
Ann Upchurch	Alabama	1991
Dave & Carol Guilford	Canada	1991
Jack & Gina Chase	Wyoming	1991
Jack Cowley	California	1991
James Burnes & Sons	Wisconsin	1991
James R. O'Neill	Iowa	1991
Jim Taylor	Kansas	1991
John Bruner	South Dakota	1991
Larry Wakefield	Minnesota	1991
N. Wehrmann/R. McClung	Virginia	1991
R.A. Brown	Texas	1991
R.M. Felts & Son Farm	Tennessee	1991
Ralph Bridges	Georgia	1991
Richard & Sharon Beitelspacher	South Dakota	1991
Rob & Gloria Thomas	Oregon	1991
Steve & Bill Florschcuetz	Illinois	1991
Summitcrest Farms	Ohio	1991
Tom Sonderup	Nebraska	1991
A.W. Compton, Jr.	Alabama	1992
Bill Rea	Pennsylvania	1992
Bob Buchanan Family	Oregon	1992
Calvin & Gary Sandmeier	South Dakota	1992
Dennis, David & Danny Geffert	Wisconsin	1992
Dick Montague	California	1992
Eugene B. Hook	Minnesota	1992
Francis & Karol Bormann	Iowa	1992
Glenn Brinkman	Texas	1992
Harold Dickson	Missouri	1992
Leonard Wulf & Sons	Minnesota	1992
Robert Elliot & Sons	Tennessee	1992
Tom & Ruth Clark	Virginia	1992
Tom Drake	Oklahoma	1992
Bob Zarn	Minnesota	1993
Clarence, Elaine & Adam Dean	South Carolina	1993
Collin Sander	South Dakota	1993
D. Eldridge & Y. Aycock	Oklahoma	1993
Harrell Watts	Alabama	1993
J. David Nichols	Iowa	1993
J. Newbill Miller	Virginia	1993
Joseph Freund	Colorado	1993
Lynn Pelton	Kansas	1993
Miles P. "Buck" Pangburn	Iowa	1993
Norman Bruce	Illinois	1993

R.A. Brown	Texas	1993
R.B. Jarrell	Tennessee	1993
Rueben Leroy & Bob Littau	South Dakota	1993
Ted Seely	Wyoming	1993
Wes & Fran Cook	North Carolina	1993
Bobby F. Hayes	Alabama	1994
Bruce Orvis	California	1994
Buell Jackson	Iowa	1994
Calvin & Gary Sandmeier	South Dakota	1994
Dave Taylor & Gary Parker	Wyoming	1994
Jere Caldwell	Kentucky	1994
John Blankers	Minnesota	1994
John Pfeiffer Family	Oklahoma	1994
Ken & Bonnie Bieber	South Dakota	1994
Mary Howe di'Zerega	Virginia	1994
Richard Janssen	Kansas	1994
Ron & Wayne Hanson	Canada	1994
Bobby Aldridge	North Carolina	1995
Chris & John Christensen	South Dakota	1995
Donald J. Hargrave	Canada	1995
Gene Bedwell	Iowa	1995
Gordon & Mary Ann Booth	Wyoming	1995
Howard & JoAnne Hillman	South Dakota	1995
John Robbins	Montana	1995
Billy Mack & Tom Maples	Alabama	1995
Mary Howe de'Zerega	Virginia	1995
Maurice Grogan	Minnesota	1995
Thomas Simmons	Virginia	1995
Tom Perrier	Kansas	1995
Ward Burroughs	California	1995
C. Knight & B. Jacobs	Oklahoma	1996
C.W. Pratt	Virginia	1996
Cam Spike & Sally Forbes	Wyoming	1996
Chris and John Christensen	South Dakota	1996
D. Borgen and B. McCulloh	Wisconsin	1996
Frank Felton	Missouri	1996
Frank Schiefelbein	Minnesota	1996
Galen & Lori Fink	Kansas	1996
Gerald & Lois Neher	Illinois	1996
Ingrid & Willy Volk	North Carolina	1996
Mose & Dave Hebbert	Nebraska	1996
Robert C. Miller	Minnesota	1996
WillIowam A. Womack, Jr.	Alabama	1996
Alan Albers	Kansas	1997
Blaine & Pauline Canning	California	1997
Bob & Gloria Thomas	Oregon	1997
Darel Spader	South Dakota	1997
E. David Pease	California	1997
Gregg & Diane Butman	Minnesota	1997
Harold Pate	Alabama	1997
James I. Smith	North Carolina	1997
Jim & JoAnn Enos	Illinois	1997
Juan Reyes	Wyoming	1997
Nicholas Wehrmann	Virginia	1997
Richard McClung	Virginia	1997
Abilgail & Mark Nelson	California	1998
Adrian Weaver & Family	Colorado	1998
Airey Family	Canada	1998
Dallis & Tammy Basel	South Dakota	1998
Dave & Cindy Judd	Kansas	1998
Dick & Bonnie Helms	Nebraska	1998
Duane L. Kruse Family	Illinois	1998
Earl & Neadra McKarns	Ohio	1998
James D. Benett Family	Virginia	1998
Tom Shaw	Idaho	1998
Wilbur & Melva Stewart	Canada	1998
Duane Schieffer	Montana	1999
John Kluge	Virginia	1999
Kelly & Lori Darr	Wyoming	1999
Kent Kline	South Dakota	1999
Kramer Farms	Illinois	1999
Lynn & Gary Pelton	Kansas	1999
Noller & Frank Charolais	Iowa	1999
Rausch Herefords	South Dakota	1999
Steve Munger	South Dakota	1999
Terry O'Neill	Montana	1999
Tony Walden	Alabama	1999
Alan & Deb Vedvei	South Dakota	2000
Banks & Margo Hernon	Alabama	2000
Blane & Cindy Nagel	South Dakota	2000
Galen. Lori and Megan Finkk	Kansas	2000
Harlin & Susan Hecht	Minnesota	2000
Jim & Janet Listen	Wyoming	2000
John & Betty Botert	Missouri	2000
John C. Curtin	Illinois	2000
Kent Kline & Steve Munger	South Dakota	2000
Larry & Jean Croissant	Colorado	2000
Mike & T.K. McDowell	Virginia	2000
Ralph Blalock, Sr., Blalock, Jr. and David Blalock	North Carolina	2000
Vaughn Meyer & Family	South Dakota	2000
Blane & Cindy Nagel	South Dakota	2001

Bob & Nedra Funk	Oklahoma	2001
Dale, Don & Mike Spencer	Nebraska	2001
Don & Priscilla Nielsen	Colorado	2001
Eddie L. Sydenstricker	Missouri	2001
George W. Lemm	Virginia	2001
Ken Stielow & Family	Kansas	2001
Kevin, Jessica and Dakota Emily Moore	Texas	2001
Marvin & Katheryn Robertson	Virginia	2001
MCallen Ranch	Texas	2001
Steve Hillman & Family	Illinois	2001
Tom Lovell	Alabama	2001
DeBruycker Charolais	Montana	2002
Ellis Farms	Illinois	2002
Holly Hill Farm	Virginia	2002
Isa Cattle Co., Inc.	Texas	2002
Lyons Ranch	Kansas	2002
Noller and Frank Charolais	Iowa	2002
Rishel Angus	Nebraska	2002
Running Creek Ranch	Colorado	2002
Shamrock Angus	Wyoming	2002
Stewart Angus	Indiana	2002
Triple “M” Farm	Alabama	2002
Bedwell Charolais	Iowa	2003
Boyd Farm	Alabama	2003
Camp Cooley Ranch	Texas	2003
Hilltop Ranch	Texas	2003
Moser Ranch	Kansas	2003
Mystic Hill Farms	Virginia	2003
Pingetzer’s Six Iron Ranch	Wyoming	2003
San Isabel Ranch	Colorado	2003
Shamrock Vale Farms	Ohio	2003
Adams Angus Farm	Alabama	2004
Byland Polled Shorthorns	Ohio	2004
Camp Cooley Ranch	Texas	2004
Eaton Charolais	Montana	2004
Flat Branch Cattle Company	Illinois	2004
Judd Ranch, Inc.	Kansas	2004
Rausch Herefords	South Dakota	2004
Reynolds Ranch	Colorado	2004
Silveira Brothers Angus and Diversified Farming	California	2004
Symens Brothers Limousin	South Dakota	2004
Touchstone Angus	Wyoming	2004
Triple U Ranch	Iowa	2004
Altenburg Super Baldy	Colorado	2005
Bar S Ranch	Kansas	2005
Ellis Farms	Illinois	2005
Ingram Cattle Company	Mississippi	2005
Moore Farms	Alabama	2005
Morrison Stock Farm	Ohio	2005
Pangburn Stock Farm	Iowa	2005
Rishel Angus	Nebraska	2005
Rogers Bar HR	Mississippi	2005
Soldiers’ Hill Angus Farm	Virginia	2005
Sunnyhill Angus Farm	Illinois	2005
Waukaru Farms, Inc.	Indiana	2005
Benoit Angus Ranch	Kansas	2006
Champion Hill	Ohio	2006
EE Ranches, Inc.	Mississippi	2006
Earhart Farms	Wyoming	2006
Figure 4 Cattle Company / Volk Ranch LLLP	Colorado	2006
Lawler Farm	Alabama	2006
Powder Creek Simmentals	Georgia	2006
Quaker Hill Farm LLC	Virginia	2006
Sauk Valley Angus	Illinois	2006
Thomas Charolais, Inc.	Texas	2006
Vorthmann Limousin	Iowa	2006
Waukaru Farms, Inc.	Indiana	2006
Pelton Simmental	Kansas	2007
5L Red Angus	Montana	2007
Bridle Bit Simmentals	Colorado	2007
Echo Ridge Farm	Virginia	2007
Heartland Cattle Co.	Iowa	2007
Lindskov-Thiel Ranch	South Dakota	2007
Star Lake Cattle Ranch	Oklahoma	2007
TC Ranch	Nebraska	2007
Tinney Farms	Alabama	2007
Tomlinson Farms	Illinois	2007
Andras Stock Farm	Illinois	2008
Croissant Red Angus	Colorado	2008
Harms Plainview Ranch	Kansas	2008
Little Mountain Farm	Alabama	2008
C. H. Morris & Sons	Virginia	2008
Nolin Red Angus	Iowa	2008
Schott Limousin Ranch	South Dakota	2008
TC Ranch	Nebraska	2008
Thomas Ranch	South Dakota	2008
Calyx Star Ranch	Mississippi	2009
Champion Hill	Ohio	2009
Gibbs Farms	Alabama	2009
Harrell Hereford Ranch	Oregon	2009
Musgrave Angus	Illinois	2009
Oak Meadow Farm Simmentals	Minnesota	2009
Oak Ridge Angus	California	2009
Quaker Hill Farm	Virginia	2009
Skarda Farms	Iowa	2009
Stucky Ranch	Kansas	2009
Circle Ranch	California	2010
Edgewood Angus	Virginia	2010

McBee Cattle Company	Missouri	2010
Rincker Simmentals	Illinois	2010
Sandhill Farms	Kansas	2010
Schuler Red Angus	Nebraska	2010
Spring Creeks Cattle Company	Wisconsin	2010
Windy Hill Angus Farm	Alabama	2010

BIF Seedstock Producer of the Year

John Crowe	California	1972
Mrs. R. W. Jones, Jr.	Georgia	1973
Carlton Corbin	Oklahoma	1974
Jack Cooper	Montana	1975
Leslie J. Holden	Montana	1975
Jorgenson Brothers	South Dakota	1976
Glenn Burrows	New Mexico	1977
James D. Bennett	Virginia	1978
Jim Wolf	Nebraska	1979
Bill Wolfe	Oregon	1980
Bob Dickinson	Kansas	1981
A.F. “Frankie” Flint	New Mexico	1982
Bill Borror	California	1983
Lee Nichols	Iowa	1984
Ric Hoyt	Oregon	1985
Leonard Lodoen	North Dakota	1986
Henry Gardiner	Kansas	1987
W.T. “Bill” Bennett	Washington	1988
Glynn Debter	Alabama	1989
Douglas & Molly Hoff	South Dakota	1990
Summitcrest Farms	Ohio	1991
Leonard Wulf & Sons	Minnesota	1992
J. David Nichols	Iowa	1993
R.A. “Rob” Brown	Texas	1993

Richard Janssen	Kansas	1994
Tom & Carolyn Perrier	Kansas	1995
Frank Felton	Missouri	1996
Bob & Gloria Thomas	Oregon	1997
Wehrmann Angus Ranch	Virginia	1997
Flying H Genetics	Nebraska	1998
Knoll Crest Farms	Virginia	1998
Morven Farms	Virginia	1999
Fink Beef Genetics	Kansas	2000
Sydenstricker Angus Farms	Missouri	2001
Circle A Ranch	Missouri	2002
Moser Ranch	Kansas	2003
Camp Cooley Ranch	Texas	2004
Rishel Angus	Nebraska	2005
Sauk Valley Angus	Illinois	2006
Pelton Simmental Red Angus	Kansas	2007
TC Ranch	Nebraska	2008
Champion Hill	Ohio	2009
Harrell Hereford Ranch	Oregon	2009
Sandhill Farms	Kansas	2010

2011 COMMERCIAL PRODUCER AWARD NOMINEES

Bambarger Cattle Farm
Owners/Managers: John and Jim Bambarger
Northport, Alabama

Bambarger Cattle Farm is a second generation cattle operation, owned and operated by John and Jim Bambarger, located near Eutaw, Alabama. The operation consists of 250 acres of pasture and hay fields with another 200 acres of timberland. The cow herd consists of 75 Angus crossed cows calving in a fall calving season ranging from late September to December. A long term performance goal of Bambarger Cattle Farm has been to establish a high-quality, uniform cow herd through decisions based primarily on performance records and through retention of the best replacement heifers. Performance records have been diligently maintained for over 10 years utilizing on-farm spreadsheets and the Alabama BCIA commercial record keeping program. Select Angus sires have been chosen for the last 12 years for calf uniformity, conformation, calving ease, growth, maternal ability, and high yield and carcass quality. Replacement heifers are selected by evaluation of both individual and dam performance records for traits that include weaning weight indexes and calving intervals. Steer calves are marketed annually in July through the Alabama Feeder Calf Marketing Association tele-auction. Bambarger Cattle Farm typically markets thirty 800 lb steers annually and partners with a fellow producer to offer a uniform truckload. Replacement heifers are marketed with complete performance and genetic data through Alabama BCIA heifer sales or by private treaty. Short term goals of Bambarger Cattle Farm are to maintain a healthy, productive cow herd and to raise a highly marketable calf crop each year. Long term goals are to keep the land productive, keep improving the quality of the cow herd through good herd management practices, and to leave the land in good condition for the next generation. Bambarger Cattle Farm is proudly nominated by the Alabama Beef Cattle Improvement Association.

Durheim Ranch
Owners/Managers: Bruce and Lynette Durheim
Ellendale, North Dakota

Northern Brown County, South Dakota is where Bruce and Lynette Durheim run a commercial herd of 275 Red Angus cows. Located in farming country, their 3,000 acres consists of 2,000 acres of pasture, 150 acres of alfalfa and 850 acres of crop ground which is leased during growing season, but does provide residue grazing. Together, the couple handles all of the ranch work. Calving season starts the last week of March and in 13 months the steer calves are hanging on the rail. The majority of the heifer calves make replacements, either retained in the herd or sold to fellow ranchers. In their 14 year history of retained ownership through slaughter, the steers have an average profit of $75/head. Since 1997, they have added value to the calves through Red Angus' FCCP program, which allows access to premium product lines in addition to receiving premiums for age and source verification. Carcass data on previously retained steers supported the decision to sell on the grid in 2003. That decision netted a grid premium of $57/head and their first Red Angus GridMaster award. The steers have received six Red Angus GridMaster awards for carcass quality and the 2005 Angus America Outstanding Cow/Calf Producer for highest grid premiums. Utilizing a combination of superior genetics and aggressive management, they continually strive to top the best set of steers produced on their ranch. Currently, the bar is set with the 2008 steers: 171 head, 95% Choice, 76% Premium Products, 30% YG 1&2, 6% YG 4. The Red Angus Association of America is proud to nominate Durheim Ranch.

E. Roen Ranches
Owner: Erik O. Roen
Manager: Paul Roen
Knights Ferry, California

Located in Calpine, Knights Ferry and LeGrand, California, E. Roen Ranches operates three operations under the partnership of Sierra Valley Ranch. The enterprise has been in production for over 15 years and focus on producing beef that is both an industry and consumer demanded product. The Roens achieve this by breeding their 2,000 head of English based cows to Lim-Flex bulls and tracking female production and beef product results. Based on available feed sources, cows calve in the fall in the Sierra Valley and then are shipped as pairs to the San Joaquin Valley to graze during the winter grass season. Calves are then weaned in the spring and grown on improved pasture ground in the Sierra Valley. Calves that aren't retained are then sold through Superior Livestock Video Auction with the assistance of Jim Davis for fall delivery as yearlings. Understanding the demand for expanded market opportunities, the Roens raise calves to work in a certified or non-hormone treated cattle (NHTC) program. Jim Davis of Superior said that of the more than 500,000 head that he had shipped, the Roen's 2010 calf crop was the best set of yearlings. The Roens have placed great emphasis on collecting feeding and carcass data from buyers to aid in bull selection, because they realize that the beef industry changes and so should their selection. They take great pride in serving as stewards of the land, by incorporating extensive water management and conservation plans. The multi-generation enterprises of Sierra Valley Ranch are environmental and beef industry leaders. E. Roen Ranches is proudly nominated by the North American Limousin Foundation.

Larson Angus Ranch
Owners/Managers: Dan and Becky Larson
Sharon Springs, Kansas

Larson Angus Ranch is located 14 miles south of Wallace in Northwest Kansas. The ranch is in close proximity to large commercial cattle feeders and processing plants. They have about 10,000 acres of farm and grassland. The cowherd originally started as a Hereford x Angus herd, then Hereford x Simmental. After a while, this breeding program caused the cowherd to lose uniformity. At that point, they decided to revamp their breeding program and build it around a registered Angus cowherd, as they believed the Angus breed had the most trouble-free traits to offer. In 1988, they bought their first registered Angus cows. Since that time, they have grown their operation to 600 spring-calving cows and 40 fall-calving cows. In addition to their commercial herd, they have a seedstock and farming business. They have an annual bull sale where they market around 100 bulls and offer a select group of registered heifers. They retain 100 to 150 replacement heifers. About 70% of the calves in their seedstock operation will not make the cut for purebred seedstock, and therefore, will be age- and source-verified and finished at the ranch. All their finished calves are shipped to U.S. Premium Beef, of which they are founding members. All carcass data is obtained on their calves. They do not sell very many replacement females as they get more premiums through harvesting the heifers than selling them for replacement individuals. The Kansas Livestock Association is proud to nominate Larson Angus Ranch.

Leavitt Lake Ranches
Owners/Managers: Darrell & Callie Wood, Ramsey Wood, and Dallice Wood
Vina, California

The Leavitt Lake Ranches is a family owned business that is a certified organic cow/calf and yearling operation. They have a winter calving herd and a summer calving herd. A benefit of these two calving dates is to have a year round supply of marketable cattle for organic grass fed meat sales. Weaning weights are from 650-750 pounds. All pasture and hay needs are raised on the ranches. After calves are weaned and backgrounded at their feeding facility, they go back on pasture until they are harvested at

approximately 1,000 pounds. Leavitt Lake Ranches run about 700 cows that includes a registered Angus herd as well as the Angus cross commercial herd. They raise their own registered Angus bulls that are selected for grass-finished efficiency. The winter range is located in Tehama County in the annual grasslands of the Vina Plains and the summer ranch is in the scenic high elevation meadows of Lassen County. Darrell and Callie started buying cows after being married in 1981. They leased property initially and when they found property they could afford, they took a chance and bought it. Their first ranch was in Lassen County and had once belonged to Darrell's great, great grandfather Benjamin Leavitt. This was the beginning of Leavitt Lake Ranches. Son, Ramsey returned to the ranch after college in 2005 and daughter, Dallice followed in 2007. Everyone has a hand in the management of the operation, which includes 11,000 acres of leased ground, 3,600 acres of deeded land, and BLM grazing permits. Leavitt Lake Ranches is proudly nominated by the California Beef Cattle Improvement Association.

Quinn Cow Company
Owners/Managers: Reuben and Connee Quinn
Chadron, Nebraska

Reuben and Connee Quinn started Quinn Cow Company as a commercial cow/calf operation in 1974 with the purchase of 50 Simmental x Angus cross heifers. The ranch is located primarily on leased land on the Pine Ridge Indian Reservation in South Dakota as well as Dawes County in northwestern Nebraska. Currently, Angus x Simmental cows are bred to Angus, Simmental and Angus x Simmental composite bulls to calve in the spring. The goal is to produce a cow with high output and relatively low inputs in a challenging environment compromised by high selenium and sulfate levels in the water and grass. Depending heavily on EPDs for selecting sires with calving ease and moderate milk yet above average growth traits, the Quinns require a cow that produces excellent replacements as well as high performing feeder cattle. Calves are retained through the feedlot phase and typically sold on a carcass merit basis. Feedlot performance and detailed carcass data have been collected on the calf crop for more than 15 years. Thirty percent of the mature cows, all of the replacement heifers and 2nd calf heifers are synchronized and bred artificially. Individual cow records and ranch production are documented for continual management improvement. Measured areas include reproductive performance, weaning percentage per cow exposed, and annual cow cost by line item. A network of experts, in various industry disciplines, is regularly consulted to achieve the Quinn's goals of profitability and production criteria.
The Nebraska Cattlemen is proud to nominate the Quinn Cow Company.

Silver Spur Ranch
Cheramie Viator
Encampment, Wyoming

Silver Spur Ranch has operations in Wyoming, Colorado and New Mexico. The headquarters ranch in Encampment, WY dates back to the 1950's with Charolais cattle and 1940's with Hereford cattle. The Silver Spur owned Bell and TO Ranches in New Mexico are two of the most historical ranches in the country and date back to the 1800's. Today the Silver Spur Ranch cowherd includes over 13,000 mother cows. A large percentage of calves are retained through the feeding process and sold as "All Natural" or non-hormone treated cattle. Replacement females for both the commercial and registered herds are predominantly selected from within the herd. The Silver Spur's seedstock herd is comprised of registered Charolais, Red Angus, Angus, and Hereford cattle. In recent years, they have added a Charolais x Red Angus composite, called Rangefires, to the herd. Commercial herds are either Angus or Red Angus based. Charolais, Angus, Red Angus and Rangefire bulls are used in terminal and replacement rotations. The Silver Spur Ranch encompasses vast geographic challenges and variations. Because of this, it is vital for their cowherd to be moderate in size, forage efficient, altitude adaptable, sound and fertile. At the same time, offspring must have the ability to gain and perform in the feedlot and on the rail. The Silver Spur Ranch is proudly nominated by the American-International Charolais Association.

Commercial Producer Honor Roll of Excellence

Chan Cooper	Montana	1972
Alfred B Cobb, Jr.	Montana	1972
Lyle Eivens	Iowa	1972
Broadbent Brothers	Kentucky	1972
Jess Kilgote	Montana	1972
Clifford Ouse	Minnesota	1973
Pat Wilson	Florida	1973
John Glaus	South Dakota	1973
Sig Peterson	North Dakota	1973
Max Kiner	Washington	1973
Donald Schott	Montana	1973
Stephen Garst	Iowa	1973
J.K. Sexton	California	1973
Elmer Maddox	Oklahoma	1973
Marshall McGregor	Missouri	1974
Dave Matti	Montana	1974
Lloyd DeBruycker	Montana	1974
Gene Rambo	California	1974
Jim Wolf	Nebraska	1974
Henry Gardiner	Kansas	1974
Johnson Brothers	South Dakota	1974
John Blankers	Minnesota	1975
Paul Burdett	Montana	1975
Oscar Burroughs	California	1975
John R. Dahl	North Dakota	1975
Eugene Duckworth	Missouri	1975
Gene Gates	Kansas	1975
V.A. Hills	Kansas	1975
Robert D. Keefer	Montana	1975
Kenneth E. Leistritz	Nebraska	1975
Ron Baker	Oregon	1976
Dick Boyle	Idaho	1976
James Hackworth	Missouri	1976
John Hilgendorf	Minnesota	1976
Kahau Ranch	Hawaii	1976
Milton Mallery	California	1976
Robert Rawson	Iowa	1976
William A. Stegner	North Dakota	1976
U.S. Range Exp. Stat.	Montana	1976
Maynard Crees	Kansas	1977
Ray Franz	Montana	1977
Forrest H. Ireland	South Dakota	1977
John A. Jameson	Illinois	1977
Leo Knoblauch	Minnesota	1977
Jack Pierce	Idaho	1977
Mary & Stephen Garst	Iowa	1977
Todd Osteross	North Dakota	1978
Charles M. Jarecki	Montana	1978
Jimmy G McDonnal	North Carolina	1978
Victor Arnaud	Missouri	1978
Ron & Malcom McGregor	Iowa	1978
Otto Uhrig	Nebraska	1978
Arnold Wyffels	Minnesota	1978
Bert Hawkins	Oregon	1978
Mose Tucker	Alabama	1978
Dean Haddock	Kansas	1978
Myron Hoeckle	North Dakota	1979
Harold & Wesley Arnold	South Dakota	1979
Ralph Neill	Iowa	1979
Morris Kuschel	Minnesota	1979
Bert Hawkins	Oregon	1979
Dick Coon	Washington	1979
Jerry Northcutt	Missouri	1979
Steve McDonnell	Montana	1979
Doug Vandermyde	Illinois	1979
Norman, Denton & Calvin Thompson	South Dakota	1979
Jess Kilgore	Montana	1980
Robert & Lloyd Simon	Illinois	1980
Lee Eaton	Montana	1980
Leo & Eddie Grubl	South Dakota	1980
Roger Winn, Jr.	Virginia	1980
Gordon McLean	North Dakota	1980
Ed Disterhaupt	Minnesota	1980
Thad Snow	Canada	1980
Oren & Jerry Raburn	Oregon	1980
Bill Lee	Kansas	1980
Paul Moyer	Missouri	1980
G.W. Campbell	Illinois	1981
J.J. Feldmann	Iowa	1981
Henry Gardiner	Kansas	1981
Dan L. Weppler	Montana	1981
Harvey P. Wehri	North Dakota	1981
Dannie O'Connell	South Dakota	1981
Wesley & Harold Arnold	South Dakota	1981
Jim Russell & Rick Turner	Missouri	1981
Oren & Jerry Raburn	Oregon	1981
Orin Lamport	South Dakota	1981
Leonard Wulf	Minnesota	1981
Wm. H. Romersberter	Illinois	1982
Milton Krueger	Missouri	1982
Carl Odegard	Montana	1982
Marvin & Donald Stoker	Iowa	1982
Sam Hands	Kansas	1982
Larry Campbel	Kentucky	1982
Earl Schmidt	Minnesota	1982
Raymond Josephson	North Dakota	1982
Clarence Reutter	South Dakota	1982
Leonard Bergen	Canada	1982
Kent Brunner	Kansas	1983

Tom Chrystal	Iowa	1983
John Freltag	Wisconsin	1983
Eddie Hamilton	Kentucky	1983
Bill Jones	Montana	1983
Harry & Rick Kline	Illinois	1983
Charlie Kopp	Oregon	1983
Duwayne Olson	South Dakota	1983
Ralph Pederson	South Dakota	1983
Ernest & Helen Schaller	Missouri	1983
Al Smith	Virginia	1983
John Spencer	California	1983
Bud Wishard	Minnesota	1983
Bob & Sharon Beck	Oregon	1984
Leonard Fawcett	South Dakota	1984
Fred & Lee Kummerfeld	Wyoming	1984
Norman Coyner & Sons	Virginia	1984
Franklyn Esser	Missouri	1984
Edgar Lewis	Montana	1984
Boyd Mahrt	California	1984
Neil Moffat	Canada	1984
William H. Moss, Jr.	Georgia	1984
Dennis P. Solvie	Minnesota	1984
Robert P. Stewart	Kansas	1984
Charlie Stokes	North Carolina	1984
Milton Wendland	Alabama	1984
Bob & Sheri Schmidt	Minnesota	1985
Delmer & Joyce Nelson	Illinois	1985
Harley Brockel	South Dakota	1985
Kent Brunner	Kansas	1985
Glenn Havery	Oregon	1985
John Maino	California	1985
Ernie Reeves	Virginia	1985
John R. Rouse	Wyoming	1985
George & Thelma Boucher	Canada	1985
Kenneth Bentz	Oregon	1986
Gary Johnson	Kansas	1986
Ralph G. Lovelady	Alabama	1986
Ramon H. Oliver	Kentucky	1986
Kay Richarson	Florida	1986
Mr. & Mrs. Clyde Watts	North Carolina	1986
David & Bev Lischka	Canada	1986
Dennis & Nancy Daly	Wyoming	1986
Carl & Fran Dobitz	South Dakota	1986
Charles Fariss	Virginia	1986
David Forster	California	1986
Danny Geersen	South Dakota	1986
Oscar Bradford	Alabama	1987
R.J. Mawer	Canada	1987
Rodney G. Oliphant	Kansas	1987
David Reed	Oregon	1987
Jerry Adamson	Nebraska	1987
Gene Adams	Georgia	1987
Hugh & Pauline Maize	South Dakota	1987
P.T. McIntire & Sons	Virginia	1987
Frank Disterhaupt	Minnesota	1987
Mac, Don and Joe Griffith	Georgia	1988
Jerry Adamson	Nebraska	1988
Ken, Wayne & Bruce Gardiner	Canada	1988
C.L. Cook	Missouri	1988
C.J. and D.A. McGee	Illinois	1988
William E. White	Kentucky	1988
Frederick M. Mallory	California	1988
Stevenson Family	Oregon	1988
Gary Johnson	Kansas	1988
John McDaniel	Alabama	1988
William Stegner	North Dakota	1988
Lee Eaton	Montana	1988
Larry D. Cundall	Wyoming	1988
Dick & Phyllis Henze	Minnesota	1988
Jerry Adamson	Nebraska	1989
J.W. Aylor	Virginia	1989
Jerry Bailey	North Dakota	1989
James G. Guyton	Wyoming	1989
Kent Koostra	Kentucky	1989
Ralph G. Lovelady	Alabama	1989
Thomas McAvory, Jr.	Georgia	1989
Bill Salton	Iowa	1989
Lauren & Mel Schuman	California	1989
Jim Tesher	North Dakota	1989
Joe Thielen	Kansas	1989
Eugene & Ylene Williams	Missouri	1989
Phillip, Patty & Greg Bartz	Missouri	1990
John C. Chrisman	Wyoming	1990
Les Herbst	Kentucky	1990
Jon C. Ferguson	Kansas	1990
Mike & Dianna Hooper	Oregon	1990
James & Joan McKinlay	Canada	1990
Gilbert Meyer	South Dakota	1990
DuWayne Olson	South Dakota	1990
Raymond R. Peugh	Illinois	1990
Lewis T. Pratt	Virginia	1990
Ken and Wendy Sweetland	Canada	1990
Swen R. Swenson Cattle	Texas	1990
Robert A Nixon & Sons	Virginia	1991

Murray A. Greaves	Canada	1991
James Hauff	North Dakota	1991
J.R. Anderson	Wisconsin	1991
Ed and Rich Blair	South Dakota	1991
Reuben & Connee Quinn	South Dakota	1991
Dave & Sandy Umbarger	Oregon	1991
James A. Theeck	Texas	1991
Ken Stielow	Kansas	1991
John E. Hanson, Jr.	California	1991
Charles & Clyde Henderson	Missouri	1991
Russ Green	Wyoming	1991
Bollman Farms	Illinois	1991
Craig Utesch	Iowa	1991
Mark Barenthsen	North Dakota	1991
Rary Boyd	Alabama	1992
Charles Daniel	Missouri	1992
Jed Dillard	Florida	1992
John & Ingrid Fairhead	Nebraska	1992
Dale J. Fischer	Iowa	1992
E. Allen Grimes Family	North Dakota	1992
Kopp Family	Oregon	1992
Harold, Barbara & Jeff Marshall	Pennsylvania	1992
Clinton E. Martin & Sons	Virginia	1992
Loyd and Pat Mitchell	Canada	1992
William Van Tassel	Canada	1992
James A. Theeck	Texas	1992
Aquilla M. Ward	West Virginia	1992
Albert Wiggins	Kansas	1992
Ron Wiltshire	Canada	1992
Andy Bailey	Wyoming	1993
Leroy Beiterspacher	South Dakota	1993
Glenn Valbaugh	Wyoming	1993
Oscho Deal	North Carolina	1993
Jed Dillard	Florida	1993
Art Farley	Illinois	1993
Jon Ferguson	Kansas	1993
Walter Hunsuker	California	1993
Nola & Steve Kielboeker	Missouri	1993
Jim Maier	South Dakota	1993
Bill & Jim Martin	West Virginia	1993
Ian & Adam McKillop	Canada	1993
George & Robert Pingetzer	Wyoming	1993
Timothy D. Sufphin	Virginia	1993
James A. Theeck	Texas	1993
Gene Thiry	Canada	1993
Fran & Beth Dobitz	South Dakota	1994
Bruce Hall	South Dakota	1994
Lamar Ivey	Alabama	1994
Gordon Mau	Iowa	1994
Randy Mills	Kansas	1994
W.W. Oliver	Virginia	1994
Clint Reed	Wyoming	1994
Stan Sears	California	1994
Walter Carlee	Alabama	1995
Nicholas Lee Carter	Kentucky	1995
Charles C. Clark, Jr.	Virginia	1995
Greg & Mary Gunningham	Wyoming	1995
Robert & Cindy Hine	South Dakota	1995
Walter Jr. & Evidean Major	Kentucky	1995
Delhert Ohnemus	Iowa	1995
Henry Stone	California	1995
Joe Thielen	Kansas	1995
Jack Turnell	Wyoming	1995
Tom Woodard	Texas	1995
Jerry and Linda Bailey	North Dakota	1996
Kory M. Bierle	South Dakota	1996
Mavis Dummermuth	Iowa	1996
Terry Stuard Forst	Oklahoma	1996
Don W. Freeman	Alabama	1996
Lois & Frank Herbst	Wyoming	1996
Mr. & Mrs. George A. Horkan, Jr.	Virginia	1996
David Howard	Illinois	1996
Virgil & Mary Jo Huseman	Kansas	1996
Q.S. Leonard	North Carolina	1996
Ken & Rosemary Mitchell	Canada	1996
James Sr., Jerry, & James Petlik	South Dakota	1996
Ken Risler	Wisconsin	1996
Merlin Anderson	Kansas	1997
Joe C. Bailey	North Carolina	1997
William R. “Bill” Brockett	Virginia	1997
Howard McAdams, Sr. & Howard McAdams, Jr.	North Carolina	1997
Rob Orchard	Wyoming	1997
David Petty	Iowa	1997
Rosemary Rounds and Marc & Pam Scarborough	South Dakota	1997
Morey and Pat Van Hoecke	Minnesota	1997
Randy and Judy Mills	Kansas	1998
Mike and Priscille Kasten	Missouri	1998

Amana Farms, Inc.	Iowa	1998
Terry and Dianne Crisp	Canada	1998
Jim and Carol Faulstich	South Dakota	1998
James Gordon Fitzhugh	Wyoming	1998
John B. Mitchell	Virginia	1998
Holzapfel Family	California	1998
Mike Kitley	Illinois	1998
Wallace & Donald Schilke	North Dakota	1998
Doug & Ann Deane and Patricia R. Spearman	Colorado	1998
Glenn Baumann	North Dakota	1999
Bill Boston	Illinois	1999
C-J-R- Christensen Ranches	Wyoming	1999
Ken Fear, Jr.	Wyoming	1999
Giles Family	Kansas	1999
Burt Guerrieri	Colorado	1999
Karlen Family	South Dakota	1999
Deseret Ranches of Alberta	Canada	1999
Nick and Mary Klintworth	North Dakota	1999
MW Hereford Ranch	Nebraska	1999
Mossy Creek Farm	Virginia	1999
Iris, Bill, & Linda Lipscomb	Alabama	1999
Amana Farms, Inc.	Iowa	2999
Tony Boothe	Alabama	2000
Glenn Clabaugh	Wyoming	2000
Connie, John & Terri Griffith	Kansas	2000
Frank B. Labato	Colorado	2000
Roger & Sharon Lamont and Doug & Shawn Lamont	South Dakota	2000
Bill and Claudia Tucker	Virginia	2000
Wayne and Chip Unsicker	Illinois	2000
Billy H. Bolding	Alabama	2001
Mike and Tom Endress	Illinois	2001
Henry and Hank Maxey	Virginia	2001
Paul McKee	Kansas	2001
3-R Ranch	Colorado	2002
Agri-Services Division, Oklahoma Department of Corrections	Oklahoma	2002
Alpine Farms	Virginia	2002

Amana Farms	Iowa	2002
Griffin Seedstock	Kansas	2002
Indian Knoll Cattle Co.	Illinois	2002
Miles Land and Livestock	Wyoming	2002
Shovel Dot Ranch	Nebraska	2002
Torbert Farms	Alabama	2002
White Farms	Iowa	2002
Voyles Farms	Indiana	2002
Clear Creek Cattle Company	Wyoming	2003
Crider Salers	North Dakota	2003
Mike Goldwasser	Virginia	2003
Patterson Ranch	Colorado	2003
W.S. Roberts and Sons	Indiana	2003
Shriver Farms	Ohio	2003
Stroud Farms	Alabama	2003
Tailgate Ranch Company	Kansas	2003
Burkhalter Cattle	Alabama	2004
Doler Farm	Mississippi	2004
LU Ranch	Wyoming	2004
Namminga Angus	South Dakota	2004
Nellwood Farms	Georgia	2004
Olsen Ranches, Inc.	Nebraska	2004
Prather Ranch (Ralphs Ranches Inc.)	California	2004
Blair Porteus and Sons	Ohio	2004
Rx Ranch	Missouri	2004
Schuette Farms	Illinois	2004
Valdez Ranches	Colorado	2004
Wickstrum Farms, Inc.	Kansas	2004
CK Ranch	Kansas	2005
Diamond V Ranch	North Dakota	2005
Dover Ranch	Montana	2005
Gaines Farm	Alabama	2005
Hillwinds Farm	Virginia	2005
Krupps Farm	Illinois	2005
Jack and Ila Mae Larson	Colorado	2005
Mule Creek Ranch	Kansas	2005
Paxton Ranch	Nebraska	2005
Pontious Farms	Ohio	2005
Prather Ranch	California	2005
Shovel Dot Ranch	Nebraska	2005
Wintergreen Farm	Iowa	2005
Duck Farm Inc.	Virginia	2006
Hunt Hill Cattle Co.	Mississippi	2006
McDorman Farms	Ohio	2006
Pitchfork Ranch	Illinois	2006
Rock Creek Ranch	Kansas	2006
Sutherland Ranches	Colorado	2006
Van Waarhuizen, Inc.	Iowa	2006
Broseco Ranch	Texas	2007
4Z Farms	Kansas	2007

CK Ranch	Kansas	2007
Barry and Larry Dowell Families	Illinois	2007
Eagle Rock Ranch	Colorado	2007
Eatinger Cattle Company, Inc.	Nebraska	2007
JHL Ranch	Nebraska	2007
Lacey Livestock	California	2007
Lerwick Brothers LLC	Wyoming	2007
MG Farms	Mississippi	2007
Stuart Land & Cattle Company	Virginia	2007
CL Ranches Ltd.	Canada	2008
Eatinger Cattle Company, Inc.	Nebraska	2008
Frank Farms	Colorado	2008
Genereux Ranch	Montana	2008
Jack Giltner	Iowa	2008
Hollow Hill Farm	Virginia	2008
JL Cattle Company	Colorado	2008
Kniebel Farms & Cattle Company	Kansas	2008
Otley Brothers Inc.	Oregon	2008
Toland's River Oak	Illinois	2008

Ranch		
Tom Bengard Ranches	California	2008
Win Parmer Ranch	Alabama	2008
Anderson Land and Cattle	Kansas	2009
Tom Bengard Ranches	California	2009
Joe Davis Cattle Farm	South Carolina	2009
Freedom Hills Ranch	Illinois	2009
JHL Ranch	Nebraska	2009
Gale Rippey Farms	Virginia	2009
Slusher Valley Farms	Virginia	2009
Stephens Farm	Alabama	2009
Stan and Lisa Buzzard	Illinois	2010
Downey Ranch	Kansas	2010
G.W. Jones and Sons Farms	Alabama	2010
M&B Limousin	Missouri	2010
Duane Martin Livestock	California	2010
Optimal Beef, LLC	Virginia	2010

BIF Commercial Producer of the Year

Chan Cooper	Montana	1972
Pat Wilson	Florida	1973
Lloyd Nygard	North Dakota	1974
Gene Gates	Kansas	1975
Ron Baker	Oregon	1976
Mary & Stephen Garst	Iowa	1977
Mose Tucker	Alabama	1978
Bert Hawkins	Oregon	1979
Jess Kilgore	Montana	1980
Henry Gardiner	Kansas	1981
Sam Hands	Kansas	1982
Al Smith	Virginia	1983
Bob & Sharon Beck	Oregon	1984
Glenn Harvey	Oregon	1985
Charles Fariss	Virginia	1986
Rodney G. Oliphant	Kansas	1987
Gary Johnson	Kansas	1988
Jerry Adamson	Nebraska	1989
Mike & Diana Hopper	Oregon	1990
Dave & Sandy Umbarger	Oregon	1991
Kopp Family	Oregon	1992
Jon Ferguson	Kansas	1993
Fran & Beth Dobitz	South Dakota	1994
Joe & Susan Thielen	Kansas	1995
Virgil & Mary Jo Huseman	Kansas	1996

Merlin & Bonnie Anderson	Kansas	1997
Mike & Priscilla Kasten	Missouri	1998
Randy & Judy Mills	Kansas	1998
Giles Family	Kansas	1999
Mossy Creek Farm	Virginia	1999
Bill & Claudia Tucker	Virginia	2000
Maxey Farms	Virginia	2001
Griffith Seedstock	Kansas	2002
Tailgate Ranch	Kansas	2003
Olsen Ranches, Inc.	Nebraska	2004
Prather Ranch	California	2005
Pitchfork Ranch	Illinois	2006
Broseco Ranch	Colorado	2007
Kniebel Farms & Cattle	Kansas	2008
JHL Ranch	Nebraska	2009
Downey Ranch	Kansas	2010